

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
22 May 2003 (22.05.2003)

PCT

(10) International Publication Number  
**WO 03/042661 A2**

(51) International Patent Classification<sup>7</sup>: **G01N**

(21) International Application Number: PCT/US02/36810

(22) International Filing Date:  
13 November 2002 (13.11.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/350,666	13 November 2001 (13.11.2001)	US
60/332,464	21 November 2001 (21.11.2001)	US
60/334,393	29 November 2001 (29.11.2001)	US
60/335,394	3 December 2001 (03.12.2001)	US
60/340,376	14 December 2001 (14.12.2001)	US
60/347,211	8 January 2002 (08.01.2002)	US
60/347,349	10 January 2002 (10.01.2002)	US
Not furnished	8 February 2002 (08.02.2002)	US
60/356,714	13 February 2002 (13.02.2002)	US
60/359,077	20 February 2002 (20.02.2002)	US
60/368,809	29 March 2002 (29.03.2002)	US
60/370,110	4 April 2002 (04.04.2002)	US
60/372,246	12 April 2002 (12.04.2002)	US
60/386,614	5 June 2002 (05.06.2002)	US
60/396,839	16 July 2002 (16.07.2002)	US
60/397,775	22 July 2002 (22.07.2002)	US
60/397,845	22 July 2002 (22.07.2002)	US
60/409,450	9 September 2002 (09.09.2002)	US

(71) Applicant (for all designated States except US): **EOS BIOTECHNOLOGY, INC.** [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **AFAR, Daniel** [CA/US]; 435 Visitacion Avenue, Brisbane, CA 94005 (US). **AZIZ, Natasha** [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). **GINSBURG, Wendy, M.** [US/US]; 655 Page Street, San Francisco, CA 94117 (US). **GISH, Kurt, C.** [US/US]; 37 Artuna Avenue, Piedmont,

CA 94611 (US). **GLYNNE, Richard** [GB/US]; 2691 Palomino Circle, La Jolla, CA 92037 (US). **HEVEZI, Peter, A.** [GB/US]; 1360 11th Avenue, San Francisco, CA 94122 (US). **MACK, David, H.** [US/US]; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). **MURRAY, Richard** [US/US]; 22643 Woodridge Court, Cupertino, CA 95014 (US). **WATSON, Susan, R.** [GB/US]; 805 Balra Drive, El Cerrito, CA 94530 (US). **WILSON, Keith, E.** [US/US]; 219 Jeter Street, Redwood City, CA 94062 (US). **ZLOTNIK, Albert** [US/US]; 507 Alger Drive, Palo Alto, CA 94306 (US).

(74) Agents: **BASTIAN, Kevin, L.** et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, Eighth Floor, San Francisco, CA 94111 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Declaration under Rule 4.17:**

— of inventorship (Rule 4.17(iv)) for US only

**Published:**

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



WO 03/042661 A2

## METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

### 5 CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/340,376, filed December 14, 2001; Attorney Docket Number 018501-006400US, filed February 8, 2002; USSN 60/347,211, filed January 8, 2002; USSN 60/334,393, filed November 29, 2001; USSN 60/335,394, filed November 15, 2001; USSN 60/347,349, filed January 10, 2002; USSN 60/368,809, filed March 29, 2002; USSN 60/409,450, filed September 9, 2002; USSN 60/359,077, filed February 20, 2002; USSN 60/386,614, filed June 5, 2002; USSN 60/356,714, filed February 13, 2002; USSN 60/397,775 filed July 22, 2002; USSN 60/332,464, filed November 21, 2001; USSN 60/397,845, filed July 22, 2002; USSN 60/370,110, filed April 4, 2002; USSN 60/396,839, filed July 16, 2002; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002; each of which is incorporated herein by reference for all purposes. The application also incorporates by reference PCT/US02/29560; PCT/US02/02242; and PCT/US02/17594.

### FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer and other diseases; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of these conditions. The invention further relates to methods for identifying and using agents and/or targets that modulate these conditions.

### BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is in Japan.

Cancers share the characteristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over



70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases. Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

5 Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis, prognosis, and treatment of cancer patients.

10 Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be  
15 tolerated, e.g., reproductive organs, especially those absent in one sex. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies  
20 (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic  
25 intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

#### SUMMARY OF THE INVENTION

30 The present invention provides methods for determining the presence or absence of a pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell.

In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-80; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is suspected of having the pathology or cancer.

Compositions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as described in Tables 2A-80; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targeting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80; and determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression

of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

5

## DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for

10 treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN:

15 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous

20 System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American

25 Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM

30 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini

- (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznick (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwer, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic

Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901;

5 Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the

10 invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g.,

15 using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also

20 be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

25 Tables 2B-76B provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in diseased samples (see Tables 1-3), particularly sequences involved in angiogenesis, arthritis, prostate cancer, breast cancer, colorectal cancer, cervical cancer, bladder cancer, head and neck cancer, esophageal cancer, lung cancer, ovarian cancer, pancreatic cancer, renal cancer, stomach cancer, skin

30 cancer, testicular cancer, uterine cancer, glioblastoma, Ewing sarcoma, soft tissue sarcoma, and lung fibrosis. Tables 2A-80 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

## Definitions

The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-80; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-80 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a "cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is

typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is about 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from about 20 to 600, usually about 50 to 200, more usually about 100 to 150, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-



scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787.

One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, [www.atcc.org](http://www.atcc.org)).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its

native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from  
5 some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing  
10 at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally  
15 occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as  
20 those amino acids that are later modified, e.g., hydroxyproline,  $\gamma$ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an  $\alpha$  carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g.,  
25 norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter  
30 symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts,

et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules

Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide.

"Secondary structure" refers to locally ordered, three dimensional structures within a

polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to

approximately 500 amino acids long. Typical domains are made up of sections of lesser

organization such as stretches of  $\beta$ -sheet and  $\alpha$ -helices. "Tertiary structure" refers to the

complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers

to the three dimensional structure formed, usually by the noncovalent association of

independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about

100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length,

including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A

nucleic acid of the present invention will generally contain phosphodiester bonds, although in

some cases, nucleic acid analogs are included that may have at least one different linkage, e.g.,

phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages

(see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ.

Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include

those with positive backbones; non-ionic backbones, and non-ribose backbones, including those

described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and

Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series

580. Nucleic acids containing one or more carbocyclic sugars are also included within one

definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a

variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological

environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and

analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of

naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g.,

phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein;

Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805, Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature ( $T_m$ ) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in  $T_m$  for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively

insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ , or  $^{125}\text{I}$ , electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including

radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; chemoattracting moieties, immune modulators (micA/B), or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is

achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid



sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength pH. The  $T_m$  is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at  $T_m$ , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to

8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times

5 background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32°-48° C depending on primer length. For  
10 high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high  
15 stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy  
20 permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar  
25 stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a cancer protein includes the determination of a parameter that is indirectly  
30 or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact

inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase,  $\beta$ -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for

inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 2A-80.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

5 Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

10 An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain ( $V_L$ ) and variable heavy chain ( $V_H$ ) refer to these  
15 light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce  $F(ab)'_2$ , a dimer of Fab which itself is a light chain joined to  $V_H-C_H1$  by a disulfide bond. The  $F(ab)'_2$  may be reduced under mild  
20 conditions to break the disulfide linkage in the hinge region, thereby converting the  $F(ab)'_2$  dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant  
25 DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies,  
30 many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in

Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, effector function, chemoattractant, immune modulator, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

#### Identification of cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis

and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the cancer sequences are from humans; however, cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained using the techniques outlined below.

Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based

upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and  
5 non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are  
10 applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and  
15 disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not  
20 necessary (e.g., where organs may be dispensable, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or  
25 non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the  
30 GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases,



e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have  
5 been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher  
10 being preferred.

#### Informatics

The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development,  
15 and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1-3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA).

Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).  
20

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access  
25 to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.  
30

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others.

Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is available. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxeianis, et al. (2001) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Wiley; Mount (2001)

- Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999)
- Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxevanis and Ouellette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999)
- 5 Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the
- 10 Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

25 The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of

30 magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention

provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method  
5 for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount  
10 of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed,  
15 Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line,  
20 wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes  
25 generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a  
30 query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute

the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

5           The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can  
10   be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal  
15   comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

          The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be  
20   stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different  
25   samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning: Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the  
30   smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

### Characteristics of cancer-associated proteins

Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus.

5 Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase  
10 activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In  
15 addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH  
20 domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.  
25 One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420 ; Bateman, et al. (1999) Nuc.  
30 Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may

have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated

molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

5 Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are  
10 typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated that a transmembrane protein can be made soluble by  
15 removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal  
20 sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion  
25 into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic  
30 markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.



### Use of cancer nucleic acids

As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally  
5 determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment  
10 may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the  
15 shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g.,  
20 moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-80, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of  
25 the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent  
30 parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or  
5 binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and  
10 the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid  
15 support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

20 The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but  
25 are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably  
30 fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., [www2.perkin-elmer.com](http://www2.perkin-elmer.com)).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Natl. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

#### Expression of cancer proteins from nucleic acids

In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The cancer protein may also be made as a fusion protein, using available techniques. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may



be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

#### Variants of cancer proteins

Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will  
5 elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are sometimes made by  
10 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's  
15 properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain,  
20 e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to  
25 modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of  
30 a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutaminyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57 and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases.

5 See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

10 Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer  
5 sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

10 In addition, cancer proteins can be made that are longer than those encoded by the nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

#### 15 Antibodies to cancer proteins

In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell  
20 receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

25 Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 2A-80 or  
30 fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

5           The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent.

10          Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line  
15          using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or  
20          more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

25           In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and  
30          preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.



Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95).

5 Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the  
10 following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

15 By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are  
20 raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the cancer proteins against which antibodies are raised are  
25 secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may  
30 bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- $\alpha$ , TNF- $\beta$ , IL-1, INF- $\gamma$ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, target a drug loaded liposome, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells. See, e.g., USSN 09/544,494.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce

deleterious side effects that may be associated with the untargeted therapeutic moiety.

Antibody fragments may be used to target toxin loaded liposomes.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a  $K_d$  of at least about 0.1 mM, more usually at least about 1  $\mu$ M, preferably at least about 0.1  $\mu$ M or better, and most preferably, 0.01  $\mu$ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

#### Detection of cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably  
5 labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl  
10 phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or  
15 corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or  
20 diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following  
25 separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with  
30 from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins.

5 Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

10 In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

15 In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes  
20 which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene  
25 expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined  
30 above for diagnosis. PCR method may provide more sensitive and accurate quantification.

### Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or  
5 by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

10 In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of  
15 drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be  
20 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal  
25 versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

30 The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically  
5 involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell.

Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for  
10 each well.

#### Modulators of cancer

Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out  
15 in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical  
20 equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator  
25 suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

30 Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or



less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

5           The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

          Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another  
10       embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially  
15       expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

          In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to  
20       modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be  
25       identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics, e.g., toxin loaded liposomes, to the treated cancer tissue sample.

          Thus, in one embodiment, a test compound is administered to a population of cancer  
30       cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

5           Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

10           Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein  
15           need to change.

          In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes  
20           are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another  
25           embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

          Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a  
30           non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or  $\beta$ -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or



the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g.,  $^{125}\text{I}$  for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

- 5           In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.
- 10          Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

- In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test
- 15          compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

- In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second
- 20          sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

- 25          Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

- 30          Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

5 A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may  
10 be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a  
15 cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including  
20 chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the  
25 compound.

In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising  
30 administration of a cancer inhibitor.

In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

#### Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss; Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) Nature Genet. 14:415-20.

#### Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (<sup>3</sup>H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (<sup>3</sup>H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (<sup>3</sup>H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

### Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al.(1970) J. Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

### Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum; Freshney (1985) Anticancer Res. 5:111-130.

### Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with  $^{125}\text{I}$  and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

#### Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about  $10^6$  cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

## Polynucleotide modulators of cancer

## Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be



effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

#### Ribozymes

5 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general  
10 review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-  
15 45; Leavitt, et al.(1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface  
20 receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the  
25 target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating cancer in cells or organisms are  
30 provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene  
5 encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386. Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other  
10 inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic  
15 purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

#### 20 Methods of identifying variant cancer-associated sequences

Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one  
25 endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to  
30 a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

5 In a preferred embodiment, the cancer genes are used as probes to determine the number of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

#### 10 Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as  
20 the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and  
25 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary,  
30 vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294.; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in  
5 immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p.  
10 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al.  
15 (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de  
20 Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance  
25 designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham,  
30 Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient.

5 This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S.  
10 Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide  
15 fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are available for therapeutic  
20 administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a  
25 cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a  
30 cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure



provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

#### Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

## EXAMPLES

### Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs affected by disease, referred to in Tables 2A and 3A, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

- 5 blood vessels/angiogenesis: hemangiomas, lymphangiomas, angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma, wound healing, tissue remodeling, psoriasis, ischemic, heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atherosclerosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, lymphadenitis, lymphangitis, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented villonodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (keloid), birth control, uterine fibroids
- 10 bladder: carcinoma in situ, papillary carcinomas, transitional cell carcinoma, squamous cell carcinoma  
bone: Ewing sarcoma, sarcomas arising from skeletal and extraskelatal connective tissues, including the peripheral nervous system (e.g. chondrosarcoma, osteosarcoma)  
brain: glioblastoma, oligodendroglioma, anaplastic astrocytoma, meningioma, medulloblastoma, neuroblastoma, ependymoma, schwannoma, craniopharyngioma, pineoblastoma, pineocytoma, neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, neuroma, ganglioneuroma
- 15 breast: ductal carcinoma in situ, lobular carcinoma in situ  
cervix: cancer of the cervix, vagina, or vulva  
colon/rectum: precancerous colorectal disease (e.g., neoplastic polyps (adenomas), familial adenomatous polyposis, ulcerative colitis), colon cancer, e.g., epithelial tumor (e.g., adenocarcinoma, mucinous adenocarcinoma, signet-ring cell adenocarcinoma, squamous cell carcinoma, adenosquamous carcinoma, undifferentiated carcinoma, unclassified carcinoma), carcinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leiomyosarcoma, others), inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease (granulomatous colitis), dysplasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary villous carcinoma, mucinous adenocarcinoma, melanoma)
- 20 esophagus: premalignant or predisposing conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, lung, or cervix), gastroduigestive carcinomas (e.g., cancers of the stomach, colon, or rectum)  
fibrosis: lung fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scleroderma, wound healing
- 25 head and neck: tumors of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, lip, larynx, hypopharynx, salivary glands, paragangliomas, esophagus  
kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypernephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, angiomyolipoma, oncocytoma  
leukocytes: acute lymphoblastic leukemia/lymphoma, chronic lymphocytic leukemia, follicular lymphoma, large B-cell lymphoma, Burkitt lymphoma, plasma cell neoplasms, mantle cell lymphoma, lymphoplasmacytic lymphoma, peripheral T-cell lymphoma, adult T-cell leukemia/lymphoma, Hodgkin disease, acute myelogenous leukemia, chronic myelogenous leukemia, thymic hyperplasia, hairy cell leukemia, malignant transformation, inappropriate activation or abnormalities of leukocytes (e.g., immature, precursor B (pre-B) or precursor T (pre-T) lymphocytes, monocytes, neutrophils, eosinophils, basophils, dendritic cells, lymphoblasts), arthritis, inflammation, leukocytosis, lymphadenitis, lymphangitis, bacteremia, chronic nonspecific lymphadenitis, psoriasis, wound healing
- 30 liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor bile conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder or bile duct
- 35 lung: lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer
- ovary: ovarian carcinoma (e.g., epithelial (serous tumors, mucinous tumors, endometrioid tumors), germ cell (e.g., teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosa stromal cell tumors)), fallopian tube carcinoma, peritoneal carcinoma, leiomyoma
- 40 pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma, pancreatoblastoma, duct-ectatic mucin-hypersecreting tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes mellitus, chronic pancreatitis  
prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumors, transitional cell carcinoma, carcinoma in situ, and basal cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia, prostatitis
- 45 skin/melanoma: melanoma, lentigo (common benign localized hyperplasia of melanocytes), nevocellular nevi (congenital or acquired neoplasm of melanocytes), actinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Merkel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histiocytes within the dermis), dermal vascular tumors, seborrheic keratoses (benign tumor), acanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinomas of the skin, lung, cervix, esophagus, uterus, head, neck, or bladder
- 50 soft tissue: soft tissue tumors (e.g., fibrosarcoma, liposarcoma, leiomyosarcoma, histiocytoma, fibrohistiocytic sarcoma) smooth muscle tumors (e.g., rhabdomyoma, rhabdomyosarcoma) tumors of the blood and lymph vessels (e.g., angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma), perivascular tumors (e.g., glomus tumors, hemangiopericytoma), synovial tumors (e.g., mesothelioma), neural tumors (e.g., neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, extraskelatal Ewing's sarcoma, schwannoma, neuroma, ganglioneuroma), paraganglioma, extraskelatal cartilaginous and osseous tumors (e.g., chondrosarcoma, osteosarcoma), pluripotent mesenchymal tumors, epithelioid sarcomas, rhabdoid tumors, desmoplastic small cell tumors, alveolar sarcoma
- 55 stomach: adenocarcinoma, squamous cell carcinoma, adenoacanthoma, carcinoid, leiomyosarcoma, gastritis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas
- 60 testicles: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, choriocarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblastomas), adnexal and paratesticular tumors (e.g., mesotheliomas, soft tissue sarcomas, and adnexal of the rete testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)
- uterus: epithelial tumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed mullerian tumors, adenosarcoma)

65

70 Tables 2B-22B, 76B, and 79B list accession numbers for Pkeys lacking UnigeneID's for Tables 2A-72A, 76A, and 79A, respectively. For each probeset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

75 Tables 2C-72C, 76C, and 79C list genomic positioning for Pkeys lacking Unigene ID's and accession numbers in Tables 2A-72A, 76A, and 79A, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Table 2A, Disease Indications and Preferred Utilities for Selected Genes

80 Table 2A provides preferred disease indications and preferred utilities for about 413 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number  
UnigeneID: Unigene ID number

Unigene Title: Unigene gene title  
 Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), leio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)  
 Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAccn; UnigenelD; Unigene Title; Disease; Utility

102892; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk; mAb+diag+s.m.  
 104865; T79340; Hs.22575; B-cell CLL/lymphoma 6, member ; angio; CTL  
 104978; A1199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, lung, pros, blad, stom; CTL  
 109424; NM\_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb+s.m.  
 110765; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag  
 110906; AA035211; Hs.17404; SOX7 SRY (sex determining regi; angio, blad; CTL  
 115522; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; GTL  
 116176; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL  
 118695; AK000465; Hs.50081; KIAA1199 protein; colon, lung; diag  
 123049; BE047680; Hs.211869; dickkopf (Xenopus laevis) homo; EWS; mAb+diag  
 131486; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.  
 133370; AF245505; Hs.72157; Adican; breast, lung, panc; diag  
 310016; AW449612; Hs.152475; ESTs; colon; CTL  
 322303; A1357412; Hs.157601; ESTs; colon, pros, fibro, breast; CTL+diag  
 400289; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, cerv, ovar, headnk, esoph; mAb+diag+s.m.  
 400297; A1127076; Hs.288381; hypothetical protein DKFZp5640; breast, blad, colon, pros; mAb  
 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regula; breast, ovar, pros, stom, uter, blad, lung, headnk; mAb  
 400843; ; NM\_003105; Homo sapiens sortil; blad; s.m.  
 402075; ; ENSP00000251056; Plasma membra; blad, lung, headnk, cerv, mela, esoph; mAb+diag  
 402901; ; NM\_025206; Homo sapiens hypoth; blad ; CTL  
 404287; ; FGENESH predicted novel CUB-do; panc, lung, colon, uter, esoph; mAb+s.m.  
 404682; ; ortholog of mouse polydomain p; panc; diag  
 404875; ; NM\_022819; Homo sapiens phosph; blad; CTL+s.m.  
 404977; ; Insulin-like growth factor 2 (; blad, ovar, sarc; mAb+diag  
 405033; ; C1002652; gij544327[sp]Q04799; blad; s.m.  
 406400; ; kallikrein 8 (neuropsin/ovasin; ovar, uter; diag  
 406964; M21305; ; FGENES predicted novel secrete; angio, blad, fibro, sarc; diag  
 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299; glio, blad; CTL  
 407792; A1077715; Hs.39384; putative secreted ligand homol; ovar, uter, cerv, panc; mAb+diag  
 407811; AW190902; Hs.40098; cysteine knot superfamily 1, B; blad, panc, stom, uter, lung, esoph; diag  
 407836; T79340; Hs.22575; B-cell CLL/lymphoma 6, member ; angio; CTL  
 407975; X89426; Hs.41716; endothelial cell-specific mole; angio, renal; diag  
 408243; Y00787; Hs.624; interleukin 8; blad, stom, headnk, cerv, lung, angio, esoph, panc; diag  
 408367; AK001178; Hs.44424; Homo sapiens orphan neurotrans; mela; mAb+s.m.  
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family ; pros, lung, fibro, uter, glio, cerv, ovar; mAb  
 408380; AF123050; Hs.44532; diubiquitin; lung, blad, headnk, panc, stom, fibro, esoph, mela; CTL  
 408482; NM\_000676; Hs.45743; adenosine A2b receptor; lung, esoph, headnk, colon; mAb+s.m.  
 408562; A1436323; Hs.31141; roundabout (axon guidance rece; uter, fibro, sarc; mAb+s.m.  
 408790; AW580227; Hs.47860; neurotrophic tyrosine kinase, ; lung; mAb+s.m.  
 408908; BE296227; Hs.250822; serine/threonine kinase 15; blad, lung, headnk, stom, colon; s.m.  
 409041; AB033025; Hs.50081; Hypothetical protein, XP\_05186; uter, ovar, lung, colon, stom, headnk, breast, panc; CTL+diag  
 409079; W87707; Hs.82065; interleukin 6 signal transduce; breast, pros; mAb+s.m.  
 409103; AF251237; Hs.112208; XAGE-1 protein; lung; CTL  
 409178; BE393948; Hs.50915; kallikrein 5; ovar, breast, mela; diag  
 409220; BE243323; Hs.51233; tumor necrosis factor receptor; angio, renal, colon, stom; mAb+s.m.  
 409420; Z15008; Hs.54451; laminin, gamma 2 (nicein (100k; lung, headnk, panc, stom, cerv, esoph, blad; diag  
 409632; W74001; Hs.55279; serine (or cysteine) proteinase; lung, blad, headnk; diag  
 409663; A1743750; Hs.98306; KIAA1862 protein; renal; CTL  
 409757; NM\_001898; Hs.123114; cystatin SN; panc, stom, lung, blad; diag  
 409889; AW630041; Hs.56937; suppression of tumorigenicity ; colon, ovar, pros; mAb+s.m.  
 409893; AW247090; Hs.57101; minichromosome maintenance def; lung, cerv, blad, test, esoph; CTL+s.m.  
 409956; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, panc, ovar, colon, headnk, lung, blad, esoph; diag  
 410001; AB041036; Hs.57771; kallikrein 11; ovar, pros, uter, cerv, lung ; diag  
 410055; AJ250839; Hs.58241; gene for serine/threonine prot; renal; s.m.  
 410153; BE311926; Hs.15830; hypothetical protein FLJ12691; renal,blad; CTL  
 410274; AA381807; Hs.336402; hypoxia-inducible protein 2; lung, renal; CTL  
 410309; BE043077; Hs.278153; alpha-2,8-sialyltransferase II; panc; s.m.  
 410407; X66839; Hs.63287; carbonic anhydrase IX; renal, lung, colon, stom, ovar, uter, blad, sarc; mAb+s.m.  
 410418; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.  
 411274; NM\_002776; Hs.69423; kallikrein 10; colon, ovar, uter, cerv, headk, panc; diag  
 411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA13; renal; mAb+s.m.  
 411773; NM\_006799; Hs.72026; protease, serine, 21 (testisin; ovar; diag  
 411975; A1916058; Hs.144583; 3'UTR of: dead ringer (Drosoph; test, colon; CTL  
 412078; X69699; Hs.73149; paired box gene 8; ovar; CTL  
 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, headnk, breast, ovar, panc, angio, test, mela; s.m.  
 412314; AA825247; Hs.356084; G protein-coupled receptor 27 ; ovar, uter, test; mAb+s.m.  
 412609; Z48804; Hs.74124; ocular albinism 1 (Nettleship; mela; s.m.  
 412628; A1972402; Hs.306051; hypothetical protein MGC2648; pros; diag  
 412709; AL022327; Hs.74518; KIAA0027 protein; glio, sarc; mAb+s.m.  
 412719; AW016610; Hs.816; ESTs; lung, headnk, blad, glio, cerv, sarc; s.m.  
 412959; D87458; Hs.75090; KIAA0282 protein; glio; CTL+s.m.  
 413048; M93221; Hs.75182; mannose receptor, C type 1; fibro, panc; mAb

- 413063; AL035737; Hs.75184; chitinase 3-like 1 (cartilage ; glio, ovar, blad, lung ; diag  
 413278; BE563085; Hs.833; interferon-stimulated protein.; panc, lung, blad, breast, cerv, ovar, headnk, esoph, mela; CTL+s.m.  
 413324; V00571; Hs.75294; corticotropin releasing hormon; blad; diag  
 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxyg; blad, lung, mela, fibro, uter, sarc; s.m.  
 413554; AA319146; Hs.75426; secretogranin II (chromogranin; panc, glio; diag  
 413719; BE439580; Hs.75498; small inducible cytokine subfa; leuk, panc, lung, headnk, cerv, colon, uter, stom, esoph; diag  
 414555; N98569; Hs.76422; phospholipase A2, group IIA (p; pros; s.m.  
 414577; AI056548; Hs.378938; hypothetical protein FLJ20992 ; angio; CTL+diag  
 414774; X02419; Hs.77274; plasminogen activator, urokina; lung, blad, headnk, panc, stom, ovar, esoph; diag  
 414812; X72755; Hs.77367; monokine induced by gamma inte; breast, blad, lung, fibro, panc, colon, headnk, cerv, stom, renal, ovar, test, mela, esoph; diag  
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; lung, ovar, stom, colon, cerv, headnk, test; s.m.  
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; blad, lung, ovar, test; s.m.  
 414991; C17898; ; Homo sapiens up-regulated by B; fibro, lung; mAb+diag  
 415138; C18356; Hs.295944; tissue factor pathway inhibito; angio, panc, stom, lung, uter; CTL+diag  
 415539; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb+s.m.  
 415668; AW957684; Hs.306814; Homo sapiens lysyl oxidase-lik; mela; diag  
 415669; NM\_005025; Hs.78589; serine (or cysteine) proteinas; lung; mAb+diag+s.m.  
 415817; U88967; Hs.78867; protein tyrosine phosphatase, ; lung, glio, headnk, cerv, mela, esoph, fibro; mAb+s.m.  
 415929; AA724373; Hs.304950; Homo sapiens mucollipin-3 (MCOL; mela; mAb  
 416091; AF295370; Hs.283082; defensin, beta 3; headnk, esoph, mela; CTL+diag  
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient; lung, headnk, colon, uter, stom; CTL+s.m.  
 416250; AA581386; Hs.73452; Kremen 2; esoph, lung, cerv, ovar; mAb+s.m.  
 416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyme); ovar, uter; diag  
 416636; N32536; Hs.42645; solute carrier family 16 (mono; breast, panc, uter, mela; mAb+s.m.  
 416658; U03272; Hs.79432; fibrillin 2 (congenital contra; lung, ovar, uter, blad, angio, test, sarc; diag  
 416836; D54745; Hs.80247; cholecystokinin; pros, EWS, glio ; diag  
 416857; AA188775; Hs.292453; FGENSESH predicted TM containin; glio; mAb+s.m.  
 416965; N26223; Hs.160436; MDAC1; fibro, ovar, uter; mAb  
 417034; NM\_006183; Hs.80962; neurotensin; lung, headnk, cerv; diag  
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; blad, lung, headnk, cerv, esoph; diag  
 417166; AA431323; Hs.42146; Paired box protein Pax-3; mela, sarc; CTL  
 417389; BE260964; Hs.82045; midkine (neurite growth-promot; ovar, lung, blad, uter, cerv, panc, stom, mela, test, colon, sarc; mAb+diag  
 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glyco; panc, breast, blad, lung, headnk, cerv, uter, ovar, stom, renal; mAb  
 417771; AA804698; Hs.82547; retinoic acid receptor respond; blad, cerv, panc, pros, ovar; mAb  
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; lung, panc, breast, ovar, headnk, stom, sarc; CTL  
 417931; W95642; Hs.82961; trefoil factor 3 (intestinal); ovar, panc, stom, colon, uter, pros; diag  
 417933; X02308; Hs.82962; thymidylate synthetase; blad, lung, angio, colon, panc, esoph; s.m.  
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (in; lung, blad, fibro, headnk, panc, stom, colon, ovar, esoph, mela; mAb+diag+s.m.  
 418030; BE207573; Hs.83321; neuromedin B; glio, panc; diag  
 418064; BE387287; Hs.83384; S100 calcium-binding protein, ; mela; diag  
 418281; U09550; Hs.1154; oviductal glycoprotein 1, 120k; uter, ovar; CTL+diag  
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk, panc, cerv, mela, sarc; s.m.  
 418506; AA084248; Hs.372651; Unknown protein for MGC:29643 ; angio, ovar, glio, uter, lung, blad, panc, mela, sarc; mAb+diag  
 418526; BE019020; Hs.85838; solute carrier family 16 (mono; lung, blad, renal, panc, stom, colon, ovar; mAb+s.m.  
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via d; esoph, headnk; s.m.  
 418678; NM\_001327; Hs.87225; cancer/testis antigen (NY-ESO-; lung, blad, stom, ovar, panc, esoph, cerv, sarc; CTL  
 418738; AW388633; Hs.6682; solute carrier family 7, (cat; angio, lung, ovar, blad, colon, stom, panc, uter, leuk; mAb+s.m.  
 418830; BE513731; Hs.348874; hypothetical protein MGC4816; lung; CTL  
 418867; D31771; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad, renal; mAb+s.m.  
 419080; AW150835; Hs.18878; hypothetical protein FLJ21620; renal, lower uter, lung; CTL  
 419121; AA374372; Hs.89626; parathyroid hormone-like hormo; lung, esoph, headnk, blad; diag  
 419171; NM\_002846; Hs.89655; protein tyrosine phosphatase, ; lung; mAb+s.m.  
 419172; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio, renal; mAb+s.m.  
 419183; U60669; Hs.89663; cytochrome P450, subfamily XXI; blad, lung, headnk, panc; CTL+s.m.  
 419216; AU076718; Hs.164021; small inducible cytokine subfa; panc, lung, stom, cerv, pros, headnk, esoph; diag  
 419235; AW470411; Hs.288433; neurotrophin; panc, fibro, headnk, lung; mAb+diag  
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ovar, pros, lung, breast, uter, test, panc, stom, sarc; mAb+s.m.  
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-fami; glio, omuc, stom, lung, panc, colon, renal, uter; mAb+s.m.  
 419556; U29615; Hs.91093; chitinase 1 (chitotriosidase); lung, fibro, test; mAb+diag  
 419704; AA429104; Hs.45057; ESTs; glio; CTL+s.m.  
 419723; AL120193; Hs.339810; longevity assurance (LAG1, S. ; glio; mAb+diag  
 419741; NM\_007019; Hs.93002; ubiquitin carrier protein E2-C; blad, lung, colon, ovar, test, esoph, mela, sarc; CTL+s.m.  
 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA; fibro, stom, blad, esoph, uter; diag  
 420159; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 fi; blad, stom; mAb  
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; lung, mela, sarc; s.m.  
 420370; Y13645; Hs.97234; uroplakin 2; blad; mAb  
 420440; NM\_002407; Hs.97644; mammaglobin 2; ovar, uter, cerv; diag  
 420602; AF060877; Hs.99236; regulator of G-protein signal; headnk, glio, cerv, mela; CTL+s.m.  
 420610; AI683183; Hs.99348; distal-less homeo box 5; uter, endo, lung; CTL  
 420737; L08096; Hs.99899; CD70 ; tumor necrosis factor ; renal; mAb+s.m.  
 420876; AA918425; Hs.177744; FGENSESH predicted novel protein; panc, blad; s.m.  
 421066; AU076725; Hs.101408; branched chain aminotransferas; blad, lung; CTL+s.m.  
 421110; AJ250717; Hs.1355; cathepsin E; blad, panc, stom, lung, fibro, ovar, esoph; sm+diag  
 421340; F07783; Hs.1369; decay accelerating factor for ; angio, panc, stom; diag  
 421379; Y15221; Hs.103982; small inducible cytokine subfa; breast, panc, headnk, lung, stom, blad, cerv, colon, leuk, fibro, test, mela, esoph; diag  
 421471; U90545; Hs.327179; solute carrier family 17 (sodi; renal; mAb+s.m.  
 421474; U76362; Hs.104637; solute carrier family 1 (gluta; lung; mAb+s.m.  
 421524; AA312082; Hs.105445; GDNF family receptor alpha 1; breast; mAb+s.m.  
 421552; AF026692; Hs.105700; secreted frizzled-related prot; breast, ovar, panc, cerv, uter, pros, lung, stom, headnk; diag  
 421563; NM\_006433; Hs.105806; granulysin; fibro; diag  
 421574; AJ000152; Hs.105924; defensin, beta 2; headnk, lung; CTL+diag  
 421582; AI910275; Hs.350470; trefoil factor 1 (breast cance; breast, panc, lung, omuc; diag

- 421659; NM\_014459; Hs.106511; protocadherin 17; fibro; mAb  
 421753; BE314828; Hs.107911; ATP-binding cassette, sub-fam1; lung; mAb+s.m.  
 421817; AF146074; Hs.108660; ATP-binding cassette, sub-fam1; lung, cerv, headnk, blad; mAb+s.m.  
 421829; AB018330; Hs.108708; calcium/calmodulin-dependent p; pros; s.m.  
 5 422048; NM\_012445; Hs.288126; spondin 2, extracellular matri; panc, pros, sarc; diag  
 422083; NM\_001141; Hs.111256; arachidonate 15-lipoxygenase, ; pros; s.m.  
 422109; S73265; Hs.1473; gastrin-releasing peptide; panc, lung, colon, fibro; diag  
 422158; L10343; Hs.112341; protease inhibitor 3, skin-der; headnk, blad, lung, cerv, stom, esoph; diag  
 10 422192; AA305159; Hs.113019; fls485; mela; s.m.  
 422260; AA315993; Hs.105484; regenerating gene type IV; colon, omuc, stom, panc; mAb+diag  
 422282; AF019225; Hs.114309; apolipoprotein L; blad, lung, headnk, renal; diag  
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45; lung, blad, test, cerv, headnk, esoph; s.m.  
 422330; D30783; Hs.115263; epiregulin; panc, colon, blad; mAb+diag  
 15 422397; AJ223366; Hs.116051; MYEOV Myeloma overexpressed ge; panc, stom, colon, esoph, renal, blad; CTL+s.m.  
 422424; AI186431; Hs.296638; prostate differentiation facto; blad, panc, pros, angio, colon, stom, lung, mela; diag  
 422578; AF239666; Hs.1545; caudal type homeo box transcrip; colon; CTL  
 422627; BE336857; Hs.118787; transforming growth factor, be; colon, renal, sarc; mAb+diag  
 422765; AW409701; Hs.1578; baculoviral IAP repeat-contain; lung, blad; s.m.  
 20 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; blad, cer, lung, uter, angio, stom, test; s.m.  
 422867; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar, pros, panc, lung, colon, uter, sarc; diag  
 422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell ; ovar, blad, panc, lung, headnk, colon, stom; CTL+s.m.  
 423161; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar, blad; mAb+s.m.  
 423184; NM\_004428; Hs.1624; ephrin-A1; pros, panc, renal, colon; mAb+s.m.  
 25 423242; AL039402; Hs.125783; DEME-6 protein; breast, renal, ovar, pros, colon; CTL  
 423508; AW604297; Hs.129711; hepatitis A virus cellular rec; renal, colon; mAb  
 423583; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.  
 423634; AW959908; Hs.1690; heparin-binding growth factor ; lung, blad, headnk, panc; diag  
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (m; blad, lung, headnk, ovar, panc, colon, stom, uter, cerv, esoph, test; mAb+diag+s.m.  
 30 423936; U77629; Hs.135639; achaete-scute complex (Drosophila; colon, stom, ovar; CTL  
 423961; D13666; Hs.136348; periostin (OSF-2os); breast, colon, blad, lung, fibro, panc, headnk, ovar, mela, sarc; mAb+diag  
 424008; R02740; Hs.137555; putative chemokine receptor; G; blad, headnk, stom, cerv, esoph; mAb+s.m.  
 424046; AF027866; Hs.138202; serine (or cysteine) proteinase; headnk, lung, cerv; diag  
 424321; W74048; Hs.1765; lymphocyte-specific protein ty; mela, fibro; s.m.  
 35 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); lung, colon, test; s.m.  
 424411; NM\_005209; Hs.146549; crystallin, beta A2; panc, sarc; s.m.  
 424502; AF242388; Hs.149585; lengsin; lung; s.m.  
 424503; NM\_002205; Hs.149609; integrin, alpha 5 (fibronectin; panc, pros, angio, blad, lung; mAb+s.m.  
 424620; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag  
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (ge; headnk, panc, lung, blad, uter, cerv, colon, stom, test, mela, sarc; diag  
 40 424735; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.  
 424825; AF207069; Hs.153357; procollagen-lysine, 2-oxogluta; mela; CTL+s.m.  
 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a); ovar, blad, lung, headnk, panc, stom; s.m.  
 424917; AI636208; Hs.96901; hypothetical protein FLJ23049; fibro, uter, ovar; CTL  
 424943; AU077260; Hs.153924; death-associated protein kinase; fibro; s.m.  
 45 425009; X58288; Hs.154151; protein tyrosine phosphatase, ; renal, fibro; mAb+s.m.  
 425071; NM\_013989; Hs.154424; deiodinase, iodothyronine, typ; pros, colon, stom, uter, cerv, headnk, esoph, panc; diag  
 425115; R44664; Hs.123956; downstream of: G protein-coupled; glio; mAb+s.m.  
 425247; NM\_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, ovar, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph, sarc; mAb+diag+s.m.  
 50 425263; NM\_001197; Hs.155419; BCL2-interacting killer (apopt; pros; s.m.  
 425322; U63630; Hs.155637; protein kinase, DNA-activated; lung, headnk; s.m.  
 425535; AB007937; Hs.158287; syndecan 3; mela, glio; mAb+s.m.  
 425650; NM\_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, headnk, cerv, esoph, blad; mAb  
 425721; AC002115; Hs.159309; uroplakin 1A; blad; mAb  
 55 425723; NM\_014420; Hs.159311; dickkopf (Xenopus laevis) homo; endo, uter, colon; CTL+diag  
 425734; AF056209; Hs.159396; peptidylglycine alpha-amidatin; lung; s.m.  
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; ovar, uter, lung; mAb+diag  
 425842; AI587490; Hs.159623; NK-2 (Drosophila) homolog B; panc, glio; s.m.  
 425852; AK001504; Hs.159651; death receptor 6, TNF superfam; blad, lung, headnk; mAb+s.m.  
 425883; AL137708; Hs.161031; Homo sapiens mRNA; cDNA DKFZp4; blad, panc; mAb  
 60 425998; AU076629; Hs.165950; fibroblast growth factor recep; renal; mAb+s.m.  
 426028; NM\_001110; Hs.172028; a disintegrin and metalloprote; blad; mAb+diag  
 426215; AW963419; Hs.155223; stanniocalcin 2; breast, lung, renal, colon, ovar, uter; mAb+diag  
 426227; U67058; Hs.154299; Human proteinase activated rec; panc, lung, colon, esoph, stom; mAb+s.m.  
 65 426322; J05068; Hs.2012; transcobalamin I (vitamin B12 ; panc, blad, stom; diag  
 426344; H41821; Hs.322469; transcriptional activator of t; glio; CTL+s.m.  
 426427; M86699; Hs.169840; TTK protein kinase; ovar, lung, headnk, cerv, colon, uter, stom, test; CTL+s.m.  
 426451; AI908165; Hs.169946; GATA-binding protein 3 (T-cell; blad, breast; s.m.  
 426514; BE616633; Hs.170195; bone morphogenetic protein 7 (; ovar, colon, blad, lung, cerv; mAb+diag  
 70 426600; NM\_003378; Hs.171014; VGF nerve growth factor induci; mela, sarc; diag  
 426761; AI015709; Hs.172089; PORIMIN Pro-oncogene receptor ; lung, esoph, pros, uter, panc, colon, ovar, headnk; mAb+s.m.  
 426812; AF105365; Hs.172613; solute carrier family 12 (pota; renal; mAb+s.m.  
 426890; AA393167; Hs.41294; ESTs; renal, colon, ovar, uter, stom; CTL  
 427239; BE270447; Hs.356512; ubiquitin carrier protein; lung, blad, test, mela, sarc; CTL+s.m.  
 427335; AA448542; Hs.278444; G antigen 7B; lung, headnk, blad, mela, esoph, sarc; CTL  
 75 427343; AI880044; Hs.176977; protein kinase C binding prote; glio; CTL+s.m.  
 427722; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, stom, panc; CTL  
 427747; AW411425; Hs.180655; serine/threonine kinase 12; blad, lung, ovar, stom, test, esoph, sarc; s.m.  
 427923; AW274357; Hs.301406; FGENSEH predicted 11 TM protei; mela; mAb  
 427969; NM\_001963; Hs.2230; epidermal growth factor (beta-; panc; mAb+diag  
 80 428093; AW594506; Hs.104830; ESTs; ovar, panc; CTL  
 428179; AI127772; Hs.380877; serum/glucocorticoid regulated; breast; s.m.  
 428187; AI687303; Hs.285529; G protein-coupled receptor 49; ovar, uter, colon, stom; mAb+s.m.  
 428242; H55709; Hs.2250; leukemia inhibitory factor (ch; ovar, panc, leuk, lung; diag

- 428296; NM\_003058; Hs.183572; solute carrier family 22 (orga; renal; mAb+s.m.  
 428330; L22524; Hs.2256; matrix metalloproteinase 7 (ma; uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela; mAb+diag+s.m.  
 428368; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk, stom, esoph, colon; diag  
 428392; H10233; Hs.2265; secretory granule, neuroendocr; panc; diag  
 5 428450; NM\_014791; Hs.184339; KIAA0175 gene product; ovar, cerv, panc, lung, blad, mela; s.m.  
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S; lung, blad, colon, uter, ovar; s.m.  
 428484; AF104032; Hs.184601; solute carrier family 7 (catio; lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela; mAb+s.m.  
 428486; AW583497; Hs.184604; pancreatic polypeptide; panc; diag  
 10 428505; AL035461; Hs.2281; chromogranin B (secretogranin ; panc, lung; diag  
 428513; BE220806; Hs.184697; plexin C1; mela, panc, breast stom, headnk; mAb  
 428579; NM\_005756; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.  
 428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosoph; blad, ovar, pros, lung, stom, test; CTL+s.m.  
 428698; AA852773; Hs.334838; KIAA1866 protein; breast, colon, lung, panc, stom, headnk, ovar, EWS; mAb  
 15 428748; AW593206; Hs.98785; Ksp37 protein; lung, sarc; diag  
 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; ovar, cerv, lung, panc, stom, renal; diag  
 428778; AK000530; Hs.193326; fibroblast growth factor recep; ovar; mAb+s.m.  
 428953; AA306610; Hs.348183; tumor necrosis factor receptor; cerv, panc, colon, stom, headnk, renal; mAb+diag  
 428969; AF120274; Hs.194689; artemin; lung, cerv; diag  
 20 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG; stom, panc, colon, ovar, fibro; mAb+s.m.  
 429149; AW193360; Hs.197962; Homolog of mouse ADP-ribosylat; glio; mAb+s.m.  
 429211; AF052693; Hs.198249; gap junction protein, beta 5 ( ; lung, blad, headnk, cerv, esoph, stom, mela; mAb+s.m.  
 429263; AA019004; Hs.198396; ATP-binding cassette, sub-fami; lung; mAb+s.m.  
 429276; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad, glio; mAb+s.m.  
 25 429353; AL117406; Hs.335891; ATP-binding cassette transport; breast, pros ; mAb+s.m.  
 429547; AW009166; Hs.99376; FGENSESH predicted novel secret; panc, headnk, lung, ovar; diag  
 429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate lu; lung, fibro; mAb+diag  
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, reg; lung, mela; s.m.  
 429910; NM\_000867; Hs.2507; 5-hydroxytryptamine (serotonin; leio; mAb+s.m.  
 30 430147; R60704; Hs.234434; hairy/enhancer-of-split relate; glio; s.m.  
 430178; AW449612; Hs.152475; 3'UTR of: achaete-scute comple; colon, stom, ovar; CTL  
 430377; NM\_001922; Hs.301865; dopachrome tautomerase (dopach; mela; CTL  
 430413; AW842182; Hs.241392; small inducible cytokine A5 (R; fibro, esoph, mela; diag  
 430486; BE062109; Hs.241551; chloride channel, calcium acti; lung, blad, headnk, cerv, esoph; mAb+s.m.  
 35 430822; AJ005371; Hs.248017; glyceraldehyde-3-phosphate deh; mela, sarc; s.m.  
 431130; NM\_006103; Hs.2719; HE4; epididymis-specific, whey; ovar, uter; diag  
 431462; AW583672; Hs.256311; granin-like neuroendocrine pep; panc, lung, glio, test; diag  
 431515; NM\_012152; Hs.258583; EDG-7 (endothelial differenti; ovar, pros, lung, blad; mAb+s.m.  
 431620; AA126109; Hs.264981; 2'-5'-oligoadenylate synthetas; esoph, cerv; CTL+s.m.  
 431629; AU077025; Hs.265827; interferon, alpha-inducible pr; panc, uter, cerv, stom, esoph, mela; mAb+diag  
 40 431630; NM\_002204; Hs.265829; integrin, alpha 3 (antigen CD4; ovar, panc, blad, headnk, mela, renal; mAb+s.m.  
 431745; AW972448; Hs.163425; Novel FGENSESH predicted cadher; fibro, ovar, uter; mAb  
 431840; AA534908; Hs.2860; POU domain, class 5, transcrip; test, renal, blad; CTL  
 431846; BE019924; Hs.271580; uroplakin 1B; lung, blad, headnk, uter, cerv, stom, ovar; mAb+diag  
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, cerv, headnk, ovar, colon, pros, panc, breast, esoph, test, mela; mAb+diag  
 45 432101; AI918950; Hs.123642; EphA3; pros, panc, EWS sarc; s.m.  
 432179; X75208; Hs.2913; EphB3; ovar, colon; mAb+s.m.  
 432196; AW300888; Hs.273230; hypothetical protein FLJ10830; renal; CTL  
 432201; AI538613; Hs.298241; Transmembrane protease, serine; breast, colon, ovar, stom, panc, uter, cerv, lung ; mAb+diag+s.m.  
 50 432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis; renal; CTL  
 432596; AJ224741; Hs.278461; matrilin 3; panc, breast, sarc; diag  
 432606; NM\_002104; Hs.3066; granzyme K (serine protease, g; renal, breast, lung, stom, hepC, fibro, leuk; CTL  
 432829; W60377; Hs.57772; ESTs; blad; CTL+s.m.  
 432874; W94322; Hs.279651; melanoma inhibitory activity; panc, stom, mela, sarc; diag  
 55 432990; AL036071; Hs.279899; tumor necrosis factor receptor; pros, renal; mAb+s.m.  
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; colon, breast, lung, blad, cerv, uter, test, mela; s.m.  
 433447; U29195; Hs.3281; neuronal pentraxin II; mela, esoph, colon, renal; diag  
 433848; AF095719; Hs.93764; carboxypeptidase A4; headnk, esoph, lung; s.m.  
 433867; AK000596; Hs.3618; hippocalcin-like 1; renal; CTL  
 434206; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung, stom; CTL+s.m.  
 60 434276; AF123659; Hs.93605; leucine zipper, putative tumor; mela; s.m.  
 434293; NM\_004445; Hs.3796; EphB6; blad, pros; s.m.  
 435013; H91923; Hs.110024; NM\_020142: Homo sapiens NADH:ub; renal, lung, sarc; CTL  
 435472; AW972330; Hs.283022; triggering receptor expressed ; glio; mAb  
 65 435505; AF200492; Hs.211238; interleukin-1 homolog 1; lung, headnk; diag  
 436456; AW292677; Hs.248122; melanin-concentrating hormone ; mela, glio; mAb+s.m.  
 436480; AJ271643; Hs.87469; putative acid-sensing ion chan; glio; mAb+s.m.  
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubi; lung, blad, colon, ovar, uter, headnk, test; s.m.  
 436576; AI458213; Hs.77542; ESTs; renal, panc, headnk, lung; mAb+s.m.  
 70 436608; AA628980; Hs.192371; down syndrome critical region ; blad, lung, sarc; CTL+s.m.  
 436895; AF037335; Hs.5338; carbonic anhydrase XII; breast, renal, ovar, glio; mAb+s.m.  
 436961; AW375974; Hs.156704; ESTs; lung, panc, renal, uter, colon ; CTL  
 436982; AB018305; Hs.5378; spondin 1, (f-spondin) extrace; ovar, fibro; diag  
 437016; AU076916; Hs.5398; guanine monophosphate synthetas; lung, blad, cerv, esoph, colon, headnk; s.m.  
 437044; AL035864; Hs.69517; differentially expressed in Fa; headnk, cerv, lung, blad, breast, pros, ovar, stom, esoph; CTL  
 75 437789; AI581344; Hs.127812; ESTs, Weakly similar to T17330; lung; CTL  
 437852; BE001836; Hs.256897; putative GPCR; blad, lung; mAb+s.m.  
 438380; T06430; Hs.6194; chondroitin sulfate proteoglyc; glio, mela; diag  
 438549; BE386801; Hs.21858; trinucleotide repeat containin; mela, sarc; CTL+diag  
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, s; uter, stom, pros, fibro; mAb  
 439223; AW238299; Hs.250618; UL16 binding protein 2; lung, headnk, cerv, esoph, leuk, blad, colon; mAb  
 439477; W69813; Hs.58042; ESTs, Moderately similar to GF; lung; mAb+s.m.  
 439569; AW602166; Hs.222399; CEGP1 protein; breast, pros, blad; diag  
 80 439606; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv, esoph; mAb+s.m.

- 439738; BE246502; Hs.9598; sema domain, immunoglobulin do; blad, lung, cerv, renal; mAb+s.m.  
 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; renal, cerv, pros, headnk, colon, test, sarc; mAb  
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containin; blad, ovar, lung, headnk, test; s.m.  
 440065; W03476; Hs.266331; Homo sapiens Fc receptor homol; mela; diag  
 440304; BE159984; Hs.125395; hepatitis A virus cellular rec; renal, colon, blad; mAb+s.m.  
 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin; glio, ovar, uter, renal, hepC; mAb+diag  
 440672; AF083811; Hs.7345; MAD1 (mitotic arrest deficient; mela; s.m.  
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog ; lung, blad, headnk, test, mela, esoph; s.m.  
 442117; AW664964; Hs.128899; ESTs; hypothetical protein for; breast, lung, blad, panc, headnk, stom, ovar, pros, sarc; mAb+s.m.  
 442133; AW874138; Hs.129017; ESTs; type Ia transmembrane p; ovar, uter; mAb  
 442275; AW449467; Hs.54795; Homo sapiens secretoglobulin, fa; fibro; diag  
 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; fibro, ovar, uter; CTL  
 443105; X96753; Hs.9004; chondroitin sulfate proteoglyc; mela; mAb+diag  
 443247; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL  
 443324; R44013; Hs.164225; ESTs; fibro; mAb+diag  
 443426; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad, stom, test, mela, sarc; CTL  
 443595; AF169312; Hs.9613; PPAR(gamma) angiotensin relat; renal; diag  
 443646; AI085198; Hs.164226; Thrombospondin 1; angio, panc, uter; diag  
 443859; NM\_013409; Hs.9914; follistatin; lung, cerv, headnk, blad, esoph; diag  
 443987; AW163123; Hs.10071; seven transmembrane protein TM; renal; mAb+s.m.  
 444006; BE395085; Hs.334762; type I transmembrane protein F; panc, colon, lung, ovar, renal, esoph, mela, blad, stom, cerv; mAb  
 444090; S69115; Hs.10306; natural killer cell group 7 se; fibro, renal, mela; diag  
 444371; BE540274; Hs.239; forkhead box M1; lung, headnk, blad, glio, test, mela; s.m.  
 444381; BE387335; Hs.283713; hypothetical protein BC014245; breast, colon, blad, lung, panc, headnk, ovar, stom, uter, renal, angio, test, mela, esoph, sarc; CTL+diag  
 444488; AW192879; Hs.355660; ancient conserved domain prote; renal; mAb+s.m.  
 444527; NM\_005408; Hs.11383; small inducible cytokine subfa; fibro, esoph; diag  
 444781; NM\_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk, cerv; mAb+diag  
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon, esoph; CTL+s.m.  
 445417; AK001058; Hs.12680; a disintegrin-like and metallo; panc, headnk, stom, lung, esoph, sarc, colon; diag  
 445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; ovar, blad, uter, breast, lung, headnk, renal, fibro, panc, cerv, sarc; mAb+diag  
 445891; AW391342; Hs.199460; DPCR1 protein; stom, panc, esoph, omuc, esoph; mAb  
 445895; D29954; Hs.13421; KIAA0056 protein; pros; CTL  
 446051; BE048061; Hs.37054; ephrin-A3; colon, breast; mAb+diag  
 446163; AA026880; Hs.25252; prolactin receptor; breast, cerv, uter; mAb+s.m.  
 446341; AL040763; Hs.310735; FGENESH prediction similar to ; mela; mAb+s.m.  
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (ost; ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter, sarc; diag  
 446650; AB016625; Hs.15813; solute carrier family 22 (orga; renal; mAb+s.m.  
 446921; AB012113; Hs.16530; small inducible cytokine subfa; breast, panc, headnk, lung, fibro, mela; diag  
 447033; AI357412; Hs.157601; Predicted gene: Eos cloned; se; colon, pros, fibro, breast, ovar, lung, panc, sarc; CTL+diag  
 447072; D61594; Hs.17279; tyrosylprotein sulfotransferas; glio, panc; CTL+s.m.  
 447131; NM\_004585; Hs.17466; retinoic acid receptor respond; renal, breast, stom, lung, mela, ovar; mAb+s.m.  
 447208; BE315291; Hs.237971; hypothetical protein MGC5627; esoph, stom, colon; CTL+diag  
 447269; NM\_004861; Hs.17958; cerebroside (3'-phosphoadenyly; renal; CTL  
 447342; AI199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, blad, pros, lung, stom, ovar; CTL  
 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag  
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; mela; s.m.  
 448243; AW369771; Hs.367688; integrin, beta 8; ovar, uter, lung, stom, headnk, glio, panc ; mAb+s.m.  
 448610; NM\_006157; Hs.21602; nel (chicken)-like 1; mela, sarc; diag  
 448733; NM\_005629; Hs.187958; solute carrier family 6 (neuro; lung, renal; mAb+s.m.  
 448844; AI581519; Hs.177164; FGENESH predicted novel cell s; panc, lung, stom, omuc; mAb+s.m.  
 449032; AA045573; Hs.22900; nuclear factor (erythroid-deri; colon, test, stom; CTL+s.m.  
 449048; Z45051; Hs.22920; similar to S68401 (cattle) glu; panc, ovar, uter, glio, headnk, lung, sarc; mAb  
 449444; AW818436; Hs.351306; solute carrier family 16 (mono; renal, panc; mAb+s.m.  
 449523; NM\_000579; Hs.54443; chemokine (C-C motif) receptor; lung, panc, renal, stom, hepC, fibro, leuk, mela; mAb+s.m.  
 449720; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL  
 449722; BE280074; Hs.23960; cyclin B1; headnk, blad, lung, panc, angio, test, mela, esoph; s.m.  
 450001; NM\_001044; Hs.406; solute carrier family 6 (neuro; renal; mAb+s.m.  
 450375; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc, lung, esoph, colon, sarc; mAb+diag+s.m.  
 450531; AW301032; Hs.203800; (BC017500) Similar to hypothet; colon; CTL  
 450701; H39960; Hs.288467; hypothetical protein XP\_098151; lung, headnk, panc, breast, stom, ovar, esoph, colon, sarc; mAb+diag  
 450726; AW204600; Hs.355462; HUMPSBA Human pulmonary surfa; fibro, lung; s.m.  
 450931; N25156; Hs.25648; tumor necrosis factor receptor; lung, renal; mAb+s.m.  
 450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; blad, lung, ovar, panc; diag  
 451310; AW250651; Hs.26213; Human DNA sequence from clone ; colon, panc; CTL  
 451527; AF022813; Hs.26518; transmembrane 4 superfamily me; renal; mAb  
 451537; R56631; Hs.26550; retinoid X receptor, gamma; mela; CTL+s.m.  
 451668; Z43948; Hs.326444; cartilage acidic protein 1; blad, ovar, lung; mAb+diag  
 451939; U80456; Hs.27311; single-minded (Drosophila) hom; pros; CTL  
 451979; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.  
 451988; AF263928; Hs.27410; papillomavirus regulatory fact; renal; CTL  
 452017; AF109302; Hs.27495; prostate cancer associated pro; pros; s.m.  
 452097; AB002364; Hs.27916; a disintegrin-like and metallo; ovar; mAb+s.m.+diag  
 452190; H26735; Hs.91668; Homo sapiens clone PP1498 unkn; breast, stom, panc; mAb  
 452194; AI694413; Hs.373599; olfactory receptor, family 2, ; stom, panc, renal, colon, mela, fibro; mAb+s.m.  
 452203; X57522; Hs.352018; transporter 1, ATP-binding cas; cerv, esoph, blad, stom, mela, renal; mAb+s.m.  
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast, headnk, panc, stom, lung, esoph, fibro; diag  
 452401; NM\_007115; Hs.29352; tumor necrosis factor, alpha-i; blad, breast, panc, headnk, stom, lung, leuk, renal, esoph; diag  
 452431; U88879; Hs.29499; toll-like receptor 3; renal, hepC; mAb  
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung, headnk, ovar, stom, uter, panc; mAb  
 452838; U65011; Hs.30743; preferentially expressed antig; lung, ovar, breast, mela, test, esoph, renal, sarc; CTL  
 452862; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like a; headnk, breast, colon, leuk, lung, blad, esoph, stom, sarc; mAb+diag  
 453195; BE241876; Hs.32352; hypothetical protein DKFZp434K; renal; CTL  
 453496; AA442103; Hs.33084; solute carrier family 2 (facil; renal, pros; mAb+s.m.



453837; AL138387; Hs.256126; baculoviral IAP repeat-contain; renal, mela, sarc; s.m.  
 453968; AA847843; Hs.62711; High mobility group (nonhiston; lung, uter, blad, test; CTL+s.m.  
 456546; A1690321; Hs.203845; KCNK15 potassium channel, subf; ovar; mAb+s.m.  
 456662; NM\_002448; Hs.1494; msh (Drosophila) homeo box hom; uter, ovar; CTL  
 457133; M54968; Hs.351221; v-Ki-ras2 Kirsten rat sarcoma; panc; s.m.  
 457489; A1693815; Hs.127179; cryptic gene; panc, pros, lung; diag  
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein; lung, cerv, headnk; mAb+diag  
 458079; A1796870; Hs.381220; Homo sapiens similar to RIKEN; mela, fibro, sarc; mAb  
 458627; AW088642; Hs.97984; SRY (sex determining region Y); ovar, uter, test; CTL

## TABLE 2B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414991	1785136_1	D78831 C17898 D78863

## TABLE 2C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
402901	8894222	Minus	175426-175667
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 3A. Disease Indications and Preferred Utilities for Selected Genes

Table 3A provides preferred disease indications and preferred utilities for about 2709 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number  
 UnigenelD: Unigene ID number  
 Unigene Title: Unigene gene title  
 Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), lei (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)  
 Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAccn; UnigenelD; Unigene Title; Disease; Utility

100125; R02740; Hs.137555; putative chemokine receptor; G; blad; mAb+s.m.  
 100131; D12485; Hs.11951; ectonucleotide pyrophosphatase; breast; mAb  
 100147; D13666; Hs.136348; periostin (OSF-2os); breast, colon, blad, lung, fibro, panc; mAb+diag  
 100241; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; blad; mAb  
 100299; D49493; Hs.2171; growth differentiation factor; EWS; diag  
 100335; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.  
 100365; A1878927; Hs.79284; mesoderm specific transcript; colon, pros; diag  
 100372; NM\_014791; Hs.184339; KIAA0175 gene product; ovar, lung, cerv, panc; s.m.  
 100405; AW291587; Hs.82733; nidogen 2; angio; diag  
 100420; D86983; Hs.118893; Melanoma associated gene; breast, pros, lung, colon, angio, leuk; diag  
 100448; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G; breast; mAb+s.m.  
 100452; D87742; Hs.241552; KIAA0268 protein; pros; diag  
 100559; NM\_000094; Hs.1640; collagen, type VII, alpha 1 (e; lung; CTL+s.m.  
 100654; A03758; Hs.184411; NM\_000477; Homo sapiens albumi; pros; diag  
 100655; A03758; Hs.184411; Empirically selected from AFFX; pros; diag  
 100668; L05424; Hs.169610; CD44 antigen (homing function; lung, breast; mAb  
 100824; A1393237; Hs.193989; runt-related transcription fac; ovar; CTL+s.m.  
 100930; J04129; Hs.82269; progesterone-associated endomet; lung; diag  
 101063; D54745; Hs.80247; cholecystokinin; pros, EWS; diag  
 101097; BE245301; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad; mAb+s.m.  
 101104; AW862258; Hs.169266; neuropeptide Y receptor Y1; breast, EWS; mAb  
 101192; BE247295; Hs.78452; solute carrier family 20 (phos; angio; mAb+s.m.  
 101193; L20861; Hs.152213; wingless-type MMTV integration; blad, lung; diag  
 101249; L18964; Hs.1904; protein kinase C, iota; ovar; s.m.

- 101261; D30857; Hs.82353; protein C receptor, endothelia; angio; mAb+s.m.  
 101389; AW951430; Hs.78888; diazepam binding inhibitor (GA; pros; mAb+s.m.  
 101431; BE185289; Hs.1076; small proline-rich protein 1B; lung, blad; diag  
 101447; M21305; ; gb:Human alpha satellite and s; angio, blad; diag  
 101461; N98569; Hs.76422; phospholipase A2, group IIA (p; pros; diag  
 101485; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, ovar; mAb  
 101506; J02931; Hs.62192; coagulation factor III (thromb; pros; mAb  
 101526; NM\_002197; Hs.220529; aconitase 1, soluble; lung, colon, headnk, panc; mAb  
 101543; M31166; Hs.2050; pentaxin-related gene, rapidly; angio, ovar; diag  
 101545; BE246154; Hs.154210; endothelial differentiation, s; angio; mAb+s.m.  
 101560; AW958272; Hs.347326; intercellular adhesion molecu; angio; mAb  
 101626; M57399; Hs.44; pleiotrophin (heparin binding ; lung; diag  
 101649; AW959908; Hs.1690; heparin-binding growth factor ; lung, blad; diag  
 101714; M68874; Hs.211587; phospholipase A2, group IVA (c; angio; s.m.  
 101724; L11690; Hs.198689; bullous pemphigoid antigen 1 (; breast, pros, blad, lung; mAb+CTL  
 101741; NM\_003199; Hs.326198; transcription factor 4; angio; CTL+s.m.  
 101748; NM\_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, blad, headnk, cerv; mAb  
 101759; M80244; Hs.184601; solute carrier family 7 (catio; lung, glio, blad, headnk; mAb+s.m.  
 101791; M83822; Hs.62354; cell division cycle 4-like; pros; s.m.  
 101804; M86699; Hs.169840; TTK protein kinase; ovar, lung, blad, cerv; CTL+s.m.  
 101806; AA586894; Hs.112408; S100 calcium-binding protein A; lung, breast, blad; diag  
 101809; M86849; Hs.323733; gap junction protein, beta 2, ; colon, blad, lung, panc, headnk; mAb  
 101839; AA446644; Hs.692; GA733-2 antigen; epithelial gl; ovar, pros; mAb  
 101845; U88967; Hs.78867; protein tyrosine phosphatase, ; lung, glio, headnk, cerv; mAb+s.m.  
 101851; BE260964; Hs.82045; midkine (neurite growth-promot; lung, blad, ovar, breast, panc; mAb+diag  
 102009; BE245149; Hs.82643; protein tyrosine kinase 9; ovar; s.m.  
 102012; BE259035; Hs.118400; singed (Drosophila)-like (sea ; angio; diag  
 102024; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag  
 102048; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb  
 102076; BE299197; Hs.179665; cyclin-dependent kinase inhibi; pros; CTL+s.m.  
 102125; NM\_006456; Hs.288215; sialyltransferase; breast, lung, ovar; s.m.  
 102136; AA300576; Hs.85769; acidic 82 kDa protein mRNA; ovar; diag  
 102151; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag  
 102154; U17760; Hs.75517; laminin, beta 3 (nicein (125kD; lung, blad, headnk; diag  
 102178; AW178761; Hs.227948; serine (or cysteine) proteinas; blad; mAb+diag  
 102187; U20325; Hs.1707; cocaine- and amphetamine-regul; breast; diag  
 102193; AL036335; Hs.313; secreted phosphoprotein 1 (ost; ovar, lung, fibro; diag  
 102200; AA232362; Hs.317432; branched chain aminotransferas; ovar; s.m.  
 102208; U22961; Hs.184411; gb:Human mRNA clone with simil; pros; diag  
 102211; BE314524; Hs.78776; putative transmembrane protein; breast, blad; mAb  
 102283; AW161552; Hs.83381; guanine nucleotide binding pro; angio; CTL+s.m.  
 102297; NM\_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb  
 102304; AF015224; Hs.46452; mammaglobin 1; breast; diag  
 102305; AL043202; Hs.90073; chromosome segregation 1 (yeas; ovar, lung, blad ; diag  
 102348; U37519; Hs.87539; aldehyde dehydrogenase 3 famil; lung, blad; s.m.  
 102380; U40434; Hs.155981; mesothelin; ovar; diag  
 102394; NM\_003816; Hs.2442; a disintegrin and metalloprote; panc; s.m.  
 102455; U48705; Hs.75562; discoidin domain receptor fami; breast; mAb  
 102457; NM\_001394; Hs.2359; dual specificity phosphatase 4; breast; s.m.  
 102522; BE250944; Hs.183556; solute carrier family 1 (neutr; pros; mAb  
 102581; AU077228; Hs.77256; enhancer of zeste (Drosophila); blad, EWS, leuk; CTL+s.m.  
 102610; U65011; Hs.30743; preferentially expressed antig; lung, ovar; CTL  
 102623; AW249285; Hs.37110; melanoma antigen, family A, 9; lung, blad; mAb+CTL  
 102669; U71207; Hs.29279; eyes absent (Drosophila) homol; lung, pros; CTL+s.m.  
 102696; BE540274; Hs.239; forkhead box M1; lung, blad; s.m.  
 102725; AB026187; Hs.374280; protocadherin 11; EWS; mAb  
 102742; U79293; Hs.159264; Human clone 23948 mRNA sequenc; breast, ovar ; diag  
 102745; AW753865; Hs.74376; olfactomedin related ER locali; EWS; diag  
 102803; H48299; Hs.26126; claudin 10; ovar; mAb  
 102829; NM\_006183; Hs.80962; neurotensin; lung, ovar, headnk; diag  
 102836; U94320; Hs.158330; neuropeptide Y receptor Y5; EWS; mAb  
 102852; V00571; Hs.75294; corticotropin releasing hormon; blad; diag  
 102898; NM\_002205; Hs.149609; integrin, alpha 5 (fibronectin; angio, blad, lung, pros; mAb+s.m.  
 102915; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, ovar; mAb+diag+s.m.  
 102917; AI016712; Hs.287797; integrin, beta 1 (fibronectin ; angio; mAb  
 102927; BE512730; Hs.65114; keralin 18; ovar; diag  
 102968; AU076611; Hs.154672; methylene tetrahydrofolate deh; ovar; s.m.  
 102994; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.  
 103003; AI910275; Hs.350470; trefoil factor 1 (breast cance; breast, panc; diag  
 103021; BE001596; Hs.85266; integrin, beta 4; lung blad; mAb  
 103036; M13509; Hs.83169; matrix metalloproteinase 1 (in; angio, colon, blad, lung, leuk, ovar, headnk, fibro, panc, stom; mAb+diag+s.m.  
 103037; BE018302; Hs.2894; placental growth factor, vascu; angio; diag  
 103060; NM\_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, lung, ovar, panc; mAb+diag+s.m.  
 103080; AU077231; Hs.82932; cyclin D1 (PRAD1: parathyroid ; breast, EWS; diag  
 103095; NM\_005424; Hs.78824; tyrosine kinase with immunoglo; angio; mAb  
 103111; NM\_006103; Hs.2719; epididymis-specific, whey-acid; ovar, uter; diag  
 103119; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, ovar, colon, pros, panc, breast; mAb+diag  
 103206; X72755; Hs.77367; monokine induced by gamma inte; breast, lung; diag  
 103210; X72925; Hs.69752; desmocollin 1; pros; mAb  
 103280; U84722; Hs.76206; cadherin 5, type 2, VE-cadheri; angio, fibro; mAb+s.m.  
 103299; NM\_005756; Hs.184942; G protein-coupled receptor 64; ovar; mAb+s.m.  
 103312; Y12642; Hs.3185; lysosomal; lung, blad; mAb  
 103365; X90908; Hs.74126; fatty acid binding protein 6, ; blad; diag

- 103408; NM\_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb  
 103478; BE514982; Hs.38991; S100 calcium-binding protein A; lung, blad, headnk; diag  
 103587; BE270266; Hs.82128; 5T4 oncofetal trophoblast glyc; breast, blad, lung; mAb  
 103594; AI368680; Hs.816; SRY (sex determining region Y); lung, glio; s.m.  
 103692; AW137912; Hs.227583; Homo sapiens chromosome X map; angio; mAb+s.m.  
 103739; AA115173; ; gb:zn30d02.s1 Stratagene neuro; pros; s.m.  
 103767; BE244667; Hs.348996; CGI-100 protein; angio; diag  
 103989; AA315993; Hs.105484; regenerating gene type IV; colon, omuc; mAb+diag  
 104052; NM\_002407; Hs.97644; mammaglobin 2; ovar; diag  
 104115; AF183810; Hs.26102; opposite strand of: trichorhi; breast; mAb  
 104252; AF002246; Hs.210863; cell adhesion molecule with ho; ovar; diag  
 104301; AA768491; Hs.6783; hypothetical protein FLJ22724; ovar; diag  
 104308; N25117; Hs.355957; ribosomal protein S26; pros; diag  
 104394; AA129551; Hs.172129; Homo sapiens cDNA: FLJ21409 fit; colon; diag  
 104542; R29657; ; gb:F1-1179D 22 week old human; pros; diag  
 104608; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb  
 104659; AW969769; Hs.100343; ESTs; EWS; diag  
 104660; BE298665; Hs.14846; Homo sapiens mRNA; cDNA DKFZp5; uter, colon, pros; mAb  
 104667; AI239923; Hs.63931; dachshund (Drosophila) homolog; breast, pros, colon; diag  
 104689; AA420450; Hs.380088; Plakophilin; lung; diag  
 104691; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.  
 104755; T49951; Hs.9029; DKFZP434G032 protein; breast, colon; diag  
 104764; AI039243; Hs.278585; ESTs; angio; diag  
 104786; AA027167; Hs.380438; KIAA0955 protein; angio; CTL+s.m.  
 104877; AI138635; Hs.22968; intron of VEGFR; renal; diag  
 104888; AW939591; Hs.5940; mucin 13, epithelial transmembr; colon, stom, uter; mAb+s.m.  
 104919; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 fit; breast, cerv, uter; mAb+s.m.  
 104943; AF072873; Hs.114218; frizzled (Drosophila) homolog; ovar; mAb+s.m.  
 104954; AW250651; Hs.26213; Human DNA sequence from clone; colon; diag  
 104971; BE311926; Hs.15830; hypothetical protein FLJ12691; blad; CTL  
 105012; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad; CTL  
 105038; AW503733; Hs.9414; KIAA1488 protein; breast, angio; CTL+s.m.  
 105039; AA907305; Hs.36475; ESTs; breast; diag  
 105093; AL137566; Hs.32405; Homo sapiens mRNA; cDNA DKFZp5; blad; diag  
 105149; BE089288; Hs.8958; Homo sapiens cDNA FLJ12024 fit; pros; diag  
 105175; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; colon, lung; mAb  
 105263; AW388633; Hs.6682; solute carrier family 7, (cat); angio, lung, ovar, blad, panc; mAb+s.m.  
 105298; BE387790; Hs.26369; hypothetical protein FLJ20287; ovar, lung; diag  
 105301; AW352357; Hs.7457; MAGE1 protein; EWS; diag  
 105316; AI671245; Hs.24835; hypothetical protein FLJ14594; EWS; mAb  
 105329; AA234561; Hs.22862; ESTs; breast, pros; CTL+s.m.  
 105330; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.  
 105370; AF179274; Hs.22791; transmembrane protein with EGF; pros; mAb+s.m.  
 105500; AW602166; Hs.222399; CEGP1 protein; breast, pros; diag  
 105503; AW963624; Hs.31707; ESTs, Weakly similar to YEW4\_Y; pros, breast, colon; CTL+s.m.  
 105507; BE268348; Hs.380963; CCR4-NOT transcription complex; colon; diag  
 105516; AK001269; Hs.30738; hypothetical protein FLJ10407; ovar; diag  
 105564; BE616694; Hs.288042; hypothetical protein FLJ14299; breast; diag  
 105645; AW294631; Hs.351270; ESTs; pros; diag  
 105715; BE621800; Hs.29444; putative small membrane protei; colon; diag  
 105743; BE246502; Hs.9598; sema domain, immunoglobulin do; breast, lung; mAb+s.m.  
 105746; AW151952; Hs.46679; hypothetical protein FLJ20739; breast; CTL+s.m.  
 105777; R42755; Hs.23096; ESTs; breast; diag  
 105782; H09748; Hs.57987; B-cell CLL/lymphoma 11B (zinc); EWS; CTL+s.m.  
 105826; AA478756; Hs.194477; E3 ubiquitin ligase SMURF2; angio; s.m.  
 105990; AI690586; Hs.29403; hypothetical protein FLJ22060; breast; diag  
 106000; AW194426; Hs.20726; ESTs; breast; diag  
 106012; AI240665; Hs.352537; ESTs; breast, lung; diag  
 106014; AF123094; Hs.180566; mucosa associated lymphoid tis; leuk; diag  
 106063; BE260415; Hs.348198; hypothetical protein FLJ20262; pros; diag  
 106066; AW274357; Hs.301406; hypothetical protein PP3501; mela; CTL+s.m.  
 106111; AW875398; Hs.6451; PRO0659 protein; EWS; CTL+s.m.  
 106124; H93366; Hs.7567; branched chain aminotransferas; angio; s.m.  
 106155; AA425414; Hs.33287; nuclear factor I/B; breast, pros, angio; diag  
 106373; AW503807; Hs.21907; histone acetyltransferase; breast; s.m.  
 106400; BE397649; Hs.279607; Homo sapiens cDNA FLJ13634 fit; colon; diag  
 106414; BE568205; Hs.28827; mitogen-activated protein kina; breast; s.m.  
 106448; Z42061; Hs.27004; ESTs; pros; diag  
 106533; AL134708; Hs.145998; ESTs; EWS; diag  
 106574; BE044325; Hs.227280; U6 snRNA-associated Sm-like pr; colon; diag  
 106579; AA456135; Hs.23023; ESTs; pros; diag  
 106632; NM\_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk; mAb+diag  
 106738; AW149266; Hs.25130; Homo sapiens cDNA FLJ14923 fit; ovar; diag  
 106793; H94997; Hs.16450; ESTs; angio; diag  
 106844; AA485055; Hs.158213; sperm associated antigen 6; breast; mAb+CTL  
 106906; AA861271; Hs.222024; transcription factor BMAL2; lung, blad; diag  
 106990; AA280722; Hs.24758; ESTs, Weakly similar to I38022; breast; diag  
 107036; AI973016; Hs.15725; hypothetical protein SBBI48; pros; diag  
 107102; AB037765; Hs.30652; KIAA1344 protein; pros, breast; diag  
 107105; AW963419; Hs.155223; stanniocalcin 2; breast; diag  
 107136; AV661958; Hs.8207; GK001 protein; breast, colon; diag  
 107151; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like a; breast, colon, leuk, blad; mAb+diag  
 107216; D51069; Hs.211579; melanoma cell adhesion molecul; angio; diag

- 107248; AW263124; Hs.350547; nuclear receptor co-repressor; breast, colon, pros; mAb+s.m.  
 107284; NM\_005629; Hs.187958; solute carrier family 6 (neuro; lung; mAb+s.m.  
 107385; NM\_005397; Hs.16426; podocalyxin-like; angio; diag  
 107901; L42612; Hs.335952; keralin 6B; breast, blad, lung; diag  
 5 107922; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung; mAb  
 107932; AW392555; Hs.18878; hypothetical protein FLJ21620; lung; CTL  
 108055; AJ404672; Hs.334483; hypothetical protein FLJ23571; breast, ovar; diag  
 108059; S69002; Hs.234773; Homo sapiens cDNA: FLJ22281 fi; ovar; CTL+s.m.  
 108153; AW519204; Hs.40808; ESTs; pros; diag  
 10 108186; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag  
 108242; AA062746; Hs.355244; gb:zm03g12.s1 Stratagene corne; pros; diag  
 108282; AA065142; ; gb:zm50h11.r1 Stratagene fibro; pros; diag  
 108505; AA083376; ; gb:zn09g08.s1 Stratagene hNT n; pros; diag  
 15 108679; AA115963; Hs.323423; ESTs, Moderately similar to B ; pros; diag  
 108695; AB029000; Hs.70823; KIAA1077 protein; breast, colon, lung; diag  
 108732; AA258888; Hs.107476; ATP synthase, H+ transporting.; pros; s.m.  
 108778; AF133123; Hs.90847; general transcription factor I; ovar; diag  
 108828; AK001693; Hs.273344; DKFZP564O0463 protein; breast; diag  
 108860; AA133334; Hs.816; ESTs; lung; s.m.  
 20 109001; AI056548; Hs.72116; hypothetical protein FLJ20992 ; angio; CTL+diag  
 109032; AI219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL  
 109077; AI732617; Hs.182362; ESTs; blad; diag  
 109112; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag  
 25 109141; AF174600; Hs.5978; ESTs, Highly similar to AF1746; colon; CTL+s.m.  
 109166; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, breast, colon, ovar, headnk, EWS; s.m.  
 109220; AW958181; Hs.189998; ESTs; pros; diag  
 109273; AA375752; Hs.348140; Homo sapiens mRNA; cDNA DKFZp5; breast; diag  
 109292; AW975746; Hs.188662; KIAA1702 protein; breast; diag  
 30 109454; AA232255; Hs.295232; ESTs, Moderately similar to A4; ovar; diag  
 109456; AW956580; Hs.42699; ESTs; angio, panc; diag  
 109514; AA234087; Hs.262346; ESTs, Weakly similar to S72482; breast ; diag  
 109530; AA908645; Hs.19597; KIAA1694 protein; pros; CTL+s.m.  
 109648; H17800; Hs.7154; ESTs; ovar; diag  
 35 109680; AB037734; Hs.4993; KIAA1313 protein; ovar; diag  
 110009; BE075297; Hs.6614; ESTs, Weakly similar to A43932; breast, colon; diag  
 110151; H18835; Hs.31608; hypothetical protein FLJ20041; pros, EWS; diag  
 110156; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag  
 110240; AI668594; Hs.176588; ESTs, Weakly similar to CP4Y\_H; breast; diag  
 40 110278; AF061573; Hs.19492; protocadherin 8; EWS; mAb+s.m.  
 110675; H89355; Hs.249159; adrenergic, alpha-2A-, recepto; pros; mAb+s.m.  
 110728; AA737108; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.  
 110844; AI740792; Hs.167531; methylcrotonyl-Coenzyme A car; pros, pros; s.m.  
 110915; BE092285; Hs.29724; hypothetical protein FLJ13187; breast, pros; diag  
 45 110971; AI760098; Hs.21411; ESTs; pros; diag  
 111157; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.  
 111179; AK000136; Hs.10760; asporin (LRR class 1); breast, colon; CTL+s.m.  
 111185; AJ245671; Hs.12844; EGF-like-domain, multiple 6; ovar, blad; mAb+diag  
 111223; AA852773; Hs.334838; KIAA1866 protein; breast, colon, lung, EWS; mAb  
 50 111299; AB033091; Hs.355925; KIAA1265 protein; ovar; diag  
 111357; BE314949; Hs.87128; hypothetical protein FLJ23309; breast; diag  
 111384; N94606; Hs.288969; HSCARG protein; breast; diag  
 111900; AF131784; Hs.25318; Homo sapiens clone 25194 mRNA ; breast; diag  
 111929; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb  
 55 112134; R41823; Hs.7413; ESTs; calyntenin-2; breast, EWS; diag  
 112244; AB029000; Hs.70823; KIAA1077 protein; breast, colon, blad, lung; diag  
 112280; AA863360; Hs.26040; ESTs, Weakly similar to fatty ; breast; s.m.  
 112283; L14561; Hs.20952; ATPase, Ca++ transporting, pla; ovar; mAb  
 112287; AB033064; Hs.236463; KIAA1238 protein; breast ; diag  
 60 112971; Z42387; Hs.83883; transmembrane, prostate androg; colon, pros, pros; mAb+s.m.  
 113003; AW292315; Hs.7215; ESTs; EWS; diag  
 113021; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.  
 113047; AI571940; Hs.7549; ESTs; breast, colon; diag  
 113073; N39342; Hs.103042; microtubule-associated protein; pros; CTL+s.m.  
 65 113168; AW002393; Hs.337629; gb:wu61d05.x1 NCL\_CGAP\_GC6 Hom; ovar; diag  
 113195; H83265; Hs.8881; ESTs, Weakly similar to S41044; angio, lung; diag  
 113230; T61430; ; gb:yc06a03.s1 Stratagene lung ; blad; diag  
 113361; T79589; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.  
 113374; T79925; Hs.269165; ESTs, Weakly similar to ALU1\_H; leuk; diag  
 70 113443; AW083920; Hs.16098; claudin 2; colon, panc; mAb  
 113471; AI765890; Hs.16341; MAWD binding protein; pros; diag  
 113490; BE178110; Hs.173374; Homo sapiens cDNA FLJ10500 fis; colon; diag  
 113950; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; breast, pros ; diag  
 113970; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag  
 75 114124; W57554; Hs.125019; lymphoid nuclear protein (LAF-; breast; diag  
 114251; H15261; Hs.21948; ESTs; breast; diag  
 114292; AI815395; Hs.184641; fatty acid desaturase 2; breast; s.m.  
 114334; AB037784; Hs.22941; KIAA1363 protein; ovar; diag  
 114407; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, colon, lung; diag  
 114452; AI369275; Hs.243010; Homo sapiens cDNA FLJ14445 fis; angio; diag  
 80 114480; BE066778; Hs.151678; UDP-N-acetyl-alpha-D-galactosa; breast; s.m.  
 114531; AA053033; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.  
 114540; AI904232; Hs.75323; prohibitin; breast; diag  
 114542; AW970128; Hs.91011; anterior gradient 2 (Xenopus l; breast, pros; diag

- 114587; AF086009; Hs.296398; gb:Homo sapiens full length in; colon; diag  
 114724; R64730.comp; Hs.155986; DEAD/H (Asp-Glu-Ala-Asp/His) b; ovar; CTL+s.m.  
 114768; AF212848; Hs.182339; ets homologous factor; pros; breast, colon; CTL+s.m.  
 114798; AA159181; Hs.54900; serologically defined colon ca; pros; CTL+s.m.  
 114908; AA454985; Hs.54973; cadherin-like protein VR20; pros; diag  
 114918; BE165762; Hs.23518; hypothetical protein from BCRA; pros; diag  
 114965; A1733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb  
 115060; AF052693; Hs.198249; gap junction protein, beta 5 (; lung, blad, headnk; mAb+s.m.  
 115221; AW365434; Hs.79741; hypothetical protein FLJ10116; ovar; diag  
 115239; BE251328; Hs.73291; hypothetical protein FLJ10881; colon; diag  
 115291; BE545072; Hs.122579; hypothetical protein FLJ10461; ovar, lung; CTL+s.m.  
 115412; AW131168; Hs.372382; ESTs, Weakly similar to I38022; pros; diag  
 115536; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon; CTL+s.m.  
 115674; AW992356; Hs.380760; Homo sapiens pyruvate dehydrog; ovar; s.m.  
 115675; W87707; Hs.82065; interleukin 6 signal transduce; breast, pros; mAb+s.m.  
 115683; AF255910; Hs.54650; junctional adhesion molecule 2; angio, glio; mAb  
 115697; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.  
 115719; AW992405; Hs.352406; Homo sapiens, clone IMAGE:3507; pros; breast, colon; CTL+s.m.  
 115819; AA486620; Hs.41135; endomucin-2; angio; diag  
 115827; AA428000; Hs.283072; actin related protein 2/3 comp; angio; diag  
 115844; A1373062; Hs.332938; hypothetical protein MGC5370; pros; diag  
 115881; NM\_005756; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.  
 115892; AA291377; Hs.50831; ESTs; ovar, blad, lung; diag  
 115909; AW872527; Hs.59761; ESTs, Weakly similar to DAP1\_H; ovar, lung; diag  
 115947; R47479; Hs.94761; KIAA1691 protein; colon; diag  
 115978; AL035864; Hs.69517; cDNA for differentially expres; lung, blad, breast, pros, ovar, headnk; CTL  
 116003; BE275469; Hs.66493; Down syndrome critical region ; colon; mAb  
 116011; AL359053; Hs.57664; Homo sapiens mRNA full length ; breast; diag  
 116028; H59799; Hs.42644; thioredoxin-like; ovar, lung; diag  
 116107; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag  
 116202; BE159395; Hs.294092; ESTs; pros; diag  
 116238; AV660717; Hs.47144; DKFZP586N0819 protein; ovar; diag  
 116301; AW969706; Hs.293332; ESTs; EWS; diag  
 116334; AL038450; Hs.48948; ESTs; pros; diag  
 116335; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk; diag  
 116393; A1972402; Hs.306051; hypothetical protein MGC2648; pros; diag  
 116399; AA889120; Hs.110637; homeo box A10; pros; CTL+s.m.  
 116401; AW893940; Hs.59698; ESTs; ovar; diag  
 116416; AW753676; Hs.39982; ESTs; ovar; diag  
 116470; A1272141; Hs.351928; SRY (sex determining region Y); colon, breast, angio, blad; diag  
 116483; A1346201; Hs.76118; ubiquitin carboxyl-terminal es; angio, lung; s.m.  
 116610; D80449; Hs.184841; ESTs; pros; diag  
 116732; AW152225; Hs.165909; ESTs, Weakly similar to I38022; colon; diag  
 116787; AW362955; Hs.356547; Homo sapiens cDNA FLJ14415 fis; pros, breast, colon, pros; mAb  
 116962; H79677; ; gb:yu76g10.s1 Soares fetal liv; pros; diag  
 117027; AW085208; Hs.130093; ESTs; breast; diag  
 117280; M18217; Hs.172129; Homo sapiens cDNA: FLJ21409 fi; breast, colon, pros; diag  
 117284; AK001701; Hs.183779; Homo sapiens cDNA FLJ10590 fis; pros; diag  
 117320; AB024937; Hs.211092; LUNX protein; PLUNC (palate lu; lung; mAb+diag  
 117367; A1041793; Hs.42502; ESTs; breast; diag  
 117412; N32536; Hs.42645; solute carrier family 16 (mono; breast, ovar ; mAb+s.m.  
 117425; AK000028; Hs.356100; ribosomal protein S24; pros; diag  
 117563; AF055634; Hs.44553; unc5 (C.elegans homolog) c; leuk ; diag  
 117602; N35020; Hs.44685; C3HC4-like zinc finger protein; EWS; CTL+s.m.  
 117921; AA021459; Hs.306480; Homo sapiens mRNA; cDNA DKFZp7; pros ; diag  
 117984; AF189723; Hs.106778; ATPase, Ca++ transporting, typ; pros, breast, colon; mAb  
 118049; N53145; ; gb:yv55f09.s1 Soares fetal liv; pros; diag  
 118314; N48580; Hs.46692; ESTs; blad, lung; diag  
 118336; BE327311; Hs.47166; HT021; breast, ovar, blad, pros; CTL+s.m.  
 118368; N64339; Hs.48956; gap junction protein, beta 6 (; lung, blad; mAb  
 118417; AF080229; ; gb:Human endogenous retrovirus; pros; s.m.  
 118472; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag  
 118511; N75620; Hs.43157; ESTs; angio; diag  
 118901; AW292577; Hs.94445; ESTs; breast; diag  
 118905; AW973708; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag  
 119018; AA631143; Hs.278695; Homo sapiens prostein mRNA, co; pros, pros; diag  
 119036; R95872; Hs.117572; chemokine binding protein 2; breast, ovar; mAb  
 119073; BE245360; Hs.45514; v-ets erythroblastosis virus E; angio, pros; CTL+s.m.  
 119082; AF252297; Hs.91546; cytochrome P450 retinoid metab; EWS; diag  
 119126; R45175; Hs.117183; ESTs; pros, breast, colon; diag  
 119279; N57568; Hs.48028; EST; breast; diag  
 119307; BE048061; Hs.37054; ephrin-A3; colon, breast; mAb+diag  
 119478; A1624342; Hs.179082; ESTs; breast; diag  
 119617; AA516531; Hs.55999; NK homeobox (Drosophila), fami; pros; diag  
 119743; AA947552; Hs.58086; branched chain aminotransferas; ovar; s.m.  
 119771; A1905687; Hs.348419; A1905687:IL-BT095-190199-019 B; breast; diag  
 119780; NM\_016625; Hs.191381; hypothetical protein; ovar, lung; CTL+s.m.  
 119789; BE393948; Hs.50915; kallikrein 5; ovar; diag  
 119845; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv; mAb+s.m.  
 119940; AL050097; Hs.272531; DKFZP586B0319 protein; pros; diag  
 120104; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, lung; diag  
 120132; W57554; Hs.126019; lymphoid nuclear protein (LAF-; pros, breast; diag  
 120147; A1917116; Hs.348941; hemoglobin, beta; EWS; diag

- 120206; H26735; Hs.91668; Homo sapiens clone PP1498 unkn; breast; mAb  
 120242; AW969587; Hs.86366; ESTs; blad; diag  
 120326; AA923278; Hs.290905; ESTs, Weakly similar to protea; pros; s.m.  
 120438; AW015242; Hs.99488; ESTs, Weakly similar to YK54\_Y; ovar; diag  
 5 120471; AA251944; Hs.104058; CGI-29 protein; colon; diag  
 120486; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk; diag  
 120588; AA703226; Hs.16193; Homo sapiens mRNA; cDNA DKFZp5; pros; diag  
 120624; AW407987; Hs.173518; M-phase phosphoprotein homolog; breast; s.m.  
 120830; AI568170; Hs.96886; ESTs; EWS; diag  
 10 120977; AA398155; Hs.97600; ESTs; breast, ovar; diag  
 121027; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 fi; blad; mAb  
 121231; AA814948; Hs.96343; ESTs, Weakly similar to ALUC\_H; EWS; diag  
 121335; AA404418; ; gb:zw37e02.s1 Soares\_total\_fet; angio; diag  
 121362; AF050147; Hs.97932; chondromodulin I precursor; EWS; mAb  
 15 121457; W07404; Hs.102558; hypothetical protein FLJ22055; colon; diag  
 121619; AA528339; Hs.178062; ESTs, Weakly similar to phosph; EWS; s.m.  
 121710; AF163474; Hs.96744; prostate androgen-regulated tr; pros; diag  
 121721; AL047051; Hs.199961; ESTs, Weakly similar to ALU7\_H; pros; diag  
 121723; AA243499; Hs.104800; hypothetical protein FLJ10134; breast; diag  
 20 121748; BE536911; Hs.234545; hypothetical protein NUF2R; breast; diag  
 121779; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag  
 121791; AA815378; Hs.293317; ESTs, Weakly similar to GGC1\_H; blad, headnk, lung, ovar; mAb+CTL  
 121792; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag  
 25 121913; AI249368; Hs.98558; ESTs; protease inhibitor 15 (i; breast, pros; s.m.  
 121920; AA428300; ; gb:zw18b02.s1 Soares ovary tum; ovar, uter, cerv; diag  
 122041; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag  
 122520; AW951324; Hs.173609; pregnancy specific beta-1-glyc; colon; diag  
 122797; AJ251027; Hs.99526; odorant-binding protein 2B (OB; breast; diag  
 30 122802; AI687303; Hs.285529; G protein-coupled receptor 49; ovar, uter; mAb+s.m.  
 122969; AW821252; Hs.104336; hypothetical protein; ovar; diag  
 123005; AW369771; Hs.367688; integrin, beta 8; ovar, lung, headnk, glio; mAb+s.m.  
 123044; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc ; lung; diag  
 123137; AI073913; Hs.100686; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom; diag  
 35 123158; AF161426; Hs.218329; hypothetical protein; breast; diag  
 123160; AA488687; Hs.284235; ESTs, Weakly similar to I38022; lung; diag  
 123169; AI950087; Hs.369628; gb:wq05c02.x1 NCL\_CGAP\_Kid12 H; ovar; diag  
 123209; AW968543; Hs.203270; ESTs, Weakly similar to ALU1\_H; pros; diag  
 123308; C14187; Hs.157208; ESTs; EWS; diag  
 40 123339; AW188464; Hs.101515; ESTs; ovar; diag  
 123475; BE439553; Hs.12329; Homo sapiens, clone IMAGE:4098; pros; diag  
 123494; AW179019; Hs.112110; mitochondrial ribosomal protein; ovar; diag  
 123520; AA608550; ; gb:ae53d12.s1 Stratagene lung ; pros; s.m.  
 123533; AA608751; ; gb:ae56h07.s1 Stratagene lung ; colon; diag  
 45 123619; AA602964; Hs.366318; gb:no97c02.s1 NCL\_CGAP\_Pr2 Hom; breast; CTL+s.m.  
 123689; AA399323; Hs.285130; Homo sapiens pinch-2 protein m; ovar; diag  
 123709; AA706910; Hs.112742; ESTs; breast; diag  
 123829; AF251237; Hs.112208; XAGE-1 protein; lung, blad, test; CTL  
 123972; T46848; Hs.70337; immunoglobulin superfamily, me; ovar; diag  
 50 124006; AI147155; Hs.279727; ESTs; homologue of PEM-3 [Cion; breast, angio, lung, ovar, EWS; diag  
 124059; BE387335; Hs.283713; ESTs, Weakly similar to S64054; breast, colon, blad, lung; CTL+diag  
 124153; AU077333; Hs.160483; erythrocyte membrane protein b; pros; mAb  
 124352; AA640891; Hs.102406; ESTs; breast, pros, ovar, lung; diag  
 124526; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros; mAb+s.m.  
 124579; AI693815; Hs.127179; cryptic gene; panc; diag  
 55 124777; R41933; Hs.140237; ESTs, Weakly similar to ALU1\_H; pros, breast; diag  
 125103; AA570056; Hs.122730; ESTs, Moderately similar to KI; colon; mAb  
 125154; W38419; ; gb:zc78a07.s1 Pancreatic Islet; ovar; diag  
 125250; W26524; Hs.356686; protein phosphatase 4 regulato; ovar; CTL+s.m.  
 60 125266; W90022; Hs.186809; ESTs, Highly similar to LCT2\_H; angio; diag  
 125453; BE385523; Hs.18048; melanoma antigen, family A, 10; blad; mAb+CTL  
 125666; AL390172; Hs.317432; Homo sapiens cDNA: FLJ21270 fi; ovar; diag  
 125770; AA143045; Hs.81665; v-kit Hardy-Zuckerman 4 feline; EWS; diag  
 125976; AA436760; Hs.35552; gb:zv67d11.r1 Soares\_total\_fet; pros; diag  
 65 126399; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.  
 126645; AA316181; Hs.61635; six transmembrane epithelial a; pros, breast, lung, panc, headnk, EWS; mAb+CTL  
 126758; AI559444; Hs.104679; ESTs; pros, breast; mAb  
 126799; AW753865; Hs.74376; olfactomedin related ER local; EWS; diag  
 126872; AW450979; ; gb:UL-H-BI3-ala-a-12-0-Ut.s1 N; blad; diag  
 70 126892; AF121856; Hs.284291; sorting nexin 6; ovar; diag  
 126960; AL390172; Hs.317432; branched chain aminotransferas; ovar; s.m.  
 126966; R38438; Hs.118747; solute carrier family 15 (H+>p; pros; mAb  
 127003; AW816515; Hs.173540; ATPase, Class V, type 10D; pros; mAb  
 127221; BE062109; Hs.241551; chloride channel, calcium acti; lung, blad, headnk, cerv; mAb+s.m.  
 75 127240; AJ005683; Hs.86998; nuclear factor of activated T-; pros; CTL+s.m.  
 127425; AF183810; Hs.26102; trichorhinophalangeal syndrome; breast; mAb  
 127479; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc; diag  
 127537; AI926047; Hs.162859; ESTs; pros; diag  
 127664; AA806164; Hs.116502; ESTs; EWS; diag  
 80 128046; AA873285; Hs.357313; gb:oh68h05.s1 NCL\_CGAP\_Kid5 Ho; pros, breast, colon; diag  
 128305; AI954968; Hs.365706; matrix Gla protein; breast; diag  
 128478; AA708205; Hs.100343; ESTs; EWS; CTL+s.m.  
 128515; BE395085; Hs.334762; type I transmembrane protein F; panc; mAb  
 128595; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.

- 128610; N48373; Hs.10247; activated leucocyte cell adhes; breast, pros, lung, ovar; diag  
 128734; AB008390; Hs.104570; kallikrein 8 (neuropsin/ovasin; ovar; diag  
 128790; AF026692; Hs.105700; secreted frizzled-related prot; breast, colon, pros, ovar, uter, panc; diag  
 128797; NM\_002975; Hs.105927; stem cell growth factor; lymph; EWS, leuk; diag  
 128854; BE159181; Hs.168232; hypothetical protein FLJ13855; breast; diag  
 128925; R67419; Hs.21851; Homo sapiens cDNA FLJ12900 fis; breast; diag  
 128949; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc; mAb+diag+s.m.  
 128969; Z42047; Hs.107479; Homo sapiens PRO2751 mRNA, com; pros; diag  
 129041; BE382756; Hs.169902; solute carrier family 2 (facil; lung, blad; mAb+s.m.  
 129097; BE243933; Hs.108642; zinc finger protein 22 (KOX 15; ovar; CTL+s.m.  
 129099; AF146074; Hs.108660; ATP-binding cassette, sub-fam; lung, blad, headnk ; mAb+s.m.  
 129184; AW161450; Hs.109201; CGI-86 protein; pros; mAb  
 129260; AF077200; Hs.279813; hypothetical protein; colon; diag  
 129284; AA318224; Hs.296141; ESTs; colon; diag  
 129362; U30246; Hs.110736; solute carrier family 12 (sodi; colon, breast, pros; mAb  
 129366; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA ; breast; diag  
 129389; NM\_012445; Hs.288126; spondin 2, extracellular matri; colon, pros; diag  
 129404; AI267700; Hs.351201; ESTs; pros, ovar, lung, blad, headnk, panc; diag  
 129466; L42583; Hs.334309; keratin 6A; lung, blad; diag  
 129482; AA188185; Hs.289043; spindlin; breast; diag  
 129534; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag  
 129571; X51630; Hs.1145; Wilms tumor 1; ovar; CTL+s.m.  
 129605; AF061812; Hs.115947; keratin 16 (focal non-epidermo; lung, blad, headnk; diag  
 129620; D79338; Hs.239720; CCR4-NOT transcription complex; breast, angio; diag  
 129628; U38945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk; s.m.  
 129650; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag  
 129689; AW748482; Hs.77873; B7 homolog 3; breast; diag  
 129703; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457; EWS, leuk; diag  
 129720; AA156214; Hs.12152; APMCF1 protein; breast; diag  
 129750; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad; mAb+s.m.  
 129869; AI222069; Hs.13015; hypothetical protein similar t; breast; diag  
 129912; AF155096; Hs.107213; hypothetical protein FLJ20585; ovar; CTL+s.m.  
 129936; AJ250717; Hs.1355; cathepsin E; blad; sm+diag  
 129953; AA412195; Hs.13740; ESTs; breast; diag  
 129977; NM\_000399; Hs.1395; early growth response 2 (Krox-; EWS; CTL+s.m.  
 130010; AA301116; Hs.142838; nucleolar phosphoprotein Nopp3; ovar; diag  
 130057; AF027153; Hs.324787; solute carrier family 5 (inosi; breast; mAb  
 130095; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag  
 130155; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag  
 130181; AF052119; Hs.151608; Homo sapiens clone 23622 mRNA ; pros; diag  
 130184; H58306; Hs.15165; retinoic acid induced 14; angio; diag  
 130262; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renal; diag  
 130343; AB040914; Hs.278628; KIAA1481 protein; breast; diag  
 130376; R40873; Hs.155174; CDC5 (cell division cycle 5, S; ovar; CTL+s.m.  
 130385; AW067800; Hs.155223; stanniocalcin 2; breast, lung; mAb+diag  
 130455; D90041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.  
 130511; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar; diag  
 130558; BE564937; Hs.15984; pp21 homolog; pros; CTL+s.m.  
 130577; M69241; Hs.162; insulin-like growth factor bin; ovar; diag  
 130604; AA383256; Hs.1657; estrogen receptor 1; breast; mAb+s.m.  
 130627; BE003054; Hs.1695; matrix metalloproteinase 12 (m; lung, colon, blad, headnk, ovar, panc; mAb+diag+s.m.  
 130637; AA356764; Hs.17109; integral membrane protein 2A; EWS; mAb+s.m.  
 130648; AI458165; Hs.17296; hypothetical protein MGC2376; colon; diag  
 130667; BE246961; Hs.17639; Homo sapiens ubiquitin protein; breast; s.m.  
 130690; AB006625; Hs.139033; paternally expressed 3; ovar; diag  
 130714; AI348274; Hs.18212; DNA segment on chromosome X (u; breast; diag  
 130760; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.  
 130800; AI187292; Hs.19574; hypothetical protein MGC5469; colon, lung; diag  
 130839; AB011169; Hs.380875; similar to S. cerevisiae SSM4; angio; diag  
 130844; U76248; Hs.20191; seven in absentia (Drosophila); breast; diag  
 130892; AL120837; Hs.20993; high-glucose-regulated protein; breast; CTL+s.m.  
 130941; NM\_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb  
 130967; AA393071; Hs.182579; leucine aminopeptidase; ovar; s.m.  
 130972; D81866; Hs.374468; Homo sapiens mRNA; cDNA DKFZp5; angio; diag  
 130987; BE613269; Hs.21893; hypothetical protein DKFZp761N; colon; diag  
 131046; AA321649; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, fibro; diag  
 131080; NM\_001955; Hs.2271; endothelin 1; angio; diag  
 131083; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros; mAb  
 131148; AW953575; Hs.303125; p53-induced protein PIGPC1; breast, colon, angio; diag  
 131216; AI815486; Hs.243901; Homo sapiens cDNA FLJ20738 fis; colon, breast; diag  
 131228; AW207469; Hs.24485; chondroitin sulfate proteoglyc; ovar; diag  
 131244; AI638429; Hs.24763; RAN binding protein 1; lung, blad, headnk; CTL+s.m.  
 131288; AA278482; Hs.25328; ESTs, Moderately similar to AL; pros; diag  
 131289; AA296696; Hs.333418; FXD domain-containing ion tra; colon; diag  
 131307; NM\_000025; Hs.2549; adrenergic, beta-3-, receptor; EWS; mAb  
 131313; R96290; Hs.75874; ribosomal protein L44; EWS; diag  
 131492; AI452601; Hs.288869; nuclear receptor subfamily 2, ; pros; mAb+s.m.  
 131544; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag  
 131559; AL078599; Hs.10784; hypothetical protein FLJ20037; breast; diag  
 131564; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast; diag  
 131603; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad; s.m.  
 131643; AW410601; Hs.30026; HSPC182 protein; breast; diag  
 131739; AF017986; Hs.31386; secreted frizzled-related prot; breast; mAb+s.m.

- 131817; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, glio; s.m.  
 131885; BE502341; Hs.3402; ESTs; breast; diag  
 131919; T15803; Hs.272458; protein phosphatase 3 (former); pros, breast; s.m.  
 131925; AF151048; Hs.183180; anaphase promoting complex sub; breast; diag  
 131965; W79283; Hs.35962; ESTs; lung, ovar; diag  
 131985; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag  
 132050; AI267615; Hs.38022; ESTs; angio; diag  
 132173; X89426; Hs.41716; endothelial cell-specific mole; angio; diag  
 132180; NM\_004460; Hs.418; fibroblast activation protein; colon, panc, esoph; mAb  
 132191; AA507576; Hs.288361; Homo sapiens cDNA: FLJ22696 fi; ovar; diag  
 132349; AW975654; Hs.181286; serine protease inhibitor, Kaz; pros, blad; s.m.  
 132354; BE185289; Hs.1076; small proline-rich protein 1B; lung; diag  
 132358; NM\_003542; Hs.46423; H4 histone family, member G; pros; CTL+s.m.  
 132371; AA235448; Hs.222088; PRO2000 protein; breast; diag  
 132454; BE296227; Hs.250822; serine/threonine kinase 15; blad, breast; s.m.  
 132490; NM\_001290; Hs.4980; LIM domain binding 2; angio; diag  
 132520; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.  
 132528; T78736; Hs.50758; SMC4 (structural maintenance o; ovar; CTL+s.m.  
 132543; BE568452; Hs.344037; protein regulator of cytokines; colon, lung; diag  
 132572; AI929659; Hs.237825; signal recognition particle 72; ovar; diag  
 132592; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22528 fi; colon; diag  
 132624; AA326108; Hs.33829; bHLH protein DEC2; ovar; diag  
 132632; AU076916; Hs.5398; guanine monphosphate synthetas; ovar, lung; s.m.  
 132669; W38586; Hs.380933; guanine nucleotide binding pro; colon; diag  
 132710; W74001; Hs.55279; serine (or cysteine) proteinas; lung, blad, colon, headnk; diag  
 132725; NM\_006276; Hs.184167; splicing factor, arginine/seri; ovar; CTL+s.m.  
 132767; BE182592; Hs.11261; small proline-rich protein 2A; lung; diag  
 132791; AB029551; Hs.7910; RING1 and YY1 binding protein; pros; CTL+s.m.  
 132837; AA307362; Hs.57958; EGF-TM7-latrophilin-related pr; angio; diag  
 132856; NM\_001448; Hs.58367; glypican 4; breast, colon, pros; mAb  
 132888; NM\_005476; Hs.5920; UDP-N-acetylglucosamine-2-epim; pros; s.m.  
 132902; AI936442; Hs.59838; hypothetical protein FLJ10808; colon; diag  
 132939; AB009284; Hs.61152; exostoses (multiple)-like 2; ovar; diag  
 132964; AI362575; Hs.303171; ESTs; pros; diag  
 132967; AA316181; Hs.61635; six transmembrane epithelial a; pros, pros; mAb+CTL  
 132990; X77343; Hs.334334; transcription factor AP-2 alpha; breast, lung; CTL+s.m.  
 132994; AA112748; Hs.279905; clone HQ0310 PRO0310p1; colon, breast; s.m.  
 133006; AW978436; Hs.62515; KIAA0494 gene product; colon; diag  
 133015; AJ002744; Hs.246315; UDP-N-acetyl-alpha-D-galactosa; breast, colon, pros; s.m.  
 133016; AI439688; Hs.6289; hypothetical protein FLJ20886; breast; diag  
 133061; AI186431; Hs.296638; prostate differentiation facto; angio, pros, blad; diag  
 133063; AI654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.  
 133070; U92649; Hs.380136; a disintegrin and metalloprote; leuk; diag  
 133179; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.  
 133199; AF231981; Hs.250175; homolog of yeast long chain po; breast, angio; CTL+s.m.  
 133260; AA403045; Hs.6906; Homo sapiens cDNA: FLJ23197 fi; angio; diag  
 133272; NM\_002776; Hs.69423; kallikrein 10; colon, ovar; diag  
 133314; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); breast, panc; mAb  
 133321; T79526; Hs.179516; integral type I protein; breast; diag  
 133391; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, blad, lung; diag  
 133415; X69699; Hs.73149; paired box gene 8; ovar; CTL  
 133477; AW502935; Hs.740; PTK2 protein tyrosine kinase 2; breast; s.m.  
 133579; X75346; Hs.75074; mitogen-activated protein kina; pros; diag  
 133626; AW836130; Hs.75277; hypothetical protein FLJ13910; pros; diag  
 133736; D49958; Hs.75819; glycoprotein M6A; pros; mAb  
 133829; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; ovar; diag  
 133860; S78296; Hs.76888; hypothetical protein MGC12702; blad; diag  
 133944; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag  
 133975; C18356; Hs.295944; tissue factor pathway inhibitor; angio, panc; CTL+diag  
 133976; AI908165; Hs.169946; GATA-binding protein 3 (T-cell; breast, blad; mAb+s.m.  
 134100; AA460085; Hs.171075; replication factor C (activato; pros; diag  
 134110; U41060; Hs.79136; LIV-1 protein, estrogen regula; breast, blad, ovar, pros; mAb  
 134169; AI690916; Hs.178137; transducer of ERBB2, 1; breast; CTL+s.m.  
 134219; NM\_000402; Hs.80206; glucose-6-phosphate dehydrogen; breast; s.m.  
 134319; BE304999; Hs.285754; fumarate hydratase; colon; s.m.  
 134326; AW903838; Hs.81800; chondroitin sulfate proteoglyc; ovar, breast, panc, lung; diag  
 134348; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.  
 134374; N22687; Hs.8236; ESTs; pros; diag  
 134390; R35528; Hs.8258; DKFZP434D1335 protein; pros; CTL+s.m.  
 134401; AI916662; Hs.211577; kinesin 1 (kinesin receptor); pros, breast; mAb+s.m.  
 134405; AW067903; Hs.82772; collagen, type XI, alpha 1; breast, lung, ovar, headnk; CTL  
 134470; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, headnk; s.m.  
 134520; BE091005; Hs.349506; activated RNA polymerase II tr; ovar; s.m.  
 134529; AW411479; Hs.848; FK506-binding protein 4 (59kD); breast; diag  
 134570; U66615; Hs.172280; SWI/SNF related, matrix associ; EWS; CTL+s.m.  
 134654; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag  
 134666; BE391929; Hs.8752; transmembrane protein 4; breast; mAb+s.m.  
 134691; AW382987; Hs.88474; prostaglandin-endoperoxide syn; ovar; s.m.  
 134727; X80507; Hs.84520; yes-associated protein 65 kDa; blad; diag  
 134731; D89377; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.  
 134786; T29618; Hs.89640; TEK tyrosine kinase, endotheli; angio; s.m.  
 134824; S78723; Hs.298623; 5-hydroxytryptamine (serotonin); blad; mAb  
 134856; BE281128; Hs.9030; TONDU; blad; CTL+s.m.



- 134868; AB020689; Hs.90419; KIAA0882 protein; breast; diag  
 134924; BE294029; Hs.279903; Ras homolog enriched in brain ; breast; mAb  
 134972; AL033527; Hs.169252; v-myc avian myelocytomatosis v; ovar; CTL+s.m.  
 134975; R50333; Hs.92186; Leman coiled-coil protein; breast; diag  
 134989; AW968058; Hs.92381; nudix (nucleoside diphosphate ; colon; diag  
 135073; W55956; Hs.94030; Homo sapiens mRNA; cDNA DKFZp5; angio; diag  
 135117; W52493; Hs.94694; Homo sapiens cDNA FLJ10561 fis; breast; diag  
 135166; AA135867; Hs.280858; ESTs, Highly similar to A35661; pros; diag  
 135235; AW298244; Hs.266195; ESTs; angio; diag  
 135242; AI583187; Hs.9700; cyclin E1; ovar; CTL+s.m.  
 135243; BE463721; Hs.97101; putative G protein-coupled rec; colon; mAb+s.m.  
 135255; Y13645; Hs.97234; uroplakin 2; blad; mAb  
 135309; AI564123; Hs.355689; ADP-ribosylation factor-like 5; pros; diag  
 135315; H81136; Hs.334604; Homo sapiens mRNA for KIAA1870; pros; diag  
 135389; U05237; Hs.99872; fetal Alzheimer antigen; pros, breast, colon; CTL+s.m.  
 135400; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.  
 300254; AW183618; Hs.55610; solute carrier family 30 (zinc; pros, breast; mAb+s.m.  
 300256; AW591433; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.  
 300318; AW444502; Hs.256982; ESTs, Weakly similar to NEL1\_H; angio; CTL+diag  
 300605; AI218847; Hs.152670; ESTs; pros; diag  
 300921; AF146747; Hs.232165; polycythemia rubra vera 1; cel; pros; mAb+s.m.  
 300923; AW136372; Hs.1852; acid phosphatase, prostate; pros; s.m.  
 301042; AI659131; Hs.366053; hypothetical protein MGC2849; pros; mAb  
 301043; AI160316; Hs.149155; voltage-dependent anion channe; pros; mAb+s.m.  
 301050; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung; CTL+s.m.  
 301341; AA887801; Hs.208229; G protein-coupled receptor; breast, lung; mAb+s.m.  
 302001; AB020711; Hs.374965; KIAA0904 protein; breast ; CTL+s.m.  
 302005; BE252922; Hs.123119; MAD (mothers against decapenta; pros; diag  
 302067; BE542706; Hs.222399; CEGP1 protein; breast; diag  
 302167; NM\_006227; Hs.283007; phospholipid transfer protein; pros; mAb  
 302225; NM\_007231; Hs.162211; solute carrier family 6 (neuro; panc; mAb+s.m.  
 302276; AW057736; Hs.323910; HER2 receptor tyrosine kinase ; breast; mAb+s.m.  
 302290; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp5; pros, breast; diag  
 302372; AL117406; Hs.335891; ATP-binding cassette transport; breast, pros ; mAb+s.m.  
 302384; AI678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag  
 302410; NM\_004917; Hs.218366; kallikrein 4 (prostase, enamel; pros; diag  
 302468; AL133561; Hs.380155; DKFZP434B061 protein; pros; diag  
 302562; BE149762; Hs.48956; gap junction protein, beta 6 (; lung, blad; mAb  
 302881; AA508353; Hs.105314; relaxin 1 (H1); pros; diag  
 303295; AA205625; Hs.208067; ESTs; blad; diag  
 303380; AW962764; Hs.303171; olfactory receptor, family 51.; pros; mAb  
 303506; AA340605; Hs.105887; ESTs, Weakly similar to Homolo; pros, breast, colon ; diag  
 303699; BE143707; Hs.19525; hypothetical protein FLJ22794; pros; diag  
 303753; AW503733; Hs.9414; KIAA1488 protein; pros, breast, colon; CTL+s.m.  
 305503; AA759177; Hs.298148; ESTs, Weakly similar to KIAA05; pros; diag  
 306273; AA936290; ; gb:on70a01.s1 Soares\_NFL\_T\_GBC; pros; diag  
 306676; AI005603; ; gb:ov15c10.s1 NCL\_CGAP\_GC3 Horn; lung; diag  
 306840; AI077477; Hs.307912; ESTs; angio; diag  
 309177; AI951118; Hs.326736; Homo sapiens breast cancer ant; breast, pros; mAb+CTL  
 309583; AW170035; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL  
 309931; AW341683; Hs.343663; gb:hd13d01.x1 Soares\_NFL\_T\_GBC; lung; mAb  
 310382; AI734009; Hs.127699; KIAA1603 protein; pros; diag  
 310431; AI420227; Hs.366053; ESTs, Weakly similar to A46010; pros; diag  
 310573; AW292180; Hs.156142; ESTs; pros; diag  
 310636; AI814373; Hs.164175; ESTs; lung; diag  
 310781; AI380797; Hs.158992; ESTs; breast ; diag  
 310955; AI476732; Hs.263912; ESTs; breast, angio; diag  
 311034; BE567130; Hs.311389; ESTs, Highly similar to NKGD\_H; lung; mAb+s.m.  
 311166; AI821005; Hs.118599; intron of. BFF9 (GDNFRa); breast ; diag  
 311251; AI655662; Hs.197698; ESTs; pros; diag  
 311557; AF200492; Hs.211238; interleukin-1 homolog 1; lung; diag  
 311596; AI682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL  
 311630; AI915444; Hs.372037; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.  
 311877; AA084248; Hs.372651; G protein-coupled receptor 39; ovar, angio, glio; mAb+s.m.  
 311911; R19175; Hs.169793; ribosomal protein L32; pros; diag  
 311928; T62216; Hs.378028; ESTs; pros; diag  
 312182; T94344; Hs.326263; ESTs; pros; diag  
 312252; AI128388; Hs.143655; ESTs; blad; diag  
 312319; AA906997; Hs.180780; TERA protein; colon; CTL+s.m.  
 312521; AI263307; Hs.356901; H2B histone family, member L; pros, breast, lung; diag  
 312544; AA516420; Hs.352340; ESTs, Weakly similar to I38022; breast; diag  
 312742; AI650363; Hs.116462; ESTs; colon; diag  
 312795; AW975014; Hs.26; ferrochelatase (protoporphyrin; pros; s.m.  
 312857; BE083868; Hs.126914; KIAA1430 protein; colon, pros; CTL+s.m.  
 312922; AA329256; Hs.378739; ESTs, Moderately similar to al; pros; diag  
 313328; AW449211; Hs.105445; GDNF family receptor alpha 1; breast ; mAb+s.m.  
 313513; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.  
 313556; AA628517; Hs.118502; ESTs; angio; diag  
 313665; AW751201; Hs.120932; ESTs; angio; diag  
 313774; AI916058; Hs.144583; ESTs; colon; CTL  
 313915; C18863; Hs.163443; intron of periostin (OSF-2os); breast; diag  
 313978; AI870175; Hs.13957; ESTs; angio; diag  
 314078; AW129357; Hs.329700; ESTs; breast; diag

- 5 314097; AA648744; Hs.269493; ESTs; breast; diag  
 314121; AI732083; Hs.187619; ESTs; pros; breast; diag  
 314171; AI821895; Hs.193481; ESTs; pros; diag  
 314506; AA833655; Hs.206868; Homo sapiens cDNA FLJ14056 fis; breast; diag  
 314547; AA399272; Hs.144341; ESTs; breast; diag  
 314558; AI873274; Hs.370280; ESTs; breast; pros; diag  
 314589; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis; lung, blad; diag  
 10 314691; AW207206; Hs.356962; ESTs; breast; pros; diag  
 314785; AI538226; Hs.32976; guanine nucleotide binding pro; colon; pros; diag  
 314907; AW971082; Hs.222886; ESTs, Weakly similar to TRHY\_H; pros; diag  
 315006; AI538613; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.  
 315033; AI493046; Hs.146133; ESTs; colon; diag  
 315051; AW292425; Hs.163484; ESTs; breast, pros, blad; diag  
 15 315052; AA876910; Hs.134427; ESTs; pros; breast; diag  
 315196; AI367347; Hs.44898; Homo sapiens clone TCCCTA00151; breast; diag  
 315368; AB037745; Hs.104696; KIAA1324 protein; pros; diag  
 315408; AW273261; Hs.216292; ESTs; pros; diag  
 315634; AA837085; Hs.372254; ESTs; breast; pros; diag  
 20 315720; AA292998; Hs.163900; ESTs; blad; diag  
 316177; AI904982; Hs.293102; downstream of breast cancer an; breast; mAb+CTL  
 316442; AA760894; Hs.125350; ESTs; pros; diag  
 316580; AA938198; Hs.146123; poly(A) polymerase gamma; breast, angio; s.m.  
 316886; AA836331; Hs.170261; ESTs; breast; diag  
 25 316943; AW014875; Hs.137007; ESTs; blad; diag  
 317079; BE159984; Hs.125395; ESTs; blad; mAb+s.m.  
 317140; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag  
 317224; X73608; Hs.93029; sparc/osteoneclin, cwcw and ka; pros, angio; diag  
 317548; BE568568; Hs.159066; ESTs; pros; CTL+s.m.  
 30 317803; AW664964; Hs.128899; ESTs; breast, lung, ovar, pros; mAb+s.m.  
 317881; AI827248; Hs.224398; Homo sapiens cDNA FLJ11469 fis; breast, lung; diag  
 318240; AI085377; Hs.143610; ESTs; lung; diag  
 318524; AK001050; Hs.159066; hypothetical protein FLJ10188; pros, colon; CTL+s.m.  
 318532; AW139377; Hs.127179; cryptic gene; panc; diag  
 35 318744; AI793124; Hs.144479; ESTs; breast; diag  
 318754; W21423; Hs.44222; CGI-90 protein; pros; diag  
 319080; AW967646; Hs.23023; ESTs; pros; diag  
 319795; AB037821; Hs.146858; protocadherin 10; pros, glio; mAb+s.m.  
 320066; BE305242; Hs.16098; claudin 2; colon, panc; diag  
 40 320167; AA984373; Hs.90790; Homo sapiens cDNA: FLJ22930 fi; breast, pros; diag  
 320203; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar, mAb+s.m.  
 320211; AL039402; Hs.125783; DEME-6 protein; breast, pros; CTL  
 320322; AF077374; Hs.139322; small proline-rich protein 3; lung; diag  
 320324; AF071202; Hs.139336; ATP-binding cassette, sub-fam1; pros; mAb  
 45 320561; AF085808; Hs.159330; uroplakin 3; pros, blad; diag  
 320590; U67058; Hs.154299; Human proteinase activated rec; pros; mAb+s.m.  
 320635; N50617; Hs.80506; small nuclear ribonucleoprotein; angio lung; diag  
 320736; AA315361; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag  
 320796; AK001541; Hs.31218; secretory carrier membrane pro; pros, colon; diag  
 50 320896; BE019924; Hs.271580; uroplakin 1B; lung, blad, ovar, headnk; mAb+diag  
 321023; AW294316; Hs.125608; ESTs; colon; diag  
 321107; AI732643; Hs.144151; downstream of breast cancer an; breast; mAb+CTL  
 321412; AI674383; Hs.22891; solute carrier family 7 (catio; pros; mAb+s.m.  
 321441; AF107493; Hs.201675; Homo sapiens LUCA-15 protein m; pros, breast; diag  
 55 321644; AW975944; Hs.237396; ESTs; breast, pros; diag  
 321717; AW956580; Hs.42699; ESTs; angio; diag  
 321906; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag  
 321911; AF026944; Hs.293797; ESTs; angio, lung, blad; diag  
 322035; AL137517; Hs.306201; hypothetical protein DKFZp564O; breast, blad; mAb  
 60 322521; AF147347; ; gb:Homo sapiens full length in; breast; diag  
 322706; AA018899; Hs.127179; cryptic gene; panc; diag  
 322782; AA056060; Hs.202577; Homo sapiens cDNA FLJ12166 fis; pros; diag  
 322818; AW043782; Hs.293616; ESTs; pros, breast, angio, glio; diag  
 322882; AW248508; Hs.279727; Homo sapiens cDNA FLJ14035 fis; breast, lung, ovar, angio, blad; diag  
 65 322975; C16391; ; intron of breast cancer antigen; breast; mAb+CTL  
 323168; AL120862; Hs.124165; programmed cell death 9 (PDCD9; breast; diag  
 323226; AF055019; Hs.355279; Homo sapiens clone 24670 mRNA; pros; diag  
 323262; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag  
 323287; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag  
 70 323332; AI829520; ; gb:wt19c06.x1 NCL\_CGAP\_Ut1 Hom; breast; diag  
 323335; AI655499; Hs.161712; ESTs; pros, breast; mAb  
 323587; AI299709; Hs.131886; Homo sapiens cDNA: FLJ22113 fi; colon; diag  
 323817; AA410943; ; NAME OMITTED ... receptor kinase; breast; mAb  
 324261; BE069341; ; gb:QV3-BT0381-270100-073-c08 B; breast; diag  
 75 324295; AA434579; Hs.143691; ESTs; pros; diag  
 324338; AA927668; Hs.145078; regulator of differentiation (; colon; diag  
 324430; AA464018; Hs.335798; Homo sapiens cDNA: FLJ23241 fi; pros, colon; diag  
 324432; AA464510; Hs.152812; ESTs; breast, lung, panc; diag  
 324603; AW993522; Hs.299867; ESTs; pros, breast; diag  
 80 324617; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros; diag  
 324658; AI694767; Hs.129179; Homo sapiens cDNA FLJ13581 fis; pros; diag  
 324718; AI557019; Hs.116467; small nuclear protein PRAC; colon, pros; diag  
 324866; AI541214; Hs.46320; Small proline-rich protein SPR; lung, blad; diag  
 324871; AI890347; Hs.271923; Homo sapiens cDNA: FLJ22785 fi; colon; diag

324987; AI375572; Hs.172634; ESTs; breast; diag  
 325372; ; Phase 2 & 3 Exons; breast; CTL+s.m.  
 325544; ; Phase 2 & 3 Exons; breast; angio; diag  
 327036; ; Phase 2 & 3 Exons; lung; angio; diag  
 327075; ; Phase 2 & 3 Exons; breast; lung; diag  
 327414; ; Phase 2 & 3 Exons; angio; diag  
 328700; ; Phase 2 & 3 Exons; breast; angio; diag  
 330211; ; Phase 2 & 3 Exons; pros; CTL+s.m.  
 330468; L10343; Hs.112341; protease inhibitor 3; skin-der; lung; colon; blad; diag  
 330493; M27826; Hs.334372; endogenous retroviral protease; lung; colon; s.m.  
 330630; NM\_002902; Hs.79088; reticulocalbin 2; EF-hand calc; pros; diag  
 330762; AW407332; Hs.13014; ADP-ribosylation factor GTPase; pros; CTL+s.m.  
 330790; AI660243; Hs.318545; Hu01 Chip Redos; pros; blad; diag  
 330814; AI955040; Hs.265398; PAR-6 beta (partitioning def; breast; diag  
 330827; AI961486; Hs.249196; ESTs; lung; uter; diag  
 330892; AF109298; Hs.118258; prostate cancer associated pro; pros; diag  
 331014; AW770994; Hs.30340; hypothetical protein KIAA1165; colon; diag  
 331151; R82331; Hs.121602; ESTs; pros; breast; diag  
 331183; T40769; Hs.8469; ESTs; colon; diag  
 331237; W87874; Hs.25277; Homo sapiens cDNA FLJ10717 fis; angio; diag  
 331490; AF216751; Hs.26813; CDA14; pros; diag  
 331578; AI246482; Hs.243010; ESTs; angio; diag  
 331614; N92293; Hs.206832; EST; Moderately similar to ALU; breast; diag  
 331811; AW885727; Hs.9914; Hu01 Chip Redos; lung; diag  
 331889; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag  
 331969; AA526911; Hs.82772; collagen; type XI; alpha 1; breast; lung; CTL  
 332180; AF134160; Hs.7327; claudin 1; lung; mAb  
 332247; AA669097; ESTs; pros; breast; diag  
 332396; AW579842; Hs.380730; hypothetical protein FLJ10697; pros; diag  
 332453; L42583; Hs.334309; Hu01 Chip Redos; lung; diag  
 332466; AB018259; Hs.118140; KIAA0716 gene product; angio; diag  
 332530; M31669; Hs.1735; inhibin; beta B (activin AB be; ovar; pros; diag  
 332535; AF167706; Hs.19280; cysteine-rich repeat-containing; angio; diag  
 332640; BE568452; Hs.344037; protein regulator of cytokines; blad; headnk; diag  
 332645; AA284371; Hs.118064; ESTs; breast; colon; diag  
 332686; X69699; Hs.73149; paired box gene 8; ovar; CTL+s.m.  
 332697; X51405; Hs.75360; carboxypeptidase E; pros; diag  
 332740; BE409869; Hs.286241; Homo sapiens cDNA: FLJ22698 fi; pros; diag  
 332798; ; C22000007.gij12314195[emb]CAB9; pros; breast; diag  
 333769; ; NM\_005940\*.Homo sapiens matrix; breast; colon; lung; mAb+diag+s.m.  
 333904; ; Chromosome 22; pros; diag  
 334223; ; NM\_005080\*.Homo sapiens X-box ; pros; breast; diag  
 334447; ; NM\_012429\*.Homo sapiens SEC14 ; pros; diag  
 335115; ; NM\_006498\*.Homo sapiens lectin; pros; CTL+s.m.  
 335809; ; NM\_014509\*.Homo sapiens kraken; breast; CTL+s.m.  
 335824; ; ENSP00000249072\*.DJ222E13.1 (N; breast; pros; CTL+s.m.  
 335825; ; ENSP00000249072\*.DJ222E13.1 (N; breast; diag  
 335936; ; Chromosome 22; lung; diag  
 336034; ; NM\_007172\*.Homo sapiens nucleop; breast; angio; CTL+s.m.  
 336152; ; NM\_014246\*.Homo sapiens cadheri; breast ; mAb  
 336636; ; C22000024\*.gij10645308[gb]AAG2; lung, breast; CTL+s.m.  
 338008; ; NM\_005940\*.Homo sapiens matrix; lung, breast; colon; mAb+diag+s.m.  
 338033; ; Chromosome 22; lung, angio; diag  
 338158; ; NM\_012399\*.Homo sapiens phosphi; lung, angio; diag  
 338255; ; NM\_014323\*.Homo sapiens zinc f; pros, breast, colon ; CTL+s.m.  
 400195; ; Hs.42650; NM\_007057\*.Homo sapiens ZW10 i; lung; CTL+s.m.  
 400269; ; Hs.253495; Eos Control; fibro; diag  
 400285; ; Eos Control; lung; diag  
 400287; S39329; Hs.181350; kallikrein 2, prostatic; pros; diag  
 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin; panc, pros, angio, blad, lung; mAb+s.m.  
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; pros, colon, EWS; mAb  
 400294; N95796; Hs.278695; Homo sapiens protein mRNA, co; pros, pros; mAb  
 400295; W72838; Hs.348419; AI905687; IL-BT095-190199-019 B; breast; diag  
 400298; AA032279; Hs.61635; six transmembrane epithelial a; panc, lung, headnk, stom, EWS, ovar; mAb+CTL  
 400328; X87344; ; transporter 2, ATP-binding cas; lung; mAb+s.m.  
 400409; AF153341; ; Homo sapiens winged helix/fork; blad; CTL+s.m.  
 400419; AF084545; ; Target; lung, sarc; diag  
 400440; X83957; Hs.83870; nebulin; sarc; diag  
 400494; ; ENSP00000238970\*.CIG30 (Fragme; angio; mAb  
 400517; ; lengsin; stom, cerv, uter, lung, pros, colon, hepC; diag  
 400651; ; ENSP00000228031\*.COPPER CHAPER; sarc; s.m.  
 400665; ; NM\_002425; Homo sapiens matrix ; lung; mAb+diag+s.m.  
 400773; ; NM\_003105\*.Homo sapiens sortil; blad; mAb  
 400844; ; NM\_003105\*.Homo sapiens sortil; blad; s.m.  
 400846; ; sortilin-related receptor, L(D; blad; mAb+s.m.  
 400881; ; NM\_025080; Homo sapiens hypothe; ovar; diag  
 401093; ; C12000586\*.gij6330167[dbj]BAA8; blad, lung; CTL+s.m.  
 401234; ; mitogen-activated protein kina; angio; diag  
 401424; ; NM\_001172; Homo sapiens arginas; pros; s.m.  
 401486; ; C4000647\*.gij4758508[ref]NP\_00; headnk; mAb  
 401704; ; NM\_021195\*.Homo sapiens claudi; test; mAb  
 401732; ; NM\_001176\*.Homo sapiens Rho GD; panc; diag  
 401747; ; Homo sapiens keratin 17 (KRT17; blad, lung, headnk, mela; diag

401760;; Target Exon; blad, lung, headnk, esoph; diag  
 401780;; NM\_005557\*:Homo sapiens kerati; lung, blad, headnk, esoph, mela; diag  
 401781;; Target Exon; lung, blad, headnk, esoph, cerv; diag  
 401785;; NM\_002275\*:Homo sapiens kerati; lung; diag  
 5 401797;; Target Exon; sarc; diag  
 401994;; Target Exon; lung; diag  
 402145;; Target Exon; test; CTL+s.m.  
 402199;; Target Exon; test; CTL+s.m.  
 10 402230;; Fgenesh predicted: CYTOCHROME ; blad; diag  
 402239;; Target Exon; blad; diag  
 402260;; NM\_001436\*:Homo sapiens fibril; blad; CTL+s.m.  
 402265;; Target Exon; lung; diag  
 402305;; C19000735\*:gil4508027[ref]NP\_0; blad; CTL+s.m.  
 15 402420;; C1000823\*:gil10432400[emb]CAC1; lung; diag  
 402424;; NM\_024901:Homo sapiens hypothe; blad; CTL+s.m.  
 402447;; C1000201:gil204416[gb]AAA02627; esoph; mAb  
 402474;; NM\_004079:Homo sapiens catheps; lung, colon, stom, fibro; diag  
 402550;; Target Exon; fibro; diag  
 20 402604;; Target Exon; glio; diag  
 402605;; Target Exon; glio; diag  
 402606;; NM\_024626:Homo sapiens hypothe; ovar, breast; mAb  
 402680;; Target Exon; test; mAb  
 402777;; C1002652\*:gil544327[sp]Q04799; blad; diag  
 25 402860;; ENSP00000239210:DJ50024.4 (nov; mela; CTL+s.m.  
 402888;; Target Exon; sarc; diag  
 402992;; Target Exon; sarc; diag  
 402994;; NM\_002463\*:Homo sapiens myxovi; esoph; diag  
 403046;; NM\_005656\*:Homo sapiens transm; pros; mAb  
 30 403047;; NM\_005656\*:Homo sapiens transm; pros, blad, colon; mAb  
 403071;; NM\_003319\*:Homo sapiens titin ; sarc; diag  
 403088;; NM\_003319\*:Homo sapiens titin ; sarc; diag  
 403171;; C2001472\*:gil5809678[gb]AAB418; test; diag  
 403328;; Target Exon; mela; diag  
 35 403329;; unnamed protein product [Homo ; lung; diag  
 403381;; ENSP00000231844\*:Ecotropic vir; blad; CTL+s.m.  
 403409;; NM\_005929:Homo sapiens antigen; mela; mAb  
 403433;; NM\_001622:Homo sapiens alpha-2; hepC; diag  
 403478;; NM\_022342:Homo sapiens kinesin; lung; CTL+s.m.  
 40 403715;; Target Exon; lung; diag  
 403740;; NM\_001076\*:Homo sapiens UDP gt; pros, hepC; s.m.  
 403776;; ENSP00000226542\*:Small inducib; panc; diag  
 403903;; C5001632\*:gil10645308[gb]AAG21; blad; CTL+s.m.  
 404029;; NM\_018936\*:Homo sapiens protoc; glio; mAb  
 45 404049;; NM\_018937\*:Homo sapiens protoc; glio; mAb  
 404210;; NM\_005936:Homo sapiens myeloid; panc, uter, cerv, lung, ovar, pros, colon, stom; diag  
 404240;; NM\_018950:Homo sapiens major h; fibro; mAb  
 404253;; NM\_021058\*:Homo sapiens H2B hi; lung; CTL+s.m.  
 404286;; C6001909:gil704441[dbj]BAA1890; panc; diag  
 50 404298;; C6001238\*:gil121715[sp]P26697; lung; s.m.  
 404403;; Target Exon; blad; diag  
 404440;; NM\_021048:Homo sapiens melanom; lung, blad; mAb+CTL  
 404866;; ENSP00000251112\*:Sodium/potass; panc; s.m.  
 404877;; NM\_005365:Homo sapiens melanom; lung, blad; CTL+s.m.  
 55 404927;; Target Exon; lung, headnk; diag  
 404996;; Target Exon; lung, headnk, esoph; diag  
 405001;; interleukin enhancer binding f; sarc; diag  
 405025;; Homo sapiens bone morphogeneti; angio; diag  
 405121;; mitogen-activated protein kina; angio, renal; s.m.  
 60 405238;; Target Exon; glio; diag  
 405239;; oxidative 3 alpha hydroxystero; glio; s.m.  
 405451;; Homo sapiens glutaminy-peptid; mela; s.m.  
 405545;; Target Exon; cerv; mAb  
 405546;; NM\_018833\*:Homo sapiens transp; cerv; mAb  
 65 405547;; NM\_018833\*:Homo sapiens transp; cerv, mela; mAb  
 405646;; C12000200:gil4557225[ref]NP\_00; lung; diag  
 405704;; NM\_001844\*:Homo sapiens collag; sarc; diag  
 405770;; NM\_002362:Homo sapiens melanom; lung, esoph; mAb+CTL  
 405849;; Target Exon; panc; diag  
 70 405932;; C15000305:gil3806122[gb]AAC691; blad, lung, headnk, cerv; CTL+s.m.  
 406081;; Target Exon; blad; diag  
 406137;; NM\_000179\*:Homo sapiens mutS (; lung; CTL+s.m.  
 406173;; ENSP00000250148\*:Growth hormon; panc; CTL+s.m.  
 406348;; Target Exon; breast; CTL+s.m.  
 75 406360;; Target Exon; lung, headnk; diag  
 406399;; NM\_003122\*:Homo sapiens serine; blad; diag  
 406434;; NM\_030579\*:Homo sapiens cytoch; blad; diag  
 406467;; Target Exon; lung, headnk, blad; diag  
 406506;; Target Exon; angio; diag  
 80 406547;; Target Exon; test; diag  
 406627; T64904; Hs.163780; ESTs; angio; CTL+s.m.  
 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte; panc; mAb  
 406672; M26041; Hs.198253; major histocompatibility compl; fibro; mAb  
 406685; M18728; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung; mAb+CTL

- 406687; M31126; Hs.352054; matrix metalloproteinase 11 (s; breast, lung, ovar, cerv, uter, panc, esoph, mela, sarc; mAb+diag+s.m.  
 406690; M29540; Hs.220529; carcinoembryonic antigen-relat; lung, headnk, panc, stom, blad, colon, cerv; mAb+CTL  
 406706; X03740; Hs.231581; myosin, heavy polypeptide 1, s; sarc; diag  
 406850; A1624300; Hs.172928; collagen, type I, alpha 1; sarc; CTL+s.m.  
 5 406906; Z25424; ; gb:H.sapiens protein-serine/th; blad, lung; s.m.  
 406937; U14622; ; gb:Human transketolase-like pr; test; s.m.  
 406967; M24349; ; gb:Human parathyroid hormone-l; lung; CTL+s.m.  
 406974; M57293; ; gb:Human parathyroid hormone-r; lung, blad; diag  
 10 407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial; sarc; diag  
 407034; U84540; ; gb:Human dystrobrevin isoform ; glio; diag  
 407103; AA424881; Hs.256301; hypothetical protein MGC13170; pros; diag  
 407118; AA156790; Hs.262036; ESTs, Weakly similar to Z223\_H; pros; diag  
 407122; H20276; Hs.31742; ESTs; pros; diag  
 15 407137; T97307; ; gb:ye53h05.s1 Soares fetal liv; lung, blad, ovar, pros, panc, headnk; diag  
 407168; R45175; Hs.117183; ESTs; pros, breast, colon; diag  
 407178; AA195651; Hs.352312; AP-2 beta transcription factor; breast ; CTL+s.m.  
 407202; N58172; Hs.109370; ESTs; pros; diag  
 407216; N91773; Hs.348385; lysyl oxidase; panc; diag  
 20 407242; M18728; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung, ovar, cerv; mAb  
 407244; M10014; ; fibrinogen, gamma polypeptide; lung; diag  
 407245; X90568; Hs.172004; titin; sarc; diag  
 407251; U67611; Mm.29182; transaldolase 1; pros; s.m.  
 407252; AA659037; Hs.163780; ESTs; angio; CTL+s.m.  
 25 407276; A1951118; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL  
 407289; AA135159; Hs.203349; Homo sapiens cDNA FLJ12149 fis; lung; diag  
 407366; AF026942; Hs.17518; gb:Homo sapiens cig33 mRNA, pa; ovar, hepC, stom, mela, esoph; diag  
 407581; R48402; Hs.173508; P3ECSL; blad; CTL+s.m.  
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gat; blad; mAb  
 30 407619; AL050341; Hs.37165; collagen, type IX, alpha 2; sarc; diag  
 407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-; lung, headnk; s.m.  
 407710; AW022727; Hs.23616; ESTs; test; diag  
 407720; AB037776; Hs.38002; KIAA1355 protein; lung; mAb  
 407746; AK001962; Hs.38114; hypothetical protein FLJ11100; lung; diag  
 35 407756; AA116021; Hs.38260; ubiquitin specific protease 18; panc, lung, esoph, fibro, mela; CTL+s.m.  
 407758; D50915; Hs.38365; KIAA0125 gene product; lung; diag  
 407777; AA161071; Hs.71465; squalene epoxidase; panc, esoph; s.m.  
 407782; AA608956; Hs.112619; ESTs, Moderately similar to PU; lung; diag  
 407786; AA687538; Hs.38972; tetraspan 1; pros, colon, uter, stom, ovar, cerv; mAb  
 40 407788; BE514982; Hs.38991; S100 calcium-binding protein A; headnk, panc, blad, lung, fibro; diag  
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; test; CTL+s.m.  
 407824; AA147884; Hs.9812; Homo sapiens cDNA FLJ14388 fis; sarc; diag  
 407839; AA045144; Hs.161566; ESTs; blad, headnk; mAb  
 407846; AA426202; Hs.40403; Cbp/p300-interacting transacti; mela; diag  
 45 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homo; colon, stom, renal, breast, ovar, uter, cerv; diag  
 407856; AA045281; Hs.266175; phosphoprotein associated with; mela; diag  
 407872; AB039723; Hs.40735; frizzled (Drosophila) homolog ; ovar; mAb  
 407881; AW072003; Hs.40968; heparan sulfate (glucosamine) ; panc; s.m.  
 407910; AA650274; Hs.41296; fibronectin leucine rich trans; fibro; mAb  
 50 407944; R34008; Hs.239727; desmocollin 2; lung, headnk, esoph; mAb  
 407949; W21874; Hs.247057; ESTs, Weakly similar to 210926; fibro, blad; diag  
 407962; A1133530; Hs.62930; ESTs, Weakly similar to S59501; angio; mAb+s.m.  
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 ( ; breast, pros, blad, lung, headnk, cerv, esoph; mAb+CTL  
 408015; AW136771; Hs.244349; epidermal differentiation comp; mela, sarc; diag  
 55 408045; AW138959; Hs.245123; ESTs; breast ; diag  
 408056; AA312329; Hs.42331; ephrin-A4; ovar; diag  
 408063; BE086548; Hs.381047; calcineurin-binding protein ca; pros, lung; diag  
 408081; AW451597; Hs.167409; intron of basic-helix-loop-hel; ovar, glio; diag  
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; breast, lung, stom; s.m.  
 408122; A1432652; Hs.42824; hypothetical protein FLJ10718; lung; diag  
 60 408209; NM\_004454; Hs.43697; ets variant gene 5 (ets-relate; mela; CTL+s.m.  
 408296; AL117452; Hs.44155; DKFZP586G1517 protein; angio; diag  
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D; panc, renal, colon; mAb  
 408353; BE439838; Hs.44298; mitochondrial ribosomal protei; lung; diag  
 65 408430; S79876; Hs.44926; dipeptidylpeptidase IV (CD26, ; pros; mAb  
 408522; A1541214; Hs.46320; Small proline-rich protein SPR; lung, blad, headnk, eosph, cerv; diag  
 408561; A1308037; Hs.84120; hypothetical protein MGC13016; mela; CTL+s.m.  
 408570; AL046406; Hs.103483; KIAA1798 protein; angio; CTL+s.m.  
 408572; AA055611; Hs.226568; ESTs, Moderately similar to AL; lung; diag  
 70 408591; AF015224; Hs.46452; mammaglobin 1; breast, cerv; diag  
 408611; NM\_004367; Hs.46468; chemokine (C-C motif) receptor; mela; mAb  
 408633; AW963372; Hs.222088; PRO2000 protein; blad, lung, headnk, pros; diag  
 408660; AA525775; Hs.89040; ESTs, Moderately similar to PC; ovar, panc, pros, esoph, sarc; diag  
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; test; diag  
 408758; NM\_003686; Hs.47504; exonuclease 1; mela; CTL+s.m.  
 75 408770; AW270608; Hs.170195; bone morphogenetic protein 7 ( ; ovar; mAb+diag  
 408771; AW732573; Hs.47584; potassium voltage-gated channe; lung; mAb  
 408780; D31797; Hs.652; tumor necrosis factor (ligand); leuk; diag  
 408795; AW749126; Hs.170345; hypothetical protein FLJ13710; ovar; diag  
 80 408826; AF216077; Hs.48376; Homo sapiens clone HB-2 mRNA s; panc, pros; diag  
 408833; AW612232; Hs.254835; ESTs; pros; diag  
 408877; AA479033; Hs.130315; ESTs, Weakly similar to A47582; breast; diag  
 408915; NM\_016651; Hs.48950; heptacellular carcinoma novel ; panc, sarc; diag  
 408930; AA146721; Hs.334686; hypothetical protein FLJ21588; blad; CTL+s.m.

- 5 408962; BE386436; Hs.44317; SRY (sex determining region Y); mela; diag  
408992; AA059325; Hs.30114; guanine nucleotide binding pro; lung; diag  
408996; AI979168; Hs.82226; glycoprotein (transmembrane) n; mela; mAb+s.m.  
10 409012; AL117435; Hs.49725; DKFZP434I216 protein; sarc; CTL+s.m.  
409038; T97490; Hs.50002; small inducible cytokine subfa; mela; diag  
409051; AA080912; ; gb:zn04d03.r1 Stratagene hNT n; pros; s.m.  
409077; AA063037; Hs.66803; ESTs; lung; diag  
409093; BE243834; Hs.50441; CGI-04 protein; lung; diag  
409123; AA063403; ; gb:zm04d12.s1 Stratagene corne; pros; s.m.  
409142; AL136877; Hs.50758; SMC4 (structural maintenance o; ovar, lung, mela; diag  
409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibro; diag  
409200; AL042914; Hs.51039; KIAA0076 gene product; sarc; CTL+s.m.  
409203; AA780473; Hs.687; cytochrome P450, subfamily IVB; fibro, blad, ovar; diag  
15 409228; R16811; Hs.22010; ESTs, Weakly similar to 210926; lung; mAb  
409231; AA446644; Hs.692; GA733-2 antigen; epithelial gl; pros, ovar, breast, uter, panc, colon, stom; mAb  
409243; AB037761; Hs.51743; KIAA1340 protein; test; diag  
409262; AK000631; Hs.52256; hypothetical protein FLJ20624; pros; CTL+s.m.  
409264; NM\_014937; Hs.52463; KIAA0966 protein; mela; CTL+s.m.  
20 409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-li; breast, ovar, lung, panc, uter; mAb  
409327; L41162; Hs.53563; collagen, type IX, alpha 3; colon, panc, sarc; CTL+s.m.  
409340; BE174629; Hs.321130; hypothetical protein MGC2771; mela; CTL+s.m.  
409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; test; CTL+s.m.  
409346; AI401535; Hs.146090; ESTs; renal, glio; diag  
25 409361; NM\_005982; Hs.54416; sine oculis homeobox (Drosophi; blad, lung, pros; CTL+s.m.  
409389; AB007979; Hs.301281; Homo sapiens mRNA, chromosome ; glio; diag  
409395; U46745; Hs.336678; dystrobrevin, alpha; glio; diag  
409402; AF208234; Hs.695; cystatin B (stefin B); blad; diag  
409415; AA579258; Hs.6083; Homo sapiens cDNA: FLJ21028 fi; mela; diag  
30 409421; AA199883; Hs.67624; ESTs; test; diag  
409430; R21945; Hs.346735; splicing factor, arginine/seri; mela; diag  
409432; D49372; Hs.54460; small inducible cytokine subfa; stom, esoph; diag  
409433; AA074382; Hs.135255; ESTs; glio, sarc; diag  
409509; AL036923; Hs.322710; ESTs; angio; diag  
35 409512; AW979187; Hs.293591; melanoma differentiation assoc; mela, esoph; CTL+s.m.  
409542; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag  
409582; R27430; Hs.271565; ESTs; lung; diag  
409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyper; headnk, mela, sarc; CTL+s.m.  
409633; AW449822; Hs.55200; ESTs; sarc; diag  
40 409637; AA323948; Hs.55407; Homo sapiens mRNA; cDNA DKFZp4; renal; diag  
409638; AW450420; Hs.21335; ESTs; glio; diag  
409670; AI368109; Hs.381163; KIAA1856 protein; test; CTL+s.m.  
409703; NM\_006187; Hs.56009; 2'-5'-oligoadenylate synthetas; panc, esoph, mela; s.m.  
409705; M37762; Hs.56023; brain-derived neurotrophic fac; lung; diag  
409719; AI769160; Hs.108681; Homo sapiens brain tumor assoc; lung; diag  
45 409731; AA125985; Hs.56145; thymosin, beta, identified in ; pros, sarc; CTL+s.m.  
409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal ; ovar, renal; CTL+s.m.  
409935; AW511413; Hs.187393; ESTs; lung; diag  
409958; NM\_001523; Hs.57697; hyaluronan synthase 1; panc, ovar; mAb  
50 409988; N27687; Hs.334334; transcription factor AP-2 alph; mela; diag  
410006; AW732308; Hs.57783; eukaryotic translation initiat; test; diag  
410037; AB020725; Hs.58009; KIAA0918 protein; pros; diag  
410044; BE566742; Hs.58169; highly expressed in cancer, ri; blad; diag  
410048; W76467; Hs.343874; proline oxidase homolog; test; s.m.  
55 410076; T05387; Hs.7991; ESTs; lung, pros; diag  
410079; U94362; Hs.380757; glycogenin 2; mela; diag  
410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; pros; diag  
410102; AW248508; Hs.279727; ESTs; homologue of PEM-3 [Cion; ovar, breast, blad, lung, angio, sarc; diag  
410174; AA306007; Hs.59461; DKFZP434C245 protein; mela; diag  
60 410240; AL157424; Hs.61289; synaptotagmin 2; angio; diag  
410247; AF181721; Hs.61345; RU2S; ovar; CTL+s.m.  
410268; AA316181; Hs.61635; six transmembrane epithelial a; panc, pros, EWS; mAb+CTL  
410290; AA402307; Hs.322844; hypothetical protein DKFZp564A; mela; diag  
65 410310; J02931; Hs.62192; coagulation factor III (thromb; pros, panc; mAb  
410361; BE391804; Hs.62661; guanylate binding protein 1, i; mela, esoph, hepC, fibro, uter; diag  
410438; AW748012; Hs.45207; hypothetical protein KIAA1335; lung; CTL+s.m.  
410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; breast, colon, uter, stom; diag  
410480; R97457; Hs.63984; cadherin 13, H-cadherin (heart; angio; mAb  
410491; AA465131; Hs.64001; Homo sapiens clone 25218 mRNA ; mela, esoph; diag  
70 410530; M25809; Hs.64173; ATPase, H transporting, lysoso; ovar; mAb  
410553; AW016824; Hs.272068; hypothetical protein MGC14128; blad, lung; diag  
410555; U92649; Hs.380136; a disintegrin and metalloprote; leuk, lung; mAb  
410561; BE540255; Hs.6994; Homo sapiens cDNA: FLJ22044 fi; lung; diag  
410566; AA373210; Hs.43047; Homo sapiens cDNA FLJ13585 fis; panc; diag  
75 410600; AW575742; Hs.351676; ESTs, Moderately similar to S6; mela; mAb+s.m.  
410621; AA194329; Hs.172004; titin; sarc; diag  
410681; AW246890; Hs.65425; calbindin 1, (28kD); lung; diag  
410687; U24389; Hs.65436; lysyl oxidase-like 1; panc; diag  
80 410733; D84284; Hs.66052; CD38 antigen (p45); pros; mAb+CTL  
410763; AF279145; Hs.8966; hypothetical protein FLJ21776; panc; mAb  
410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; test; CTL+s.m.  
410867; X63556; Hs.750; fibrillin 1 (Marfan syndrome); panc; diag  
410870; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.  
410883; D43767; Hs.66742; CCL17 chemokine (TARC) (SCYA1; leuk; diag

- 410889; X91662; Hs.66744; twist (Drosophila) homolog (ac; sarc; CTL+s.m.  
 410929; H47233; Hs.30643; ESTs; ovar, test; diag  
 411078; A1222020; Hs.182364; CocoaCrisp; pros, glo, breast; diag  
 411089; AA456454; Hs.214291; cell division cycle 2-like 1 (; lung, fibro; CTL+s.m.  
 411243; AB039886; Hs.69319; CA11; esoph; diag  
 411248; AA551538; Hs.69321; Homo sapiens cDNA FLJ14408 fis; blad; diag  
 411257; AA628967; Hs.115274; Indian hedgehog protein (IHH) ; ovar; diag  
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centro; lung, blad, headnk; CTL+s.m.  
 411296; BE207307; Hs.10114; growth suppressor 1; sarc; diag  
 411358; R47479; Hs.94761; KIAA1691 protein; mela,renal, sarc; mAb  
 411388; X72925; Hs.69752; desmocollin 1; headnk, mela; mAb  
 411393; AW797437; Hs.69771; B-factor, properdin (COMPLEMEN; ovar; diag  
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); panc, pros, stom, breast, uter, cerv, ovar; mAb  
 411573; AB029000; Hs.70823; KIAA1077 protein; panc, headnk, lung, stom; diag  
 411579; AC005258; Hs.70830; U6 snRNA-associated Sm-like pr; lung; diag  
 411732; U47924; Hs.71642; guanine nucleotide binding pro; lung; diag  
 411768; NM\_013371; Hs.71979; interleukin 19; ovar, uter, cerv; diag  
 411789; AF245505; Hs.72157; Adican; breast, panc, lung, stom, headnk, ovar, uter, esoph, sarc; diag  
 411825; AK000334; Hs.352415; solute carrier family 39 (zinc; colon, ovar; mAb  
 411828; AW161449; Hs.72290; wingless-type MMTV integration; ovar; diag  
 411869; W20027; Hs.23439; ESTs; angio; diag  
 411874; AA096106; Hs.20403; ESTs; blad; diag  
 411880; AW872477; ; gb:hm30f03.x1 NCI\_CGAP\_Thy4 Ho; blad; diag  
 411945; AL033527; Hs.92137; L-my-2 protein (MYCL2); blad, ovar; CTL+s.m.  
 412006; AW451618; Hs.380683; ESTs; sarc; diag  
 412026; AA383618; Hs.73073; testis-specific ankyrin motif ; test; diag  
 412045; AA099802; Hs.83883; transmembrane, prostate androg; pros; mAb+s.m.  
 412099; U64198; Hs.73165; interleukin 12 receptor, beta ; leuk, mela; mAb  
 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN; panc, fibro; diag  
 412115; AK001763; Hs.73239; hypothetical protein FLJ10901; lung, blad; CTL+s.m.  
 412116; AW402166; Hs.784; Epstein-Barr virus induced gen; panc; mAb  
 412133; U83460; Hs.380728; solute carrier family 31 (copp; pros; mAb  
 412228; AW503785; Hs.73792; complement component (3d/Epste; mela; mAb  
 412247; AF022375; Hs.73793; vascular endothelial growth fa; renal, glo, blad, colon; diag  
 412265; AA101325; Hs.86154; hypothetical protein FLJ12457; test; CTL+s.m.  
 412326; R07566; Hs.73817; small inducible cytokine A3 (h; pros, leuk; diag  
 412351; AL135960; Hs.73828; T-cell acute lymphocytic leuke; angio; CTL+s.m.  
 412420; AL035668; Hs.73853; bone morphogenetic protein 2; blad, glo, lung, stom, angio; diag  
 412448; L12964; Hs.73895; tumor necrosis factor receptor; leuk; mAb  
 412471; M63193; Hs.73946; endothelial cell growth factor; cerv, mela, esoph; diag  
 412490; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22528 fi; mela; diag  
 412519; AA196241; Hs.73980; troponin T1, skeletal, slow; sarc; diag  
 412530; AA766268; Hs.266273; hypothetical protein FLJ13346; blad, lung; diag  
 412564; X83703; Hs.355934; cardiac ankyrin repeat protein; angio; diag  
 412580; AA113262; Hs.17901; similar to CABLES [Homo sapien; mela; diag  
 412610; X90908; Hs.74126; fatty acid binding protein 6 ; blad; diag  
 412661; N32860; Hs.24611; ESTs, Weakly similar to I54374; blad; CTL+s.m.  
 412715; NM\_000947; Hs.74519; primase, polypeptide 2A (58kD); pros; s.m.  
 412723; AA648459; Hs.335951; hypothetical protein AF301222; lung, blad, headnk, colon, stom, uter; diag  
 412755; BE144306; Hs.179891; ESTs, Weakly similar to P4HA\_H; angio; s.m.  
 412811; H06382; Hs.349705; ESTs; lung; diag  
 412817; AL037159; Hs.74619; proteasome (prosome, macropain; lung; s.m.  
 412843; AF007555; Hs.74624; protein tyrosine phosphatase, ; pros; mAb  
 412856; BE386745; Hs.74631; basigin (OK blood group); mela; mAb  
 412926; A1879076; Hs.75061; macrophage myristoylated alani; mela; CTL+s.m.  
 412939; AW411491; Hs.75069; eukaryotic translation elongat; mela, renal; diag  
 412970; AB026436; Hs.177534; dual specificity phosphatase 1; breast, mela; s.m.  
 412986; X81120; Hs.75110; cannabinoid receptor 1 (brain); glo; mAb  
 413004; T35901; Hs.75117; interleukin enhancer binding f; lung; diag  
 413011; AW068115; Hs.821; biglycan; lung; CTL+s.m.  
 413049; NM\_002151; Hs.823; hepsin (transmembrane protease; pros; mAb  
 413095; AA494359; Hs.30715; potassium voltage-gated channe; panc, stom, renal, colon; mAb+s.m.  
 413125; BE244589; Hs.75207; glyoxalase I; pros; s.m.  
 413126; AW419203; Hs.174174; ESTs; angio; diag  
 413129; AF292100; Hs.104613; RP42 homolog; lung; diag  
 413132; NM\_006823; Hs.75209; protein kinase (cAMP-dependent; angio; CTL+s.m.  
 413142; M81740; Hs.75212; ornithine decarboxylase 1; lung; s.m.  
 413163; Y00815; Hs.75216; protein tyrosine phosphatase, ; pros; mAb  
 413171; AA318325; Hs.75219; tyrosinase-related protein 1; mela; mAb  
 413190; AA151802; Hs.40368; adaptor-related protein comple; mela; diag  
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis; esoph, cerv; diag  
 413223; A1732182; Hs.191866; ESTs; lung; diag  
 413268; AL039079; Hs.75256; regulator of G-protein signal; headnk; CTL+s.m.  
 413281; AA861271; Hs.222024; transcription factor BMAL2; lung, blad, headnk, panc, angio; diag  
 413313; NM\_002047; Hs.293885; glycyl-tRNA synthetase; test; s.m.  
 413328; Y15723; Hs.75295; guanylate cyclase 1, soluble, ; pros; s.m.  
 413335; A1613318; Hs.48442; ESTs; ovar; diag  
 413364; BE536218; Hs.137516; fidgetin-like 1; lung; diag  
 413372; H55532; Hs.349695; tubulin, alpha 2; test; diag  
 413435; X51405; Hs.75360; carboxypeptidase E; pros, glo, panc, sarc; diag  
 413436; AF238083; Hs.68061; sphingosine kinase 1; sarc; s.m.  
 413472; BE242870; Hs.75379; solute carrier family 1 (glial; glo; mAb  
 413566; AW604451; Hs.381153; sprouty (Drosophila) homolog 4; sarc; CTL+s.m.

- 413573; AI733859; Hs.149089; ESTs; lung; diag  
 413582; AW295647; Hs.71331; hypothetical protein MGC5350; lung; diag  
 413597; AW302885; Hs.117183; ESTs; pros; diag  
 413623; AA825721; Hs.246973; intron of Bicaudal D homolog 1; ovar, pros; diag  
 413691; AB023173; Hs.75478; ATPase, Class VI, type 11B; lung; mAb  
 413711; AW291765; Hs.75486; heat shock transcription facto; renal; diag  
 413753; U17760; Hs.75517; laminin, beta 3 (nicein (125kD; lung, blad, headnk, panc, cerv, esoph, colon; diag  
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); test; diag  
 413778; AA090235; Hs.75535; myosin, light polypeptide 2, r; sarc; diag  
 413794; AF234532; Hs.61638; myosin X; mela; diag  
 413804; T64682; ; gb:yc48b02.r1 Stratagene liver; blad; diag  
 413808; J00287; Hs.350038; Homo sapiens mRNA for caldesmo; esoph; diag  
 413813; M96956; Hs.75561; teratocarcinoma-derived growth; colon; diag  
 413833; Z15005; Hs.75573; centromere protein E (312kD); lung; CTL+s.m.  
 413842; M29383; Hs.856; interferon, gamma; leuk; diag  
 413869; NM\_000878; Hs.75596; interleukin 2 receptor, beta; fibro, renal; mAb  
 413880; AI660842; Hs.110915; interleukin 22 receptor; panc, colon; mAb+s.m.  
 413924; AL119964; Hs.75616; seladin-1; pros, breast, ovar; diag  
 413943; AW294416; Hs.144687; Homo sapiens cDNA FLJ12981 fis; blad, lung; CTL+s.m.  
 413985; AI018666; Hs.75667; synaptophysin; glio, sarc; mAb  
 414004; AA737033; Hs.7155; ESTs, Moderately similar to 21; panc, mela; diag  
 414020; NM\_002984; Hs.75703; CCL4 Chemokine (C-C motif) lig; pros; diag  
 414034; U89277; Hs.305985; early development regulator 1; test; CTL+s.m.  
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase; lung, cerv, headnk, blad; s.m.  
 414053; BE391635; Hs.75725; transgelin 2; blad; diag  
 414061; NM\_000699; Hs.300280; amylase, alpha 2A; pancreatic; ovar; diag  
 414065; AW515373; Hs.271249; Homo sapiens cDNA FLJ13580 fis; pros; diag  
 414085; AA114016; Hs.75746; aldehyde dehydrogenase 1 famil; pros, panc, sarc; s.m.  
 414142; AW368397; Hs.334485; hemicentin (fibulin 6); fibro, panc, sarc; diag  
 414161; AA136106; Hs.184852; KIAA1553 protein; test; diag  
 414166; AW888941; Hs.75789; N-myc downstream regulated; pros, renal; diag  
 414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fi; glio; diag  
 414219; W20010; Hs.75823; ALL1-fused gene from chromosom; sarc; diag  
 414221; AW450979; ; gb:U1-H-BI3-ala-a-12-0-U1.s1 N; blad; diag  
 414251; AL042306; Hs.97689; VASA protein; test; CTL+s.m.  
 414259; W44633; Hs.301296; integrin, beta-like 1 (with EG; panc; diag  
 414334; AA824298; Hs.21331; hypothetical protein FLJ10036; test; diag  
 414359; M62194; Hs.75929; cadherin 11, type 2, OB-cadher; breast, ovar, uter, pros, colon, panc, sarc; mAb  
 414368; W70171; Hs.75939; uridine monophosphate kinase; lung; s.m.  
 414386; X00442; Hs.75990; haptoglobin; ovar; diag  
 414416; AW409985; Hs.76084; hypothetical protein MGC2721; blad, lung; CTL+s.m.  
 414420; AA043424; Hs.76095; immediate early response 3; panc, colon; diag  
 414430; AI346201; Hs.76118; ubiquitin carboxyl-terminal es; lung; s.m.  
 414443; AU077268; Hs.76144; platelet-derived growth factor; sarc, panc, headnk; mAb  
 414476; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag  
 414477; U41635; Hs.76228; amplified in osteosarcoma; sarc; diag  
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antig; mela; mAb  
 414521; D28124; Hs.76307; neuroblastoma, suppression of; breast, ovar, uter, pros, blad, panc, colon, stom, fibr; diag  
 414565; AA502972; Hs.183390; hypothetical protein FLJ13590; pros; diag  
 414569; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag  
 414575; H11257; Hs.375743; Homo sapiens clone IMAGE:45193; renal; diag  
 414595; AA641726; Hs.289015; hypothetical protein MGC4171; blad; diag  
 414602; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; pros; mAb  
 414683; S78296; Hs.76888; hypothetical protein MGC12702; blad, lung, test; diag  
 414732; AW410976; Hs.77152; minichromosome maintenance def; test, blad; diag  
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila); lung, blad, test; CTL+s.m.  
 414776; AA155598; Hs.212839; hypothetical protein FLJ14195; angio; diag  
 414786; AI246482; Hs.243010; Homo sapiens cDNA FLJ14372 fis; angio; diag  
 414799; AI752416; Hs.77326; insulin-like growth factor bin; renal; diag  
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; lung; mAb  
 414807; AI738616; Hs.77348; hydroxyprostaglandin dehydroge; blad; s.m.  
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD7; lung; mAb+s.m.  
 414825; X06370; Hs.77432; epidermal growth factor recept; glio, lung, renal, esoph, panc, headnk, leuk; mAb+s.m.  
 414915; NM\_002462; Hs.76391; myxovirus (influenza) resistar; esoph; diag  
 414918; AI219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL  
 414921; BE390551; Hs.77628; steroidogenic acute regulatory; breast; diag  
 414945; BE076358; Hs.77667; lymphocyte antigen 6 complex, ; mela; mAb  
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; blad, panc, esoph; diag  
 414998; NM\_002543; Hs.77729; oxidised low density lipoprote; fibro, ovar, panc, colon; mAb  
 415003; M11437; Hs.77741; kininogen; panc; diag  
 415025; AW207091; Hs.72307; ESTs; blad; diag  
 415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-Co; lung, headnk; s.m.  
 415178; D80503; Hs.46692; ESTs; blad; diag  
 415214; AI445236; Hs.125124; EphB2; colon, stom; mAb  
 415314; N88802; Hs.5422; glycoprotein M6B; mela; mAb  
 415457; AW081710; Hs.7369; Homo sapiens testes specific A; fibro, ovar, uter; CTL+s.m.  
 415511; AI732617; Hs.182362; ESTs; blad, ovar, renal; diag  
 415542; R13474; Hs.290263; ESTs, Weakly similar to I38022; blad; diag  
 415724; NM\_003580; Hs.78687; neutral sphingomyelinase (N-SM; test; CTL+s.m.  
 415752; BE314524; Hs.78776; putative transmembrane protein; endo, uter, breast, stom, blad, mela; mAb  
 415786; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag  
 415787; H01463; Hs.93534; ESTs; pros; diag  
 415819; AU077330; Hs.360791; transcription elongation facto; test; CTL+s.m.



- 415829; AW450198; Hs.163742; ESTs; test; diag  
 415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fis; lung, test; diag  
 415910; U20350; Hs.78913; chemokine (C-X3-C) receptor 1; glio; mAb  
 415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colo; test; diag  
 415989; AI267700; Hs.351201; ESTs; pros, ovar, blad, lung, headnk, panc, colon, sarc; diag  
 415992; C05837; Hs.145807; hypothetical protein FLJ13593; pros, fibro; mAb  
 415999; AA172179; Hs.294029; ESTs; pros, uter; diag  
 416018; AW138239; Hs.78977; proprotein convertase subtilis; colon, panc, lung; diag  
 416030; H15261; Hs.21948; ESTs; breast, fibro; diag  
 416065; BE267931; Hs.78996; proliferating cell nuclear ant; blad, lung, headnk, mela; CTL+s.m.  
 416111; AA033813; Hs.79018; chromatin assembly factor 1, s; lung, stom; CTL+s.m.  
 416188; BE157260; Hs.79070; v-myc avian myelocytomatosis v; pros; diag  
 416201; AA467752; Hs.195161; ESTs; test; diag  
 416208; AW291168; Hs.41295; ESTs, Weakly similar to MUC2\_H; lung; diag  
 416224; NM\_002902; Hs.79088; reticulocalbin 2, EF-hand calc; ovar; diag  
 416225; AA577730; Hs.188684; ESTs, Weakly similar to PC4259; pros, blad; diag  
 416350; AF188625; Hs.189507; phospholipase A2, group IID; test, mela, fibro; diag  
 416370; N90470; Hs.203697; CD38 antigen (p45); pros, glio; mAb+CTL  
 416373; AA195845; Hs.73680; ESTs, Weakly similar to S12658; sarc; diag  
 416402; NM\_000715; Hs.1012; complement component 4-binding; fibro; diag  
 416448; L13210; Hs.79339; lectin, galactoside-binding, s; ovar, colon, stom; diag  
 416498; U33632; Hs.79351; potassium channel, subfamily K; panc, stom, breast, ovar, colon; mAb  
 416539; Y07909; Hs.79368; epithelial membrane protein 1; pros, headnk; diag  
 416602; NM\_006159; Hs.367895; Protein kinase C-binding prote; breast; diag  
 416640; BE262478; Hs.13406; neuron-specific protein; mela; diag  
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; blad, lung, headnk, cerv, panc, angio; diag  
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; test; CTL+s.m.  
 416815; U41514; Hs.80120; UDP-N-acetyl-alpha-D-galactosa; angio; s.m.  
 416819; U77735; Hs.80205; pim-2 oncogene; lung, test; diag  
 416881; N32520; Hs.141358; ESTs; mela; diag  
 416929; N20535; Hs.43265; melastatin 1; mela; diag  
 416975; NM\_004131; Hs.1051; granzyme B (granzyme 2, cyto; mela; s.m.  
 417003; AL038170; Hs.80756; betaine-homocysteine methyltra; blad; s.m.  
 417070; Z19077; Hs.172004; titin; sarc; diag  
 417105; X60992; Hs.81226; CD6 antigen; fibro; mAb  
 417115; AVW952792; Hs.334612; small nuclear ribonucleoprotei; test; CTL+s.m.  
 417124; BE122762; Hs.25338; ESTs; angio; diag  
 417148; AA359896; Hs.374554; hypothetical protein FLJ14902; panc; diag  
 417151; AA194055; Hs.293858; ESTs; blad; diag  
 417153; X57010; Hs.81343; collagen, type II, alpha 1 (pr; pros, sarc; diag  
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte; lung; mAb+s.m.  
 417237; H86385; Hs.81737; palmitoyl-protein thioesterase; mela; s.m.  
 417259; AW903838; Hs.81800; chondroitin sulfate proteoglyc; panc, breast; diag  
 417275; X63578; Hs.295449; parvalbumin; blad; diag  
 417295; AW993524; Hs.43148; epithelial membrane protein 1; pros; diag  
 417308; H60720; Hs.81892; KIAA0101 gene product; lung, headnk, blad, cerv, angio, mela, sarc; diag  
 417312; AW888411; Hs.250811; leukemia-associated phosphopro; blad; CTL+s.m.  
 417333; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag  
 417355; D13168; Hs.82002; endothelin receptor type B; glio, mela; mAb  
 417365; D50683; Hs.82028; transforming growth factor, be; fibro, angio; mAb  
 417366; BE185289; Hs.1076; small proline-rich protein 1B; lung, blad, headnk, panc, esoph, mela; diag  
 417370; T28651; Hs.374466; tryptophanyl-tRNA synthetase; fibro, mela; diag  
 417391; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.  
 417400; AA663486; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag  
 417407; AA923278; Hs.290905; ESTs, Weakly similar to protea; test, pros; s.m.  
 417409; BE272506; Hs.82109; syndecan 1; blad; diag  
 417412; X16896; Hs.82112; interleukin 1 receptor, type I; fibro, pros, panc; mAb  
 417426; NM\_002291; Hs.82124; laminin, beta 1; angio; diag  
 417437; U52682; Hs.82132; interferon regulatory factor 4; mela; CTL+s.m.  
 417512; X76534; Hs.82226; glycoprotein (transmembrane) n; lung, mela, headnk, panc, breast; mAb  
 417515; L24203; Hs.82237; ataxia-telangiectasia group D; lung, headnk, blad; diag  
 417542; J04129; Hs.82269; progesterone-associated endomet; lung, mela; diag  
 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383; test; diag  
 417599; AA204688; Hs.62954; ESTs; blad, esoph; diag  
 417621; AV654694; Hs.82316; interferon-induced, hepatitis; esoph; diag  
 417696; BE241624; Hs.82401; CD69 antigen (p60, early T-cell; pros; mAb  
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; test; mAb  
 417715; AW969587; Hs.86366; ESTs; blad, lung, headnk; diag  
 417720; AA205625; Hs.208067; ESTs; blad, lung, esoph, headnk; diag  
 417750; AI267720; Hs.260523; synovial sarcoma, translocated; sarc; diag  
 417777; AI823763; Hs.7055; ESTs, Weakly similar to I78885; test; s.m.  
 417791; AW965339; Hs.44269; ESTs; ovar, blad, lung, headnk; CTL+s.m.  
 417801; AA417383; Hs.82582; integrin, beta-like 1 (with EG; panc, fibro; diag  
 417805; U38545; Hs.82587; phospholipase D1, phosphatidylc; angio; s.m.  
 417831; H16423; Hs.82685; CD47 antigen (Rh-related antig; ovar; mAb  
 417843; W07361; Hs.22545; Homo sapiens cDNA FLJ12935 fis; pros; diag  
 417847; AI521558; Hs.7331; hypothetical protein FLJ22316; ovar; diag  
 417849; AW291587; Hs.82733; nidogen 2; angio, headnk; diag  
 417874; BE616160; Hs.82829; protein tyrosine phosphatase; panc; mAb+s.m.  
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesio; mela; mAb  
 417886; AA214584; ESTs; test, ovar; diag  
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20; lung, stom, test, blad, headnk, cerv, esoph; CTL+s.m.  
 417911; AA333387; Hs.82916; chaperonin containing TCP1, su; test; diag

- 417944; AU077196; Hs.82985; collagen, type V, alpha 2; sarc; diag  
 417975; AA641836; Hs.30085; hypothetical protein FLJ23186; colon, stom, lung; mAb  
 417976; BE565892; Hs.83077; interleukin 18 (interferon-gam; colon, stom, fibros; diag  
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 famii; lung, headnk, esoph; s.m.  
 418036; Z37976; Hs.83337; latent transforming growth fac; angio; diag  
 418054; NM\_002318; Hs.83354; lysyl oxidase-like 2; lung, angio, test, sarc; diag  
 418067; A1127958; Hs.83393; cystatin E/M; headnk, panc, blad; diag  
 418068; AW971155; Hs.293902; ESTs, Weakly similar to 1SHUSS; blad; s.m.  
 418113; A1272141; Hs.83484; SRY (sex determining region Y); blad, breast, uter, colon, lung, ovar, glio, test, sarc; CTL+s.m.  
 418134; AA397769; Hs.86617; ESTs; test; diag  
 418140; BE613836; Hs.83551; microfibrillar-associated prot; lung, headnk, esoph, ovar, sarc; diag  
 418156; W17056; Hs.83623; nuclear receptor subfamily 1, ; fibro; mAb+s.m.  
 418203; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, test, mela, stom; s.m.  
 418216; AA662240; Hs.283099; AF15q14 protein; headnk, lung, blad; diag  
 418245; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.  
 418283; S79895; Hs.83942; cathepsin K (pseudosclerosis); breast, cerv, ovar, uter, pros, headnk, lung, panc, colon, stom; diag  
 418318; U47732; Hs.84072; transmembrane 4 superfamily me; panc, pros, colon, stom, omuc; mAb  
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibi; headnk, lung, blad; s.m.  
 418338; NM\_002522; Hs.84154; neuronal pentraxin I; sarc; diag  
 418339; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag  
 418345; A1001696; Hs.241407; serine (or cysteine) proteinases; cerv, lung; s.m.  
 418371; M13560; Hs.84298; CD74 antigen (invariant polype; renal; mAb  
 418379; AA218940; Hs.137516; fidgetin-like 1; lung; diag  
 418394; AF132818; Hs.84728; Kruppel-like factor 5 (intesti; panc; CTL+s.m.  
 418396; A1765805; Hs.26691; SLC2A12 Solute carrier family ; pros; mAb  
 418397; NM\_001269; Hs.84746; chromosome condensation 1; lung; diag  
 418399; AF131781; Hs.84753; hypothetical protein FLJ12442; test, blad, sarc; diag  
 418406; X73501; Hs.84905; cytokeratin 20; blad, colon; diag  
 418432; M14156; Hs.85112; insulin-like growth factor 1 ( ; pros, fibro; diag  
 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide; fibro; mAb  
 418462; BE001596; Hs.85266; integrin, beta 4; lung, blad, cerv, headnk, ovar; mAb  
 418543; NM\_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb  
 418576; AW968159; Hs.302740; Epithelial calcium channel 2, ; pros; mAb+s.m.  
 418610; AW245993; Hs.32417; hypothetical protein MGC2742; pros; diag  
 418641; BE243136; Hs.86947; a disintegrin and metalloprote; cerv, lung, panc, blad, headnk, stom; mAb  
 418655; AA226354; Hs.111240; ESTs; pros; diag  
 418661; NM\_001949; Hs.1189; E2F transcription factor 3; ovar, lung, mela; CTL+s.m.  
 418663; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk, cerv, esoph; mAb  
 418683; U90908; Hs.87241; hypothetical protein from clon; angio; CTL+s.m.  
 418686; Z36830; Hs.87268; annexin A8; blad, lung; diag  
 418693; A1750878; Hs.87409; thrombospondin 1; angio, panc; diag  
 418696; AW959433; Hs.326290; hypothetical protein FLJ12581; test; diag  
 418739; AA310964; Hs.88012; SHP2 interacting transmembrane; mela; diag  
 418756; AA252254; Hs.226949; ESTs; test ; diag  
 418825; AA228881; Hs.22394; hypothetical protein FLJ10893; angio; diag  
 418829; AA516531; Hs.55999; NK homeobox (Drosophila), fami; pros; diag  
 418882; NM\_004996; Hs.89433; ATP-binding cassette, sub-fami; ovar, pros, breast, lung; diag  
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate r; fibro; s.m.  
 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (live; colon, stom, ovar, uter, panc; mAb+s.m.  
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red b; mela, fibro; mAb  
 418932; L34059; Hs.89484; cadherin 4, type 1, R-cadherin; glio; mAb  
 418941; AA452970; Hs.239527; E1B-55kDa-associated protein 5; angio, blad; diag  
 418968; NM\_000078; Hs.89538; cholesteryl ester transfer pro; mela; diag  
 418994; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, angio; mAb  
 419038; AW134924; Hs.58290; ESTs; pros; diag  
 419073; AW372170; Hs.183918; transmembrane receptor Unc5H2 ; ovar, renal, blad, lung; mAb  
 419078; M93119; Hs.89584; insulinoma-associated 1; blad, lung, panc, sarc; diag  
 419079; AW014836; Hs.18844; ESTs; esoph, lung, stom, colon; diag  
 419086; NM\_000216; Hs.89591; Kallmann syndrome 1 sequence; fibro; diag  
 419092; J05581; Hs.89603; mucin 1, transmembrane; breast, panc, lung, blad, fibro; mAb  
 419222; AD001528; Hs.89718; spermine synthase; pros; s.m.  
 419223; X60111; Hs.1244; CD9 antigen (p24); breast, pros, ovar; mAb  
 419231; AL046294; Hs.136245; ESTs, Weakly similar to T17227; fibro; diag  
 419261; X07876; Hs.89791; wingless-type MMTV integration; panc; diag  
 419264; AA877104; Hs.293672; ESTs, Weakly similar to ALUB\_H; pros; diag  
 419290; A1128114; Hs.112885; spinal cord-derived growth fac; panc; diag  
 419356; A1656166; Hs.7331; hypothetical protein FLJ22316; uter, ovar; diag  
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeas; lung, blad, test; diag  
 419440; AB020689; Hs.90419; KIAA0882 protein; breast; diag  
 419485; AA489023; Hs.99807; ESTs, Weakly similar to unname; mela; diag  
 419490; NM\_006144; Hs.90708; granzyme A (granzyme 1, cytoto; fibro; s.m.  
 419519; A1198719; Hs.176376; ESTs; mela; diag  
 419551; AW582256; Hs.91011; anterior gradient 2 (Xenopus I; panc, pros, breast; diag  
 419559; Y07828; Hs.91096; ring finger protein; blad, colon, stom; CTL+s.m.  
 419568; AB026116; Hs.283078; hOAT4; renal; mAb  
 419569; A1971651; Hs.91143; jagged 1 (Alagille syndrome); headnk, lung; diag  
 419628; H67546; Hs.49768; ESTs; mela, sarc; diag  
 419667; AU077005; Hs.92208; a disintegrin and metalloprote; breast, cerv, angio; mAb  
 419693; AA133749; Hs.301350; FXYD domain-containing ion tra; pros, breast, ovar, panc, lung; mAb  
 419721; NM\_001650; Hs.315369; aquaporin 4; glio, lung, fibro; mAb  
 419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA ; blad, headnk; diag  
 419749; X73608; Hs.93029; sparc/osteoneclin, cwcw and ka; pros, panc, lung; diag  
 419752; AA249573; Hs.152618; ESTs, Moderately similar to ZN; lung; diag

- 5 419839; U24577; Hs.93304; phospholipase A2, group VII (p; pros; lung; diag  
419870; AW403911; Hs.266175; phosphoprotein associated with; mela; diag  
419875; AA853410; Hs.93557; proenkephalin; sarc; diag  
419948; AB0411035; Hs.93847; NM\_016931: Homo sapiens NADPH o; angio; mAb  
10 419956; AL137939; Hs.40096; cadherin 19, type 2; mela; mAb  
419968; X04430; Hs.93913; interleukin 6 (interferon, bet; lung, panc, esoph; diag  
419981; AA897581; Hs.128773; ESTs; angio; diag  
420005; AW271106; Hs.133294; ESTs; lung, test, blad, colon; diag  
420062; AW411096; Hs.94785; TGF(beta)-induced transcriptio; test; CTL+s.m.  
420067; T52431; Hs.94795; Homo sapiens mRNA; cDNA DKFZp5; sarc; diag  
420137; AA306478; Hs.95327; CD3D antigen, delta polypeptid; fibro; mAb  
420154; AI093155; Hs.95420; G antigen family C 1 protein (; pros; leio; CTL+s.m.  
420174; AI824144; Hs.199749; ESTs; angio; CTL+s.m.  
15 420208; BE276055; Hs.95972; silver (mouse homolog) like; mela; sarc; mAb  
420209; AA256444; Hs.126485; hypothetical protein FLJ12604; angio; diag  
420218; AW958037; Hs.381105; ribosomal protein L4; mela; pros; diag  
420255; NM\_007289; Hs.1298; membrane metallo-endopeptidase; pros; mAb  
420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadheri; angio; fibro; mAb  
20 420267; N37030; Hs.173337; ESTs; mela; sarc; diag  
420281; AI623693; Hs.323494; Predicted cation efflux pump; lung, blad, ovar, panc; mAb  
420301; AA767526; Hs.22030; paired box gene 5 (B-cell line; mela; diag  
420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339; mela; mAb  
420340; NM\_000734; Hs.97087; CD3Z antigen, zeta polypeptide; fibro; mAb  
25 420344; BE463721; Hs.97101; putative G protein-coupled rec; colon, pros, blad, headnk, panc, stom, ovar; mAb  
420347; AL033539; Hs.97124; Human DNA sequence from clone ; test; diag  
420360; U83171; Hs.97203; small inducible cytokine subfa; leuk; diag  
420367; AA259090; Hs.257028; ESTs; test; diag  
420376; AL137471; Hs.97266; protocadherin 18; sarc; mAb+s.m.  
30 420378; NM\_014143; Hs.97269; B7-H1 protein; leuk; mAb  
420380; AA640891; Hs.102406; ESTs; lung; diag  
420424; AB033036; Hs.97594; KIAA1210 protein; pros; diag  
420462; AF050147; Hs.97932; chondromodulin I precursor; lung, EWS, sarc; mAb  
420474; L09753; Hs.1313; tumor necrosis factor (ligand); leuk; mAb  
35 420544; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag  
420576; AA297634; Hs.54925; KIAA1858 protein; sarc; diag  
420596; NM\_002692; Hs.99185; polymerase (DNA directed), eps; test; CTL+s.m.  
420633; NM\_014581; Hs.274480; odorant-binding protein 2B (OB; breast, endo; diag  
420656; AA279098; Hs.187636; ESTs; fibro; diag  
40 420710; NM\_007009; Hs.99875; zona pellucida binding protein; test; diag  
420729; AW964897; Hs.290825; ESTs; pros; diag  
420757; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.  
420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 fis; test; diag  
420783; AI659838; Hs.99923; lectin, galactoside-binding, s; lung, blad, headnk; diag  
45 420789; AI670057; Hs.199882; ESTs; renal; diag  
420859; AW468397; Hs.100000; S100 calcium-binding protein A; sarc; diag  
420908; AL049974; Hs.100261; Homo sapiens mRNA; cDNA DKFZp5; panc; diag  
420923; AF097021; Hs.273321; differentially expressed in he; blad, colon; diag  
420931; AF044197; Hs.100431; small inducible cytokine B sub; breast, lung, mela; diag  
50 420981; L40904; Hs.100724; peroxisome proliferative activ; colon; mAb+s.m.  
421016; AA504583; Hs.101047; transcription factor 3 (E2A im; test; CTL+s.m.  
421044; AF061871; Hs.101302; Human DNA sequence from clone ; panc; diag  
421059; AI654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.  
421064; AI245432; Hs.101382; tumor necrosis factor, alpha-i; blad, uter; diag  
55 421070; AA283185; Hs.19327; ESTs; blad; diag  
421100; AW351839; Hs.124660; Homo sapiens cDNA: FLJ21763 fi; blad; diag  
421133; AA814971; Hs.26410; ESTs; lung; diag  
421154; AA284333; Hs.287631; Homo sapiens cDNA FLJ14269 fis; BPH; diag  
421155; H87879; Hs.102267; lysyl oxidase; headnk, panc, renal, sarc; diag  
60 421218; NM\_000499; Hs.72912; cytochrome P450, subfamily I (; blad, angio; diag  
421233; AA209534; Hs.284243; tetraspan NET-6 protein; pros, breast, ovar; mAb  
421241; X91817; Hs.102866; transketolase-like 1; test; s.m.  
421302; T34462; Hs.103291; neuritin; uter, endo ; diag  
421305; BE397354; Hs.324830; diphtheria toxin resistance pro; ovar; diag  
65 421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, lung, angio, test, sarc; diag  
421341; AJ243212; Hs.279611; deleted in malignant brain tum; panc, lung; diag  
421350; AW301608; Hs.278188; ESTs, Moderately similar to I5; test; diag  
421373; AA808229; Hs.222088; ESTs; blad; diag  
421433; AI829192; Hs.22380; ESTs; pros; diag  
70 421451; AA291377; Hs.50831; ESTs; ovar, blad, lung; diag  
421458; NM\_003654; Hs.104576; carbohydrate (keratan sulfate ; sarc; s.m.  
421478; AI683243; Hs.97258; ESTs, Moderately similar to S2; ovar, blad, renal, uter; diag  
421481; AW391972; Hs.104696; KIAA1324 protein; pros; diag  
421502; AF111856; Hs.105039; solute carrier family 34 (sodi; ovar, fibro; mAb  
75 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; lung, headnk, esoph; s.m.  
421508; NM\_004833; Hs.105115; absent in melanoma 2; blad, esoph, lung, mela; CTL+s.m.  
421535; AB002359; Hs.105478; phosphoribosylformylglycinamid; test; s.m.  
421537; BE383488; Hs.105547; neural proliferation, differen; pros; diag  
421566; NM\_000399; Hs.1395; early growth response 2 (Krox-; pros; CTL+s.m.  
80 421579; NM\_002975; Hs.105927; stem cell growth factor; lymph; sarc; mAb  
421633; AF121860; Hs.106260; sorting nexin 10; mela; diag  
421650; AA781795; Hs.343800; ESTs; mela; diag  
421666; AL035250; Hs.1408; endothelin 3; mela; diag  
421727; Y13153; Hs.107318; kynurenine 3-monooxygenase (ky; breast; s.m.

- 421773; W69233; Hs.112457; ESTs; mela, esoph, sarc; diag  
 421777; BE562088; Hs.108196; HSPC037 protein; esoph, cerv, lung; diag  
 421779; AI879159; Hs.108219; wingless-type MMTV integration; colon, ovar; diag  
 421798; N74880; Hs.355462; N-acylsphingosine amidohydrolase; fibro; s.m.  
 5 421814; L12350; Hs.108623; thrombospondin 2; panc; diag  
 421831; AA298836; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.  
 421887; AW161450; Hs.109201; CGI-86 protein; pros; mAb  
 421896; N62293; Hs.45107; ESTs; pros; diag  
 10 421917; AB028943; Hs.109445; KIAA1020 protein; test; diag  
 421920; BE551245; Hs.1438; gamma-aminobutyric acid (GABA); sarc; mAb  
 421924; BE514514; Hs.109606; coronin, actin-binding protein; fibro; diag  
 421948; L42583; Hs.334309; keratin 6A; lung, headnk, blad, esoph, cerv, mela; diag  
 421952; AA300900; Hs.98849; dynein light chain 2B (DNLC2B); fibro; diag  
 15 421991; NM\_014918; Hs.110488; KIAA0990 protein; panc; diag  
 421996; AW583807; Hs.1460; glucagon; panc; diag  
 422002; X70070; Hs.110642; neurotensin receptor 1 (high a; colon; mAb  
 422027; AL043100; Hs.288828; fatty acid amide hydrolase; pros; s.m.  
 20 422033; AW245805; Hs.110903; claudin 5 (transmembrane prote; glio; mAb  
 422087; X58968; Hs.111301; matrix metalloproteinase 2 (ge; sarc; diag  
 422089; AA523172; Hs.103135; ESTs, Weakly similar to SFR4\_H; pros; diag  
 422094; AF129535; Hs.272027; F-box only protein 5; blad, lung; CTL+s.m.  
 422095; AI868872; Hs.282804; hypothetical protein FLJ22704; lung, panc, ovar, breast; CTL+s.m.  
 422099; AA156022; Hs.111518; hypothetical protein; angio; CTL+s.m.  
 25 422100; AI096988; Hs.111554; ADP-ribosylation factor-like 7; lung, esoph; CTL+s.m.  
 422110; AI376736; Hs.121555; secreted protein, acidic, cyst; panc; diag  
 422119; AI277829; Hs.111862; KIAA0590 gene product; blad; diag  
 422134; AW179019; Hs.112110; mitochondrial ribosomal protei; lung; diag  
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc; blad; mAb+s.m.  
 30 422163; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb  
 422164; NM\_014312; Hs.112377; cortic al thymocyte receptor (; blad; mAb+s.m.  
 422168; AA586894; Hs.112408; S100 calcium-binding protein A; lung, blad, headnk, breast, mela, esoph, sarc, cerv; CTL+s.m.  
 422170; AI791949; Hs.112432; anti-Mullerian hormone; uter, blad; diag  
 422173; BE385828; Hs.250619; phorbol-like protein MDS019 ; mela; diag  
 35 422247; U18244; Hs.113602; solute carrier family 1 (high ; blad; mAb  
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog ; ovar, headnk, blad, cerv, lung, panc, stom; mAb  
 422309; U79745; Hs.114924; solute carrier family 16 (mono; mela; mAb+s.m.  
 422311; AF073515; Hs.114948; cytokine receptor-like factor ; lung, fibro; diag  
 422355; AW403724; Hs.300697; coagulation factor VII (serum ; fibro; diag  
 40 422363; T55979; Hs.115474; replication factor C (activato; mela, colon; diag  
 422398; AI476149; Hs.334489; hypothetical protein FLJ21992; fibro; CTL+s.m.  
 422406; AF025441; Hs.116206; Opa-interacting protein 5; blad, lung; diag  
 422420; U03398; Hs.1524; tumor necrosis factor (ligand); colon, panc, stom, leuk; mAb  
 422423; AF283777; Hs.116481; CD72 antigen; spleen, leuk; mAb  
 45 422440; NM\_004812; Hs.116724; aldo-keto reductase family 1, ; lung, headnk; s.m.  
 422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; lung, headnk, panc, sarc; diag  
 422532; AL008726; Hs.118126; protective protein for beta-ga; renal, mela; s.m.  
 422565; BE259035; Hs.118400; singed (Drosophila)-like (sea ; panc, test, mela; diag  
 422573; AW297985; Hs.295726; integrin, alpha V (vitronecti; panc; mAb+s.m.  
 50 422596; AF063611; Hs.118633; 2'-5'-oligoadenylate synthetas; esoph, mela; s.m.  
 422603; BE242587; Hs.118651; hematopoietically expressed ho; angio; CTL+s.m.  
 422633; X56832; Hs.118804; enolase 3, (beta, muscle); sarc; s.m.  
 422658; AF231981; Hs.250175; homolog of yeast long chain po; pros; diag  
 422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 C; test; diag  
 55 422726; U11690; Hs.1572; faciogenital dysplasia (Aarsko; test; diag  
 422728; AW937826; Hs.103262; MAD (mothers against decapenta; pros; diag  
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; test; CTL+s.m.  
 422835; BE218705; Hs.121378; metallothionein-like 5, testis; breast; diag  
 422871; AL031228; Hs.121509; collagen, type XI, alpha 2; sarc; diag  
 422887; AI751848; Hs.49215; ESTs; sarc; CTL+s.m.  
 60 422938; NM\_001809; Hs.1594; centromere protein A (17kD); lung, test; CTL+s.m.  
 422963; M79141; Hs.13234; ESTs; lung, panc; diag  
 422997; BE018212; Hs.122908; DNA replication factor; test; CTL+s.m.  
 423017; AW178761; Hs.227948; serine (or cysteine) proteinase; blad, headnk, mela; mAb+diag  
 65 423052; M28214; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag  
 423189; M59371; Hs.171596; EphA2; colon, ovar; mAb  
 423196; AK001866; Hs.125139; hypothetical protein FLJ11004; fibro; CTL+s.m.  
 423198; M81933; Hs.1634; cell division cycle 25A; test; CTL+s.m.  
 423201; NM\_000163; Hs.125180; growth hormone receptor; pros; mAb  
 70 423217; NM\_000094; Hs.1640; collagen, type VII, alpha 1 (e; lung, esoph; diag  
 423271; W47225; Hs.126256; interleukin 1, beta; blad, stom, esoph; diag  
 423309; BE006775; Hs.126782; sushi-repeat protein; lung, colon; diag  
 423354; AB011130; Hs.127436; calcium channel, voltage-depen; test, fibro; mAb  
 423387; AJ012074; Hs.348500; vasoactive intestinal peptide ; pros; mAb  
 75 423397; NM\_001838; Hs.1652; chemokine (C-C motif) receptor; blad, mela; mAb  
 423412; AF109300; Hs.351615; prostate cancer associated pro; pros; diag  
 423422; AC005175; Hs.128425; NY-REN-24 antigen; glio; mAb+CTL  
 423445; NM\_014324; Hs.128749; alpha-methylacyl-CoA racemase; pros; s.m.  
 423453; AW450737; Hs.128791; CGI-09 protein; lung; CTL+s.m.  
 80 423458; AI204212; Hs.351113; ESTs; test; CTL+s.m.  
 423511; AF036329; Hs.129715; gonadotropin-releasing hormone; lung; diag  
 423515; AA327017; Hs.176594; ESTs; ovar; diag  
 423541; AA296922; Hs.129778; serine protease inhibitor, Kaz; colon, panc; diag  
 423575; C18863; Hs.163443; intron of periostin (OSF-2os); headnk, breast, panc, lung, fibro, esoph; diag

- 423605; AF047826; Hs.129887; cadherin 19, type 2; mela; mAb  
 423642; AW452650; Hs.157148; hypothetical protein MGC13204; lung; diag  
 423662; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc); lung; diag  
 423685; BE350494; Hs.49753; uveal autoantigen with coiled; panc, uter, colon; CTL+s.m.  
 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; lung, headnk, blad; diag  
 423739; AA398155; Hs.97600; ESTs; breast, ovar, panc; diag  
 423761; NM\_006194; Hs.132576; paired box gene 9; headnk; CTL+s.m.  
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840; test; diag  
 423778; Y09267; Hs.132821; flavin containing monooxygenase; fibro; s.m.  
 423779; AW071837; Hs.57971; TRANSCRIPTION FACTOR HES-5; glio; diag  
 423787; AJ295745; Hs.236204; nuclear pore complex protein; test, esoph; diag  
 423798; AF047033; Hs.132904; solute carrier family 4, sodium; angio; mAb  
 423799; AW026300; Hs.132906; 19A24 protein; mela; mAb  
 423849; AL157425; Hs.133315; Homo sapiens mRNA; cDNA DKFZp7; lung; diag  
 423887; AL080207; Hs.134585; DKFZP434G232 protein; headnk, lung; diag  
 423899; NM\_001427; Hs.134989; engrailed homolog 2; mela; CTL+s.m.  
 423905; AW579960; Hs.135150; lung type-I cell membrane-asso; test; mAb  
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, me; test; diag  
 423934; U89995; Hs.159234; forkhead box E1 (thyroid trans; lung; CTL+s.m.  
 424001; W67883; Hs.137476; paternally expressed 10; breast, ovar; diag  
 424012; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk, esoph; diag  
 424036; AA770688; Hs.348495; H2A histone family, member L; panc, ovar; CTL+s.m.  
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, s; pros, fibro; mAb  
 424078; AB006625; Hs.139033; paternally expressed 3; ovar, uter; CTL+s.m.  
 424081; NM\_006413; Hs.139120; ribonuclease P (30kD); test; s.m.  
 424098; AF077374; Hs.139322; small proline-rich protein 3; lung, blad, headnk, esoph, cerv; diag  
 424125; M31669; Hs.1735; inhibin, beta B (activin AB be; ovar, pros; diag  
 424144; AA454033; Hs.41644; AKAP-associated sperm protein; fibro; diag  
 424153; AA451737; Hs.141496; MAGE-like 2; mela; CTL+s.m.  
 424165; AW582904; Hs.142255; islet amyloid polypeptide; panc; mAb  
 424212; NM\_005814; Hs.143131; glycoprotein A33 (transmembran; colon, stom, ovar; mAb  
 424218; AF031824; Hs.143212; cystatin F (leukocystatin); mela, fibro; diag  
 424244; AV647184; Hs.143601; hypothetical protein hCLA-iso; blad; diag  
 424252; AK000520; Hs.143811; hypothetical protein FLJ20513; colon, stom; diag  
 424264; D80400; Hs.239388; Human DNA sequence from clone; blad; mAb  
 424308; AW975531; Hs.154443; minichromosome maintenance def; blad, lung, test; diag  
 424310; AA338648; Hs.50334; testes development-related NYD; fibro; diag  
 424332; AA338919; Hs.101615; ESTs; pros; diag  
 424339; BE257148; Hs.145416; endoglycan; pros, lung; diag  
 424343; AW956360; Hs.4748; adenylate cyclase activating p; glio, ovar, uter; mAb  
 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763; lung, blad, headnk, cerv; diag  
 424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 B; breast, uter, headnk; diag  
 424420; BE614743; Hs.146688; prostaglandin E synthase; lung, blad; s.m.  
 424440; AA340743; Hs.133208; ESTs; sarc; diag  
 424441; X14850; Hs.147097; H2A histone family, member X; lung; diag  
 424450; AL137526; Hs.147472; dynein intermediate chain 2; fibro; diag  
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 9; breast, cerv, ovar, uter, blad, colon, stom; s.m.  
 424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374; fibro; diag  
 424578; AK001973; Hs.150890; hypothetical protein; test; CTL+s.m.  
 424581; M62062; Hs.150917; catenin (cadherin-associated p; glio, ovar, uter; mAb+s.m.  
 424586; NM\_003401; Hs.150930; X-ray repair complementing def; panc; CTL+s.m.  
 424629; M90656; Hs.151393; glutamate-cysteine ligase, cat; lung; CTL+s.m.  
 424635; AA420687; Hs.115455; Homo sapiens cDNA FLJ14259 fis; glio; diag  
 424676; Y08565; Hs.151678; UDP-N-acetyl-alpha-D-galactose; breast; s.m.  
 424704; AI263293; Hs.152096; cytochrome P450, subfamily IIJ; renal; s.m.  
 424711; NM\_005795; Hs.152175; calcitonin receptor-like; angio; mAb  
 424717; H03754; Hs.152213; wingless-type MMTV integration; blad, lung, headnk; diag  
 424800; AL035588; Hs.153203; MyoD family inhibitor; test, pros; diag  
 424806; AA382523; Hs.105689; MSTP031 protein; angio; mAb  
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis; lung, blad, ovar, headnk, esoph, cerv, uter; diag  
 424846; AU077324; Hs.1832; neuropeptide Y; pros; diag  
 424897; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renal; diag  
 424902; NM\_003866; Hs.153687; inositol polyphosphate-4-phosp; panc, leuk, mela; CTL+s.m.  
 424954; NM\_000546; Hs.1846; tumor protein p53 (Li-Fraumeni; mela, colon; CTL+s.m.  
 424971; AA479005; Hs.154036; tumor suppressing subtransfera; panc, mela; CTL+s.m.  
 424998; U58515; Hs.154138; chitinase 3-like 2; glio; diag  
 425023; AW956889; Hs.154210; EDG-1 (endothelial different); angio; mAb  
 425048; H05468; Hs.164502; ESTs; lung, blad; diag  
 425057; AA826434; Hs.1619; achaete-scute complex (Drosoph; glio, lung; CTL+s.m.  
 425088; AA663372; Hs.169395; hypothetical protein FLJ12015; glio, mela; diag  
 425154; NM\_001851; Hs.154850; collagen, type IX, alpha 1; sarc; diag  
 425159; NM\_004341; Hs.154868; carbamoyl-phosphate synthetase; lung, test; s.m.  
 425200; BE255203.comp; Hs.155101; ATP synthase, H transporting, ; panc; s.m.  
 425206; NM\_002153; Hs.155109; hydroxysteroid (17-beta) dehyd; blad; mAb  
 425211; M18667; Hs.1867; progastricsin (pepsinogen C); fibro, esoph, pros; diag  
 425234; AW152225; Hs.165909; ESTs, Weakly similar to I38022; lung, angio, blad, mela; diag  
 425235; AA353113; Hs.105468; Homo sapiens cDNA: FLJ22743 fi; angio; diag  
 425237; U07695; Hs.155227; EphB4; test; mAb  
 425245; AI751768; Hs.155314; KIAA0095 gene product; lung; diag  
 425259; AL049280; Hs.145010; Homo sapiens mRNA; cDNA DKFZp5; pros; diag  
 425262; D87119; Hs.155418; GS3955 protein; mela, renal; CTL+s.m.  
 425266; J00077; Hs.155421; alpha-fetoprotein; lung; diag  
 425274; BE281191; Hs.155462; minichromosome maintenance def; test; diag

- 425289; AW139342; Hs.155530; interferon, gamma-inducible pr; mela; CTL+s.m.  
 425308; M97639; Hs.155585; receptor tyrosine kinase-like ; pros; sarc; mAb  
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, ; fibro; diag  
 425371; D49441; Hs.155981; mesothelin; ovar, lung, fibro; mAb  
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (; lung, blad, panc, angio, test, mela, esoph; CTL+s.m.  
 425427; A1652662; Hs.317432; branched chain aminotransferas; test; s.m.  
 425428; AL110261; Hs.157211; DKFZP586B0621 protein; panc; diag  
 425465; L18964; Hs.1904; protein kinase C, iota; ovar, pros, colon; s.m.  
 425525; AA358883; Hs.23871; ESTs; sarc; diag  
 425545; N98529; Hs.158295; Homo sapiens, clone MGC:12401,; sarc; diag  
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 fi; fibro; CTL+s.m.  
 425572; AB011076; Hs.158307; undifferentiated embryonic cel; test; CTL+s.m.  
 425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; test; CTL+s.m.  
 425606; U52112; Hs.158331; renin-binding protein; mela; diag  
 425628; NM\_004476; Hs.1915; folate hydrolase (prostate-spe; pros; s.m.  
 425638; NM\_012337; Hs.158450; nasopharyngeal epithelium spec; fibro; CTL+s.m.  
 425679; X05997; Hs.159177; lipase, gastric; esoph; s.m.  
 425692; D90041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.  
 425695; NM\_005401; Hs.159238; protein tyrosine phosphatase, ; lung; mAb+s.m.  
 425709; AA383076; Hs.159274; outer dense fibre of sperm tai; test; diag  
 425710; AF030880; Hs.159275; solute carrier family, member ; pros; mAb  
 425722; A1659076; Hs.97031; hypothetical protein MGC13047; mela; diag  
 425726; AF085808; Hs.159330; uroplakin 3; pros, blad; diag  
 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA,; test; diag  
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort; test; diag  
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated; lung, headnk; s.m.  
 425921; NM\_007231; Hs.162211; solute carrier family 6 (neuro; stom, panc; mAb  
 425976; C75094; Hs.334514; NG22 protein; pros, ovar; mAb  
 426027; NM\_002608; Hs.1976; platelet-derived growth factor; sarc; diag  
 426050; AF017307; Hs.166096; E74-like factor 3 (ets domain ; ovar, blad, stom; CTL+s.m.  
 426059; BE292842; Hs.166120; interferon regulatory factor 7; esoph, cerv; CTL+s.m.  
 426067; AW664691; Hs.97053; ESTs; lung; diag  
 426088; AF038007; Hs.166196; ATPase, Class I, type 8B, memb; blad, lung; mAb  
 426094; AF034611; Hs.166206; cubilin (intrinsic factor-coba; renal; diag  
 426116; AA868729; Hs.144694; ESTs; fibro; diag  
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophi; colon, stom, panc, pros, renal, fibro, cerv; mAb  
 426156; BE244537; Hs.167382; natriuretic peptide receptor A; ovar; mAb  
 426158; NM\_001982; Hs.199067; v-erb-b2 avian erythroblastic ; breast, ovar, uter, pros, blad, panc, colon, fibro, mela; diag  
 426172; AA371307; Hs.125056; ESTs; pros; diag  
 426174; AA547959; Hs.115838; Homo sapiens similar to Echino; breast, pros, fibro; diag  
 426212; S71824; Hs.167988; neural cell adhesion molecule ; glio; mAb  
 426271; AF026547; Hs.169047; chondroitin sulfate proteoglyc; glio; diag  
 426274; D38122; Hs.2007; tumor necrosis factor (ligand); fibro, mela; mAb  
 426300; U15979; Hs.169228; delta-like homolog (Drosophila; ovar, sarc; mAb  
 426310; NM\_000909; Hs.169266; neuropeptide Y receptor Y1; breast; mAb  
 426312; AF026939; Hs.181874; interferon-induced protein wit; esoph, mela; diag  
 426320; W47595; Hs.169300; transforming growth factor, be; ovar, pros, blad, panc; diag  
 426350; NM\_003245; Hs.2022; transglutaminase 3 (E polypept; cerv; s.m.  
 426363; M58524; Hs.2025; transforming growth factor, be; pros; diag  
 426370; R98288; Hs.281706; sortilin 1; sarc; diag  
 426416; AW612744; Hs.169824; killer cell lectin-like recept; fibro; mAb  
 426440; BE382756; Hs.169902; solute carrier family 2 (facil; lung, panc, ovar, blad, headnk, esoph; mAb  
 426462; U59111; Hs.169993; dermatan sulphate proteoglycan; sarc; diag  
 426470; AA528794; Hs.128644; ESTs; mela; diag  
 426471; M22440; Hs.170009; transforming growth factor, al; headnk, renal, panc; diag  
 426490; NM\_001621; Hs.170087; aryl hydrocarbon receptor; panc; mAb+s.m.  
 426501; AW043782; Hs.293616; ESTs; pros, breast, glio, lung, mela; mAb  
 426502; Y07759; Hs.170157; myosin VA (heavy polypeptide 1; mela; diag  
 426534; U58096; Hs.2051; testis specific protein, Y-lin; test; CTL+s.m.  
 426535; AU077012; Hs.170279; ESTs, Weakly similar to ubiqui; angio; diag  
 426555; NM\_000372; Hs.2053; tyrosinase (oculocutaneous alb; mela, sarc; mAb  
 426559; AB001914; Hs.170414; paired basic amino acid cleavi; hepC, breast, ovar, renal; diag  
 426575; M74826; Hs.170808; glutamate decarboxylase 2 (pan; panc; s.m.  
 426627; AF012359; Hs.195685; ESTs; test; diag  
 426635; BE395109; Hs.129327; hypothetical protein MGC13057; ovar; CTL+s.m.  
 426682; AV660038; Hs.2056; UDP glycosyltransferase 1 fami; blad, lung; s.m.  
 426691; NM\_006201; Hs.171834; PCTAIRE protein kinase 1; ovar; CTL+s.m.  
 426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 fi; angio; mAb  
 426721; AA383588; Hs.288545; ESTs, Weakly similar to T29012; fibro; diag  
 426726; AA488915; Hs.171955; trophinin associated protein (; test; diag  
 426747; AA535210; Hs.171995; kallikrein 3, (prostate specif; pros; diag  
 426752; X69490; Hs.172004; titin; sarc; diag  
 426759; A1590401; Hs.21213; ESTs; mela; diag  
 426793; X89887; Hs.172350; HIR (histone cell cycle regula; pros; CTL+s.m.  
 426828; NM\_000020; Hs.172670; activin A receptor type II-lik; angio; mAb  
 426866; U02330; Hs.172816; neuregulin 1; esoph; CTL+s.m.  
 426897; AW976570; Hs.97387; ESTs; lung; diag  
 426900; AW163564; Hs.142375; ESTs; blad, pros; mAb  
 426935; NM\_000088; Hs.172928; collagen, type I, alpha 1; test, sarc; CTL+s.m.  
 426966; A1493134; Hs.349204; sclerostin; lung; diag  
 426968; U07616; Hs.173034; amphiphysin (Stiff-Mann syndro; blad; mAb+CTL  
 426991; AK001536; Hs.214410; Homo sapiens cDNA FLJ10674 fis; ovar, sarc; diag  
 427080; AW068287; Hs.301175; ras-related C3 botulinum toxin; mela; diag

- 427099; AB032953; Hs.173560; odd Oz/ten-m homolog 2 (Drosop; headnk, esoph; diag  
427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase; breast; mAb  
427244; AA402400; Hs.178045; ESTs; esoph; diag  
5 427260; AA663848; ; gb:ae70b06.s1 Stratagene schiz; lung; diag  
427274; NM\_005211; Hs.174142; colony stimulating factor 1 re; pros, sarc; mAb  
427298; AA400495; ; ESTs; test; diag  
427318; AF186081; Hs.175783; zinc transporter; pros; mAb  
427333; AF067797; Hs.176658; aquaporin 8; panc, colon; mAb  
10 427344; NM\_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb  
427356; AW023482; Hs.97849; ESTs; ovar, breast, pros, blad, lung; diag  
427398; AW390020; Hs.20415; chromosome 21 open reading fra; pros; diag  
427427; AF077345; Hs.177936; lectin, superfamily member 1 (; breast; diag  
427441; AA412605; Hs.293266; SPANX family, member C; lung, esoph; CTL+s.m.  
15 427461; AA531527; Hs.332040; hypothetical protein MGC13010; pros; mAb  
427474; U13192; Hs.2159; aggrecan 1 (chondroitin sulfat; sarc; diag  
427486; AA974433; Hs.362432; fibroblast growth factor 4 (he; test; diag  
427510; Z47542; Hs.179312; small nuclear RNA activating c; lung; CTL+s.m.  
427515; T79526; Hs.179516; integral type I protein; pros; diag  
20 427521; AW973352; ; ESTs; test; diag  
427528; AU077143; Hs.179565; minichromosome maintenance def; mela; CTL+s.m.  
427535; R29543; Hs.2164; pro-platelet basic protein (in; fibro; diag  
427546; AA405280; Hs.36793; hypothetical protein FLJ23188; lung; diag  
427550; BE242818; Hs.311609; nuclear RNA helicase, DECD var; mela; CTL+s.m.  
25 427557; NM\_002659; Hs.179657; plasminogen activator, urokina; panc, colon, stom, ovar, cerv, blad, lung, headnk, esoph; mAb  
427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3\_H; test; diag  
427583; M82962; Hs.179704; meprin A, alpha (PABA peptide; colon; mAb  
427584; BE410293; Hs.179718; v-myb avian myeloblastosis vir; test; CTL+s.m.  
427585; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc, stom, colon, ovar, cerv, sarc; diag  
30 427615; BE410107; Hs.179817; CGI-82 protein, PSDR1; pros; diag  
427634; AI399745; Hs.18449; hypothetical protein MGC10820; mela, sarc; diag  
427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20653 fis; sarc; diag  
427666; AI791495; Hs.180142; calmodulin-like skin protein (; breast, cerv, blad, lung, headnk, esoph; diag  
427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis; test; diag  
35 427668; AA298760; Hs.180191; hypothetical protein FLJ14904; lung, test; diag  
427681; AB018263; Hs.284232; tumor necrosis factor receptor; ovar; mAb+s.m.  
427698; AW972594; Hs.335499; ESTs; fibro; CTL+s.m.  
427701; AA411101; Hs.243886; nuclear autoantigenic sperm pr; lung; mAb+CTL  
427715; BE245274; Hs.180428; KIAA1181 protein; pros; diag  
40 427719; AI393122; Hs.134726; ESTs; test, blad; diag  
427730; AW250549; Hs.180577; granulin; mela; diag  
427786; BE407863; Hs.256871; ESTs; esoph, blad; diag  
427809; M26380; Hs.180878; lipoprotein lipase; ovar; mAb  
427811; M81057; Hs.180884; carboxypeptidase B1 (tissue); breast; s.m.  
45 427897; NM\_017413; Hs.303084; apelin; peptide ligand for APJ; angio, renal, pros; diag  
427912; AL022310; Hs.181097; tumor necrosis factor (ligand); angio; mAb  
427958; AA418000; Hs.376771; potassium intermediate/small c; pros, glio; mAb  
427961; AW293165; Hs.143134; ESTs; lung, sarc; diag  
428001; H97428; Hs.219907; ESTs, Moderately similar to Tr; mela; diag  
50 428004; AA449563; Hs.151393; glutamate-cysteine ligase, cat; lung; s.m.  
428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fi; lung; diag  
428046; AW812795; Hs.337534; ESTs, Moderately similar to I3; lung, colon; diag  
428062; AA420683; Hs.98321; hypothetical protein FLJ14103; angio; diag  
428087; AA100573; Hs.182421; troponin C2, fast; sarc; CTL+s.m.  
55 428141; D50402; Hs.182611; solute carrier family 11 (prot; glio; mAb  
428153; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag  
428169; AI928984; Hs.182793; golgi phosphoprotein 2; pros; diag  
428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1\_H; blad, headnk, lung, ovar, sarc; CTL+s.m.  
428183; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag  
60 428206; AB020643; Hs.183006; KIAA0836 protein; angio; mAb  
428221; U96781; Hs.183075; ATPase, Ca transporting, cardi; sarc; s.m.  
428227; AA321649; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, headnk, fibro, colon, stom, cerv, leuk, renal, test, mela, esoph, hepC; diag  
428248; AI126772; Hs.40479; ESTs; sarc; diag  
428293; BE250944; Hs.183556; solute carrier family 1 (neutr; pros; mAb  
65 428305; AA446628; Hs.2799; cartilage linking protein 1; sarc; diag  
428329; AA426091; Hs.98453; ESTs, Moderately similar to R2; test; diag  
428336; AA503115; Hs.183752; microseminoprotein, beta-; pros; diag  
428355; BE256452; Hs.2257; vitronectin (serum spreading f; colon; diag  
428398; AI249368; Hs.98558; ESTs; pros, breast; diag  
70 428405; Y00762; Hs.2266; cholinergic receptor, nicotini; esoph, sarc; mAb  
428423; AU076517; Hs.184276; solute carrier family 9 (sodi; ovar; CTL+s.m.  
428434; AW363590; Hs.65551; Homo sapiens, Similar to DNA s; lung, fibro; diag  
428467; AK002121; Hs.184465; hypothetical protein FLJ11259; fibro; mAb  
428471; X57348; Hs.184510; stratifin; lung, headnk, colon, panc; diag  
75 428645; AA431400; Hs.98729; ESTs, Weakly similar to 201720; lung; s.m.  
428651; AF196478; Hs.188401; annexin A10; blad, stom, panc; diag  
428667; AI375550; Hs.346868; nucleolar protein p40; homolog; fibro, uter; diag  
428722; U76456; Hs.190787; tissue inhibitor of metallopro; glio; diag  
428728; NM\_016625; Hs.191381; hypothetical protein; ovar, lung, BPH; CTL+s.m.  
80 428771; AB028992; Hs.193143; KIAA1069 protein; lung; CTL+s.m.  
428784; Y12851; Hs.193470; purinergic receptor P2X, ligand; glio, mela; mAb  
428800; M57627; Hs.193717; interleukin 10; fibro; diag  
428801; AW277121; Hs.254881; ESTs; pros; diag  
428804; AK000713; Hs.193736; hypothetical protein FLJ20706; mela; diag

- 428810; AF068236; Hs.193788; nitric oxide synthase 2A (indu; lung; s.m.  
 428819; AL135623; Hs.193914; KIAA0575 gene product; pros; CTL+s.m.  
 428824; W23624; Hs.173059; ESTs; panc; diag  
 428832; AA578229; Hs.324239; ESTs, Moderately similar to ZN; panc, uter; diag  
 428841; A1418430; Hs.104935; ESTs; renal; diag  
 428848; NM\_000230; Hs.194236; leptin (murine obesity homolog; sarc; diag  
 428862; NM\_000346; Hs.2316; SRY (sex determining region Y); pros, sarc; CTL+s.m.  
 428927; AA441837; Hs.90250; Homo sapiens hypothetical prot; fibro; mAb+diag  
 428928; BE409838; Hs.194657; cadherin 1, type 1, E-cadherin; pros, breast, stom, blad; mAb  
 428949; AA442153; Hs.104744; hypothetical protein DKFZp434J; sarc; diag  
 428957; NM\_003881; Hs.194679; WNT1 inducible signaling pathw; cerv; diag  
 428959; AF100779; Hs.194680; WNT1 inducible signaling pathw; sarc; diag  
 428977; AK001404; Hs.194698; cyclin B2; test; CTL+s.m.  
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2\_H; sarc; diag  
 429002; AW248439; Hs.2340; junction plakoglobin; blad; CTL+s.m.  
 429010; Y18198; Hs.194725; one cut domain, family member ; panc; diag  
 429038; AL023513; Hs.194766; seizure related gene 6 (mouse); lung; mAb  
 429058; AF138863; Hs.35254; hypothetical protein FLB6421; esoph; diag  
 429065; A1753247; Hs.29643; Homo sapiens cDNA FLJ13103 fis; lung; diag  
 429083; Y09397; Hs.227817; BCL2-related protein A1; mela; diag  
 429113; D28235; Hs.196384; prostaglandin-endoperoxide syn; angio, blad, stom; s.m.  
 429120; AK001673; Hs.196530; hypothetical protein FLJ10811; test; diag  
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolo; ovar; mAb  
 429163; AA884766; ; gb:am20a10.s1 Soares\_NFL\_T\_GBC; pros; diag  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; breast, panc, stom, lung, mela; s.m.  
 429201; X03178; Hs.198246; group-specific component (vita; panc; diag  
 429220; AW207206; Hs.356962; ESTs; breast, pros, BPH; diag  
 429228; A1553633; Hs.356828; ESTs; lung, fibro, headnk, esoph; diag  
 429259; AA20450; Hs.380088; Plakophilin; lung, headnk; diag  
 429290; AF203032; Hs.198760; neurofilament, heavy polypepti; pros; CTL+s.m.  
 429299; A1620463; Hs.347408; hypothetical protein MGC13102; pros, cerv; diag  
 429329; AA456140; Hs.99235; Homo sapiens pannexin 3 (PANX3; sarc; mAb  
 429345; R11141; Hs.199695; hypothetical protein; blad; diag  
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (m; headnk, breast, cerv, ovar, blad, lung, esoph, mela, sarc; mAb  
 429413; NM\_014058; Hs.201877; DESC1 protein; lung, blad; diag  
 429415; NM\_002593; Hs.202097; procollagen C-endopeptidase en; sarc; diag  
 429423; A1016712; Hs.380983; integrin, beta 1 (fibronectin ; angio; mAb  
 429432; A1678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag  
 429441; AJ224172; Hs.204096; lipophilin B (uteroglobin fami; breast, pros, ovar; diag  
 429466; M85835; Hs.12827; ESTs; glio, uter; CTL+s.m.  
 429469; M64590; Hs.380791; glycine dehydrogenase (decarbo; test; s.m.  
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; blad, lung, headnk, test; diag  
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cyto; lung, glio, headnk, mela, sarc; diag  
 429504; X99133; Hs.204238; lipocalin 2 (oncogene 24p3) (N; ovar, lung, blad; diag  
 429505; AW820035; Hs.278679; a disintegrin and metalloprote; colon, leuk; mAb  
 429538; BE182592; Hs.139322; small proline-rich protein 2A; lung, esoph; diag  
 429563; BE19413; Hs.2437; eukaryotic translation initiat; lung; diag  
 429586; T73510; Hs.209153; angiopoietin-like 3; hepC; CTL+s.m.  
 429597; NM\_003816; Hs.2442; a disintegrin and metalloprote; panc, colon, stom, lung; mAb  
 429609; AF002246; Hs.210863; cell adhesion molecule with ho; ovar, mela; diag  
 429612; AF062649; Hs.252587; pituitary tumor-transforming 1; lung, blad, headnk; diag  
 429655; U48959; Hs.211582; myosin, light polypeptide kina; pros; s.m.  
 429663; M68874; Hs.211587; phospholipase A2, group IVA (c; angio, lung; s.m.  
 429664; L20433; Hs.211588; POU domain, class 4, transcrip; sarc; CTL+s.m.  
 429736; AF125304; Hs.212680; tumor necrosis factor receptor; lung; mAb  
 429747; M87507; Hs.2490; caspase 1, apoptosis-related c; colon, stom, fibro; s.m.  
 429764; BE245076; Hs.216958; KIAA0194 protein; pros; mAb  
 429769; NM\_004917; Hs.218366; kallikrein 4 (prostase, enamel; pros; s.m.  
 429784; M89796; Hs.30; membrane-spanning 4-domains, s; fibro; mAb  
 429823; AA459443; Hs.181400; ESTs; sarc; diag  
 429859; NM\_007050; Hs.225952; protein tyrosine phosphatase ; breast; mAb+s.m.  
 429918; AW873986; Hs.119383; ESTs; pros, glio; diag  
 429921; AA526911; Hs.82772; collagen, type XI, alpha 1; headnk, panc, sarc; CTL  
 429983; W92620; Hs.260855; ESTs; blad; diag  
 429986; AF092047; Hs.227277; sine oculis homeobox (Drosophi; lung; CTL+s.m.  
 430014; H59354; Hs.374303; actinin, alpha 4; renal; diag  
 430016; NM\_004736; Hs.227656; xenotropic and polytropic retr; ovar; mAb  
 430044; AA464510; Hs.152812; ESTs; breast, lung, panc, headnk, ovar, stom, esoph; diag  
 430056; X97548; Hs.228059; KRAB-associated protein 1; test; CTL+s.m.  
 430129; BE301708; Hs.233955; hypothetical protein FLJ20401; angio; diag  
 430130; AL137311; Hs.234074; Homo sapiens mRNA; cDNA DKFZp7; pros; mAb  
 430144; A1732722; Hs.98927; ERGL protein; ERGL-53-like pr; pros; diag  
 430152; AB001325; Hs.234642; aquaporin 3; blad, fibro; mAb  
 430154; AW583058; Hs.234726; serine (or cysteine) proteinas; pros; diag  
 430157; BE348706; Hs.278543; ESTs; blad; diag  
 430168; AW968343; Hs.145582; DKFZP4341735 protein; blad; diag  
 430223; NM\_002514; Hs.235935; nephroblastoma overexpressed g; mela; diag  
 430226; BE245562; Hs.2551; adrenergic, beta-2-, receptor;; pros; mAb  
 430228; AW950939; Hs.6382; ESTs, Highly similar to T00391; glio; diag  
 430252; A1638774; Hs.105328; testes development-related NYD; test; CTL+s.m.  
 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; test; CTL+s.m.  
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551; test; CTL+s.m.  
 430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse h; ovar; CTL+s.m.



- 430280; AA361258; Hs.237868; interleukin 7 receptor; mela, lung, panc, stom, esoph, headnk, fibro; mAb+s.m.  
 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5\_H; test; diag  
 430294; AI538226; Hs.32976; guanine nucleotide binding pro; pros; diag  
 430337; M36707; Hs.239600; calmodulin-like 3; lung; diag  
 430354; AA954810; Hs.239784; human homolog of Drosophila Sc; ovar; diag  
 430378; Z29572; Hs.2556; tumor necrosis factor receptor; lung, fibro, breast headnk, blad, breast, colon, stom; diag  
 430393; BE185030; Hs.241305; estrogen-responsive B box prot; lung; diag  
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; panc; diag  
 430407; H23551; Hs.30974; ESTs; panc; diag  
 430439; AL133561; Hs.380155; DKFZP434B061 protein; lung, test; diag  
 430451; AA836472; Hs.297939; cathepsin B; ovar, lung, headnk, panc, stom; diag  
 430454; AW469011; Hs.105635; ESTs; lung; diag  
 430476; AA447465; Hs.2563; tachykinin, precursor 1 (subst; sarc; diag  
 430487; D87742; Hs.241552; KIAA0268 protein; pros; diag  
 430491; AL109791; Hs.241559; Homo sapiens mRNA full length ; ovar; diag  
 430498; X02910; Hs.241570; tumor necrosis factor (TNF sup; leuk; diag  
 430508; AI015435; Hs.104637; ESTs; lung; mAb+s.m.  
 430521; NM\_016383; Hs.242183; HOM-TES-85 tumor antigen; test; CTL+s.m.  
 430540; AW245422; Hs.106357; Homo sapiens cDNA: FLJ22105 f; mela; mAb  
 430563; AA481269; Hs.348628; ATP-binding cassette, sub-fami; lung; diag  
 430594; AK000790; Hs.246885; hypothetical protein FLJ20783; mela; diag  
 430634; AI860651; Hs.26685; calyphosine; ovar; diag  
 430637; BE160081; Hs.256290; S100 calcium-binding protein A; mela; diag  
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211\_H; test; diag  
 430676; AF084866; Hs.372585; gb:Homo sapiens envelope prote; test; diag  
 430677; Z26317; Hs.359784; desmoglein 2; lung, colon; mAb  
 430678; AI458174; Hs.192855; ESTs; lung; diag  
 430686; NM\_001942; Hs.2633; desmoglein 1; lung, headnk, mela; mAb  
 430691; C14187; Hs.157208; aristaless-related homeobox pr; EWS, ovar, panc; diag  
 430704; AW813091; Hs.335799; ESTs; stom; diag  
 430770; AA765694; Hs.123296; ESTs; mela; diag  
 430832; AI073913; Hs.100886; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom, fibro; diag  
 430838; N46664; Hs.169395; hypothetical protein FLJ12015; mela; CTL+s.m.  
 430890; X54232; Hs.2699; glypican 1; glio, lung, cerv, blad, esoph; mAb  
 430985; AA490232; Hs.27323; ESTs, Weakly similar to I78885; lung; mAb  
 431009; BE149762; Hs.48956; gap junction protein, beta 6 (; lung, blad, headnk, esoph; mAb  
 431053; S40369; Hs.249141; Glutamate receptor subunit; glio; mAb  
 431070; AW408164; Hs.249184; transcription factor 19 (SC1); blad; diag  
 431089; BE041395; Hs.374629; ESTs, Weakly similar to unknow; blad, lung, pros, angio, fibro; diag  
 431099; Y13367; Hs.249235; phosphoinositide-3-kinase, cla; pros; CTL+s.m.  
 431103; M57399; Hs.44; pleiotrophin (heparin binding ; sarc, mela; diag  
 431124; AF284221; Hs.59506; doublesex and mab-3 related tr; lung; CTL+s.m.  
 431151; BE207083; Hs.366053; gb:ba10d10.y1 NIH\_MGC\_7 Homo s; pros; mAb  
 431164; AA493650; Hs.94367; thyroid transcription factor 1; fibro; CTL+s.m.  
 431183; NM\_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endopla; mela, pros, panc, colon, stom; mAb  
 431211; M86849; Hs.323733; gap junction protein, beta 2 ; colon, blad, lung, panc, headnk, esoph; mAb  
 431217; NM\_013427; Hs.250830; Rho GTPase activating protein ; pros; CTL+s.m.  
 431221; AA449015; Hs.286145; SRB7 (suppressor of RNA polyme; lung; CTL+s.m.  
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A; pros; diag  
 431250; BE264649; Hs.251377; taxol resistance associated ge; esoph; diag  
 431322; AW970622; Hs.376626; gb:EST382704 MAGE resequenc.; blad, ovar, uter; diag  
 431347; AI133461; Hs.251664; insulin-like growth factor 2 (; blad; mAb+diag  
 431354; BE046956; Hs.251673; DNA (cytosine-5)-methyltransf; test; CTL+s.m.  
 431360; NM\_000427; Hs.251680; Ioricrin; mela, sarc; diag  
 431362; AI874223; Hs.293560; ESTs; angio; diag  
 431369; BE184455; Hs.251754; secretory leukocyte protease i; ovar, blad; diag  
 431384; BE158000; Hs.334372; gb:MR2-HT0377-150200-202-e03 H; lung; diag  
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, s; panc; diag  
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gat; ovar, pros, blad; mAb  
 431448; AL137517; Hs.306201; hypothetical protein DKFZp5640; blad; mAb  
 431457; NM\_012211; Hs.256297; integrin, alpha 11; headnk; mAb  
 431474; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag  
 431494; AA991355; Hs.298312; hypothetical protein DKFZp434A; lung; diag  
 431512; BE270734; Hs.2795; lactate dehydrogenase A; panc; s.m.  
 431548; AI834273; Hs.9711; novel protein; lung, angio, pros; diag  
 431553; X78075; Hs.2799; cartilage linking protein 1; sarc; diag  
 431579; AW971082; Hs.222886; ESTs, Weakly similar to TRHY\_H; pros; diag  
 431616; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros, panc, colon ; mAb  
 431674; AA098901; Hs.301642; G-protein coupled receptor; ovar; mAb+s.m.  
 431723; AW058350; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; fibro; diag  
 431728; NM\_007351; Hs.268107; multimerin; angio; diag  
 431808; M30703; Hs.270833; amphiregulin (schwannoma-deriv; breast, headnk, panc, colon; diag  
 431836; AF178532; Hs.271411; beta-site APP-cleaving enzyme ; mela; mAb  
 431870; AW449902; Hs.105500; ESTs; renal; diag  
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alph; blad, headnk, lung, panc, cerv, stom; mAb  
 431938; AA938471; Hs.54431; specific granule protein (28 k; panc; diag  
 431939; AW008061; Hs.231994; ESTs; renal, colon; diag  
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis; cerv, glio; diag  
 431989; AW972870; Hs.291069; ESTs; ovar; diag  
 431992; NM\_002742; Hs.2891; protein kinase C, mu; pros, glio; s.m.  
 432004; BE018302; Hs.2894; placental growth factor, vascu; renal; diag  
 432015; AL157504; Hs.159115; Homo sapiens mRNA; cDNA DKFZp5; blad; diag  
 432023; AW273128; Hs.300268; EST; lung; diag

- 432097; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.  
 432117; AL036195; Hs.2909; prolamine 1; test; CTL+s.m.  
 432128; AA127221; Hs.66; ESTs; angio; diag  
 432141; BE410964; Hs.272736; nuclear receptor binding prote; test; mAb+s.m.  
 432189; AA527941; ; gb:nh30c04.s1 NCI\_CGAP\_Pr3 Hom; pros; diag  
 432199; AI693815; Hs.127179; cryptic gene; panc; diag  
 432210; AI567421; Hs.273330; Homo sapiens, clone IMAGE:3544; ovar, lung, blad; diag  
 432222; AI204995; ; gb:an03c03.x1 Stratagene schiz; angio, blad, fibro; diag  
 432231; AA339977; Hs.274127; CLST 11240 protein; fibro; diag  
 432239; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad, lung, headnk, esoph, sarc; s.m.  
 432240; AI694767; Hs.129179; Homo sapiens cDNA FLJ13581 fis; pros; diag  
 432305; M62402; Hs.274313; insulin-like growth factor bin; cerv; diag  
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis; cerv, lung, fibro, pros; diag  
 432407; AA221036; ; gb:zr03f12.r1 Stratagene NT2 n; lung, test,colon; diag  
 432415; T16971; ; ESTs, Weakly similar to A43932; ovar, pros; diag  
 432432; AA541323; Hs.115831; ESTs; uter, pros; diag  
 432435; BE218886; Hs.282070; ESTs; pros, uter, colon, stom, fibro; diag  
 432441; AW292425; Hs.163484; intron of hepatocyte nuclear f; blad, fibro, pros; diag  
 432473; AI202703; Hs.152414; ESTs; pros; diag  
 432481; AW451645; Hs.151504; intron of collagen, type XI, a; sarc; diag  
 432512; NM\_003284; Hs.3017; transition protein 1 (during h; test; CTL+s.m.  
 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUIA; fibro, ovar, uter; CTL+s.m.  
 432527; AW975028; Hs.102754; ESTs; pros, uter, ovar, cerv; diag  
 432542; AW083920; Hs.16098; claudin 2; colon, panc; diag  
 432583; AW023624; Hs.162282; potassium channel TASK-4; pota; lung; mAb  
 432615; AA557191; Hs.55028; ESTs, Weakly similar to I54374; pros; diag  
 432621; AI298501; Hs.21192; ESTs, Weakly similar to T46428; pros; mAb  
 432629; AW860548; Hs.280658; ESTs; ovar; diag  
 432653; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros, lung; mAb+s.m.  
 432666; AW204069; Hs.351118; ESTs, Weakly similar to unname; test; diag  
 432706; NM\_013230; Hs.286124; CD24 antigen (small cell lung; colon, ovar, pros; mAb+CTL  
 432730; AI066520; Hs.131358; ESTs; test; diag  
 432731; R31178; Hs.287820; fibronectin 1; panc, fibro; diag  
 432788; AA521091; Hs.178499; Homo sapiens cDNA: FLJ23117 fi; lung, ovar; CTL+s.m.  
 432800; BE391046; Hs.278962; AIM-1 protein; mela, pros; mAb  
 432842; AW674093; Hs.334822; hypothetical protein MGC4485; blad, lung, headnk; CTL+s.m.  
 432850; X87723; Hs.3110; angiotensin receptor 2 (AT2); leio; mAb  
 432855; AF017988; Hs.279565; secreted frizzled-related prot; panc; diag  
 432867; AW016936; Hs.233364; ESTs; stom, colon; diag  
 432878; BE386490; Hs.279663; Pirin; mela; CTL+s.m.  
 432887; AI926047; Hs.162859; AK056805; Homo sapiens cDNA FL; pros; diag  
 432938; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag  
 432966; AA650114; Hs.325198; ESTs; pros; diag  
 433012; NM\_004045; Hs.279910; ATX1 (antioxidant protein 1, y; mela; diag  
 433013; AI697890; Hs.127337; axin 2 (conductin, axil); colon; CTL+s.m.  
 433043; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag  
 433068; NM\_006456; Hs.288215; sialyltransferase; breast, ovar, mela; s.m.  
 433078; AW015188; Hs.121575; Homo sapiens cDNA FLJ12231 fis; blad; diag  
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, ; blad, lung, headnk, cerv; mAb  
 433147; AF091434; Hs.43080; platelet derived growth factor; ovar, panc, fibro; diag  
 433159; AB035898; Hs.150587; kinesin-like protein 2; ovar, uter, colon, blad; diag  
 433170; AB037816; Hs.8982; KIAA1395; angio; diag  
 433183; AF231338; Hs.222024; transcription factor BMAL2; lung; diag  
 433228; F28212; Hs.14953; KIAA1491 protein; test; CTL+s.m.  
 433258; AI806626; Hs.207300; ESTs, Weakly similar to ALUB\_H; lung; diag  
 433285; AW975944; Hs.237396; ESTs; breast, pros; diag  
 433293; AF007835; Hs.32417; hypothetical protein MGC2742; fibro, pros, stom, panc; CTL+s.m.  
 433323; AA805132; Hs.159142; ESTs; pros; diag  
 433334; AI927208; Hs.231958; matrix metalloproteinase 28; panc; s.m.  
 433336; AF017986; Hs.31386; secreted frizzled-related prot; ovar, fibro, headnk, lung, panc, blad; diag  
 433364; AI075407; Hs.296083; ESTs, Moderately similar to I5; mela; diag  
 433365; AF026944; Hs.293797; ESTs; blad; diag  
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related c; angio; s.m.  
 433388; AI432672; Hs.288539; hypothetical protein FLJ22191; ovar; CTL+s.m.  
 433404; T32982; Hs.352670; Homo sapiens cDNA FLJ32064 fis; pros; diag  
 433437; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, glio, colon; s.m.  
 433444; AW975324; Hs.129816; ESTs; pros; diag  
 433466; AA508353; Hs.105314; relaxin 1 (H1); pros; diag  
 433485; AI493076; Hs.306098; aldo-keto reductase family 1, ; lung; s.m.  
 433495; AW373784; Hs.71; alpha-2-glycoprotein 1, zinc; breast, pros; diag  
 433576; BE080715; Hs.161091; ESTs; mela; diag  
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene; colon; diag  
 433671; AW138797; Hs.132906; 19A24 protein; fibro; mAb  
 433701; AW445023; Hs.15155; ESTs; test; diag  
 433724; AI827749; Hs.144924; serine/threonine protein kinas; test; CTL+s.m.  
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM-; pros, ovar; diag  
 433800; AI034361; Hs.135150; lung type-I cell membrane-asso; glio, lung, test; mAb  
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homo; test; s.m.  
 434011; AW953437; Hs.5486; clone FLB5214; pros; diag  
 434105; AW952124; Hs.13094; presenilins associated rhombol; lung; diag  
 434217; AW014795; Hs.23349; ESTs; angio; diag  
 434262; AF121858; Hs.12169; sorting nexin 8; mela; CTL+s.m.  
 434274; AA628539; Hs.57783; ESTs, Moderately similar to AL; test; diag

- 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis; test; diag  
 434340; AI193043; Hs.353146; ESTs, Weakly similar to T17226; lung; diag  
 434360; AW015415; Hs.127780; ESTs; lung; diag  
 434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic re; colon, stom; diag  
 434377; AW137148; Hs.306593; intron of periostin (OSF-2os); headnk; diag  
 434398; AA121098; Hs.3838; serum-inducible kinase (SNK); angio, breast; CTL+s.m.  
 434411; AA632649; Hs.201372; ESTs; stom, leuk; diag  
 434414; AI798376; ; gb:tr34b07.x1 NCL\_CGAP\_Ov23 Ho; lung, test, colon; diag  
 434423; NM\_006769; Hs.3844; LIM domain only 4; panc; diag  
 434449; AW953484; Hs.3849; hypothetical protein FLJ22041 ; sarc; diag  
 434487; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb+s.m.  
 434596; T59538; ; gb:yb65g12.s1 Stratagene ovary; angio; s.m.  
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; test; CTL+s.m.  
 434609; R76593; ; gb:yi60c11.r1 Soares placenta ; pros; diag  
 434636; AA083764; Hs.349208; hypothetical protein MGC3178; angio; diag  
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350; test; diag  
 434665; AA642125; Hs.74502; gb:nr60c01.s1 NCL\_CGAP\_Lym3 Ho; panc; diag  
 434666; AF151103; Hs.112259; T cell receptor gamma locus; pros; mAb+s.m.  
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis; panc; diag  
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phospho; mela; s.m.  
 434846; AW295389; Hs.119768; ESTs; angio; diag  
 434876; AF160477; Hs.61460; Ig superfamily receptor LNIR; lung, blad; mAb  
 434927; H46612; Hs.293815; Homo sapiens HSPC285 mRNA, par; angio; diag  
 434973; AW449285; Hs.313636; EST; pros; diag  
 435045; BE297155; Hs.143698; ESTs; test; diag  
 435047; AA454985; Hs.54973; cadherin-like protein VR20; pros; mAb  
 435066; BE261750; Hs.4747; dyskeratosis congenita 1, dysk; colon; CTL+s.m.  
 435080; AI831760; Hs.155111; hypothetical protein FLJ14428; renal; mAb  
 435094; AI560129; Hs.289008; EST; ovar, cerv; diag  
 435099; AC004770; Hs.4756; flap structure-specific endonu; blad, test, mela; CTL+s.m.  
 435140; AA668123; Hs.134170; ESTs; fibro; diag  
 435159; AA668879; Hs.116649; ESTs; lung; diag  
 435206; AI432364; Hs.160594; ESTs; test; diag  
 435243; AW292886; Hs.348932; hypothetical protein DJ434014; cerv, headnk; diag  
 435292; N20514; Hs.172965; ESTs; mela; diag  
 435299; AI745458; Hs.343026; ESTs, Weakly similar to T20593; fibro; diag  
 435479; AF197137; Hs.155101; ATP synthase, H transporting, ; pros; s.m.  
 435496; AW840171; Hs.265398; PAR-6 beta; breast, panc, ovar; diag  
 435563; AF210317; Hs.95497; solute carrier family 2 (facil; blad; mAb+s.m.  
 435575; AF213457; Hs.44234; triggering receptor expressed ; fibro; mAb+s.m.  
 435602; AF217515; Hs.283532; uncharacterized bone marrow pr; test; diag  
 435615; Y15065; Hs.4975; potassium voltage-gated channe; glio; mAb  
 435652; N32388; Hs.334370; uncharacterized hypothalamus p; panc; diag  
 435793; AB037734; Hs.4993; KIAA1313 protein; ovar, lung, uter; diag  
 435849; BE305242; Hs.16098; claudin 2; colon, panc; diag  
 435876; AW612586; Hs.160271; G protein-coupled receptor 48; pros; mAb  
 435897; AF269223; Hs.128322; t-complex 11 (a murine tcp hom; test; diag  
 435904; AF261655; Hs.8910; 1,2-alpha-mannosidase IC; blad; s.m.  
 435918; AF263538; Hs.86232; growth differentiation factor ; test; diag  
 435974; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.  
 436032; AA150797; Hs.109276; latexin protein; panc, angio; diag  
 436063; AK000028; Hs.356100; ribosomal protein S24; pros; diag  
 436120; AI248193; Hs.119860; ESTs; fibro; diag  
 436199; R38946; Hs.127951; hypothetical protein FLJ14503; renal; diag  
 436246; AW450963; Hs.119991; ESTs; blad; diag  
 436251; BE515065; Hs.296585; nucleolar protein (KKE/D repea; colon, test, blad; CTL+s.m.  
 436278; BE396290; Hs.5097; synaptogyrin 2; pros; mAb  
 436291; BE568452; Hs.344037; protein regulator of cytokines; lung, blad, headnk; diag  
 436293; AI601188; Hs.306201; ESTs; blad; diag  
 436302; AL355841; Hs.99330; hypothetical protein FLJ23588; lung; diag  
 436315; BE390513; Hs.27935; hypothetical protein MGC4837; mela; diag  
 436396; AI683487; Hs.152213; wingless-type MMTV integration; lung, headnk, pros, panc; diag  
 436420; AA443966; Hs.31595; ESTs; angio; mAb  
 436476; AA326108; Hs.33829; bHLH protein DEC2; panc; diag  
 436511; AA721252; Hs.291502; ESTs; lung; diag  
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; lung; diag  
 436569; BE439539; Hs.301961; glutathione S-transferase M2 (; blad; s.m.  
 436614; AW104388; Hs.149091; ESTs; mela; CTL+s.m.  
 436700; AI693690; Hs.301406; hypothetical protein PP3501; mela; mAb  
 436729; BE621807; Hs.351316; transmembrane 4 superfamily me; panc, colon, stom, ovar, lung, blad; mAb  
 436772; AW975688; Hs.348918; metallothionein 1E (functional; angio; diag  
 436775; AA731111; Hs.372225; ESTs; uter, ovar; diag  
 436839; AA767346; Hs.372277; ESTs; lung; diag  
 436856; AI469355; Hs.127310; ESTs; mela; diag  
 436954; AA740151; Hs.130425; ESTs; fibro, uter, ovar; diag  
 436972; AA284679; Hs.25640; claudin 3; ovar, lung, pros; mAb  
 437052; AA661697; Hs.120591; ESTs; pros; diag  
 437099; N77793; Hs.48659; ESTs, Highly similar to S14458; test; diag  
 437100; AI761073; Hs.14535; Homo sapiens cDNA: FLJ22314 fi; panc, renal; diag  
 437119; AI379921; Hs.177043; XP\_171387 similar to rhotekin; fibro; diag  
 437145; AF007216; Hs.5462; solute carrier family 4, sodiu; panc, pros, stom; mAb  
 437156; AI916600; Hs.121194; Homo sapiens cDNA: FLJ21569 fi; stom, renal, colon; diag  
 437181; AI306615; Hs.125343; ESTs, Weakly similar to KIAA07; blad; mAb+s.m.

- 437204; AL110216; Hs.355961; ESTs, Weakly similar to I55214; lung; CTL+s.m.  
 437212; AI765021; Hs.210775; ESTs; renal, uter, ovar; diag  
 437224; AL117628; Hs.97808; ESTs; test; diag  
 437259; AI377755; Hs.120695; ESTs; lung; diag  
 437267; AW511443; Hs.258110; ESTs; BPH; diag  
 437269; AA334384; Hs.149420; ESTs; angio; diag  
 437330; AL353944; Hs.50115; Homo sapiens mRNA; cDNA DKFZp7; sarc; diag  
 437381; NM\_003684; Hs.5591; MAP kinase-interacting serine; glio; CTL+s.m.  
 437390; AI125859; Hs.112607; ESTs; lung; diag  
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp5; lung; diag  
 437435; AA249439; Hs.27027; hypothetical protein DKFZp762H; lung; diag  
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L; test; CTL+s.m.  
 437478; AL390172; Hs.317432; branched chain aminotransferase; angio; s.m.  
 437553; AI829935; Hs.130497; ESTs, Weakly similar to MAT8\_H; blad; mAb  
 437571; AA760894; Hs.125350; ESTs; pros; diag  
 437623; D63880; Hs.5719; chromosome condensation-relate; test; diag  
 437740; AA810265; Hs.122915; ESTs; mela; diag  
 437802; AI475995; Hs.122910; ESTs; panc; diag  
 437862; AW978107; Hs.5884; Homo sapiens mRNA; cDNA DKFZp5; mela; CTL+s.m.  
 437908; AI082424; Hs.351043; ESTs; test; diag  
 437915; AI637993; Hs.202312; Homo sapiens clone N11 Ntera2D; lung, headnk, ovar, blad, uter; diag  
 437931; AI249468; Hs.124434; ESTs; blad; diag  
 437935; AW939591; Hs.5940; mucin 13, epithelial transmembr; colon, stom, uter, panc; mAb+s.m.  
 437938; AI950087; Hs.369628; gb:wq05c02.x1 NCI\_CGAP\_Kid12 H; renal, ovar, uter, cerv, blad; diag  
 437939; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.  
 437960; AI669586; Hs.369312; ESTs; uter, ovar; diag  
 438167; R28363; Hs.24286; chemokine binding protein 2 (C; ovar, breast, uter; mAb  
 438199; AW016531; Hs.122147; hypothetical protein FLJ13189; breast; diag  
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nucl; mela; mAb+s.m.  
 438233; W52448; Hs.56147; ESTs; pros, cerv; diag  
 438274; AI918906; Hs.55080; ESTs; headnk; diag  
 438403; AA806607; Hs.292206; ESTs; lung; mAb  
 438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.  
 438450; AI050866; Hs.65853; nodal, mouse, homolog; test; diag  
 438456; AA913381; Hs.279763; ESTs; test; diag  
 438552; AJ245820; Hs.6314; type I transmembrane receptor; pros, ovar; diag  
 438670; AI275803; Hs.123428; ESTs; fibro; CTL+s.m.  
 438702; AI879064; Hs.7164; ESTs; lung; diag  
 438707; L08239; Hs.5326; amino acid system N transporte; ovar; mAb  
 438746; AI885815; Hs.184727; Human melanoma-associated anti; panc, blad, mela, ovar; mAb+CTL  
 438817; AI023799; Hs.163242; ESTs; ovar, uter, blad, renal; diag  
 438859; AI559626; Hs.93522; Homo sapiens mRNA for KIAA1647; renal; diag  
 438866; U44385; Hs.6441; tissue inhibitor of metallopro; mela; diag  
 438873; AI302471; Hs.124292; Homo sapiens cDNA: FLJ23123 fi; fibro; diag  
 438898; AI819863; Hs.106243; ESTs; lung; diag  
 438915; AA280174; Hs.355711; Williams-Beuren syndrome chrom; lung, test, mela; diag  
 438929; AW195515; Hs.253177; ESTs; renal; diag  
 438956; W00847; Hs.135056; Human DNA sequence from clone; lung; diag  
 438966; AW979074; ; gb:EST391184 MAGE resequences.; renal; diag  
 438983; AF085884; Hs.20029; proacrosin binding protein sp3; test; CTL+s.m.  
 438993; AA828995; ; gb:od77b08.s1 NCI\_CGAP\_Ov2 Hom; ovar; mAb+s.m.  
 439053; BE244588; Hs.6456; chaperonin containing TCP1, su; test; diag  
 439092; AA830149; ; gb:oc44f08.s1 NCI\_CGAP\_GCB1 Ho; pros; diag  
 439176; AI446444; Hs.190394; ESTs, Weakly similar to B28096; pros; diag  
 439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic; breast, ovar, uter, pros, blad, panc, colon, fibro, mela; mAb  
 439221; AA737106; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.  
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582; mela, fibro; diag  
 439239; AI031540; Hs.235331; ESTs; blad; diag  
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag  
 439310; AF086120; Hs.102793; ESTs; mela; diag  
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; colon, breast, ovar, uter, cerv, pros, lung, headnk, blad, mela; mAb+s.m.  
 439335; AA742697; Hs.62492; NM\_052863; Homo sapiens secreto; fibro, uter; diag  
 439366; AF100143; Hs.6540; fibroblast growth factor 13; pros; CTL+s.m.  
 439382; BE247684; Hs.103070; ESTs; angio; diag  
 439394; AA149250; Hs.56105; ESTs; lung; diag  
 439410; AA632012; Hs.188746; ESTs; angio; diag  
 439453; BE264974; Hs.6566; thyroid hormone receptor inter; lung, esoph, ovar; mAb+s.m.  
 439496; BE616501; Hs.32343; Homo sapiens, Similar to RIKEN; mela, esoph; diag  
 439559; AW970780; Hs.59483; leucine-rich repeat-containing; ovar, stom, mela, colon; mAb  
 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog; ovar, uter; mAb  
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC0048; lung, headnk, cerv; diag  
 439702; AW085525; Hs.55964; ESTs; mela; diag  
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1\_H; ovar, lung, headnk; diag  
 439735; AI635386; Hs.142846; hypothetical protein; pros; diag  
 439737; AI751438; Hs.41271; Homo sapiens mRNA full length; panc; diag  
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length; panc, fibro, breast; diag  
 439755; AW748482; Hs.77873; B7 homolog 3; sarc; mAb  
 439759; AL359055; Hs.67709; Homo sapiens mRNA full length; colon, stom, panc, leuk, lung; diag  
 439778; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.  
 439780; AL109688; ; gb:Homo sapiens mRNA full leng; blad, esoph; diag  
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length; ovar, uter, cerv, breast, pros; diag  
 439864; AI720078; Hs.291997; ESTs, Weakly similar to A47582; test; diag  
 439867; AA847510; Hs.161292; ESTs; panc; diag

- 439920; H05430; Hs.288433; neurotrimin; panc; mAb+diag  
 439926; AW014875; Hs.137007; ESTs; blad, esoph, lung, cerv; diag  
 439963; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.  
 440042; A1073387; Hs.133898; ESTs; ovar; CTL+s.m.  
 440086; NM\_005402; Hs.6906; v-rat simian leukemia viral on; angio; diag  
 440099; AL080058; Hs.6909; DKFZP564G202 protein; panc; diag  
 440119; AA865455; Hs.125331; ESTs, Moderately similar to un; test; diag  
 440138; AB033023; Hs.318127; hypothetical protein FLJ10201; lung; CTL+s.m.  
 440151; AA868167; ; gb:ak38e07.s1 Soares\_testis\_NH; sarc; diag  
 440207; A1371978; Hs.128326; ESTs; test; diag  
 440209; H05049; Hs.247837; neurexin 3; fibro; diag  
 440210; AW674562; Hs.122128; ESTs; glio; diag  
 440225; BE295782; Hs.159; tumor necrosis factor receptor; glio; mAb  
 440238; AW451970; Hs.155644; paired box gene 2; ovar; diag  
 440260; A1972867; Hs.7130; copine IV; pros; diag  
 440273; A1805392; Hs.325335; Homo sapiens cDNA: FLJ23523 fi; lung, fibro; diag  
 440274; R24595; Hs.7122; scrapie responsive protein 1; sarc; diag  
 440311; A1733079; Hs.125407; ESTs, Moderately similar to AL; renal; diag  
 440325; NM\_003812; Hs.7164; a disintegrin and metalloprote; lung; mAb  
 440333; A1378424; Hs.288761; hypothetical protein FLJ21749; pros; CTL+s.m.  
 440449; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag  
 440452; A1925136; Hs.55150; ESTs, Weakly similar to CAYP\_H; fibro; diag  
 440457; BE387593; Hs.21321; Homo sapiens clone FLB9213 PRO; mela; diag  
 440484; BE328156; Hs.150356; ESTs; panc; diag  
 440529; AW207640; Hs.16478; Homo sapiens cDNA: FLJ21718 fi; pros; diag  
 440659; AF134160; Hs.7327; claudin 1; lung; mAb  
 440704; M69241; Hs.162; insulin-like growth factor bin; lung, glio, ovar; diag  
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN; test; diag  
 440801; AA906366; Hs.370038; ESTs; pros; diag  
 440819; A1809444; Hs.202108; ESTs; pros; diag  
 440901; AA909358; Hs.128612; ESTs; ovar; pros; diag  
 440943; AW082298; Hs.146161; hypothetical protein MGC2408; lung; diag  
 440983; M20681; Hs.7594; solute carrier family 2 (facil; test; mAb  
 441020; W79283; Hs.35962; ESTs; lung, panc; diag  
 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; lung, panc, colon; CTL+s.m.  
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis; panc, ovar, stom, uter, lung; diag  
 441134; W29092; Hs.346950; cellular retinoic acid-binding; sarc; diag  
 441247; AW118681; Hs.128051; Homo sapiens thymic stromal ly; pros; diag  
 441321; H17182; Hs.7771; B-cell associated protein; test; diag  
 441345; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag  
 441350; AB020690; Hs.7782; paraneoplastic antigen MA2; panc; mAb+CTL  
 441377; BE218239; Hs.202656; ESTs; uter, endo, lung; diag  
 441384; AA447849; Hs.288660; retinoic acid induced 3; ovar; mAb+s.m.  
 441392; AW451831; Hs.222119; ESTs, Weakly similar to S30433; renal; diag  
 441457; AW996651; Hs.43838; ESTs; angio; diag  
 441495; AW294603; Hs.127039; ESTs; blad; diag  
 441525; AW241867; Hs.127728; ESTs; lung; diag  
 441553; AA281219; Hs.121296; ESTs; lung, test, ovar; CTL+s.m.  
 441633; AW958544; Hs.112242; normal mucosa of esophagus spe; blad, lung, cerv, headnk, colon, panc; diag  
 441790; AW294909; Hs.132208; ESTs; lung; diag  
 441801; AW242799; Hs.86366; ESTs; blad; diag  
 441835; AB036432; Hs.184; advanced glycosylation end pro; fibro; mAb  
 441859; AW194364; Hs.380444; interleukin-4 induced gene-1 p; ovar, mela, fibro; mAb  
 441878; A1801869; Hs.127982; ESTs; test; diag  
 442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482; fibro, angio; CTL+s.m.  
 442082; R41823; Hs.7413; calyntenin-2; breast, pros, ovar; diag  
 442104; L20971; Hs.188; phosphodiesterase 4B, cAMP-spe; angio; CTL+s.m.  
 442108; AW452649; Hs.343259; ESTs; lung; diag  
 442242; AV647908; Hs.90424; Homo sapiens cDNA: FLJ23285 fi; BPH; diag  
 442323; AW016669; Hs.29190; ESTs; breast; diag  
 442333; A1650877; Hs.129302; ESTs; test; diag  
 442432; BE093589; Hs.38178; hypothetical protein FLJ23468; blad, lung, panc, esoph, mela; CTL+s.m.  
 442438; AA995998; Hs.370007; gb:os26b03.s1 NCI\_CGAP\_Kid5 Ho; uter, ovar, renal; diag  
 442441; A1820662; Hs.129598; ESTs; breast; diag  
 442503; AF147078; Hs.375031; p53-responsive gene 5; mela; diag  
 442506; BE566411; Hs.41726; ESTs; angio; diag  
 442573; H93366; Hs.7567; branched chain aminotransferas; ovar, panc, angio, test; s.m.  
 442577; AA292998; Hs.163900; ESTs; blad, panc, colon, stom, ovar; diag  
 442580; A1733682; Hs.130239; ESTs; breast; diag  
 442609; AL020996; Hs.8518; selenoprotein N; mela; diag  
 442613; A1004002; Hs.130522; Kv channel-interacting protein; glio; diag  
 442622; NM\_000435; Hs.8546; Notch (Drosophila) homolog 3; ovar; mAb  
 442711; AF151073; Hs.8645; hypothetical protein; angio, mela, sarc; diag  
 442739; NM\_007274; Hs.8679; cytosolic acyl coenzyme A thio; mela; s.m.  
 442757; A1739528; Hs.28345; ESTs; mela; diag  
 442818; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag  
 442821; BE391929; Hs.8752; transmembrane protein 4; ovar; diag  
 442832; AW206560; Hs.253569; ESTs; pros, fibro; diag  
 442896; R37725; Hs.283093; ESTs; panc; diag  
 442994; A1026718; Hs.16954; ESTs; blad, fibro; diag  
 443054; A1745185; Hs.84520; yes-associated protein 65 kDa; blad; diag  
 443162; T49951; Hs.9029; DKFZP434G032 protein; blad, lung; CTL+s.m.  
 443171; BE281128; Hs.9030; TONDU; blad, ovar; diag

- 443184; AI638728; Hs.135159; ESTs; sarc; diag  
 443211; AI128388; Hs.143655; ESTs; blad, ovar, lung, headnk, stom, colon; diag  
 443216; W80487; Hs.324521; hypothetical protein DC50; test; diag  
 443257; AI334040; Hs.11614; HSPC065 protein; fibro; CTL+s.m.  
 443400; R28424; Hs.250648; ESTs; lung; diag  
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; test; CTL+s.m.  
 443537; D13305; Hs.203; cholecystokinin B receptor; test; mAb  
 443648; AI085377; Hs.143610; ESTs; lung, headnk; diag  
 443709; AI082692; Hs.134662; ESTs; fibro; diag  
 443715; AI583187; Hs.9700; cyclin E1; lung, stom, ovar, colon; CTL+s.m.  
 443785; AW449952; Hs.190125; basic-helix-loop-helix-PAS pro; glio, uter, ovar; CTL+s.m.  
 443802; AW504924; Hs.9805; KIAA1291 protein; sarc; diag  
 443883; AA114212; Hs.9930; serine (or cysteine) proteinase; sarc; s.m.  
 443885; H91806; Hs.15284; ESTs; mela; diag  
 443892; AI889572; Hs.246875; ESTs; lung; diag  
 443950; NM\_001425; Hs.9999; epithelial membrane protein 3; mela; mAb  
 443968; AA287702; Hs.10031; KIAA0955 protein; angio; diag  
 443983; H04482; Hs.163724; ESTs; mela; mAb  
 443991; NM\_002250; Hs.10082; potassium intermediate/small c; pros, colon, uter; mAb  
 444009; AI380792; Hs.135104; ESTs; angio; diag  
 444151; AW972917; Hs.128749; alpha-methylacyl-CoA racemase; pros; mAb  
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like ; test; CTL+s.m.  
 444163; AI126098; ; FGENESH predicted RNaseH domain; blad; s.m.  
 444301; AK000136; Hs.10760; asporin (LRR class 1); panc; diag  
 444325; AW152618; Hs.16757; ESTs; esoph; diag  
 444330; AI597655; Hs.49265; ESTs; angio; diag  
 444342; NM\_014398; Hs.10887; similar to lysosome-associated; hepC, lung, fibro, blad, esoph; diag  
 444378; R41339; Hs.47860; neurotrophic tyrosine kinase, ; lung, glio; mAb+s.m.  
 444409; AI792140; Hs.49265; ESTs; angio; diag  
 444444; AI149332; Hs.14855; ESTs; blad; diag  
 444471; AB020684; Hs.11217; KIAA0877 protein; glio, lung, colon ; mAb  
 444476; AF020038; Hs.11223; isocitrate dehydrogenase 1 (NA; blad; s.m.  
 444484; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag  
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ovar, uter, breast, cerv, blad, headnk; mAb  
 444649; AW207523; Hs.371001; ESTs; blad; diag  
 444670; H58373; Hs.332938; hypothetical protein MGC5370; sarc; diag  
 444754; T83911; Hs.11881; transmembrane 4 superfamily me; panc, omuc, stom, lung, colon; mAb+s.m.  
 444809; BE207568; Hs.208219; ocuolspanin; mela; mAb  
 444823; BE262989; Hs.12045; putative protein; test; diag  
 444863; AW384082; Hs.104879; serine (or cysteine) proteinase; mela; s.m.  
 444895; AI674383; Hs.22891; solute carrier family 7 (catio; ovar; mAb+s.m.  
 444995; AJ272265; Hs.12230; secreted phosphoprotein 2, 24k; hepC, panc; diag  
 445019; AI205540; Hs.281295; ESTs; headnk, lung, colon; diag  
 445070; NM\_000677; Hs.258; adenosine A3 receptor; glio, renal; mAb  
 445076; AI206888; Hs.154131; ESTs; test; diag  
 445084; H38914; Hs.250848; hypothetical protein FLJ14761; sarc; mAb  
 445093; AI207197; Hs.156905; ESTs; test; diag  
 445109; AF039916; Hs.12330; ectonucleoside triphosphate di; pros; s.m.  
 445119; AF035121; Hs.12337; kinase insert domain receptor ; angio; mAb  
 445160; AI299144; Hs.101937; sine oculis homeobox (Drosophi; sarc; CTL+s.m.  
 445182; AW189787; Hs.361778; ESTs; blad; diag  
 445247; AW274290; Hs.153997; ESTs; mela; diag  
 445279; R41900; Hs.22245; ESTs; angio; diag  
 445363; NM\_005993; Hs.12570; tubulin-specific chaperone d; test; diag  
 445413; AA151342; Hs.12677; CGI-147 protein; pros, colon, uter, ovar, lung, panc ; diag  
 445418; AW139377; Hs.127179; cryptic gene; panc; diag  
 445424; AB028945; Hs.12696; cortactin SH3 domain-binding p; pros ; diag  
 445443; AV653838; Hs.295131; ESTs; lung; diag  
 445654; X91247; Hs.13046; thioredoxin reductase 1; lung; s.m.  
 445684; AK001696; Hs.13109; Ran binding protein 11; angio; diag  
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; angio; CTL+s.m.  
 445784; AI253155; Hs.146065; ESTs; mela; CTL+s.m.  
 445885; AI734009; Hs.127699; KIAA1603 protein; pros, fibro; diag  
 445900; AF070526; Hs.125036; Homo sapiens clone 24787 mRNA ; renal, leuk; mAb  
 445911; AI985987; Hs.145645; ESTs, Moderately similar to AL; blad; diag  
 445982; BE410233; Hs.13501; pescadillo (zebrafish) homolog; mela; diag  
 446057; AI420227; Hs.366053; Trp-p8 transient receptor pote; pros; mAb  
 446082; AI274139; Hs.156452; ESTs; blad; diag  
 446098; AW072215; Hs.208470; ESTs; angio; diag  
 446100; AW967109; Hs.13804; hypothetical protein DJ462023; pros; diag  
 446102; AW168067; Hs.317694; ESTs; lung; diag  
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083; test; mAb  
 446269; AW263155; Hs.14559; hypothetical protein FLJ10540; lung, headnk; CTL+s.m.  
 446291; BE397753; Hs.14623; interferon, gamma-inducible p; mela; diag  
 446292; AF081497; Hs.279682; Rh type C glycoprotein; lung, cerv; mAb  
 446293; AI420213; Hs.149722; LIM domain transcription facto; ovar, test; diag  
 446320; AF126245; Hs.14791; acyl-Coenzyme A dehydrogenase ; pros; s.m.  
 446332; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag  
 446342; BE298665; Hs.14846; solute carrier family 7 (catio; uter, colon, pros, mela; mAb  
 446428; AW082270; Hs.12496; ESTs, Weakly similar to ALU4\_H; fibro; diag  
 446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); lung, test; diag  
 446608; N75217; Hs.175622; ESTs; uter, fibro; diag  
 446626; AW292180; Hs.156142; ESTs; pros; diag

- 446636; AC002563; Hs.15767; citron (rho-interacting, serin; lung; CTL+s.m.  
 446644; NM\_003272; Hs.21065; transmembrane 7 superfamily me; mela; mAb  
 446673; NM\_016361; Hs.15871; LPAP for lysophosphatidic acid; blad; diag  
 446727; AB011095; Hs.16032; KIAA0523 protein; angio; CTL+s.m.  
 5 446733; AA863360; Hs.26040; ESTs, Weakly similar to fatty ; breast; s.m.  
 446755; AW451473; Hs.16134; serine/threonine kinase 10; mela; CTL+s.m.  
 446791; A1632278; Hs.195922; ESTs; test; diag  
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil re; test; diag  
 10 446856; A1814373; Hs.164175; ESTs; lung; diag  
 446868; AV660737; Hs.348297; ESTs; panc; diag  
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G; lung; mAb  
 446932; AA961459; Hs.125644; ESTs; fibro; diag  
 446967; A1699629; Hs.156781; ESTs; fibro; diag  
 15 446979; A1654443; Hs.197683; ESTs; test; diag  
 446984; AB020722; Hs.16714; Rho guanine exchange factor (G; angio; CTL+s.m.  
 446989; AK001898; Hs.16740; hypothetical protein FLJ11036; lung, headnk; diag  
 446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; panc, fibro; diag  
 446999; AA151520; Hs.351416; hypothetical protein MGC4485; headnk; diag  
 20 447004; AW296968; Hs.157539; FGENESH predicted secreted pro; glio; diag  
 447078; AW885727; Hs.9914; ESTs; lung; diag  
 447126; AW150632; Hs.170307; Rat guanine nucleotide exchang; angio; diag  
 447164; AF026941; Hs.17518; vipirin; similar to inflammat; colon, lung, breast, stom, hepC, esoph, mela; diag  
 447178; AW594641; Hs.192417; ESTs; mela; diag  
 25 447188; H65423; Hs.17631; hypothetical protein DKFZp434E; test; diag  
 447210; AF035269; Hs.17752; phosphatidylserine-specific ph; pros, mela; s.m.  
 447289; AW247017; Hs.36978; melanoma antigen, family A, 3; lung, mela; mAb+CTL  
 447334; AA515032; Hs.91109; ESTs; blad; diag  
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392; lung, blad, panc, headnk, mela; mAb+s.m.  
 30 447350; A1375572; Hs.172634; v-erb-a avian erythroblastic l; breast, ovar, uter; diag  
 447377; X77343; Hs.334334; transcription factor AP-2 alpha; breast, lung, mela; CTL+s.m.  
 447395; A1418412; Hs.184793; Homo sapiens cDNA: FLJ21880 fi; panc; diag  
 447437; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb  
 447499; AW262580; Hs.147674; protocadherin beta 16; pros, glio, ovar ; mAb+s.m.  
 35 447532; AK000614; Hs.18791; hypothetical protein FLJ20607; lung, blad; CTL+s.m.  
 447534; AW953935; Hs.288655; ESTs; lung, test; diag  
 447578; AA912347; Hs.136585; ESTs, Weakly similar to JC5314; ovar; s.m.  
 447595; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.  
 447604; AW089933; Hs.301342; hypothetical protein MGC4342; mela; diag  
 447636; Y10043; Hs.19114; high-mobility group (nonhiston; lung; CTL+s.m.  
 40 447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient; test; diag  
 447749; T53260; Hs.8297; ESTs; renal; diag  
 447761; AF061573; Hs.19492; protocadherin 8; EWS; glio; mAb  
 447768; X86400; Hs.19520; FXFD domain-containing ion tra; renal; mAb  
 447818; W79940; Hs.355279; Homo sapiens clone 24670 mRNA ; renal; diag  
 45 447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022; renal, ovar, uter; diag  
 447881; BE620886; Hs.355279; GCN1 (general control of amino; renal; diag  
 447937; AL109716; Hs.20034; Homo sapiens mRNA full length ; mela; mAb  
 447993; AW139525; Hs.170362; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.  
 50 448030; N30714; Hs.325960; membrane-spanning 4-domains, s; panc, leuk, renal, stom lung; mAb  
 448045; AJ297436; Hs.20166; prostate stem cell antigen; blad, panc, pros; mAb  
 448105; AW591433; Hs.298241; Transmembrane protease, serine; breast, panc, colon, lung, ovar, stom; mAb+diag+s.m.  
 448133; AA723157; Hs.73769; folate receptor 1 (adult); ovar, fibro; mAb  
 448140; AF146761; Hs.20450; BCM-like membrane protein prec; fibro, mela, leuk; mAb  
 55 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase.; test; CTL+s.m.  
 448181; AF272833; Hs.279763; hypothetical protein FLJ10504; test; diag  
 448204; A1475124; Hs.170561; ESTs; sarc; diag  
 448231; A1701916; Hs.202509; ESTs; angio; diag  
 448258; BE386983; Hs.343214; hypothetical protein FLJ20396; mela, ovar; mAb  
 60 448262; AW880830; Hs.186273; ESTs; blad; diag  
 448275; BE514434; Hs.20830; kinesin-like 2; ovar, esoph, mela; diag  
 448278; W07369; Hs.11782; ESTs; lung; diag  
 448290; AK002107; Hs.20843; Homo sapiens cDNA FLJ11245 fis; pros; diag  
 448321; NM\_005883; Hs.20912; adenomatous polyposis coli lik; glio; CTL+s.m.  
 65 448357; N20169; Hs.108923; RAB38, member RAS oncogene fam; lung, mela; diag  
 448410; AK000227; Hs.21126; hypothetical protein FLJ20220; mela; diag  
 448437; AW470125; Hs.220529; gb:wx60c04.x1 NCI\_CGAP\_Pan1 Ho; panc, colon; diag  
 448499; BE613280; Hs.77550; p53-regulated DDA3; glio; diag  
 448569; BE382657; Hs.21486; signal transducer and activato; panc, headnk, fibro, cerv, mela, renal; CTL+s.m.  
 70 448588; A1970276; Hs.156905; KIAA1676; test; CTL+s.m.  
 448595; AB014544; Hs.21572; KIAA0644 gene product; breast, glio; mAb  
 448664; A1879317; Hs.334691; splicing factor 3a, subunit 1.; mela; CTL+s.m.  
 448674; W31178; Hs.154140; ovary-specific acidic protein; angio; diag  
 448692; AW013907; Hs.167531; methylcrotonoyl-Coenzyme A car; pros, pros; s.m.  
 448706; AW291095; Hs.21814; interleukin 20 receptor, alpha; pros, uter, blad, colon; mAb  
 75 448719; AA033627; Hs.21858; trinucleotide repeat containin; mela, sarc; CTL+diag  
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate ) ; test; diag  
 448811; A1590371; Hs.199460; ESTs; esoph, panc; mAb  
 448939; BE267795; Hs.22595; hypothetical protein FLJ10637; test; CTL+s.m.  
 448966; AW372914; Hs.86149; phosphoinositol 3-phosphate-bi; mela; CTL+s.m.  
 80 448981; A1968719; Hs.195387; ESTs; test; diag  
 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros, cerv, colon, lung, stom, blad, headnk, ovar, breast; mAb  
 448993; A1471630; Hs.355952; KIAA0144 gene product; lung, blad; diag  
 448999; AF179274; Hs.22791; transmembrane protein with EGF; pros, glio ; mAb

- 5 449003; X76342; Hs.389; alcohol dehydrogenase 7 (class; lung, headnk; s.m.  
449019; A1949095; Hs.67776; ESTs, Weakly similar to T22341; blad, lung; diag  
449027; AJ271216; Hs.22880; dipeptidylpeptidase III; blad, colon, ovar; s.m.  
449040; NM\_012191; Hs.22919; putative tumor suppressor; lung; CTL+s.m.  
449078; AK001256; Hs.22975; KIAA1576 protein; mela; diag  
449101; AA205847; Hs.23016; G protein-coupled receptor; lung, headnk; mAb  
449109; AW270992; Hs.120949; ESTs, Weakly similar to ALU7\_H; sarc; diag  
449156; AF103907; Hs.171353; prostate cancer antigen 3, non; pros; mAb+CTL  
10 449207; AL044222; Hs.23255; nucleoporin 155kD; lung; diag  
449228; AJ403107; Hs.148590; protein related with psoriasis; lung; diag  
449230; BE613348; Hs.356392; melanoma cell adhesion molecule; lung, cerv, headnk, blad, ovar, colon; mAb  
449317; AW293413; Hs.132906; 19A24 protein; mela; mAb  
449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN; headnk, lung, angio; CTL+s.m.  
15 449322; A1638616; Hs.196566; ESTs; test; diag  
449338; H73444; Hs.394; adrenomedullin; renal; diag  
449394; AA004368; Hs.18160; Homo sapiens cDNA FLJ11550 fis; angio; mAb  
449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fi; test; diag  
449448; D60730; Hs.57471; ESTs; blad, lung, headnk, breast; diag  
449467; AW205006; Hs.197042; ESTs; lung; diag  
20 449494; AW237014; Hs.315369; aquaporin 4; fibro; diag  
449569; A1656634; Hs.195389; ESTs; test; diag  
449592; A1655494; Hs.195718; ESTs; panc; diag  
449618; A1076459; Hs.15978; KIAA1272 protein; angio; diag  
25 449625; NM\_014253; Hs.349094; odz (odd Oz/ten-m, Drosophila); pros; diag  
449650; AF055575; Hs.23838; calcium channel, voltage-depen; pros; mAb  
449680; A1033821; Hs.12160; ESTs; renal; diag  
449691; AW265634; Hs.133100; ESTs; glio, esoph, lung, blad ; diag  
449697; H06350; Hs.135056; Human DNA sequence from clone ; lung; diag  
30 450096; A1682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL  
450098; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag  
450149; AW969781; Hs.132863; Zic family member 2 (odd-paire; sarc; CTL+s.m.  
450152; A1138635; Hs.22968; intron of VEGFR; renal; diag  
450377; AB033091; Hs.355925; KIAA1265 protein; ovar, colon; diag  
35 450382; AA397658; Hs.60257; Homo sapiens cDNA FLJ13598 fis; pros; diag  
450400; A1694722; Hs.279744; ESTs; panc; diag  
450431; AW136797; Hs.266041; ESTs; test; diag  
450451; AW591528; Hs.202072; ESTs; uter, endo; diag  
450506; NM\_004460; Hs.418; fibroblast activation protein.; panc, esoph; diag  
40 450534; A1570189; Hs.25132; KIAA0470 gene product; angio; CTL+s.m.  
450581; AF081513; Hs.25195; TGF-beta 4; uter, cerv, test; diag  
450635; AW403954; Hs.25237; mesenchymal stem cell protein ; blad; mAb  
450642; R39773; Hs.7130; copine IV; pros; diag  
450656; AA010539; Hs.18912; unnamed protein product; fibro, uter; CTL+s.m.  
45 450663; H43540; Hs.25292; ribonuclease H1, large subunit; mela; s.m.  
450676; A1147155; Hs.279727; ESTs; sarc; diag  
450684; AA872605; Hs.25333; interleukin 1 receptor, type I; blad, lung, headnk; mAb  
450690; AA296696; Hs.333418; FXFD domain-containing ion tra; mela; diag  
450693; AW450461; Hs.203965; ESTs; pros, uter; diag  
50 450719; A1096837; Hs.21349; ESTs, Weakly similar to RB8B\_H; test; diag  
450737; AW007152; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.  
450785; AA852713; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.  
450832; AW970602; Hs.105421; ESTs; lung; diag  
451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN; pros, uter, glio; diag  
55 451035; AU076785; Hs.430; plastin 1 (I isoform); panc; diag  
451050; AW937420; Hs.351869; ESTs; mela; diag  
451099; R52795; Hs.25954; interleukin 13 receptor, alpha; glio, fibro, mela; mAb  
451106; BE382701; Hs.25960; N-MYC oncogene; test, ovar; CTL+s.m.  
451110; A1955040; Hs.265398; PAR-6 beta (partitioning def; breast, ovar, lung, colon; CTL+s.m.  
60 451181; A1796330; Hs.207461; ESTs; panc; diag  
451253; H48299; Hs.26126; claudin 10; lung, ovar, panc; mAb  
451291; R39288; Hs.6702; ESTs; lung; diag  
451295; A1557212; Hs.17132; ESTs, Moderately similar to I5; panc; diag  
451320; AW118072; Hs.350251; diacylglycerol kinase, zeta (1; lung; s.m.  
65 451346; NM\_006338; Hs.26312; glioma amplified on chromosome; ovar; mAb  
451386; AB029006; Hs.26334; spastic paraplegia 4 (autosoma; lung; diag  
451398; A1793124; Hs.144479; ESTs; breast, ovar; diag  
451411; AA017492; Hs.135655; EST; pros; diag  
451497; H83294; Hs.284122; Wnt inhibitory factor-1; uter, fibro, pros, colon, sarc; diag  
70 451541; BE279383; Hs.26557; plakophilin 3; lung, blad, ovar; diag  
451592; A1805416; Hs.213897; ESTs; lung, headnk; diag  
451635; AA018899; Hs.127179; cryptic gene; panc; diag  
451663; A1872360; Hs.209293; ESTs; pros; diag  
451720; AW970985; Hs.290853; ESTs; pros; diag  
451743; AW074266; Hs.336428; ESTs; lung; diag  
75 451820; AW058357; Hs.199248; ESTs; panc; mAb  
451844; T61430; ; gb:yc06a03.s1 Stratogene lung ; blad; diag  
451982; F13036; Hs.27373; Homo sapiens mRNA; cDNA DKFZp5; pros, blad; mAb  
451999; AW176401; Hs.380623; DEAD/H (Asp-Glu-Ala-Asp/His) b; test; CTL+s.m.  
80 452046; AB018345; Hs.27657; KIAA0802 protein; lung, uter; CTL+s.m.  
452208; AA024792; Hs.31895; hypothetical protein MGC4093; renal; diag  
452240; A1591147; Hs.61232; ESTs; blad, lung, headnk, panc, cerv; diag  
452243; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag  
452244; N33530; Hs.176674; ESTs; mela; diag



- 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S; test; CTL+s.m.  
 452295; BE379936; Hs.28866; programmed cell death 10; lung; diag  
 452298; AI039243; Hs.278585; ESTs; angio; diag  
 452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590; lung, panc, blad, stom, esoph, fibro, colon; s.m.  
 452316; AA298484; Hs.61265; ESTs, Moderately similar to G7; blad; diag  
 452340; NM\_002202; Hs.505; ISL1 transcription factor, LIM; panc, pros; CTL+s.m.  
 452353; C18825; Hs.29191; epithelial membrane protein 2; pros, breast; mAb  
 452355; N54926; Hs.29202; G protein-coupled receptor 34; glio, fibro, panc; mAb  
 452367; U71207; Hs.29279; eyes absent (Drosophila) homolog; lung, pros, ovar, uter; CTL+s.m.  
 452416; AA026115; Hs.114777; ESTs; fibro; diag  
 452461; N78223; Hs.108106; transcription factor; blad, lung, headnk, ovar, glio, stom, colon, cerv; CTL+s.m.  
 452571; W31518; Hs.34665; ESTs; stom, lung, panc, colon, fibro; diag  
 452594; AU076405; Hs.29981; solute carrier family 26 (sulf); ovar; mAb  
 452613; AA461599; Hs.23459; ESTs; lung; diag  
 452679; Z42387; Hs.83883; transmembrane, prostate androg; pros, colon, panc, pros; mAb  
 452705; H49805; Hs.246005; ESTs; panc; diag  
 452717; AW160399; Hs.30376; hypothetical protein; pros; diag  
 452721; AJ269529; Hs.301871; solute carrier family 37 (glyc); pros; mAb  
 452732; BE300078; Hs.80449; Homo sapiens, clone IMAGE:3535; blad; diag  
 452744; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; mela; diag  
 452792; AB037765; Hs.30652; KIAA1344 protein; pros, uter, breast; diag  
 452795; AW392555; Hs.18878; hypothetical protein FLJ21620; renal, headnk, colon, lung, panc; CTL  
 452796; AB011100; Hs.30656; KIAA0528 gene product; test; diag  
 452833; BE559681; Hs.30736; KIAA0124 protein; lung, mela; CTL+s.m.  
 452865; AI924046; Hs.119567; ESTs, Weakly similar to A47582; lung; diag  
 452899; M96739; Hs.30956; nescent helix loop helix 1; sarc; CTL+s.m.  
 452924; AW580939; Hs.97199; complement component C1q recep; angio; diag  
 452933; AW391423; Hs.288555; Homo sapiens cDNA: FLJ22425 fi; angio; CTL+s.m.  
 452934; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag  
 452955; AW390282; Hs.31130; transmembrane 7 superfamily me; pros; mAb+s.m.  
 453006; AI362575; Hs.303171; ESTs; pros; diag  
 453028; AB006532; Hs.31442; RecQ protein-like 4; blad, lung, test; CTL+s.m.  
 453085; AW954243; Hs.351573; KIAA0251 protein; angio; diag  
 453096; AW294631; Hs.351270; ESTs; pros; diag  
 453102; NM\_007197; Hs.31664; frizzled (Drosophila) homolog; lung, headnk, colon; mAb  
 453107; NM\_016113; Hs.279746; vanilloid receptor-like protei; mela; mAb  
 453134; AA032211; Hs.118493; ESTs; blad; diag  
 453142; AA033648; Hs.7473; Homo sapiens gap junction prot; fibro; mAb  
 453160; AI263307; Hs.356901; H2B histone family, member L; lung, panc, pros; diag  
 453210; AL133161; Hs.32360; hypothetical protein FLJ10867; lung; CTL+s.m.  
 453216; AL137566; Hs.32405; progesterone receptor (PR); blad; mAb+s.m.  
 453256; AI565587; Hs.32556; KIAA0379 protein; mela; diag  
 453310; X70697; Hs.553; solute carrier family 6 (neuro; fibro; mAb  
 453321; AI984381; Hs.232521; ESTs; blad; diag  
 453323; AF034102; Hs.32951; solute carrier family 29 (nucl; ovar; CTL+s.m.  
 453331; AI240665; Hs.352537; ESTs; breast, lung, panc, esoph; mAb+diag+s.m.  
 453344; BE349075; Hs.44571; ESTs; mela; diag  
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; test; CTL+s.m.  
 453365; AA035211; Hs.17404; SOX7 SRY (sex determining regi; angio, blad; CTL+s.m.  
 453370; AI470523; Hs.139336; ATP-binding cassette, sub-fami; pros; mAb  
 453389; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; renal, ovar, blad; mAb+s.m.  
 453392; U23752; Hs.32964; SRY (sex determining region Y); ovar, lung, glio, sarc; CTL+s.m.  
 453459; BE047032; Hs.257789; ESTs; ovar, cerv, blad, uter, panc, angio, lung; diag  
 453464; AI884911; Hs.32989; receptor (calcitonin) activity; pros; mAb  
 453633; AA357001; Hs.34045; hypothetical protein FLJ20764; lung, esoph, test; diag  
 453637; NM\_002589; Hs.34073; BH-protocadherin (brain-heart); headnk; mAb  
 453642; AI370936; Hs.34074; dipeptidylpeptidase VI; glio; mAb  
 453779; N35187; Hs.43388; 28kD interferon responsive pro; mela; diag  
 453789; AA628517; Hs.118502; ESTs; angio; diag  
 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1; glio, lung, uter, headnk, cerv, panc, pros, sarc; mAb  
 453883; AI638516; Hs.347524; cofactor required for Sp1 tran; blad, lung; diag  
 453884; AA355925; Hs.36232; KIAA0186 gene product; lung, ovar, test, esoph; diag  
 453912; AL121031; Hs.356843; SWI/SNF related, matrix associ; mela; diag  
 453922; AF053306; Hs.36708; budding uninhibited by benzimid; colon, stom, lung, test; CTL+s.m.  
 453935; AI633770; Hs.42572; ESTs; panc; diag  
 453941; U39817; Hs.36820; Bloom syndrome; lung, cerv, headnk; CTL+s.m.  
 453964; AI961486; Hs.249196; ESTs; lung; diag  
 453966; BE148734; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.  
 453985; N44545; Hs.251865; ESTs; test; diag  
 454034; NM\_000691; Hs.575; aldehyde dehydrogenase 3 famit; lung, headnk; s.m.  
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; lung; diag  
 454066; X00356; Hs.37058; calcitonin/calcitonin-related; lung; diag  
 454071; AI041793; Hs.42502; ESTs; breast; diag  
 454077; AC005952; Hs.37062; insulin-like 3 (Leydig cell); test; diag  
 454098; W27953; Hs.217493; Plakophilin; lung; diag  
 454117; BE410100; Hs.40368; adaptor-related protein comple; mela; CTL+s.m.  
 454360; L78207; Hs.54470; ATP-binding cassette, sub-fami; glio; mAb  
 454429; BE273437; Hs.301406; hypothetical protein PP3501; mela; mAb  
 454439; AW819152; Hs.154320; DKFZP566O1646 protein; lung; diag  
 454478; AW805749; Hs.372783; superoxide dismutase 2, mitoch; mela; s.m.  
 455601; AI368680; Hs.816; SRY (sex determining region Y); lung, cerv, esoph; s.m.  
 456034; AW450979; ; gb:Ul-H-BI3-ala-a-12-O-Ul.s1 N; blad, fibro; diag  
 456062; AI866286; Hs.71962; ESTs, Weakly similar to B36298; fibro, ovar, uter; diag

456177; NM\_012391; Hs.79414; prostate epithelium-specific E; breast, pros; diag  
 456266; L29073; Hs.198726; cold shock domain protein A; panc; CTL+s.m.  
 456321; NM\_001327; Hs.87225; cancer/testis antigen; lung; CTL  
 456553; AA721325; Hs.189058; ESTs, Highly similar to Simila; panc; diag  
 456723; Z43902; Hs.4748; adenylate cyclase activating p; glio; mAb+s.m.  
 456736; AW248217; Hs.1619; achaete-scute complex (Drosoph); lung; diag  
 456759; BE259150; Hs.127792; delta (Drosophila)-like 3; glio; lung; mAb  
 456847; AI360456; Hs.86088; ESTs; test; diag  
 456938; X52509; Hs.161640; tyrosine aminotransferase; breast; s.m.  
 456977; AK000252; Hs.169758; hypothetical protein FLJ20245; angio; diag  
 457200; U33749; Hs.197764; thyroid transcription factor 1; fibro; CTL+s.m.  
 457211; AW972565; Hs.32399; ESTs, Weakly similar to S51797; mela, pros; CTL+s.m.  
 457292; AI921270; Hs.281462; hypothetical protein FLJ14251; blad; mAb  
 457313; AF047002; Hs.241520; transcriptional coactivator; test; CTL+s.m.  
 457411; AW085961; Hs.130093; iroquois-class homeobox protein; breast, fibro; diag  
 457465; AW301344; Hs.122908; DNA replication factor; test, mela; diag  
 457498; AI732230; Hs.191737; ESTs; pros; diag  
 457561; AA331517; Hs.286055; chimerin (chimaerin) 2; glio; mAb  
 457590; AI612809; Hs.5378; hypothetical protein MGC10724; ovar; diag  
 457869; AU077186; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.  
 458092; W67353; Hs.350558; KIAA0251 protein; lung; diag  
 458124; AW005548; Hs.124590; ESTs; fibro; diag  
 458435; AI418718; Hs.144121; ESTs, Weakly similar to T46916; glio; diag  
 458471; AV648609; Hs.194240; ESTs; renal, panc, hepC; diag  
 458933; AI638429; Hs.24763; RAN binding protein 1; lung, test; diag  
 459373; BE408266; Hs.301406; hypothetical protein PP3501; mela; mAb  
 459578; AW612538; Hs.304491; EST; mela; diag  
 459702; AI204995; ; gb:an03c03.x1 Stratagene schiz; blad, fibro; diag  
 459705; BE082764; Hs.270252; ESTs, Weakly similar to androg; fibro; mAb+s.m.

TABLE 3B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
103739	49403_2	AA115173 AA075709 AA076354 AA083101 AA076396 AA085391 AA070684 AA083368 AA075779 AA075221 AA076395 AA650486 AA083500
108282	108971_1	AA065143 AA065142
113230	2327174_1	AI820546 AI821336 T61430
118417	35983_1	AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594
		AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614951
		N29986 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611
		AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833
		AA207155 BI004756 AA206262 AI365204 H77608 AW590511
		AA404418 AI217248
	121335	1369289_1
	126872	685586_1
	322521	14637_1
	322975	1784158_1
	323332	245301_1
	323817	887879_1
	324261	1026976_1
	406685	0_0
	409051	107934_1
		AA075419 AA082953 AA080912 AA062835 AA071252 AA084926 AA078992 AA113913 AA081881 AA070343 AA083821 AA062836 AA113892
		AA075318 AA076594 AA078900 AA1134801 AA063293 AA083403 AW974305
	409123	108378_1
	409745	MH1944_5
		AI070050 AA070823 AA063403
		BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722
		BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762
		BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
	411880	1139083_1
	413804	1556661_1
	414221	685586_1
	417886	1031334_1
	427260	11272_50
	427298	115241_1
	427521	513212_1
		BE088101 T05990 AW872477
		BE168256 BE168190 T64682
		AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
		AA210987 D57294 AA214584 AA207006 D56572
		AA401424 AA400100 AA663848
		AA933717 BF061897 AW628327 AA641788 AA400495
		AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165
		AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
	429163	1238297_1
	432189	112710_1
	432222	539529_1
	432407	MH1429_12
		AW974271 AA592975 AA447312 AA884766
		AA527941 AA635266 AI810608 AI620190
		BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
		BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104
		AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279
		BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849
		AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859
		BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
		AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
	432415	11371_1
		BG166382 AW161086 N42363 BE935013 BE934998 BG291451 AV700520 BG152773 AI224956 AI079635 AW054706 AA843979 AI744193 F04060
		T23457 F04044 AA723859 AA977643 AA283764 AI123609 N21561 BF055052 BE856661 AI804220 AA843394 AI472045 AI740490 AA578830
		H09495 AI283334 AA609495 AI122773 AW162643 AW161798 BF940077 AI808825 AI360866 AI123189 R40236 R20726 AW975899 BE764052
		N31709 N31708 AI031947 AW194138
	434414	35978_1
		AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422
		AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298

AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175  
 BF854337  
 AF147374 T59538 T59589 T59598 T59542  
 AF147390 R76593 R76594  
 AW979074 AA834841 AA828650  
 AI926361 AA834879 AA828995  
 AW978407 AA830149 M85983 AW503637 BF352096  
 AL109688 R23665 R26578  
 AA868167 F21558 F31418 F35624  
 BG403189 AI148521 AI184746 AI126098 R05933 BI057330  
 AI820546 AI821336 T61430  
 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945  
 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354

## TABLE 3C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
325372	5866920	Minus	1117061-1117304
325544	6682452	Plus	171228-171286
327036	6531965	Plus	319951-320040
327075	6531965	Plus	4041318-4041431
327414	5867750	Plus	102461-102586
328700	5868264	Plus	764089-764203
330211	6013592	Plus	59158-59215
332798	Dunham, I. et.al.	Minus	232147-231974
333769	Dunham, I. et.al.	Plus	7696625-7696707
333904	Dunham, I. et.al.	Minus	8217374-8217261
334223	Dunham, I. et.al.	Minus	12734365-12734269
334447	Dunham, I. et.al.	Plus	14308764-14308824
335115	Dunham, I. et.al.	Minus	21388250-21388146
335809	Dunham, I. et.al.	Plus	26310772-26310909
335824	Dunham, I. et.al.	Plus	26376860-26376942
335825	Dunham, I. et.al.	Plus	26378175-26378268
335936	Dunham, I. et.al.	Minus	27360474-27360400
336034	Dunham, I. et.al.	Plus	29014404-29014590
336152	Dunham, I. et.al.	Minus	30156053-30155870
336636	Dunham, I. et.al.	Plus	988418-989185
338008	Dunham, I. et.al.	Plus	7697068-7697236
338033	Dunham, I. et.al.	Plus	8092128-8092271
338158	Dunham, I. et.al.	Minus	11794465-11794343
338255	Dunham, I. et.al.	Minus	15242294-15242231
400494	9714719	Plus	169845-170272
400517	9796686	Minus	49996-50346
400651	8117978	Minus	81488-81646
400665	8118496	Plus	16879-17023
400773	8131629	Minus	44116-44238,48208-48321
400844	9188605	Plus	24746-24872,25035-25204
400846	9188605	Plus	39310-39474
400881	2842777	Minus	91446-91603,92123-92265
401093	8516137	Minus	22335-23166
401234	9929642	Plus	120173-120337
401424	8176894	Plus	24223-24428
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
401704	3097841	Plus	24712-25374
401732	1200312	Plus	19346-19525,19625-19708,19897-19973,2006
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
401797	6730720	Plus	6973-7118
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
402145	8018280	Plus	113086-114800
402199	8576116	Minus	84187-84744
402230	9966312	Minus	29782-29932
402239	7690131	Plus	38175-38304,42133-42266
402260	3399665	Minus	113765-113910,115653-115765,116808-11694
402265	3287673	Plus	21059-21168
402305	7328724	Plus	40832-41362
402420	9796339	Plus	129750-129919
402424	9796344	Minus	64925-65073
402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402550	7652009	Minus	80413-80673
402604	9909420	Plus	20393-20767
402605	9909420	Minus	47680-47973

	402606	9909429	Minus	81747-82094
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	402777	9588235	Plus	126786-126948
5	402860	9588237	Minus	76423-76560
	402888	9930892	Minus	54727-54901
	402992	7767907	Minus	42137-42515
	402994	2996643	Minus	4727-4969
	403046	3540153	Minus	55707-55859,56369-56511
10	403047	3540153	Minus	59793-59968
	403071	8954241	Plus	136688-137096
	403088	8954241	Plus	169894-170193,170504-170806
	403171	9838164	Minus	74502-74703
	403328	8469086	Minus	120428-120703
	403329	8516120	Plus	96450-96598
15	403381	9438267	Minus	26009-26178
	403409	9438598	Plus	6860-7054,12573-12771
	403433	9719611	Minus	72225-72437
	403478	9958258	Plus	116458-116564
	403715	7239669	Plus	85128-85292
20	403740	7630882	Plus	86504-87227
	403776	7770611	Minus	1414-1513,1624-1756
	403903	7710671	Minus	101165-102597
	404029	7671252	Plus	108716-111112
25	404049	3688074	Minus	75765-78155
	404210	5006246	Plus	169926-170121
	404240	5002624	Minus	116132-116407,116653-116922
	404253	9367202	Minus	55675-56055
	404286	2326514	Plus	51086-51301
30	404298	9944263	Minus	73591-73723
	404403	7272157	Minus	72053-72238
	404440	7528051	Plus	80430-81581
	404866	9366919	Minus	11743-11929
	404877	1519284	Plus	1095-2107
35	404927	7342002	Plus	68690-69563
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	405001	6015406	Minus	104646-104819
	405025	7107727	Plus	105267-105343,106184-106294,106387-10653
	405121	8102330	Minus	35816-36004,36587-36684
40	405238	7249119	Minus	51728-51836
	405239	7249119	Plus	144345-144464,144690-144836,151750-15188
	405451	7622517	Minus	145949-146227
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405546	1054740	Plus	124010-124183
45	405547	1054740	Plus	124361-124520,124914-125050
	405646	4914350	Plus	741-969
	405704	4204244	Plus	138842-139051
	405770	2735037	Plus	61057-62075
	405849	7651817	Minus	17705-18287
50	405932	7767812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
	406137	9166422	Minus	30487-31058
	406173	7230224	Plus	12925-13213
	406348	9255985	Minus	71754-71944
55	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406434	9256651	Minus	17803-17931
	406467	9795551	Plus	182212-182958
	406506	7711374	Minus	6843-8077
60	406547	7711513	Minus	172780-174358

Table 4A lists about 425 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues. These genes were selected from a starting collection of about 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 75th percentile value amongst non-malignant adult tissues. Certain predicted protein domains are noted.

Table 5A lists about 231 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected similarly as for Table 1. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 50th percentile value amongst non-malignant adult tissues. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7Im, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

TABLE 4A: ABOUT 425 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar accession number, GenBank accession number  
 UniGeneID: Unigene number  
 Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).  
 UniGene Title: Unigene gene title  
 R1: Ratio of 90th percentile of tumor to 75th percentile of normal body tissue

Pkey	ExAccn	UniGeneID	Pred.Prot.Domains	UniGeneTitle	R1
------	--------	-----------	-------------------	--------------	----

5	419551	AW582256	Hs.91011	TM=M;SS=M	anterior gradient 2 (Xenopus laevis	9.7
	426174	AA547959	Hs.115838		Homo sapiens similar to Echinoidin	7.0
	409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	6.8
	428471	X57348	Hs.184510	14-3-3;TM=M;SS=N	stratiffin	6.4
	417931	W95642	Hs.82961	trefoil;TM=N;SS=M	trefoil factor 3 (intestinal)	6.3
10	447966	AA340605	Hs.105887	Jacalin;TM=N;SS=M	ESTs, Weakly similar to Homolog of	6.1
	406387				Target Exon	6.0
	421814	L12350	Hs.108623	EGF,isp_1,vwc,TSPN,isp_3;	thrombospondin 2	5.8
	406867	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	5.8
	426104	AI204418	Hs.190080		ESTs	5.8
15	421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	5.8
	422511	AU076442	Hs.117938	Collagen,none	collagen, type XVII, alpha 1	5.7
	426539	AB011155	Hs.170290	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	5.6
	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXD domain-containing ion transpor	5.5
	419329	AY007220	Hs.288998	S_100;TM=M;SS=N	S100-type calcium binding protein A	5.4
20	418344	AA216387			gb:nc16b02.s1 NCI_CGAP_Pr1 Homo sap	5.2
	407116	AA130986	Hs.271627		ESTs	5.1
	417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midkine (neurite growth-promoting f	5.1
	419452	U33635	Hs.90572	ig,ptkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	5.1
	421552	AF026692	Hs.105700	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 4	5.1
25	409453	AI885516	Hs.95612	cadherin,cadherin,Cadheri	ESTs	5.1
	409632	W74001	Hs.55279	serpin;TM=N;SS=N	serine (or cysteine) proteinase inh	5.1
	417515	L24203	Hs.82237	zf-B_box,zf-UBR1;TM=M;SS=	ataxia-telangiectasia group D-assoc	5.0
	411573	AB029000	Hs.70823	Sulfatase;TM=M;SS=N	KIAA1077 protein	5.0
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regulato	5.0
30	422087	X58968	Hs.111301	fn2,hemopexin,Peptidase_M	matrix metalloproteinase 2 (gelatin	5.0
	421143	AB024536	Hs.102171	ig,LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily containi	4.9
	408491	AI089063	Hs.7882		ESTs	4.9
	417944	AU077196	Hs.82985	vwc,Collagen,COLFI;TM=N;S	collagen, type V, alpha 2	4.9
	409062	AL157488	Hs.50150		Homo sapiens mRNA; cDNA DKFZp564B18	4.9
35	422281	M36803	Hs.346935	hemopexin;TM=N;SS=M	hemopexin	4.9
	425308	M97639	Hs.155585	ig,kringle,ptkinase,Fz;TM=	receptor tyrosine kinase-like orpha	4.8
	408349	BE546947	Hs.44276	homeobox;TM=M;SS=N	homeo box C10	4.8
	449019	AI949095	Hs.67776		ESTs, Weakly similar to T22341 hypo	4.8
	435561	AA351978	Hs.4943	MAGE,Cys_knot,EGF,laminin	hepatocellular carcinoma associated	4.8
40	410687	U24389	Hs.65436	Lysyl_oxidase;TM=N;SS=M	lysyl oxidase-like 1	4.8
	429455	AI472111	Hs.278694	lectin_c	CD209 antigen	4.8
	414407	AA147026	Hs.76704		ESTs	4.8
	419390	AI701162	Hs.331904	PMP22_Claudin,PMP22_Claud	hypothetical protein MGC11138	4.7
	453902	BE502341	Hs.3402		ESTs	4.7
45	411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	4.7
	450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	4.7
	449717	AB040935	Hs.23954	Glyco_transf_25;TM=N;SS=N	cerebral cell adhesion molecule	4.6
	451529	AI917901	Hs.208641	actin,none	ESTs	4.6
	435370	AI964074	Hs.225838	EGF,fn3,fibrinogen_C,toxi	ESTs	4.6
50	411761	AI733848	Hs.71935	zf-C2H2;TM=M;SS=N	putative zinc finger protein from E	4.6
	424223	AJ243706	Hs.143323	PHD,ARID,jmjC,jmjN,zf-C5H	putative DNA/chromatin binding moti	4.6
	426935	NM_000088	Hs.172928	vwc,Collagen,COLFI;TM=M;S	collagen, type I, alpha 1	4.5
	408796	AA688292	Hs.170345	hormone_rec,zf-C4	ESTs	4.5
	407230	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	4.4
55	422830	AC007954	Hs.121371		hypothetical protein DKFZp434P0111	4.4
	447528	AI612027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	4.4
	430168	AW968343	Hs.145582	efhand,efhand	DKFZP43411735 protein	4.4
	423225	AA852604	Hs.125359	ig,Ribosomal_S19;TM=M;SS=	Thy-1 cell surface antigen	4.4
	414822	AA156542	Hs.72127	homeobox,HLH	ESTs	4.4
60	452683	AI089575	Hs.374574	homeobox,none	progesterone membrane binding prote	4.4
	444784	D12485	Hs.11951	Somatomedin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	4.4
	453957	AL080235	Hs.35861	TM=Y;SS=M	Ras-induced senescence 1 (RIS1)	4.4
	413859	AW992356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	4.3
	440369	AW176150	Hs.132449		downstream of breast cancer antigen	4.3
65	418140	BE613836	Hs.83551	TM=M;SS=M	microfibrillar-associated protein 2	4.3
	441384	AA447849	Hs.288660	7tm_3,none	retinoic acid induced 3	4.3
	424464	R68537	Hs.17962	homeobox,none	ESTs	4.3
	423582	BE000831	Hs.23837	TGFb_propeptide,TGF-beta,	Homo sapiens cDNA FLJ11812 fis, clo	4.3
	432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	4.2
70	433320	D60647	Hs.250879	rrm	ESTs, Highly similar to CTXN RAT CO	4.2
	429165	AW009886	Hs.118258		prostate cancer associated protein	4.2
	416984	H38765	Hs.80706	Flavodoxin_2;TM=M;SS=N	diaphorase (NADH/NADPH) (cytochrome	4.2
	448913	AA194422	Hs.22564	rrm,zf-RanBP,ptkinase,GST_	myosin VI	4.2
	430154	AW583058	Hs.234726	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	4.2
75	400496			TM=Y;SS=N	ENSP00000224716*:GTP-binding protei	4.2
	442599	AF078037	Hs.324051	SH3,ank;TM=M;SS=N	RelA-associated inhibitor	4.2
	448520	AB002367	Hs.21355	ptkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	4.2
	431309	AW451711	Hs.313760	homeobox,none	ESTs, Weakly similar to I38022 hypo	4.2
	426485	NM_006207	Hs.170040	ig;TM=N;SS=M	platelet-derived growth factor rece	4.2
80	435858	AF254260	Hs.283009	bZIP;TM=M;SS=N	tufelin 1	4.2
	446051	BE048061	Hs.37054	Ephrin_A_deamin,dsrm,z-al	ephrin-A3	4.2
	451982	F13036	Hs.27373	NA;NA	Homo sapiens mRNA; cDNA DKFZp564O17	4.2
	450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	4.1
	431890	X17033	Hs.271986	vwa,Integrin_A,FG-GAP;TM=	integrin, alpha 2 (CD49B, alpha 2 s	4.1
	434449	AW953484	Hs.3849	efhand,FKBP;TM=M;SS=N	hypothetical protein FLJ22041 simil	4.1
	422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	4.1

5	423057	AW961597	Hs.130816		ESTs, Moderately similar to I38022	4.1
	452063	R53185	Hs.32366	HLH;TM=M;SS=N	ESTs, Weakly similar to TWST_HUMAN	4.1
	450680	AF131784	Hs.25318	ras,none	Homo sapiens clone 25194 mRNA seque	4.1
	418283	S79895	Hs.83942	Peptidase_C1;TM=N;SS=M	cathepsin K (pseudosyndosis)	4.1
	416361	AW204907	Hs.6872		ESTs, Weakly similar to CA13_HUMAN	4.1
	426255	BE262530	Hs.2006	GST_C,GST_N;TM=M;SS=N	glutathione S-transferase M3 (brain	4.1
	408113	T82427	Hs.194101	7tm_3,none	Homo sapiens cDNA: FLJ20869 fis, cl	4.1
10	407792	AI077715	Hs.39384	TM=M;SS=Y	putative secreted ligand homologous	4.1
	422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	4.1
	429359	W00482	Hs.2399	hemopexin,Peptidase_M10;T	matrix metalloproteinase 14 (membra	4.1
	442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	4.0
	448826	AI580252	Hs.255565		ESTs, Weakly similar to putative p1	4.0
	419648	T73661	Hs.91877	TM=N;SS=M	thyroid hormone responsive SPOT14 (	4.0
15	421485	AA243499	Hs.104800	TM=Y;SS=M	hypothetical protein FLJ10134	4.0
	440273	AI805392	Hs.325335		Homo sapiens cDNA: FLJ23523 fis, cl	4.0
	417363	AW129357	Hs.329700		ESTs	4.0
	451277	AK001123	Hs.26176	TM=Y;SS=M	hypothetical protein FLJ10261	4.0
	421823	N40850	Hs.28625		ESTs	4.0
20	452239	AW379378	Hs.356289		protein tyrosine phosphatase, recep	4.0
	444286	AI625304	Hs.201008		ESTs	4.0
	451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	4.0
	451304	M92642	Hs.26208	Collagen,TSPN;TM=M;SS=M	collagen, type XVI, alpha 1	4.0
	429556	AW139399	Hs.314807	TM=M;SS=N	ESTs	4.0
25	441094	U33819	Hs.7647	zf-C2H2,LIM,PHD,TFIIS;TM=	MYC-associated zinc finger protein	4.0
	407788	BE514982	Hs.38991	efhand,S_100,S_100,efhand	S100 calcium-binding protein A2	4.0
	451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	3.9
	437762	T78028	Hs.154679	C2,none	synaptotagmin I	3.9
	433399	N46406	Hs.84700	START;TM=M;SS=N	similar to phosphatidylcholine tran	3.9
30	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	3.9
	404578	AF183810	Hs.26102	zf-C2H2,ubredoxin;TM=M;S	trichorhinophalangeal syndrome I gene	3.9
	443883	AA114212	Hs.9930	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	3.9
	445084	H38914	Hs.250848	TM=Y;SS=M	hypothetical protein FLJ14761	3.9
	453880	AI803166	Hs.135121	HSP70,none	ESTs, Weakly similar to I38022 hypo	3.9
35	424125	M31669	Hs.1735	TGF-beta,TGFb_propeptide;	inhibin, beta B (activin AB beta po	3.9
	437377	AL359573	Hs.124940	ras;TM=M;SS=N	GTP-binding protein	3.9
	422562	AI962060	Hs.118397	Zn_carbOpept,F5_F8_type_C	AE-binding protein 1	3.9
	422320	AI745249	Hs.23650	TM=Y;SS=N	ESTs, Weakly similar to AAB47496 NG	3.9
40	433078	AW015188	Hs.121575	asp	Homo sapiens cDNA FLJ12231 fis, clo	3.9
	411894	M57609	Hs.72916	zf-C2H2;TM=N;SS=M	GLI-Kruppel family member GLI3 (Gre	3.9
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	3.9
	418113	AI272141	Hs.83484	HMG_box,homeobox;TM=M;SS=	SRY (sex determining region Y)-box	3.9
	418753	BE217818	Hs.87016		hypothetical protein FLJ22938	3.8
	452679	Z42387	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.8
45	421030	AW161357	Hs.101174	tubulin-binding;TM=N;SS=M	microtubule-associated protein tau	3.8
	431567	N51357	Hs.260855	TM=M;SS=N	Homo sapiens cDNA: FLJ21410 fis, cl	3.8
	426363	M58524	Hs.2025	TGF-beta,TGFb_propeptide;	transforming growth factor, beta 3	3.8
	447151	AI022813	Hs.92679	kinesin;TM=M;SS=M	Homo sapiens clone CDABP0014 mRNA s	3.8
	448717	R67419	Hs.21851	HLH,homeobox,none	Homo sapiens cDNA FLJ12900 fis, clo	3.8
50	425867	D60385	Hs.12079	cadherin;TM=Y;SS=M	calysentin-2	3.8
	423940	NM_012429	Hs.277728	CRAL_TRIO;TM=M;SS=N	SEC14 (S. cerevisiae)-like 2	3.8
	426742	AA383828	Hs.181131		ESTs	3.8
	435818	AA700553	Hs.368614	arf,ras,RecR,none	ESTs	3.8
	420005	AW271106	Hs.133294		ESTs	3.8
55	410867	X63556	Hs.750	EGF,TB,wnt,EB,TIL;TM=N;SS	fibrillin 1 (Marfan syndrome)	3.8
	402531	AB037745	Hs.104696	TM=M;SS=M	KIAA1324 protein	3.8
	449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	3.8
	424806	AA382523	Hs.105689	TM=Y;SS=N	MSTP031 protein	3.8
	443933	AI091631	Hs.203845	ion_trans;TM=Y;SS=M	two pore potassium channel KT3.3	3.8
60	432952	AA813887	Hs.188173		Homo sapiens cDNA FLJ12187 fis, clo	3.8
	424036	AA770688	Hs.348495	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member L	3.7
	453828	AW970960	Hs.293821	Pep_M12B_propep,Repolysi	ESTs	3.7
	407112	AA070801	Hs.51615	hormone_rec,zf-C4	ESTs, Weakly similar to ALU7_HUMAN	3.7
	445669	AI570830	Hs.174870		ESTs	3.7
65	446091	AW022192	Hs.200197	homeobox,none	ESTs	3.7
	424651	AI493206	Hs.120785		ESTs	3.7
	409178	BE393948	Hs.50915	trypsin;TM=M;SS=Y	kallikrein 5	3.7
	417059	AL037672	Hs.81071	TM=N;SS=Y	extracellular matrix protein 1	3.7
70	431194	D43704	Hs.250712	Ca_channel_B,RepB_protein	calcium channel, voltage-dependent,	3.7
	430397	AI924533	Hs.105607	HCO3_cotransp;TM=Y;SS=N	bicarbonate transporter related pro	3.7
	418969	W33191	Hs.28907	SH3;TM=M;SS=N	hypothetical protein FLJ20258	3.7
	427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	3.7
	424012	AW368377	Hs.137569	SAM,P53;TM=M;SS=N	tumor protein 63 kDa with strong ho	3.7
	418840	AI821614	Hs.185831		ESTs	3.7
75	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamini	cadherin, EGF LAG seven-pass G-type	3.7
	433430	AI863735	Hs.369982	thyroglobulin_1,IGFBP,zf-	ESTs	3.7
	422491	AA338548	Hs.117546	TM=M;SS=Y	neuronatin	3.7
	435114	AA775483	Hs.288936	ODC_AZ,Ribosomal_L9_N;TM=	mitochondrial ribosomal protein L9	3.7
80	416899	BE262645	Hs.80420	IL8;TM=M;SS=M	small inducible cytokine subfamily	3.7
	422110	AI376736	Hs.121555	kazal,none	secreted protein, acidic, cysteine-	3.7
	448560	BE613183	Hs.23213	zf-RanBP,MDM2,Ndr	ESTs	3.6
	414945	BE076358	Hs.77687	UPAR_LY6;TM=M;SS=M	lymphocyte antigen 6 complex, locus	3.6
	422119	AI277829	Hs.111862	WD40;TM=M;SS=N	KIAA0590 gene product	3.6
	447335	BE617695	Hs.286192	TM=M;SS=N	hypothetical protein FLJ20940	3.6

5	450663	H43540	Hs.25292	RNase_HII;TM=N;SS=M	ribonuclease HI, large subunit	3.6
	417387	AW021102	Hs.21509	zf-C2H2,none	ESTs	3.6
	450825	AC005954	Hs.25527	PDZ,Guanylate_kin;TM=N;SS	tight junction protein 3 (zona occl	3.6
	439755	AW748482	Hs.77873	ig;TM=Y;SS=M	B7 homolog 3	3.6
	439873	BE159253	Hs.300638		ESTs	3.6
	439039	AI656707	Hs.48713		ESTs	3.6
	419235	AW470411	Hs.288433		neurotrophin	3.6
	445033	AV652402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	3.6
10	404394	AF332975	Hs.307004	EGF,fn1,vwc,vwd,MAM,Kerat	Zonadhesin	3.6
	452222	AW806287	Hs.21432	Sema,TIG,PSI,GDI	SEX gene	3.6
	422961	Y13620	Hs.122607	TM=M;SS=N	B-cell CLL/lymphoma 9	3.6
	420988	AW006352	Hs.159643		ESTs, Weakly similar to T32554 hypo	3.6
	439680	AW245741	Hs.58461	zf-C2H2,TFIIS,KRAB;TM=M;S	ESTs, Weakly similar to A35659 krue	3.6
15	426815	D59505	Hs.351344	ig,SET,PHD,zf-CXXC,Adap_c	ESTs, Weakly similar to K1Cl_HUMAN	3.6
	437446	AA788946	Hs.101302	fn3,vwa,Collagen,TSPN;TM=	ESTs, Moderately similar to CA1C RA	3.6
	421690	AW162667	Hs.106857	efhand;TM=M;SS=N	calbindin 2, (29kD, calretinin)	3.5
	453939	AA418160	Hs.86043		Homo sapiens cDNA FLJ13558 fis, clo	3.5
	426158	NM_001982	Hs.199067	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	3.5
20	439246	AI498072	Hs.351474	ank,pkinase,UPF0073;TM=N;	membrane-associated tyrosine- and t	3.5
	410653	BE383768	Hs.65238	zf-C3HC4,AIP3;TM=M;SS=N	95 kDa retinoblastoma protein bindi	3.5
	412703	AW984744			gb:RC1-HN0015-040400-011-d03 HN0015	3.5
	427871	AW992405	Hs.352406	TM=M;SS=N	Homo sapiens, clone IMAGE:3507281,	3.5
	444273	AI903474	Hs.230	LRR,LRRNT;TM=M;SS=M	fibromodulin	3.5
25	434936	AI285970	Hs.183817	UCH-2	ESTs	3.5
	457869	AU077186	Hs.108885	vwa,Collagen;TM=M;SS=M	Homo sapiens, alpha-1 (VI) collagen	3.5
	422575	AK000546	Hs.118552	PTR2;TM=Y;SS=M	hypothetical protein FLJ20539	3.5
	428343	AL043021	Hs.12705	WD40;TM=N;SS=M	ESTs	3.5
	426716	NM_006379	Hs.171921	ig,Sema,PSI;TM=N;SS=M	sema domain, immunoglobulin domain	3.5
30	423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	3.5
	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	3.5
	407926	AW956382	Hs.59771	TYA;TM=N;SS=M	ESTs	3.5
	447041	AL135480	Hs.250705		Homo sapiens cDNA FLJ11685 fis, clo	3.5
	419073	AW372170	Hs.183918	death,ZU5;TM=N;SS=M	Homo sapiens cDNA FLJ12797 fis, clo	3.5
35	446945	AI193115	Hs.16611	TM=M;SS=N	tumor protein D52-like 1	3.5
	416322	BE019494	Hs.79217	P5CR,NAD_Gly3P_dh,Octopin	pyrroline-5-carboxylate reductase 1	3.5
	447347	AA570056	Hs.122730	NA;NA	ESTs, Moderately similar to KIAA121	3.5
	448984	AW751955	Hs.22753	TM=M;SS=N	hypothetical protein FLJ22318	3.5
	421778	AA428000	Hs.283072	NA;NA	actin related protein 2/3 complex,	3.5
40	423363	BE544348	Hs.127562	homeobox;TM=M;SS=N	homeo box C11	3.5
	432545	X52486	Hs.3041	cyclin,none	uracil-DNA glycosylase 2	3.5
	408495	W68796	Hs.237731		ESTs	3.5
	406851	AA609784	Hs.352392	ig,MHC_II_beta;TM=M;SS=Y	major histocompatibility complex, c	3.5
	418736	T18979	Hs.87908	helicase_C,AT_hook,SNF2_N	Snf2-related CBP activator protein	3.4
45	410197	NM_005518	Hs.59889	HMG_CoA_synt;TM=N;SS=N	3-hydroxy-3-methylglutaryl-Coenzyme	3.4
	453597	BE281130	Hs.33713	KH-domain,Ribosomal_S3_C,	myo-inositol 1-phosphate synthase A	3.4
	417259	AW903838	Hs.81800	EGF,ig,lectin_c,sushi,Xli	chondroitin sulfate proteoglycan 2	3.4
	453985	N44545	Hs.251865	PH,none	ESTs	3.4
	412634	U55984	Hs.356531		heat shock 90kD protein 1, alpha	3.4
50	407204	R41933	Hs.140237	histone,histone	ESTs, Weakly similar to ALU1_HUMAN	3.4
	444371	BE540274	Hs.239	Fork_head;TM=M;SS=N	forkhead box M1	3.4
	447334	AA515032	Hs.91109		ESTs	3.4
	426530	U24578	Hs.278625	A2M,NTR,ANATO,A2M_N,preny	complement component 4A	3.4
	419749	X73608	Hs.93029	kazal,thyroglobulin_1;TM=	sparc/osteonectin, cwcv and kazal-I	3.4
55	423595	R82826	Hs.220702	homeobox,none	ESTs	3.4
	406673	M34996	Hs.198253	ig,MHC_II_alpha;TM=M;SS=M	major histocompatibility complex, c	3.4
	434241	AF119913		TM=N;SS=M	Homo sapiens PRO3077 mRNA, complete	3.4
	412490	AW803564	Hs.288850		Homo sapiens cDNA: FLJ22528 fis, cl	3.4
	452277	AL049013	Hs.28783	ank;TM=M;SS=N	KIAA1223 protein	3.4
60	431457	NM_012211	Hs.256297	FG-GAP,vwa;TM=Y;SS=M	integrin, alpha 11	3.4
	421777	BE562088	Hs.108196	TM=M;SS=N	HSPC037 protein	3.4
	453082	H18835	Hs.31608	ion_trans;TM=Y;SS=M	hypothetical protein FLJ20041	3.4
	414085	AA114016	Hs.75746	aldedh;TM=N;SS=M	aldehyde dehydrogenase 1 family, me	3.4
	440300	N39760	Hs.8859	TM=M;SS=N	Homo sapiens, Similar to RIKEN cDNA	3.4
65	400290	H18836	Hs.31608	Cys_knot	hypothetical protein FLJ20041	3.4
	433339	AF019226	Hs.8036	ras,arf;TM=M;SS=N	glioblastoma overexpressed	3.4
	419301	AA236166	Hs.132957	TM=Y;SS=M	tenomodulin protein	3.4
	414792	BE314949	Hs.87128	TM=Y;SS=M	hypothetical protein FLJ23309	3.4
	451428	AW083384	Hs.11067		ESTs, Highly similar to T46395 hypo	3.4
70	432210	AI567421	Hs.273330	EGF,kazal,laminin_EGF,lam	Homo sapiens, clone IMAGE:3544662,	3.4
	452242	R50956	Hs.159993		glycosyltransferase	3.4
	450676	AI147155	Hs.279727		ESTs	3.4
	413014	AW250533	Hs.75139	TM=M;SS=N	partner of RAC1 (arfpapin 2)	3.4
	427919	AA173942	Hs.326416	CTF_NFI,none	Homo sapiens mRNA; cDNA DKFZp564H19	3.4
75	424005	AB033041	Hs.137507	TM=Y;SS=N	vang (van gogh, Drosophila)-like 2	3.4
	422072	AB018255	Hs.111138	RhoGAP;TM=M;SS=N	KIAA0712 gene product	3.4
	440995	T57773	Hs.10263		ESTs	3.4
	426150	NM_003658	Hs.167218	homeobox;TM=N;SS=M	BarH-like homeobox 2	3.3
	416877	BE386266	Hs.85658	zf-C2H2;TM=M;SS=N	hypothetical protein FLJ23436	3.3
80	452191	AU076408	Hs.28309	UDPG_MGDP_dh,UDPG_MGDP_dh	UDP-glucose dehydrogenase	3.3
	450273	AW296454	Hs.24743	rrm,none	hypothetical protein FLJ20171	3.3
	456177	NM_012391	Hs.79414	Ets,SAM_PNT;TM=M;SS=N	prostate epithelium-specific Ets tr	3.3
	423062	NM_003655	Hs.5637	chromo;TM=N;SS=M	ESTs	3.3
	421848	X15880	Hs.108885	vwa,Collagen;TM=M;SS=M	collagen, type VI, alpha 1	3.3

5	433577	AW007080	Hs.284192		ESTs	3.3
	409636	AA305729	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	3.3
	404730	AA486704	Hs.33287	CTF_NFI:none	Nuclear factor I/B	3.3
	422940	BE077458		Sec7,PH,ANF_receptor,lig_	gb:RC1-BT0606-090500-015-b04 BT0606	3.3
	410001	AB041036	Hs.57771	trypsin;TM=M;SS=M	kallikrein 11	3.3
	427461	AA531527	Hs.332040	TM=Y;SS=M	hypothetical protein MGC13010	3.3
	453468	W00712	Hs.32990	TM=M;SS=N	DKFZP566F084 protein	3.3
	443807	W52930	Hs.9822	HAT;TM=N;SS=M	HCNP protein; XPA-binding protein 2	3.3
10	456034	AW450979			gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CG	3.3
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	3.3
	412755	BE144306	Hs.179891		ESTs, Weakly similar to P4HA_HUMAN	3.3
	429690	AW956329	Hs.23721	sugar_tr,Ribosomal_S25	ESTs	3.3
	423472	AF041260	Hs.129057	TM=M;SS=N	breast carcinoma amplified sequence	3.3
15	424118	BE269041	Hs.140452	perilipin;TM=N;SS=M	cargo selection protein (mannose 6	3.3
	437275	AW976035	Hs.292396	Frizzled,Fz	ESTs, Weakly similar to A47582 B-ca	3.3
	437464	AA323296	Hs.97837		Homo sapiens mRNA; cDNA DKFZp547J04	3.3
	433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	3.3
	434931	AW968941	Hs.166254		hypothetical protein DKFZp566I133	3.3
20	451691	AI809278	Hs.208152	C2	ESTs	3.3
	430433	AA478883	Hs.273766	VW,none	ESTs	3.3
	429343	AK000785	Hs.199480	VHS,ENTH,UIM;TM=N;SS=M	Homo sapiens, Similar to epsin 3, c	3.3
	450835	BE262773	Hs.25584	ArfGap;TM=N;SS=M	hypothetical protein FLJ10767	3.3
	414591	AI888490	Hs.248107		ESTs, Weakly similar to ALU8_HUMAN	3.3
25	452579	AA131657	Hs.23830	CN_hydrolase	ESTs	3.3
	409960	BE261944	Hs.355264		hexokinase 1	3.3
	406850	AI624300	Hs.172928	vwc, Collagen, COLFI;TM=M;S	collagen, type I, alpha 1	3.3
	453874	AW591783	Hs.36131		collagen, type XIV, alpha 1 (unduli	3.2
	425964	AW889928	Hs.9071	homeobox,none	progesterone membrane binding prote	3.2
30	428412	AA428240	Hs.126083		ESTs	3.2
	430316	NM_000875	Hs.239176	fn3,Furin-like, pkinase, Re	insulin-like growth factor 1 recept	3.2
	440087	W28969	Hs.7718	KOW,Ribosomal_S4e,S4,rm;	hypothetical protein FLJ22678	3.2
	449933	AW157098	Hs.324104	DUF176,efhand;TM=M;SS=N	Human DNA sequence from clone RP1-6	3.2
	441128	AA570256	Hs.348504	TM=Y;SS=M	ESTs, Weakly similar to T23273 hypo	3.2
35	434182	W20309	Hs.8107	G-gamma;TM=M;SS=N	G-protein gamma-12 subunit	3.2
	422737	M26939	Hs.119571	Collagen, COLFI;TM=N;SS=M	collagen, type III, alpha 1 (Ehlers	3.2
	408202	AA227710	Hs.43658	OLF;TM=M;SS=N	DKFZP586L151 protein	3.2
	424971	AA479005	Hs.154036	PH;TM=M;SS=N	tumor suppressing subtransferable c	3.2
	407869	AI827976	Hs.24391	efhand;TM=M;SS=N	hypothetical protein FLJ13612	3.2
40	444734	NM_001360	Hs.11806	ERG4_ERG24;TM=Y;SS=M	7-dehydrocholesterol reductase	3.2
	426991	AK001536	Hs.214410		Homo sapiens cDNA FLJ10674 fis, clo	3.2
	414081	AW969976	Hs.365706	gla;TM=N;SS=Y	matrix Gla protein	3.2
	408795	AW749126	Hs.170345	hormone_rec,zf-C4	hypothetical protein FLJ13710	3.2
45	452345	AA293279	Hs.29173	DSPc;TM=M;SS=N	hypothetical protein FLJ20515	3.2
	437879	BE262082	Hs.5894	TM=N;SS=N	hypothetical protein FLJ10305	3.2
	407872	AB039723	Hs.40735	Fz,Frizzled,7tm_2,DUF81;T	frizzled (Drosophila) homolog 3	3.2
	427289	AI097346	Hs.323878	aminotran_5,SDF,none	phosphoserine aminotransferase	3.2
	432375	BE536069	Hs.2962	efhand,S_100;TM=N;SS=M	S100 calcium-binding protein P	3.2
	429415	NM_002593	Hs.202097	CUB,NTR;TM=N;SS=M	procollagen C-endopeptidase enhance	3.2
50	412774	AA120865	Hs.380149	hormone_rec,zf-C4	ESTs	3.2
	445942	T80334	Hs.13479	TM=M;SS=N	hypothetical protein FLJ20847	3.2
	439456	AI752409	Hs.109314	zf-C2H2;TM=N;SS=M	hypothetical protein FLJ20980	3.2
	414774	X02419	Hs.77274	kringle,trypsin,plant_thi	plasminogen activator, urokinase	3.2
	433336	AF017986	Hs.31386	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 2	3.2
55	439905	AW799755	Hs.110953	HLH;TM=M;SS=N	retinoic acid induced 1	3.2
	420251	AW374968	Hs.379829		Human DNA sequence from clone RP5-1	3.2
	413004	T35901	Hs.75117	TM=M;SS=N	interleukin enhancer binding factor	3.2
	418686	Z36830	Hs.87268	annexin;TM=M;SS=N	annexin A8	3.2
	410279	BE271977	Hs.61809	ras;TM=M;SS=N	hypothetical protein FLJ14117	3.2
60	424391	BE550112	Hs.158549		ESTs, Weakly similar to T2D3_HUMAN	3.2
	440409	AW294316	Hs.125608	thiored	ESTs	3.2
	452689	F33868	Hs.284176	transferrin,KH-domain,rm	transferrin	3.2
	418154	BE165866	Hs.352403	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	3.2
	434384	AA631910	Hs.370133		ESTs	3.2
65	413436	AF238083	Hs.68061	DAGKc;TM=M;SS=N	sphingosine kinase 1	3.2
	431663	NM_016569	Hs.267182	T-box;TM=M;SS=N	TBX3-iso protein	3.2
	432874	W94322	Hs.279651	SH3;TM=M;SS=Y	melanoma inhibitory activity	3.2
	436252	AI539519	Hs.142827		Homo sapiens cDNA FLJ11562 fis, clo	3.2
70	421044	AF061871	Hs.101302	fn3,vwa, Collagen, TSPN;TM=	Human DNA sequence from clone RP1-2	3.2
	419102	AA234098	Hs.42424		ESTs, Weakly similar to 2004399A ch	3.2
	419359	AI043202	Hs.90073	CAS_CSE1;TM=M;SS=N	chromosome segregation 1 (yeast hom	3.2
	441859	AW194364	Hs.9877	Amino_oxidase,FAD_binding	interleukin-4 induced gene-1 protei	3.1
	426418	M90464	Hs.169825	Collagen,C4,VPR;TM=N;SS=M	collagen, type IV, alpha 5 (Alport	3.1
	413076	U10564	Hs.75188	pkinae;TM=M;SS=N	wee1 (S. pombe) homolog	3.1
75	407874	AI766311	Hs.289047	COQ7	Homo sapiens cDNA FLJ14059 fis, clo	3.1
	448019	AW947164	Hs.195641		ESTs, Moderately similar to I38022	3.1
	427024	AA397572	Hs.348902	vwc,W2,MA3,MIF4G	chromosome 11 open reading frame 14	3.1
	410281	AF076612	Hs.166186	LEA,perilipin;TM=M;SS=N	Homo sapiens clone 23928 mRNA seque	3.1
	447205	BE617015	Hs.11006		ESTs, Moderately similar to T17372	3.1
80	434433	AW629759			gb:hh70e05.y1 NCI_CGAP_GU1 Homo sap	3.1
	439737	AI751438	Hs.41271	C1q, Collagen,none	Homo sapiens mRNA full length inser	3.1
	450157	AW961576	Hs.60178	PH,Band_41,RhoGEF,none	ESTs	3.1
	445989	H97754	Hs.11108		ESTs	3.1
	442213	N36110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	3.1



	402496				Target Exon	3.1
	438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	3.1
	439335	AA742697	Hs.62492	TM=N;SS=M	NM_052863:Homo sapiens secretoglobi	3.1
5	412276	BE262621	Hs.73798	MIF,sugar_lr,none	macrophage migration inhibitory fac	3.1
	416950	AL049798	Hs.80552		dermatopontin	3.1
	456157	AW979153	Hs.336881	transmembrane4,none	ESTs	3.1
	452753	AA028049	Hs.277728	CRAL_TRIO,none	SEC14 (S. cerevisiae)-like 2	3.1
10	414420	AA043424	Hs.76095	TM=M;SS=N	immediate early response 3	3.1
	446229	AI744964	Hs.14449	TM=M;SS=N	KIAA1609 protein	3.1
	453143	AA382234	Hs.356289	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	3.1
	411441	AL042355	Hs.70202	WD40;TM=M;SS=N	WD repeat domain 10	3.1
	422921	BE062045	Hs.351625	AAA,hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23260 fis, cl	3.1
	444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	3.1
15	436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	3.1
	427890	AA435761	Hs.373623	RFX_DNA_binding,none	ESTs	3.1
	444838	AV681680	Hs.208558	integrin_A,FG-GAP,none	ESTs	3.1
	427876	AI494291	Hs.369171		ESTs	3.1
	413040	AA193338	Hs.12321	Na_Ca_Ex;TM=Y;SS=M	sodium calcium exchanger	3.1
20	427515	T79526	Hs.179516	EMP24_GP25L;TM=Y;SS=M	integral type I protein	3.1
	451092	AI207256	Hs.13766	filament;TM=N;SS=N	Homo sapiens mRNA for FLJ00074 prot	3.1
	442222	AI061301	Hs.164773	trypsin,kingle,UPAR_LY6	ESTs	3.1
	452613	AA461599	Hs.23459		ESTs	3.1
	447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	3.1
25	412890	T85247	Hs.351875	COX6C;TM=M;SS=M	cytochrome c oxidase subunit VIc	3.1
	418313	BE244231	Hs.84038	TM=Y;SS=N	CGI-06 protein	3.1
	440006	AK000517	Hs.6844	AAA,NB-ARC,PAAD_DAPIN;NA;	NALP2 protein; PYRIN-Containing APA	3.1
	434042	AI589941	Hs.8254		Homo sapiens, Similar to tumor diff	3.1
	420576	AA297634	Hs.54925		KIAA1858 protein	3.1
30	432269	NM_002447	Hs.2942	pk kinase,Sema,PSI,TIG,A4_E	macrophage stimulating 1 receptor (	3.1
	424927	AW973666	Hs.153850		hypothetical protein C321D2.4	3.1
	440100	BE382685	Hs.158549		ESTs, Weakly similar to T2D3_HUMAN	3.1
	452408	AA306477	Hs.29379	TM=M;SS=N	hypothetical protein FLJ10687	3.1
	441362	BE614410	Hs.23044	TM=N;SS=N	RAD51 (S. cerevisiae) homolog (E co	3.1
35	418444	AI902899	Hs.85155	zf-CCCH;TM=M;SS=N	butyrate response factor 1 (EGF-res	3.1
	423464	NM_016240	Hs.128856	Collagen;TM=Y;SS=N	CSR1 protein	3.1
	424604	AW865388	Hs.151076	TM=M;SS=N	KIAA1243 protein	3.1
	420059	AF161486	Hs.94769	ras,none	RAB23, member RAS oncogene family	3.1
	453271	AA903424	Hs.6786	LIM;TM=M;SS=N	ESTs	3.1
40	411274	NM_002776	Hs.69423	trypsin;TM=M;SS=N	kallikrein 10	3.1
	434095	AA011117	Hs.3745	EGF,F5_F8_type_C;TM=N;SS=	milk fat globule-EGF factor 8 prote	3.1
	403439			ank;TM=M;SS=N	NM_031419*:Homo sapiens molecule po	3.1
	413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Repro	kruppel-related zinc finger protein	3.1
45	411756	BE294350	Hs.71891	pk kinase,F5_F8_type_C;TM=Y	discoidin domain receptor family, m	3.1
	409007	AL122107	Hs.49599		Homo sapiens mRNA; cDNA DKFZp434G08	3.1
	452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	3.1
	414359	M62194	Hs.75929	cadherin,Cadherin_C_term;	cadherin 11, type 2, OB-cadherin (o	3.1
	433212	BE218049	Hs.121820		ESTs	3.1
	449123	D50920	Hs.23106	TM=M;SS=N	KIAA0130 gene product	3.1
50	431176	AI026984	Hs.293662	MCPsignal,laminin_B,lamin	ESTs	3.0
	419245	AI732742	Hs.87440		ESTs	3.0
	434493	AA635305	Hs.375591		ESTs	3.0
	449177	BE616694	Hs.288042		hypothetical protein FLJ14299	3.0
	430449	AA352723	Hs.241471	WH1;TM=M;SS=N	RNB6	3.0
55	452887	AI702223	Hs.107253	K-box;TM=N;SS=M	hypothetical protein DKFZp761F241	3.0
	451678	AA374181	Hs.26799		DKFZP564D0764 protein	3.0
	445457	AF168793	Hs.12743	Carn_acyltransf;TM=M;SS=N	camitine O-octanoyltransferase	3.0
	407597	AA043925	Hs.339352	fn3,jg;TM=Y;SS=M	Homo sapiens brother of CDO (BOC) m	3.0
	431629	AU077025	Hs.265827	TM=M;SS=Y	interferon, alpha-inducible protein	3.0
60	432302	AA345857	Hs.274307	TIG;TM=M;SS=N	KIAA1442 protein	3.0
	442549	AI751601	Hs.8375	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	3.0
	437959	AI472068	Hs.375604	elf5_elf2B,W2;TM=M;SS=N	KIAA1856 protein	3.0
	447400	AK000322	Hs.18457	zf-C3HC4;TM=Y;SS=M	hypothetical protein FLJ20315	3.0
	411734	AW374954	Hs.71779		Homo sapiens DNA from chromosome 19	3.0
65	443547	AW271273	Hs.356487	fn3,none	hypothetical protein FLJ12666	3.0
	417000	BE277919	Hs.306019	TM=Y;SS=M	ESTs, Weakly similar to ALU7_HUMAN	3.0
	416987	D86957	Hs.80712	GTP_CDC;TM=N;SS=M	KIAA0202 protein	3.0
	424494	U78575	Hs.149255	PIP5K;TM=N;SS=M	phosphatidylinositol-4-phosphate 5-	3.0
	414496	W73853	Hs.355424	pk kinase,F5_F8_type_C,adh_	ESTs	3.0
70	413336	AI569936	Hs.296178	Occludin;TM=M;SS=N	hypothetical protein FLJ22637	3.0
	434314	BE392921	Hs.3797	ras,arf;TM=M;SS=N	RAB26, member RAS oncogene family	3.0
	401038			TM=M;SS=N	C11000425:gi 4507721 ref NP_003310.	3.0
	418245	AA088767	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.0
	407688	W25317	Hs.37616		Human D9 splice variant B mRNA, com	3.0
75	456906	AF117646	Hs.156637	zf-C3HC4,Cbl_N,Cbl_N2,Cbl	Cas-Br-M (murine) ectropic retrovir	3.0
	424744	AW175781	Hs.152720	TM=M;SS=N	M-phase phosphoprotein 6	3.0
	452195	AA994712	Hs.116878		ESTs	3.0
	415988	BE407713	Hs.78943	Pept_C1-like;TM=N;SS=M	bleomycin hydrolase	3.0
	418399	AF131781	Hs.84753	TM=N;SS=N	hypothetical protein FLJ12442	3.0
80	420568	F09247	Hs.247735	cadherin,lipocalin;TM=M;S	protocadherin alpha 10	3.0
	404661			TM=M;SS=N	C9000306:gi 12737280 ref XP_006682	3.0
	414152	NM_003248	Hs.75774	EGF,TSPN,isp_3;TM=M;SS=M	thrombospondin 4	3.0
	421307	BE539976	Hs.103305	chromo	Homo sapiens mRNA; cDNA DKFZp434B04	3.0
	444868	BE560471	Hs.12101	TM=N;SS=M	hypothetical protein	3.0

450214	BE439763	Hs.227571	RGS;TM=M;SS=N	regulator of G-protein signalling 4	3.0
452664	AA398859	Hs.18397	TM=M;SS=M	hypothetical protein FLJ23221	3.0
422105	AI929700	Hs.111680	TM=M;SS=N	endosulfine alpha	3.0
422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	3.0
434067	H18913	Hs.124023		Homo sapiens cDNA FLJ14218 fis, clo	3.0
412676	NM_000165	Hs.74471	connexin,Connexin43;TM=Y;	gap junction protein, alpha 1, 43kD	3.0
426801	AA486846	Hs.271795		ESTs, Weakly similar to I38022 hypo	3.0
421983	AI252640	Hs.110364	pro_isomerase,none	peptidylprolyl isomerase C (cycloph	3.0
429299	AI620463	Hs.347408	TM=Y;SS=N	hypothetical protein MGC13102	3.0
408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	3.0
438746	AI885815	Hs.184727	transferrin,Guanylate_kin	Human melanoma-associated antigen p	3.0

TABLE 4B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
418344	245371_1	AA216387 T63548 AA228676
412703	1243670_1	AW984759 AW984744
434241	63414_1	AF119913 AI207698 R57074
422940	58443_1	BC012771 BG397153 BF366196 AA337277 AA319285 AW843252
456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
434433	111338_1	AA633408 AW749955 AW629759 AI651005

TABLE 4C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406387	9256180	Plus	116229-116371,117512-117651
400496	9743564	Plus	41515-41695
402496	9797769	Minus	8615-9103
403439	9719679	Plus	91463-91632
401038	7232177	Minus	4277-4469
404661	9797073	Plus	33374-33675,33769-34008

TABLE 5A: ABOUT 231 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES THAT MAY ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar accession number, GenBank accession number  
UniGeneID: UniGene number  
Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).  
UniGene Title: UniGene gene title  
R1: Ratio of 90th percentile tumor to 50th percentile of normal body tissue

Pkey	ExAccn	UniGeneID	Pred.Prot.Domains	UniGeneTitle	R1
409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	20.5
421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	16.3
419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXD domain-containing ion transpor	13.7
417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midkine (neurite growth-promoting f	13.7
414521	D28124	Hs.76307	DAN;TM=M;SS=M	neuroblastoma, suppression of tumor (DAN)	13.7
438091	AW373062	Hs.351546	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	13.4
413815	AL046341	Hs.75562	pkinase,F5_F8_type_C;TM=Y	discoidin domain receptor family, m	13.2
439180	AI393742	Hs.119257	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	13.2
431441	U81961	Hs.2794	ASC;TM=Y;SS=N	sodium channel, nonvoltage-gated 1	12.5
452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	12.4
452239	AW379378	Hs.356289		protein tyrosine phosphatase, recep	12.1
441384	AA447849	Hs.288660	7tm_3,none	retinoic acid induced 3	11.9
419223	X60111	Hs.1244	transmembrane4;TM=Y;SS=M	CD9 antigen (p24)	11.7
413859	AW992356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	11.5
410687	U24389	Hs.65436	Lysyl_oxidase;TM=N;SS=M	lysyl oxidase-like 1	11.2
422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	10.1
419452	U33635	Hs.90572	ig,pkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	9.9
427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	9.9
444784	D12485	Hs.11951	Somatostatin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	9.9
436972	AA284679	Hs.25640	PMP22_Claudin;TM=Y;SS=M	claudin 3	9.7
412926	AI879076	Hs.75061	MARCKS;TM=N;SS=M	macrophage myristoylated alanine-ri	9.5
425280	U31519	Hs.1872	PEPCK;TM=M;SS=N	phosphoenolpyruvate carboxykinase 1	9.5
432636	AA340864	Hs.278562	PMP22_Claudin;TM=Y;SS=M	claudin 7	9.4
423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	9.4
424206	NM_003734	Hs.198241	Cu_amine_oxid,Cu_amine_ox	amine oxidase, copper containing 3	9.4
444797	AB018333	Hs.12002	SH3,SAM;TM=M;SS=N	KIAA0790 protein	9.0

	402559	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphat.type 2B	9.0
	443932	AW888222	Hs.9973	SH2,WW,PID,none	tensin	8.9
	421143	AB024536	Hs.102171	ig,LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily containi	8.8
5	433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	8.7
	410668	BE379794	Hs.159651	death,TNFR_c6;TM=Y;SS=M	hypothetical protein	8.7
	433662	W07162	Hs.150826	ras,ABC_tran,arf;TM=M;SS=	RAB25 RAB25, member RAS oncogene fa	8.6
	421853	AL117472	Hs.108924	SH3,Sorb;TM=M;SS=N	SH3-domain protein 5 (ponsin)	8.6
	425335	BE394327	Hs.296267	efhand,kazal,arf,ras,7tm_	folistatin-like 1	8.5
10	400290	H18836	Hs.31608	Cys_knot	hypothetical protein FLJ20041	8.5
	438089	W05391	Hs.351546	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	8.4
	426158	NM_001982	Hs.199067	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	8.3
	447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	8.2
	439941	AI392640	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	8.2
15	439318	AW837046	Hs.6527	7tm_2,CytC_asm,GPS;TM=Y;S	G protein-coupled receptor 56	8.1
	442213	N36110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	8.1
	412649	NM_002206	Hs.74369	integrin_A,FG-GAP;TM=M;SS	integrin, alpha 7	8.1
	448913	AA194422	Hs.22564	rrm,zf-RanBP,pkinase,GST_	myosin VI	8.1
	420166	AW732276	Hs.95583	transmembrane4;TM=Y;SS=M	transmembrane 4 superfamily member	8.0
20	407102	AA007629	Hs.348601	transport_prot,SWIB,ASC	glycerol-3-phosphate dehydrogenase	7.9
	452516	AA058630	Hs.29759	TM=N;SS=M	RNA POLYMERASE I AND TRANSCRIPT REL	7.9
	413076	U10564	Hs.75188	pkinase;TM=M;SS=N	wee1 (S. pombe) homolog	7.9
	443604	C03577	Hs.9615	efhand;TM=M;SS=N	myosin regulatory light chain 2, sm	7.7
	429002	AW248439	Hs.2340	Armadillo_seg;TM=M;SS=N	junction plakoglobin	7.6
25	432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	7.6
	426359	AA376409	Hs.10862	adenylatekinase,none	Homo sapiens cDNA: FLJ23313 fis, cl	7.5
	417733	AL048678	Hs.82503	NA;NA	H.sapiens mRNA for 3'UTR of unknown	7.5
	451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	7.4
	443951	F13272	Hs.356835	PMP22_Claudin,none	ferritin, light polypeptide	7.4
	409960	BE261944	Hs.355264		hexokinase 1	7.3
30	423184	NM_004428	Hs.1624	Ephrin;TM=M;SS=M	ephrin-A1	7.3
	405121	X04385	Hs.110802	Cys_knot,TGF-beta,vwa,vcv	von Willebrand factor (VWF), mRNA	7.1
	438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	7.1
	417771	AA804698	Hs.82547		retinoic acid receptor responder (t	7.0
35	424118	BE269041	Hs.140452	perilipin;TM=N;SS=M	cargo selection protein (mannose 6	7.0
	402705	X67951	Hs.180909	AhpC-TSA;TM=M;SS=M	peroxiredoxin 1 (PRDX1)	7.0
	417115	AW952792	Hs.334612	Sm,pkinase;TM=N;SS=N	small nuclear ribonucleoprotein pol	7.0
	442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	6.9
40	447216	R75812	Hs.169248	cytochrome_c;NA;NA	p75NTR-associated cell death execut	6.9
	422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	6.9
	414657	AA424074	Hs.76780	TM=M;SS=N	protein phosphatase 1, regulatory (	6.9
	447528	AI612027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	6.9
	436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	6.9
	428013	AF151020	Hs.181444	TM=Y;SS=M	hypothetical protein	6.9
45	444143	AW747996	Hs.160999	Bcl-2,none	ESTs, Moderately similar to A56194	6.8
	414443	AU077268	Hs.76144	ig,pkinase;TM=Y;SS=N	platelet-derived growth factor rece	6.7
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regulato	6.7
	448479	H96115	Hs.21293	UDPGP;TM=M;SS=N	UDP-N-acteylglucosamine pyrophospho	6.6
	410552	X66945	Hs.748	ig,pkinase,SH2,SH3,C2,PH,	fibroblast growth factor receptor 1	6.6
50	414883	AA926960	Hs.348669	CKS;TM=N;SS=N	CDC28 protein kinase 1	6.6
	417426	NM_002291	Hs.82124	laminin_EGF,laminin_Nterm	laminin, beta 1	6.6
	428179	AI127772	Hs.279696	pkinase,PX,pkinase_C;TM=N	serum/glucocorticoid regulated kina	6.6
	443195	BE148235	Hs.193063	Aa_trans,none	Homo sapiens cDNA FLJ14201 fis, clo	6.5
	424512	X53002	Hs.149846	integrin_B,EGF;TM=Y;SS=M	integrin, beta 5	6.5
55	421733	AL119671	Hs.1420	ig,pkinase;TM=Y;SS=M	fibroblast growth factor receptor 3	6.5
	428950	BE311879	Hs.194673	DED;TM=M;SS=N	phosphoprotein enriched in astrocyt	6.5
	450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	6.5
	416078	AL034349	Hs.79005		protein tyrosine phosphatase, recep	6.5
	408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	6.4
60	428373	AI751656	Hs.183986	ig;TM=Y;SS=M	poliovirus receptor-related 2 (herp	6.4
	449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	6.4
	406621	X57809	Hs.181125	ig,HSP70,Ppx-GppA;TM=M;SS	immunoglobulin lambda locus	6.4
	431629	AU077025	Hs.265827	TM=M;SS=Y	interferon, alpha-inducible protein	6.4
	428169	AI928984	Hs.182793	photoRC,UPF0118;TM=Y;SS=N	golgi phosphoprotein 2	6.4
65	443337	Y07604	Hs.9235	NDK;TM=N;SS=N	non-metastatic cells 4, protein exp	6.4
	451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	6.4
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	6.4
	426539	AB011155	Hs.170290	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	6.3
	417208	S67773	Hs.81665	ig,pkinase;TM=Y;SS=M	v-kit Hardy-Zuckerman 4 feline sarc	6.3
70	438278	BE409248	Hs.57988	TFIIS,RNA_POL_M_15KD,UPF0	hypothetical protein FLJ22357 simil	6.3
	429455	AI472111	Hs.278694	lectin_c	CD209 antigen	6.3
	431685	AW296135	Hs.267659	CH,DAG_PE-bind,PH,RhoGEF,	vav 3 oncogene	6.3
	445033	AV652402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	6.3
	411756	BE294350	Hs.71891	pkinase,F5_F8_type_C;TM=Y	disoidin domain receptor family, m	6.3
75	453902	BE502341	Hs.3402		ESTs	6.3
	418005	AI186220	Hs.83164	Collagen,TSPN;TM=M;SS=M	collagen, type XV, alpha 1	6.2
	449924	W30681	Hs.146233	SH3,none	Homo sapiens cDNA: FLJ22130 fis, cl	6.2
	426520	BE545684	Hs.343566	aa_permeases,pyridoxal_de	KIAA0251 protein	6.2
80	453064	R40334	Hs.89463		potassium large conductance calcium	6.2
	448520	AB002367	Hs.21355	pkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	6.2
	452683	AI089575	Hs.374574	homeobox,none	progesterone membrane binding prote	6.2
	402575	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphat. type 2B	6.2
	444672	Z95636	Hs.11669	laminin_EGF,laminin_G,EGF	laminin, alpha 5	6.2
	450440	AB024334	Hs.25001	14-3-3;TM=M;SS=N	tyrosine 3-monooxygenase/tryptophan	6.2

5	432314	AA533447	Hs.285173	Xlink,none	ESTs	6.1
	438564	AA381553	Hs.198253	ig,MHC,IL_alpha,none	major histocompatibility complex, c	6.1
	444252	R21135	Hs.54985		ESTs	6.1
	425184	BE279288	Hs.155048	ig;TM=Y;SS=M	Lutheran blood group (Auberger b an	6.1
	431890	X17033	Hs.271986	vwa,integrin_A,FG-GAP;TM=	integrin, alpha 2 (CD49B, alpha 2 s	6.1
	449475	AI348027	Hs.129826	transmembrane4;TM=Y;SS=M	hypothetical protein PP1057	6.1
	449538	AI559444	Hs.104679	TM=M;SS=M	ESTs	6.0
	414496	W73853	Hs.355424	pkinase,F5_F8_type_C,adh_	ESTs	6.0
10	414217	AI309298	Hs.279898	NA;NA	Homo sapiens cDNA: FLJ23165 fis, cl	6.0
	445333	BE537641	Hs.44278	ras,arf,TK;TM=N;SS=M	hypothetical protein FLJ12538 simil	5.9
	431183	NM_006855	Hs.250696	ER_lumen_recept;TM=M;SS=M	KDEL (Lys-Asp-Glu-Leu) endoplasmic	5.9
	409645	AI142265	Hs.55498	polyprenyl_synt;TM=M;SS=N	geranylgeranyl diphosphate synthase	5.9
	412276	BE262621	Hs.73798	MIF,sugar_tr,none	macrophage migration inhibitory fac	5.9
15	416137	BE279513	Hs.278607	pkinase,UBA,ThiF;TM=M;SS=	ubiquitin activating enzyme E1-like	5.9
	412969	AI373162	Hs.75103	14-3-3;TM=N;SS=M	tyrosine 3-monooxygenase/tryptophan	5.9
	414504	AW069181	Hs.115175	pkinase,SAM;TM=M;SS=N	sterile-alpha motif and leucine zip	5.9
	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamini	cadherin, EGF LAG seven-pass G-type	5.9
	436415	BE265254	Hs.343258	Peptidase_M24,Furin-like,	proliferation-associated 2G4, 38kD	5.9
20	413900	AW409747	Hs.75612	TPR,PDZ,WW,Guanylate_kin;	stress-induced-phosphoprotein 1 (Hs	5.9
	441455	AJ271671	Hs.7854	Zip;TM=Y;SS=M	zinc/iron regulated transporter-lik	5.9
	444006	BE395085	Hs.334762	Idl_recept_a,PKD,MHC_I;TM	type I transmembrane protein Fn14	5.8
	408269	AW888219	Hs.44077	CH;TM=M;SS=N	parvin, alpha	5.8
	411372	AI147861	Hs.213289	Glyco_transf_11,EGF,Idl_r	low density lipoprotein receptor (f	5.8
25	450825	AC005954	Hs.25527	PDZ,Guanylate_kin;TM=N;SS=	tight junction protein 3 (zona ocl	5.8
	456534	X91195	Hs.100623	LIM,PDZ,pkinase;TM=N;SS=M	phospholipase C, beta 3, neighbor p	5.7
	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.7
	446812	AL042279	Hs.16206	pkinase	uncharacterized hypothalamus protei	5.7
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	5.7
30	405484	XM_093451		TM=N;SS=M	C3002124*.gii12737280[ref]XP_006682	5.7
	425367	BE271188	Hs.155975	TM=M;SS=Y	protein tyrosine phosphatase, recep	5.7
	444607	AW405635	Hs.293687	PI-PLC-X,PH,PI-PLC-Y	ESTs	5.7
	421456	AW579842	Hs.104557	zf-C2H2,DUF18,efhand,C2,P	hypothetical protein FLJ10697	5.6
	412810	M21574	Hs.74615	ig,pkinase,DUF11;TM=M;SS=	platelet-derived growth factor rece	5.6
35	450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	5.6
	453880	AI803166	Hs.135121	HSP70,none	ESTs, Weakly similar to I38022 hypo	5.6
	439578	AW263124	Hs.350547	WD40;TM=M;SS=N	nuclear receptor co-repressor/HDAC3	5.6
	450954	AI904740	Hs.25691	TM=Y;SS=M	receptor (calcitonin) activity modi	5.6
	414555	N98569	Hs.76422	phoslip;TM=M;SS=Y	phospholipase A2, group IIA (platel	5.6
40	409963	AA133590	Hs.377830	MBOAT,none	calcium/calmodulin-dependent protei	5.6
	450463	AW952018	Hs.201398	C1q,Collagen;TM=M;SS=Y	G protein coupled receptor interact	5.6
	425177	AF127577	Hs.155017	TM=N;SS=M	nuclear receptor interacting protei	5.5
	445496	AB007860	Hs.12802	SH3,ank,PH,ArfGap;TM=M;SS	development and differentiation enh	5.5
	428981	BE313077	Hs.93135	rm	ESTs, Weakly similar to ALU2_HUMAN	5.5
45	424441	X14850	Hs.147097	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member X	5.5
	415662	AW972481	Hs.170610	pkinase,none	ESTs, Highly similar to G01887 MEK	5.5
	422105	AI929700	Hs.111680	TM=M;SS=N	endosulfine alpha	5.5
	429556	AW139399	Hs.314807	TM=M;SS=N	ESTs	5.5
50	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	5.5
	425205	NM_005854	Hs.155106	TM=Y;SS=N	receptor (calcitonin) activity modi	5.5
	444633	AF111713	Hs.12284	ig;TM=Y;SS=M	junctional adhesion molecule 1	5.5
	431565	AF161470	Hs.260622	TM=Y;SS=N	butyrate-induced transcript 1	5.5
	429655	U48959	Hs.211582	pkinase,fn3,ig,none	myosin, light polypeptide kinase	5.5
55	431886	L77964	Hs.271980	pkinase;TM=M;SS=N	mitogen-activated protein kinase 6	5.5
	453143	AA382234	Hs.356289	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	5.4
	451863	AL120634	Hs.331803	cpn60,TCP1,E1-E2_ATPase,C	ATPase, Ca transporting, plasma mem	5.4
	422293	X94453	Hs.114366	aldedh,aakinas;TM=M;SS=N	pyrroline-5-carboxylate synthetase	5.4
	432179	X75208	Hs.2913	EPH_lbd,fn3,pkinase,SAM;T	EphB3	5.4
	408048	NM_007203	Hs.42322	Paralemmmin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.4
60	448153	Y10805	Hs.20521	NusG;TM=N;SS=M	HMT1 (hnRNP methyltransferase, S. c	5.4
	421251	Z28913	Hs.102948	LIM,PDZ;TM=N;SS=M	enigma (LIM domain protein)	5.4
	439039	AI656707	Hs.48713	pkinase,none	ESTs	5.4
	409882	AJ243191	Hs.56874	HSP20;TM=N;SS=M	heat shock 27kD protein family, mem	5.4
65	451295	AI557212	Hs.17132	pkinase,DAG_PE-bind,pkina	ESTs, Moderately similar to I54374	5.4
	442549	AI751601	Hs.8375	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	5.4
	445930	AF055009	Hs.13456	DAGKc,DAGKa,ank,WD40,bZIP	Homo sapiens clone 24747 mRNA seque	5.4
	453082	H18835	Hs.31608	ion_trans;TM=Y;SS=M	hypothetical protein FLJ20041	5.4
	426432	AF001601	Hs.169857	Arylesterase;TM=M;SS=N	paraoxonase 2	5.4
	415753	U52819	Hs.78781	PDGF;TM=M;SS=M	vascular endothelial growth factor	5.4
70	450778	U81375	Hs.25450	Nucleoside_tran;TM=Y;SS=M	solute carrier family 29 (nucleosid	5.4
	414739	U83867	Hs.77196	efhand,SH3,spectrin;TM=N;	spectrin, alpha, non-erythrocytic 1	5.3
	421233	AA209534	Hs.284243	transmembrane4;TM=Y;SS=M	tetraspan NET-6 protein	5.3
	414774	X02419	Hs.77274	kringle,trypsin,plant_thi	plasminogen activator, urokinase	5.3
	414368	W70171	Hs.75939	PRK,CoaE;TM=N;SS=N	uridine monophosphate kinase	5.3
75	446051	BE048061	Hs.37054	Ephrin_A_deamin,dsm,z-al	ephrin-A3	5.3
	423619	T48691	Hs.249159	7tm_1,7tm_2;TM=Y;SS=M	adrenergic, alpha-2A-, receptor	5.3
	440188	AK001812	Hs.7036	ROK;TM=M;SS=N	N-Acetylglucosamine kinase	5.3
	414135	NM_004419	Hs.2128	Rhodanese,DSPc,Y_phosphat	dual specificity phosphatase 5	5.3
80	444838	AV651680	Hs.208558	integrin_A,FG-GAP,none	ESTs	5.3
	447918	AI129320	Hs.115175	pkinase,SAM,none	ESTs, Highly similar to JC5818 gamm	5.3
	405517	AF000974	Hs.119498	LIM;TM=M;SS=N	thyroid hormone receptor interactor 6	5.3
	413588	AA971014	Hs.75432	IMPDH_C,CBS,IMPDH_N;TM=M;	IMP (inosine monophosphate) dehydro	5.2
	411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	5.2
	416157	NM_003243	Hs.342874	zona_pellucida;TM=Y;SS=M	transforming growth factor, beta re	5.2

5	407744	AB020629	Hs.38095	ABC_tran,PRK;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.2
	446108	AL036596	Hs.42322	Paralemmin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.2
	422034	AC006486	Hs.333069	Ets;TM=M;SS=N	Ets2 repressor factor	5.2
	417098	AB017365	Hs.173859	Frizzled,Fz,7tm_2,toxin_2	frizzled (Drosophila) homolog 7	5.2
	430526	AF181862	Hs.242407	7tm_3;TM=Y;SS=M	G protein-coupled receptor, family	5.2
	414176	BE140638	Hs.75794	7tm_1,CRCB;TM=Y;SS=N	EDG-2 (endothelial differentiation	5.2
	416710	AI268325	Hs.54890	Peptidase_M49,EGF,ig,Neur	hypothetical protein FLJ23590	5.2
	417896	AA379770	Hs.82890	DAD;TM=Y;SS=M	defender against cell death 1	5.2
10	413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Repro	kruppel-related zinc finger protein	5.2
	421837	AF135168	Hs.108802	AAA,cdc48_N,cdc48_2,NB-AR	N-ethylmaleimide-sensitive factor	5.2
	429379	NM_014840	Hs.200598	kinase,RIO1;TM=M;SS=N	KIAA0537 gene product	5.2
	429619	AL120751	Hs.211568		eukaryotic translation initiation f	5.2
	437275	AW976035	Hs.292396	Frizzled,Fz	ESTs, Weakly similar to A47582 B-ce	5.1
15	421071	AI311238	Hs.104476	TM=Y;SS=M	ESTs, Weakly similar to CGHU1E coll	5.1
	448581	NM_002709	Hs.21537		protein phosphatase 1, catalytic su	5.1
	452568	AA805634	Hs.300870	PI3_PI4_kinase;TM=M;SS=M	Homo sapiens mRNA; cDNA DKFZp547M07	5.1
	452069	AB028949	Hs.183994	Metallophos;TM=M;SS=N	KIAA1026 protein	5.1
	437175	AW968078	Hs.87773	kinase,kinase_C,none	protein kinase, cAMP-dependent, cat	5.1
20	437056	AI147061		spectrin,SH3,PH,CH	gb:ok33a11.s1 Soares_NSF_F8_9W_OT_P	5.1
	450998	BE387614	Hs.25797	rrm;TM=M;SS=N	splicing factor 3b, subunit 4, 49kD	5.1
	444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	5.1
	448528	BE613248	Hs.172084	PHD;TM=M;SS=N	Homo sapiens, clone IMAGE:3627860,	5.1
	452345	AA293279	Hs.29173	DSPC;TM=M;SS=N	hypothetical protein FLJ20515	5.1
25	443412	W84893	Hs.9305		angiotensin receptor-like 1	5.1
	412853	M34175	Hs.74626	Adaptin_N,Alpha_adaptinC2	adaptor-related protein complex 2,	5.1
	439866	AA280717	Hs.6727	rrm,NTF2;TM=M;SS=N	Ras-GTPase activating protein SH3 d	5.1
	439975	AW328081	Hs.6817	Ham1p_like;TM=M;SS=N	inosine triphosphatase (nucleoside	5.1
	435523	T62849	Hs.11090	TM=Y;SS=M	membrane-spanning 4-domains, subfam	5.1
30	433423	BE407127	Hs.8997	HSP70,ig,Ppx-GppA;TM=M;SS	heat shock 70kD protein 1A	5.1
	412641	M16660	Hs.74335	HSP90,HATPase_c;TM=M;SS=N	heat shock 90kD protein 1, beta	5.1
	431236	AV656840	Hs.285115	fn3;TM=Y;SS=M	interleukin 13 receptor, alpha 1	5.1
	438552	AJ245820	Hs.6314		type I transmembrane receptor (seiz	5.0
	422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	5.0
35	427502	AI811865	Hs.71133	TM=M;SS=N	Homo sapiens, clone IMAGE:3161564,	5.0
	414166	AW888941	Hs.75789	DEAD,helicase_C,rrm,Ndr,C	N-myc downstream regulated	5.0
	424954	NM_000546	Hs.1846	P53,WD40,IRK;TM=M;SS=N	tumor protein p53 (Li-Fraumeni synd	5.0
	422089	AA523172	Hs.103135	REJ,PLAT,PKD,WSC,LRR	ESTs, Weakly similar to SFR4_HUMAN	5.0
	426636	BE242634	Hs.2055	ThiF,UBACT;TM=M;SS=N	ubiquitin-activating enzyme E1 (A1S	5.0
40	410793	AW581906	Hs.66392	SH3,efhand,C2,PH,RhoGEF,M	intersectin 1 (SH3 domain protein)	5.0

TABLE 5B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
437056	428504_3	AW976398 AI147061 AA765223 AA743380 AI803927

TABLE 5C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405484	5922025	Plus	199214-199579,199672-199920,200262-20049

TABLE 6A: 777 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL ADULT TISSUES

Table 6A lists 777 genes up-regulated in colon cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" colon cancer level was set to the 90<sup>th</sup> percentile amongst 95 colon cancers. The "average" normal adult tissue level was set to the 90<sup>th</sup> percentile amongst 209 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15<sup>th</sup> percentile value amongst the 209 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UnigeneID: Unigene number  
Unigene Title: Unigene gene title  
R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
5	447033	AI357412	Hs.157601	ESTs	31.35
	409041	AB033025	Hs.50081	KIAA1199 protein	29.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	26.41
	422330	D30783	Hs.115263	epiregulin	24.38
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
10	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	23.55
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	22.70
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	21.60
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	21.15
	415989	AI267700	Hs.317584	ESTs	20.95
15	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.35
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	18.68
	421470	R27496	Hs.1378	annexin A3	18.05
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.30
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.15
20	450531	AW301032	Hs.203800	ESTs	16.60
	432867	AW016936	Hs.233364	ESTs	16.35
	443211	AI128388	Hs.143655	ESTs	15.80
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	15.10
	406964	M21305		gb:Human alpha satellite and satellite 3	15.00
25	410355	S58544	Hs.153057	sperm associated antigen 1	14.70
	441377	BE218239	Hs.202656	ESTs	14.45
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	14.35
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	14.35
	440304	BE159984	Hs.125395	ESTs	14.25
30	426427	M86699	Hs.169840	TTK protein kinase	13.60
	451561	N52812	Hs.177403	ESTs	12.80
	434032	AW009951	Hs.206892	ESTs	12.75
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	12.65
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	12.55
35	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.40
	446232	AI281848	Hs.194691	retinoic acid induced 3	12.25
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	12.18
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.85
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	11.80
40	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	11.65
	452461	N78223	Hs.108106	transcription factor	11.42
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	11.35
	400534				11.00
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	10.75
45	453688	AW381270	Hs.194110	hypothetical protein PRO2730	10.75
	426890	AA393167	Hs.41294	ESTs	10.60
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	10.50
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
50	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFp564F093 (fr	10.40
	425761	AW664214	Hs.196729	ESTs	10.25
	404567				10.15
	428536	AI143139	Hs.2288	visinin-like 1	10.10
	414972	BE263782	Hs.77695	KIAA0008 gene product	10.05
55	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.95
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	9.90
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.85
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	9.85
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	9.78
60	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	9.73
	420900	AL045633	Hs.44269	ESTs	9.68
	438639	AI278360	Hs.31409	ESTs	9.55
	439521	AI808955	Hs.58248	ESTs	9.55
	445676	AI247763	Hs.16928	ESTs	9.50
65	408489	AI082437	Hs.26690	ESTs	9.50
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	9.37
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.00
	423349	AF010258	Hs.127428	homeo box A9	8.96
	400195	NA		NA	8.90
70	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	8.90
	418895	AA894638	Hs.14600	ESTs	8.85
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.80
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.75
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	8.65
75	414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	8.64
	445436	AI224105	Hs.151408	ESTs	8.50
	403776				8.50
	433447	U29195	Hs.3281	neuronal pentraxin II	8.50
	407168	R45175	Hs.117183	ESTs	8.31
80	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	8.30
	422505	AL120862	Hs.124165	ESTs	8.25
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.20
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	8.15
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	409687	T51125	Hs.8493	ESTs	8.05

	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.93
	406360	NA		NA	7.80
5	443450	N66045	Hs.133529	ESTs	7.75
	414422	AA147224	Hs.337232	ESTs	7.75
	442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	7.70
	438604	AA811896	Hs.44604	ESTs	7.60
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	7.55
	400250	NA		NA	7.53
10	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.50
	404996				7.50
	450459	AI697193	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	7.45
	445019	AI205540	Hs.281295	ESTs	7.30
15	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.25
	448816	AB033052	Hs.22151	KIAA1226 protein	7.25
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	7.25
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	7.20
	433859	AW896758	Hs.273789	ESTs	7.20
20	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	7.20
	456120	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.20
	419751	AW195581	Hs.93121	KIAA0761 protein	7.16
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	7.15
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	7.15
25	421373	AA808229	Hs.167771	ESTs	7.10
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.00
	423248	AA380177	Hs.125845	ribose-5-phosphate-3-epimerase	6.96
	444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E (OABP	6.95
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.95
30	413573	AI733859	Hs.149089	ESTs	6.95
	442660	AW138174	Hs.130651	ESTs	6.93
	427878	C05766	Hs.181022	CGI-07 protein	6.90
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.85
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp5861518 (f	6.82
35	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.80
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	6.75
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	6.75
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	6.71
	401644				6.70
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	6.70
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	6.69
	406747	AI925153	Hs.217493	annexin A2	6.65
45	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.60
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	6.60
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	6.55
	427072	H38046	Hs.303193	ESTs	6.55
	452588	AA889120	Hs.110637	homeo box A10	6.53
50	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.50
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	6.50
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	6.50
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	6.50
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.50
55	410908	AA121686	Hs.10592	ESTs	6.47
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	6.47
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.45
	452838	U65011	Hs.30743	preferentially expressed antigen in meta	6.42
	451389	N73222	Hs.279009	matrix Gla protein	6.40
60	438202	AW169287	Hs.22588	ESTs	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	6.37
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.36
	436539	AI005457	Hs.275048	ESTs	6.35
65	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	6.34
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	6.32
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	6.31
	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.30
	413597	AW302885	Hs.117183	ESTs	6.30
70	429529	AA454190	Hs.24283	ESTs, Moderately similar to reduced expr	6.30
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.25
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.20
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.20
	438050	BE262816	Hs.6061	protein kinase, AMP-activated, beta 1 no	6.20
75	416857	AA188775	Hs.292453	ESTs	6.20
	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	6.18
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.15
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.15
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.15
80	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	6.11
	424745	AA214618	Hs.152759	activator of S phase kinase	6.10
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.10
	454438	AA224053	Hs.172405	cell division cycle 27	6.08
	407771	AL138272	Hs.62713	ESTs	6.08

	416057	AI927382	Hs.29857	ESTs	6.05
	442917	AA314907	Hs.85950	ESTs	6.00
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	6.00
5	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	5.96
	412246	AI160873	Hs.69233	zinc finger protein	5.96
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.95
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.95
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	5.95
10	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.90
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	5.87
	408908	BE296227	Hs.250822	serine/threonine kinase 15	5.86
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	5.86
15	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	5.85
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.85
	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.85
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	5.85
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.85
20	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.82
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	459309	AA040620	Hs.5672	hypothetical protein AF140225	5.80
	410060	NM_001448	Hs.58367	glypican 4	5.79
	423806	AA331247	Hs.86617	ESTs	5.77
25	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	5.75
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	5.75
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.75
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	5.75
	442957	AI949952	Hs.49397	ESTs	5.75
30	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	5.70
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	409757	NM_001898	Hs.123114	cystatin SN	5.69
35	433687	AA743991		gb:ny57g01.s1 NCI_CGAP_Pr18 Homo sapiens	5.68
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.60
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.60
	438777	AA825487	Hs.142179	ESTs	5.60
	417235	AA810278	Hs.24250	ESTs	5.60
40	451177	AI969716	Hs.13034	ESTs	5.60
	415227	AW821113	Hs.72402	ESTs	5.58
	436217	T53925	Hs.107	fibrinogen-like 1	5.56
	452881	AW135220	Hs.241921	ESTs	5.55
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.55
45	426235	AI631964	Hs.34447	ESTs	5.55
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	5.53
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	5.52
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
50	453884	AA355925	Hs.36232	KIAA0186 gene product	5.47
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.47
	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	5.47
	420218	AW958037	Hs.286	ribosomal protein L4	5.45
	421155	H87879	Hs.102267	lysyl oxidase	5.45
55	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	5.45
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.45
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	5.44
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	5.42
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.41
60	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	5.41
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	5.35
	430217	N47863	Hs.336901	ribosomal protein S24	5.33
	417372	T99755	Hs.334728	ESTs	5.30
	415139	AW975942	Hs.48524	ESTs	5.30
65	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	5.29
	424086	AI351010	Hs.102267	lysyl oxidase	5.27
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.27
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	5.26
	452131	AI860677	Hs.72325	Human DNA sequence from clone RP1-187J11	5.25
70	436016	AA806465	Hs.121536	Human DNA sequence from clone RP11-472E5	5.25
	449347	AV649748	Hs.295901	KIAA0493 protein	5.25
	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.25
	453921	AI824009	Hs.44577	ESTs	5.25
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.25
75	421076	AW007988	Hs.233299	ESTs, Weakly similar to I38022 hypotheti	5.25
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	5.24
	433384	AI021992	Hs.124244	ESTs	5.23
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	5.21
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.20
80	441795	N58115	Hs.21137	AD024 protein	5.20
	449416	AI651016	Hs.246311	ESTs	5.20
	418379	AA218940	Hs.137516	fidgetin-like 1	5.20
	426753	T89832	Hs.170278	ESTs	5.18
	422109	S73265	Hs.1473	gastrin-releasing peptide	5.17



	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	5.17
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	5.17
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	5.15
5	427728	AJ245600	Hs.180545	Homo sapiens mRNA for hypothetical prote	5.15
	447713	AI420733	Hs.207083	ESTs	5.15
	425739	T19016	Hs.159410	molybdopterin synthase sulfurylase	5.15
	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	5.15
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	5.13
10	441139	AW449009	Hs.126647	ESTs	5.13
	451121	AW973795	Hs.128927	Homo sapiens cDNA FLJ13903 fis, clone TH	5.10
	435202	AI971313	Hs.170204	KIAA0551 protein	5.10
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	5.10
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	5.09
15	422805	AA436989	Hs.121017	H2A histone family, member A	5.07
	411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	5.06
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	5.06
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	5.05
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.05
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.05
20	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.05
	441675	AI914329	Hs.5461	ESTs	5.00
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.00
	401480	NA		NA	5.00
25	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	4.95
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	4.92
	414718	H95348	Hs.107987	ESTs	4.91
	419139	AI123517	Hs.269940	ESTs	4.90
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	4.90
30	425420	BE536911	Hs.234545	hypothetical protein NUF2R	4.90
	408758	NM_003686	Hs.47504	exonuclease 1	4.90
	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDN	4.90
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	4.90
	433927	AI557019	Hs.116467	small nuclear protein PRAC	4.89
35	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	4.88
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	4.87
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	4.87
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	4.86
	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	4.85
40	418396	AI765805	Hs.26691	ESTs	4.85
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.84
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	4.80
	406414				4.75
	430178	AW449612	Hs.152475	ESTs	4.71
45	411901	AA166730	Hs.6966	Human DNA sequence from clone RP1-187J11	4.70
	404025	NA		NA	4.70
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	4.68
	436662	AI582393	Hs.126695	ESTs	4.68
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	4.68
50	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	4.65
	431041	AA490967	Hs.197955	KIAA0704 protein	4.65
	417860	AW408557	Hs.235498	hypothetical protein FLJ14075	4.65
	410658	AW105231	Hs.192035	ESTs	4.65
	425895	AI269484	Hs.161427	zinc finger protein 215	4.65
55	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	4.65
	436397	AA715013	Hs.169835	ESTs	4.60
	439225	AA192669	Hs.45032	ESTs	4.60
	423197	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	4.60
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.60
60	412723	AA648459	Hs.335951	hypothetical protein AF301222	4.59
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	4.59
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.58
	430704	AW813091	Hs.335799	ESTs	4.56
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	4.55
65	433326	AI379486	Hs.159430	ESTs	4.55
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	4.55
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	4.55
	423343	AA324643	Hs.246106	ESTs	4.55
	416467	H57585	Hs.37467	ESTs	4.55
70	408867	AA437199	Hs.656	cell division cycle 25C	4.54
	419423	D26488	Hs.90315	KIAA0007 protein	4.54
	414132	AI801235	Hs.48480	ESTs	4.53
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	4.53
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	4.50
75	451009	AA013140	Hs.115707	ESTs	4.50
	431064	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	4.50
	432725	AL137496	Hs.9001	ESTs	4.50
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	4.50
80	410486	AW235094	Hs.69233	zinc finger protein	4.50
	428532	AF157326	Hs.184786	TBP-interacting protein	4.50
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.50
	408390	AF123050	Hs.44532	diubiquitin	4.49
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	4.47
	434294	AJ271379	Hs.76194	ribosomal protein S5	4.47

	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.46
	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypotheti	4.45
	410142	AA081924	Hs.124918	KIAA1795 protein	4.45
5	434894	AW977850	Hs.23856	hypothetical protein MGC5297	4.45
	420092	AA814043	Hs.88045	ESTs	4.45
	400115	NA		NA	4.45
	430967	H16791	Hs.31445	ESTs	4.41
	438078	AI016377	Hs.131693	ESTs	4.41
10	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	4.40
	429774	AI522215	Hs.50883	KIAA1804 protein	4.40
	426214	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	4.40
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.40
	450480	X82125	Hs.25040	zinc finger protein 239	4.40
15	421211	AA284966	Hs.266308	mosaic serine protease	4.40
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	4.40
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	4.37
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT	4.35
	410568	AW162948	Hs.64542	cleavage and polyadenylation specific fa	4.35
20	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	4.35
	448243	AW369771	Hs.52620	integrin, beta 8	4.35
	438069	N80701	Hs.33790	ESTs	4.35
	446152	AI292036	Hs.150028	ESTs	4.34
	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	4.32
25	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.30
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.30
	422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	4.30
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.30
	439619	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	4.30
30	458076	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	4.30
	450192	AA263143	Hs.24596	RAD51-interacting protein	4.29
	443232	AF161521	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	4.28
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibito	4.26
	434217	AW014795	Hs.23349	ESTs	4.26
35	409723	AW885757	Hs.257862	ESTs	4.25
	417956	AA210704	Hs.190465	ESTs	4.25
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	4.25
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.24
40	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	4.22
	424583	AF017445	Hs.150926	fucose-1-phosphate guanylyltransferase	4.20
	429436	AA452934	Hs.279813	hypothetical protein	4.20
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila inaD-like	4.20
	448912	D83781	Hs.22559	KIAA0197 protein	4.20
	442671	AI005668	Hs.134779	EST	4.20
45	411893	R82845	Hs.273789	ESTs	4.20
	456281	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.20
	421106	AA877124	Hs.172844	ESTs	4.20
	451401	AI793163		gb:on52g03.y5 NCI_CGAP_Co8 Homo sapiens	4.20
	404516	NA		NA	4.20
50	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	4.20
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.20
	419229	AI827237	Hs.282884	ESTs	4.18
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	4.16
	453911	AW503857	Hs.4007	Sarcolemmal-associated protein	4.16
55	433159	AB035898	Hs.150587	kinesin-like protein 2	4.15
	419247	S65791	Hs.89764	fragile X mental retardation 1	4.15
	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	4.15
	422093	AF151852	Hs.111449	CGI-94 protein	4.15
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	4.15
60	446999	AA151520	Hs.334822	hypothetical protein MGC4485	4.15
	414538	AW612228	Hs.107987	ESTs	4.14
	453931	AL121278	Hs.25144	ESTs	4.12
	427718	AI798680	Hs.25933	ESTs	4.11
	453863	X02544	Hs.572	orosomucoid 1	4.10
65	440209	HI05049	Hs.22269	neurexin 3	4.10
	435148	AI918049	Hs.124961	ESTs	4.10
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.10
	448692	AW013907	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	4.10
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	4.10
70	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.10
	457059	BE561665	Hs.177677	exosome component Rrp40	4.10
	407162	N63855	Hs.142634	zinc finger protein	4.10
	406117				4.10
	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	4.09
75	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	4.08
	448666	NM_014953	Hs.323346	KIAA1008 protein	4.07
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	4.07
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	4.07
	456030	AA136106	Hs.184852	KIAA1553 protein	4.05
80	434082	AI373481	Hs.131715	hypothetical protein PRO1777	4.05
	443646	AI085198	Hs.164226	ESTs	4.05
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.05
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	4.05
	432619	AW291722	Hs.278526	related to the N terminus of tre	4.05

	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.05
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	4.04
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	4.04
5	424176	AL137273	Hs.142307	hypothetical protein	4.04
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.04
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.03
	435420	AI928513	Hs.59203	ESTs	4.03
	406666	V00495	Hs.184411	albumin	4.02
10	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	4.00
	449448	D60730	Hs.57471	ESTs	4.00
	421037	AI684808	Hs.197653	ESTs	4.00
	448310	AI480316		gb:tm26h09.x1 Soares_NFL_T_GBC_S1 Homo s	4.00
	408155	AB014528	Hs.43133	KIAA0628 gene product	4.00
	413841	M34276	Hs.75576	plasminogen	3.98
15	400110	NA		NA	3.98
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.97
	443715	AI583187	Hs.9700	cyclin E1	3.97
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.97
	450164	AI239923	Hs.30098	ESTs	3.97
20	451592	AI805416	Hs.213897	ESTs	3.95
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome delta	3.95
	426199	AA371865	Hs.97090	ESTs	3.95
	414148	BE084049		gb:PM0-BT0651-270400-003-f02 BT0651 Homo	3.95
25	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	3.94
	449532	W74653	Hs.271593	ESTs, Moderately similar to A47582 B-cel	3.93
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.93
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.92
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.91
30	416185	AW975861	Hs.47367	KIAA1785 protein	3.91
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.90
	432596	AJ224741	Hs.278461	matrilin 3	3.90
	451229	AW967707	Hs.48473	ESTs	3.90
	413583	AL120806	Hs.5888	ESTs	3.90
35	432702	AW973953	Hs.293744	ESTs	3.90
	437207	T27503	Hs.15929	hypothetical protein FLJ12910	3.90
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.90
	423697	BE088697	Hs.131834	Homo sapiens mRNA; cDNA DKFZp434B0328 (f	3.90
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	3.90
40	432289	AI860145	Hs.55118	ESTs	3.89
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.88
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.88
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.88
	410094	BE147897	Hs.58593	general transcription factor IIF, polype	3.88
45	441826	AW503603	Hs.129915	phosphotriesterase related	3.87
	444059	R69743	Hs.116774	integrin, alpha 1	3.86
	426262	AI792141	Hs.196270	folate transporter/carrier	3.85
	452641	AW952893	Hs.237825	signal recognition particle 72kD	3.85
50	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	3.85
	448315	AW290912	Hs.20797	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.85
	411343	U77949	Hs.69563	CDC6 (cell division cycle 6, S. cerevisi	3.85
	409734	BE161664	Hs.56155	hypothetical protein	3.85
	454014	AW016670	Hs.233275	ESTs	3.84
	453116	AI276680	Hs.146086	ESTs	3.83
55	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	3.82
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.82
	435040	AI932350	Hs.152825	ESTs	3.81
	426249	F05422	Hs.168352	nucleoporin-like protein 1	3.81
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	3.81
60	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.81
	437631	AA764749	Hs.267245	hypothetical protein FLJ14803	3.80
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	3.80
	405769				3.80
	438295	AI394151	Hs.37932	ESTs	3.80
65	453628	AW243307	Hs.83937	hypothetical protein	3.80
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	3.80
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.76
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	3.75
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.75
70	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.75
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.74
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	3.74
	418413	R95735	Hs.117753	ESTs, Weakly similar to A48666 cell prol	3.73
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	3.73
75	406667	M12523	Hs.184411	albumin	3.72
	436411	AW674352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	3.72
	417246	AI760098	Hs.21411	ESTs	3.72
	410664	NM_006033	Hs.65370	lipase, endothelial	3.71
	432686	BE223007	Hs.152460	Homo sapiens cDNA FLJ12909 fis, clone NT	3.70
80	442881	AI023175	Hs.167022	ESTs	3.70
	432356	AA831032	Hs.111670	ESTs, Highly similar to JC2257 prolyl ol	3.70
	450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	3.70
	405460	NA		NA	3.70
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.70

	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-1	3.70
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	3.69
	439857	AA847194	Hs.232002	ESTs	3.69
5	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.69
	444471	AB020684	Hs.11217	KIAA0877 protein	3.69
	419559	Y07828	Hs.91096	ring finger protein	3.69
	437641	AA811452	Hs.291911	ESTs	3.68
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.67
10	417791	AW965339	Hs.111471	ESTs	3.66
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.66
	432023	AW273128	Hs.330144	EST	3.66
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.65
	450600	BE079478	Hs.24880	ESTs	3.65
15	420595	AA278865	Hs.88523	ESTs	3.65
	404477	NA	NA	NA	3.65
	457003	S78234	Hs.172405	cell division cycle 27	3.65
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	3.65
	452220	BE158006	Hs.212296	ESTs	3.65
20	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	3.65
	457465	AW301344	Hs.122908	DNA replication factor	3.64
	436149	AI754308	Hs.159452	ESTs	3.63
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	3.63
	427920	Z11502	Hs.181107	annexin A13	3.63
25	424841	AB001106	Hs.151413	glia maturation factor, beta	3.63
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.62
	411975	AI916058	Hs.144583	ESTs	3.61
	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	3.61
	429628	H09604	Hs.13268	ESTs	3.61
30	449722	BE280074	Hs.23960	cyclin B1	3.60
	428389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheti	3.60
	419945	AW290975	Hs.118923	ESTs	3.60
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	3.60
	420585	AW505139	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	3.60
35	407809	AW082279	Hs.244106	ESTs	3.60
	457708	AA805443	Hs.179909	hypothetical protein FLJ22995	3.60
	427943	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.60
	428771	AB028992	Hs.193143	KIAA1069 protein	3.60
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	3.59
40	418688	T85017	Hs.1192	KIAA0074 protein	3.59
	436961	AW375974	Hs.156704	ESTs	3.58
	430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1	3.58
	415245	N59650	Hs.27252	ESTs	3.57
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.55
45	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	3.55
	401165	NA	NA	NA	3.55
	415382	AI743539	Hs.72465	ESTs, Weakly similar to non-lens beta ga	3.55
	433968	AL157518	Hs.90421	PRO2463 protein	3.55
	421528	AB037837	Hs.105461	hypothetical protein FLJ20357	3.55
50	443325	BE398006	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.55
	444355	BE383686	Hs.191621	ESTs, Moderately similar to ALU6_HUMAN A	3.55
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.55
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.55
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	3.55
55	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.54
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.54
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.53
	432542	AW083920	Hs.16098	claudin 2	3.53
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.52
60	423441	R68649	Hs.278359	absent in melanoma 1 like	3.51
	452940	AA029722	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.51
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	3.50
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.48
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.48
65	449915	NM_004529	Hs.404	myeloid/lymphoid or mixed-lineage leukem	3.47
	427975	AI536065	Hs.122460	ESTs	3.46
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	3.45
	404253				3.45
	435567	AW504944	Hs.162990	Homo sapiens cDNA FLJ14193 fis, clone NT	3.45
70	432158	W33165	Hs.22983	UDP-glucose:glycoprotein glucosyltransfe	3.45
	417315	AI080042	Hs.336901	ribosomal protein S24	3.45
	419140	AI982647	Hs.215725	ESTs	3.44
	446901	AI347274		gb:tc05d02.x1 NCL_CGAP_Co16 Homo sapiens	3.43
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.42
75	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.42
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	3.41
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.41
	419131	AA406293	Hs.41167	ESTs	3.41
	430264	AA470519		gb:nc71f10.s1 NCL_CGAP_Pr1 Homo sapiens	3.40
80	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	3.40
	453531	AA417940	Hs.271400	ESTs, Weakly similar to JC5795 CDEP prot	3.40
	444826	AI674482	Hs.148441	ESTs	3.40
	445354	AV653485	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA,	3.40
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.40

	418939	AW630803	Hs.89497	lamin B1	3.40
	418134	AA397769	Hs.86617	ESTs	3.40
	430544	AA481066	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	3.39
5	427927	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.39
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.39
	410406	AI969703	Hs.1466	glycerol kinase	3.38
	408494	AA554714	Hs.187578	Homo sapiens cDNA FLJ11639 fis, clone HE	3.38
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypotheti	3.38
10	446432	AI377320	Hs.150058	ESTs	3.36
	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	3.35
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.35
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	3.35
	421039	NM_003478	Hs.101299	cullin 5	3.35
15	407819	R42185	Hs.274803	ESTs	3.35
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	3.35
	433361	AW469373	Hs.300141	ribosomal protein L39	3.35
	435022	AW183385	Hs.54627	ESTs, Weakly similar to FTDH_HUMAN 10-FO	3.35
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	3.35
20	454018	AW016892	Hs.100855	ESTs	3.35
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	3.35
	453941	U39817	Hs.36820	Bloom syndrome	3.34
	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.33
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.33
25	438008	AA775026	Hs.203802	ESTs	3.33
	421246	AW582962	Hs.102897	CGI-47 protein	3.33
	451707	AW051061	Hs.60973	ESTs	3.33
	457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0	3.31
	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.31
30	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.31
	438746	AI885815	Hs.184727	ESTs	3.30
	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	3.30
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	3.30
	458855	AW361299	Hs.107000	hypothetical protein FLJ11294	3.30
35	417221	AW379029	Hs.118338	ESTs, Weakly similar to unnamed protein	3.30
	424770	AA425562	Hs.11065	Homo sapiens HDCME13P mRNA, partial cds	3.30
	417720	AA205625	Hs.208067	ESTs	3.29
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	3.29
	452862	AW378065	Hs.8687	ESTs	3.28
40	414343	AL036166	Hs.323378	coated vesicle membrane protein	3.28
	437222	AL117588	Hs.12778	ESTs	3.28
	422665	AJ011812	Hs.119018	transcription factor NRF	3.28
	414706	AW340125	Hs.76589	KIAA0097 gene product	3.28
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	3.27
45	447829	AI433029	Hs.164104	ESTs	3.27
	427576	BE242611	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.27
	456132	BE219771	Hs.237146	hypothetical protein FLJ12752	3.26
	407305	AA715284		gb:nv35f03.r1 NCL_CGAP_Br5 Homo sapiens	3.26
50	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.26
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	3.25
	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypotheti	3.25
	453320	AW450240	Hs.257274	ESTs	3.25
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.25
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	3.25
55	410659	AI080175	Hs.68826	ESTs	3.25
	446202	AI279706	Hs.149474	ESTs	3.25
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	3.25
	439262	AA832333	Hs.333045	ESTs	3.25
	401823	NA		NA	3.25
60	441264	AA927170	Hs.23290	ESTs	3.25
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.24
	408321	AW405882	Hs.44205	cortistatin	3.24
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	3.24
	404519				3.24
65	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.23
	422660	AW297582	Hs.103267	hypothetical protein FLJ22548 similar to	3.23
	427961	AW293165	Hs.143134	ESTs	3.22
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	3.22
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.21
70	458652	AW375610	Hs.117102	hypothetical protein FLJ13046 similar to	3.21
	426472	BE246138	Hs.30853	ESTs	3.21
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.21
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.21
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.20
75	443162	T49951	Hs.9029	DKFZP434G032 protein	3.20
	431678	AW072372	Hs.267446	hypothetical protein FLJ11184	3.20
	430439	AL133561	Hs.241426	DKFZP434B061 protein	3.20
	407201	N31998	Hs.164256	hypothetical protein FLJ20657	3.20
	437905	AW363121	Hs.175596	ESTs, Weakly similar to T26935 hypotheti	3.20
80	434160	BE551196	Hs.114275	ESTs	3.20
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	3.20
	412966	BE243311	Hs.8024	IK cytokine, down-regulator of HLA II	3.19
	414386	X00442	Hs.75990	haptoglobin	3.19
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	3.18

	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.18
	433764	AW753676	Hs.39982	ESTs	3.17
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypotheti	3.17
5	429616	AI982722	Hs.120845	ESTs	3.17
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.16
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.16
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.16
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.15
10	443830	AI142095	Hs.143273	ESTs	3.15
	413516	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo	3.15
	433527	AW235613	Hs.133020	ESTs	3.15
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.15
	457453	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.15
15	427687	AW003867	Hs.1570	histamine receptor H1	3.15
	455068	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.15
	441720	AI346487	Hs.28739	ESTs	3.15
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	3.15
	445921	AW015211	Hs.146181	ESTs	3.15
20	429957	AW204530	Hs.99500	ESTs	3.15
	403137				3.14
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	3.14
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	3.14
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.14
25	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.14
	439277	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	3.13
	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	3.13
	406668	T62745	Hs.184411	albumin	3.13
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	3.13
30	437594	AA761431	Hs.74335	heat shock 90kD protein 1, beta	3.13
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.13
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	3.13
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	3.11
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	3.11
35	441790	AW294909	Hs.132208	ESTs	3.11
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	3.10
	449664	R06212	Hs.127733	ESTs	3.10
	435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.10
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.10
40	402963				3.10
	428967	AW978441	Hs.296100	ESTs	3.10
	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo	3.10
	407502	U52096		gb:Human zinc finger protein (kr-znf1) m	3.10
45	426853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	3.10
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.10
	421056	AI076890	Hs.146847	TRAF family member-associated NFKB activ	3.10
	420617	AK001652	Hs.99423	ATP-dependent RNA helicase	3.10
	421841	AA908197	Hs.108850	MAK-related kinase	3.10
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	3.10
50	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	3.10
	433037	NM_014158	Hs.279938	HSPC067 protein	3.09
	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	3.09
	457726	AI217477	Hs.194591	ESTs	3.09
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	3.08
55	433013	AI697890	Hs.127337	axin 2 (conductin, axil)	3.08
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.08
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL_HUMAN SORTI	3.07
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.07
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	3.07
60	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	3.07
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.07
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	3.06
	436554	AI985810	Hs.301173	ESTs	3.06
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	3.06
65	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	3.06
	445413	AA151342	Hs.12677	CGI-147 protein	3.06
	452909	NM_015368	Hs.30985	pannexin 1	3.06
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	3.05
	425942	AU077195	Hs.164036	glucosamine (N-acetyl)-6-sulfatase (Sanf	3.05
70	406333				3.05
	428454	U55936	Hs.184376	synaposomal-associated protein, 23kD	3.05
	411864	AW948147		gb:RC0-MT0013-280300-031-e03 MT0013 Homo	3.05
	458632	AI744445	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.05
	448292	BE281316	Hs.47334	hypothetical protein FLJ14495	3.05
75	459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypotheti	3.05
	402167				3.05
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	3.05
	437828	AW976806	Hs.73149	paired box gene 8	3.05
	404232				3.05
80	418164	AI761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	3.05
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.05
	452787	AW294022	Hs.222707	KIAA1718 protein	3.05
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.05
	410718	AI920783	Hs.191435	ESTs	3.04

	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.04
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.03
	425492	AL021918	Hs.158174	zinc finger protein 184 (Krueppel-like)	3.02
5	452834	AI638627	Hs.105685	KIAA1688 protein	3.02
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.02
	416568	H64844	Hs.138558	ESTs	3.02
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.02
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	3.01
10	412719	AW016610	Hs.129911	ESTs	3.01
	439586	AA922936	Hs.110039	ESTs	3.01
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	3.01
	429703	T93154	Hs.28705	ESTs	3.00
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.00
	415261	T40928	Hs.8346	ESTs	3.00
15	419435	AI200540	Hs.14877	ESTs, Weakly similar to (define not ava	3.00
	429985	NM_015836	Hs.227274	tryptophanyl tRNA synthetase 2 (mitochon	3.00
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.00
	407182	AA312551	Hs.230157	ESTs	3.00
	424202	BE350295	Hs.15032	RAN binding protein 17	3.00
20	444585	AW170015	Hs.6594	ESTs	3.00
	420552	AK000492	Hs.98806	hypothetical protein	3.00
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	3.00
	441928	AI370188	Hs.211454	ESTs	3.00
	430888	BE155293	Hs.76064	ribosomal protein L27a	3.00
25	417806	AI867277	Hs.183733	ESTs	3.00
	447175	AI365208	Hs.293606	ESTs	3.00
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	3.00
	435447	AI872932		gb:wm72e03.x1 NCL_CGAP_U12 Homo sapiens	3.00
	405394				3.00
30	454975	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.00
	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	3.00
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.00

TABLE 6B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT number	Accession
45	411765	125700_1 H43346 AA248302 AA095182
	411864	1262055_1 AW948147 BE092318 AW948138 AW948130 AW948148 AW948129 AW948136 AW948152 AW948144 AW948137 AW948160
	412359	129085_1 AW837985 AW837938 AA101955 AW837913 AW837935
	413516	1374595_1 BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856
	414148	142133_1 BE084049 AW292907 AA135984
50	424492	240008_1 AI133482 AI207619 AA341626
	430264	315008_1 AA470519 BE303010 BE302954 BE384120
	431064	327472_1 AI903735 AA491283 AI694953 AW976903 AA761362
	433687	373061_1 AA743991 AA604852 AW272737
	434414	38585_1 AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
55		AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
		AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730
		AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957
		N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
		BE081531 H59570
60	435447	406400_1 AI872932 AA682306 BE220163 W88695 T81307 H91447
	436411	419334_1 AW674352 AA715374 Z25205
	443613	575391_1 AI079356 W23287
	446901	697809_1 AI347274 AW844024
	448310	757918_1 AI480316 AW847535
65	451401	868474_1 AI793163 AW875182 AW875178 AW875176
	454403	1170435_1 BE065985 BE065944 BE066008 BE066083 BE066093
	454975	1247077_1 AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
		AW848214
70	455838	1374605_1 BE145808 BE145807 BE181883

TABLE 6C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NT\_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	400534	6981826	Minus	278637-279292
	401165	9438376	Minus	168244-168423
	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401644	8576138	Plus	82655-83959
	401823	2262095	Minus	42575-42697,43189-43287,45830-45974
10	402167	8571795	Plus	109122-110357
	402963	5419653	Minus	12950-15959
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403776	7770611	Minus	1414-1513,1624-1756
	404025	7341444	Plus	131740-131905
15	404232	8218045	Minus	71800-71956
	404253	9367202	Minus	55675-56055
	404477	8080699	Plus	113390-113577
	404516	8151967	Plus	114153-114322
	404519	8152000	Plus	12817-13000
20	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405394	6624123	Minus	31900-32373
	405460	7684569	Minus	52223-52389
	405769	3046270	Minus	76844-77193
25	406117	9142932	Plus	54304-54584
	406333	9213235	Plus	64689-64798
	406360	9256107	Minus	7513-7673
	406414	9256407	Plus	49593-49850

### 30 TABLE 7A: 516 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

Table 7A lists 516 genes up-regulated in colon cancer compared to normal colon. These were selected as for Table 6A except for using all CEP and colon sample in the normal body tissue list as the normal samples in determining the denominator value and the ratio was equal to or greater than 5.0.

35	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title
	R1:	Ratio of tumor to normal colon

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
45	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	57.52
	406667	M12523	Hs.184411	albumin	49.94
	409041	AB033025	Hs.50081	KIAA1199 protein	49.18
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	42.22
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	34.64
50	429201	X03178	Hs.198246	group-specific component (vitamin D bind	33.38
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	33.10
	447033	AI357412	Hs.157601	ESTs	31.24
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	26.84
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	25.40
55	413841	M34276	Hs.75576	plasminogen	24.68
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	23.18
	452862	AW378065	Hs.8687	ESTs	21.34
	415989	AI267700	Hs.317584	ESTs	20.92
60	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.22
	421470	R27496	Hs.1378	annexin A3	17.92
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	17.36
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.28
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.08
65	421462	AF016495	Hs.104624	aquaporin 9	17.02
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	16.98
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	16.70
	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	16.64
	433447	U29195	Hs.3281	neuronal pentraxin II	16.59
70	414386	X00442	Hs.75990	haptoglobin	16.19
	425260	L47726	Hs.1870	phenylalanine hydroxylase	16.08
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	15.82
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	15.80
	443211	AI128388	Hs.143655	ESTs	15.78
75	439608	AW864696	Hs.301732	hypothetical protein MGC5306	15.52
	414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	15.42
	412719	AW016610	Hs.129911	ESTs	15.24
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	15.18
	448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	15.03



	416402	NM_000715	Hs.1012	complement component 4-binding protein,	14.60
	453863	X02544	Hs.572	orosomucoid 1	14.35
	441243	AI767056	Hs.193002	ESTs	14.30
5	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	14.30
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	13.91
	433213	AW665130	Hs.137190	ESTs	13.80
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	13.52
	438578	AA811244	Hs.164168	ESTs	13.40
10	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	13.36
	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	13.00
	449199	AI990122	Hs.196988	ESTs	12.98
	436393	AW022213	Hs.143617	ESTs	12.90
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	12.83
15	451561	N52812	Hs.177403	ESTs	12.72
	420734	AW972872	Hs.293736	ESTs	12.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	12.50
	441377	BE218239	Hs.202656	ESTs	12.45
	435981	H74319	Hs.188620	ESTs	12.38
20	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	12.38
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.38
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypotheti	12.34
	430290	AI734110	Hs.136355	ESTs	12.30
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.26
25	450628	AW382884	Hs.204715	ESTs	12.24
	446232	AI281848	Hs.194691	retinoic acid induced 3	12.16
	428223	AA424313	Hs.98402	ESTs	12.08
	432582	AI623817	Hs.168457	ESTs	12.08
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	12.02
30	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	12.01
	407202	N58172	Hs.109370	ESTs	11.84
	422109	S73265	Hs.1473	gastrin-releasing peptide	11.68
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	11.68
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	11.67
35	443162	T49951	Hs.9029	DKFZP434G032 protein	11.67
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.62
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	11.46
	453909	AW004045	Hs.203365	ESTs	11.42
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	11.34
40	452903	AI953425	Hs.246911	ESTs, Weakly similar to I38022 hypotheti	11.32
	433011	H07960	Hs.306044	CGI-05 protein	11.30
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	11.22
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	11.20
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	11.08
45	407168	R45175	Hs.117183	ESTs	10.91
	407633	NM_007069	Hs.37189	similar to rat HREV107	10.90
	400534				10.88
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	10.76
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	10.68
50	440526	AI832243	Hs.211471	ESTs	10.63
	427544	AI767152	Hs.181400	ESTs, Weakly similar to I78885 serine/th	10.62
	447794	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	10.52
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	10.52
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
55	457065	AI476318	Hs.192480	ESTs	10.40
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.38
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	10.34
	414718	H95348	Hs.107987	ESTs	10.29
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	10.28
60	404567				10.14
	428536	AI143139	Hs.2288	visinin-like 1	10.06
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.05
	437267	AW511443	Hs.258110	ESTs	10.00
	420583	H77859	Hs.65450	reticulon 4	10.00
65	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	9.99
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	9.97
	449655	AI021987	Hs.59970	ESTs	9.91
	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.90
	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	9.90
70	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	9.88
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.84
	448106	AI800470	Hs.171941	ESTs	9.64
	439192	AW970536	Hs.105413	ESTs	9.64
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	9.61
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	9.50
75	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	9.44
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	9.40
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	9.36
	401742	NA		NA	9.30
80	416393	N54037	Hs.262869	plasminogen-like	9.28
	413339	AI818080	Hs.194290	ESTs	9.28
	437641	AA811452	Hs.291911	ESTs	9.28
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	9.22
	431319	AA873350	Hs.302232	ESTs	9.21

	434008	AA740878	Hs.112982	ESTs	9.20
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.16
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	9.16
5	413597	AW302885	Hs.117183	ESTs	9.15
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	9.14
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	9.14
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	9.05
	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	8.98
10	450164	AI239923	Hs.30098	ESTs	8.95
	432867	AW016936	Hs.233364	ESTs	8.93
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	8.92
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	8.92
	452712	AW838616		gb:RC5-LT0054-140200-013-D01 LT0054 Homo	8.90
15	419131	AA406293	Hs.41167	ESTs	8.86
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	8.82
	418895	AA894638	Hs.14600	ESTs	8.82
	422665	AJ011812	Hs.119018	transcription factor NRF	8.82
	409757	NM_001898	Hs.123114	cystatin SN	8.78
20	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	8.74
	412446	AI768015	Hs.92127	ESTs	8.71
	433285	AW975944	Hs.237396	ESTs	8.68
	414538	AW612228	Hs.107987	ESTs	8.64
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	8.62
25	430835	AI240006	Hs.192326	ESTs	8.60
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	8.59
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	8.52
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	8.52
	428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	8.50
30	444478	W07318	Hs.240	M-phase phosphoprotein 1	8.47
	439398	AA284267	Hs.221504	ESTs	8.44
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	8.43
	403776				8.42
	418973	AA233056	Hs.191518	ESTs	8.42
35	445436	AI224105	Hs.151408	ESTs	8.38
	417958	AA767382	Hs.193417	ESTs	8.34
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	8.34
	425761	AW664214	Hs.196729	ESTs	8.33
	449419	R34910	Hs.119172	ESTs	8.29
40	407007	U22961		gb:Human mRNA clone with similarity to L	8.28
	420900	AL045633	Hs.44269	ESTs	8.25
	452503	AB000509	Hs.29736	TNF receptor-associated factor 5	8.23
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.18
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.16
45	432363	AA534489		gb:nf76g11.s1 NCL_CGAP_Co3 Homo sapiens	8.16
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	8.12
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	418379	AA218940	Hs.137516	fidgeline-like 1	8.07
	424560	AA158727	Hs.150555	protein predicted by clone 23733	8.06
50	453116	AI276680	Hs.146086	ESTs	8.04
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.04
	409687	T51125	Hs.8493	ESTs	8.00
	407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	8.00
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
55	418036	Z37976	Hs.83337	latent transforming growth factor beta b	7.99
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	7.96
	421633	AF121860	Hs.106260	sorting nexin 10	7.92
	432542	AW083920	Hs.16098	claudin 2	7.86
	414869	AA157291	Hs.21479	ubiquitin 1	7.84
60	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	7.80
	406666	V00495	Hs.184411	albumin	7.78
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.78
	439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT	7.77
	406360	NA		NA	7.76
65	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	7.76
	431510	AA580082	Hs.112264	ESTs	7.76
	414312	AA155694	Hs.191060	ESTs	7.71
	443450	N66045	Hs.133529	ESTs	7.70
	449870	AI672487	Hs.15423	hypothetical protein HDCMC04P	7.64
70	425681	AB018297	Hs.159183	KIAA0754 protein	7.63
	408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	7.62
	443285	AI301918	Hs.334264	ESTs	7.60
	420807	AA280627	Hs.57846	ESTs	7.60
	424650	AW576156	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	7.60
75	410718	AI920783	Hs.191435	ESTs	7.60
	430848	AW021726		gb:df27e02.y1 Morton Fetal Cochlea Homo	7.60
	434294	AJ271379	Hs.76194	ribosomal protein S5	7.60
	445808	AV655234	Hs.298083	ESTs, Moderately similar to PC4259 ferri	7.56
	438604	AA811896	Hs.44604	ESTs	7.54
80	458997	AW937420	Hs.69662	ESTs	7.54
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.54
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	7.52
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	7.49
	404996				7.48

	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.48
	433859	AW896758	Hs.273789	ESTs	7.44
	423952	AW877787	Hs.136102	KIAA0853 protein	7.44
5	431193	AW749505	Hs.296770	KIAA1719 protein	7.43
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	7.40
	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	7.40
	424613	AL079850	Hs.151236	highly charged protein	7.37
	417720	AA205625	Hs.208067	ESTs	7.35
10	449347	AV649748	Hs.295901	KIAA0493 protein	7.34
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	7.34
	447499	AW262580	Hs.147674	protocadherin beta 16	7.32
	426890	AA393167	Hs.41294	ESTs	7.31
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	7.28
	445019	AI205540	Hs.281295	ESTs	7.28
15	419474	AW968619	Hs.155849	ESTs	7.24
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	7.24
	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	7.24
	448816	AB033052	Hs.22151	KIAA1226 protein	7.18
20	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	7.18
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	7.18
	420777	AA280223	Hs.130865	ESTs	7.16
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	7.14
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.14
25	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.14
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	7.13
	441124	T97717	Hs.119563	ESTs	7.12
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	7.10
	446432	AI377320	Hs.150058	ESTs	7.10
30	439295	AW206091	Hs.253536	ESTs	7.08
	436902	AW247145	Hs.192729	ESTs	7.08
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	7.08
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	7.08
	421373	AA808229	Hs.167771	ESTs	7.06
35	432435	BE218866	Hs.282070	ESTs	7.05
	427933	AW974643	Hs.190571	ESTs	7.04
	436330	NM_004413	Hs.109	dipeptidase 1 (renal)	7.04
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	7.01
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	6.98
40	446322	N23033	Hs.155814	ESTs	6.98
	442577	AA292998	Hs.163900	ESTs	6.96
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.94
	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	6.92
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	6.90
45	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	6.90
	453204	R10799	Hs.191990	ESTs	6.90
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.88
	427878	C05766	Hs.181022	CGI-07 protein	6.88
	454438	AA224053	Hs.172405	cell division cycle 27	6.86
50	424402	M63108	Hs.1769	lutinizing hormone/choriogonadotropin r	6.86
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.84
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	419629	AB020695	Hs.91662	KIAA0888 protein	6.80
55	451686	AA059246	Hs.110293	ESTs	6.80
	430829	AW451999	Hs.194024	ESTs	6.78
	446501	AI302616	Hs.150819	ESTs	6.78
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.78
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.76
60	437773	U24186	Hs.283018	replication protein A complex 34 kd subu	6.73
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	6.72
	425478	AB007953	Hs.268840	ESTs	6.70
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	6.70
	418555	AI17215	Hs.87159	hypothetical protein FLJ12577	6.67
65	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	6.62
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.62
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.60
	450480	X82125	Hs.25040	zinc finger protein 239	6.58
	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.56
70	414575	H11257	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	6.54
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	6.54
	410116	AW630671	Hs.58636	squamous cell carcinoma antigen recogniz	6.54
	449894	AK001578	Hs.24129	CLLL7 protein	6.53
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	6.53
75	424745	AA214618	Hs.152759	activator of S phase kinase	6.52
	441801	AW242799	Hs.86366	ESTs	6.52
	435542	AA687376	Hs.269533	ESTs	6.51
	427072	H38046	Hs.303193	ESTs	6.50
	418051	AW192535	Hs.19479	ESTs	6.46
80	436217	T53925	Hs.107	fibrinogen-like 1	6.46
	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.46
	430704	AW813091	Hs.335799	ESTs	6.44
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.43
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	6.41

	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	438202	AW169287	Hs.22588	ESTs	6.38
5	458311	AF069478		gb:AF069478 Homo sapiens astrocytoma lib	6.36
	451389	N73222	Hs.279009	matrix Gla protein	6.36
	427899	AA829286	Hs.332053	serum amyloid A1	6.35
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.34
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.34
10	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	6.32
	433908	AW298141	Hs.157975	ESTs	6.32
	430114	AA847744	Hs.99640	ESTs	6.32
	434032	AW009951	Hs.206892	ESTs	6.31
	444656	AI277924	Hs.145199	ESTs	6.30
	433607	AA602004	Hs.23260	ESTs	6.26
15	440659	AF134160	Hs.7327	claudin 1	6.25
	435663	AI023707	Hs.134273	ESTs	6.24
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.24
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	6.24
	447500	AI381900	Hs.159212	ESTs	6.24
20	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.22
	417715	AW969587	Hs.86366	ESTs	6.22
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	6.20
	438138	R98299	Hs.177502	ESTs	6.20
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	6.20
25	416857	AA188775	Hs.292453	ESTs	6.20
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.18
	429598	AA811257	Hs.269710	ESTs	6.18
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.18
30	438940	AF075045	Hs.271609	ESTs	6.18
	400195	NA		NA	6.15
	430473	AW130690	Hs.59962	ESTs	6.12
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.10
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.10
	427513	AI476318	Hs.192480	ESTs	6.10
35	448934	AI598134	Hs.225592	ESTs, Highly similar to T51146 ring-box	6.10
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	6.08
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	6.08
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	6.08
40	409048	H59990	Hs.37699	ESTs	6.08
	427674	NM_003528	Hs.2178	H2B histone family, member Q	6.08
	452689	F33868	Hs.284176	transferrin	6.06
	453804	AA300204	Hs.35276	KIAA0852 protein	6.06
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	6.05
45	408243	Y00787	Hs.624	interleukin 8	6.04
	420721	AA927802	Hs.159471	ZAP3 protein	6.04
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	6.04
	435420	AI928513	Hs.59203	ESTs	6.04
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	6.04
50	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.02
	442116	AI884570	Hs.128813	ESTs	6.00
	423568	NM_005256	Hs.129818	growth arrest-specific 2	6.00
	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	5.99
	441794	AW197794	Hs.253338	ESTs	5.99
55	434739	AA804487	Hs.144130	ESTs	5.98
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.96
	420218	AW958037	Hs.286	ribosomal protein L4	5.96
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	5.94
	445546	AW468821	Hs.156054	ESTs	5.94
60	439095	AA830185	Hs.269680	ESTs	5.94
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.94
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.94
	417246	AI760098	Hs.21411	ESTs	5.94
	433190	M26901	Hs.3210	renin	5.92
65	418744	AI887288	Hs.196379	ESTs, Weakly similar to putative p150 [H	5.92
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.92
	434342	AI791138	Hs.116768	ESTs	5.92
	406668	T62745	Hs.184411	albumin	5.92
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.90
70	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	5.90
	408867	AA437199	Hs.656	cell division cycle 25C	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.88
	450380	AI863675	Hs.114017	ESTs	5.88
	413026	AA809485	Hs.124219	hypothetical protein FLJ12934	5.88
75	454653	AW812227		gb:RC2-ST0173-201099-011-g09 ST0173 Homo	5.87
	457876	AI821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	5.86
	437222	AL117588	Hs.12778	ESTs	5.86
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	5.86
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	5.84
80	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	5.84
	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.84
	401352				5.84
	419088	AI538323	Hs.52620	integrin, beta 8	5.84
	431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	5.83

	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	5.82
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.82
	419220	AA811938	Hs.291759	ESTs	5.82
5	439303	W00605	Hs.102784	ESTs	5.80
	415954	AA171850	Hs.42251	ESTs	5.80
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	5.80
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	439527	AW298119	Hs.202536	ESTs	5.78
10	435380	AA679001	Hs.192221	ESTs	5.78
	424086	AI351010	Hs.102267	lysyl oxidase	5.76
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	5.76
	428460	AA428865	Hs.98563	ESTs	5.74
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	5.74
	413982	BE503035	Hs.279193	ESTs	5.74
15	453240	AI969564	Hs.166254	hypothetical protein DKFZp566i133	5.74
	410505	AW752139	Hs.314323	ESTs	5.72
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.72
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	5.72
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	5.71
20	433384	AI021992	Hs.124244	ESTs	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	5.68
25	448666	NM_014953	Hs.323346	KIAA1008 protein	5.68
	412246	AI160873	Hs.69233	zinc finger protein	5.68
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.66
	418269	AA806113	Hs.189025	ESTs	5.64
	443316	AI478463	Hs.18443	aldehyde dehydrogenase 8 family, member	5.64
	422805	AA436989	Hs.121017	H2A histone family, member A	5.62
30	442252	AI733395	Hs.129124	ESTs	5.60
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.60
	435040	AI932350	Hs.152825	ESTs	5.59
	438777	AA825487	Hs.142179	ESTs	5.58
	433849	BE465884	Hs.280728	ESTs	5.58
35	438639	AI278360	Hs.31409	ESTs	5.58
	411274	NM_002776	Hs.69423	kallikrein 10	5.55
	435008	AF150262	Hs.162898	ESTs	5.55
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	5.54
40	452881	AW135220	Hs.241921	ESTs	5.54
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.54
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.54
	418971	AA360392	Hs.87113	ESTs	5.52
	453716	AA037675	Hs.152675	ESTs	5.52
45	406972	M32053		gb:Human H19 RNA gene, complete cds.	5.51
	417543	AA203620	Hs.110153	ESTs	5.51
	419423	D26488	Hs.90315	KIAA0007 protein	5.51
	434674	AA831879	Hs.136985	ESTs	5.50
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
50	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
	404227	NA		NA	5.49
	412766	BE544475	Hs.54347	ESTs	5.49
	441708	AI469911	Hs.26498	hypothetical protein FLJ21657	5.49
	408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	5.48
55	437440	AA846804	Hs.123694	ESTs	5.48
	410486	AW235094	Hs.69233	zinc finger protein	5.46
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.44
	437378	AI198823	Hs.160473	ESTs	5.44
	436907	AA737171	Hs.131809	ESTs	5.44
60	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.44
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.42
	441795	N58115	Hs.21137	AD024 protein	5.42
	452449	AW068658	Hs.20943	ESTs	5.42
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.40
65	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	5.40
	441217	AI922183	Hs.213246	ESTs	5.40
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone CO	5.40
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	5.40
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	5.40
70	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	5.39
	446142	AI754693	Hs.145968	ESTs	5.38
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	5.36
	433929	AI375499	Hs.27379	ESTs	5.36
	421155	H87879	Hs.102267	lysyl oxidase	5.34
75	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.34
	453931	AL121278	Hs.25144	ESTs	5.34
	409091	AW970386	Hs.269423	ESTs	5.33
	416057	AI927382	Hs.29857	ESTs	5.33
	438647	AA813118	Hs.163230	ESTs	5.32
80	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.32
	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.30
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.30
	403432				5.29
	435820	AA700580	Hs.189000	ESTs	5.28

	401714	NA	NA	5.28
	449508	AK001566	Hs.23618 hypothetical protein FLJ10704	5.28
	413151	H47969	Hs.141971 ESTs, Weakly similar to ALU1_HUMAN ALU S	5.28
	414853	U31116	Hs.77501 sarcoglycan, beta (43kD dystrophin-assoc	5.28
5	417372	T99755	Hs.334728 ESTs	5.28
	443613	AI079356	gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	5.28
	412610	X90908	Hs.74126 fatty acid binding protein 6, ileal (gas	5.27
	408943	NM_007070	Hs.49105 FKBP-associated protein	5.26
10	415139	AW975942	Hs.48524 ESTs	5.26
	447982	H22953	Hs.137551 ESTs	5.26
	430789	AA632577	Hs.310235 ESTs, Weakly similar to I78885 serine/th	5.24
	453921	AI824009	Hs.44577 ESTs	5.24
	409582	R27430	Hs.271565 ESTs	5.24
	420911	U77413	Hs.100293 O-linked N-acetylglucosamine (GlcNAc) tr	5.23
15	422956	BE545072	Hs.122579 hypothetical protein FLJ10461	5.23
	418661	NM_001949	Hs.1189 E2F transcription factor 3	5.22
	446271	D82484	Hs.330994 ESTs	5.22
	435905	AW997484	Hs.5003 KIAA0456 protein	5.21
20	434551	BE387162	Hs.280858 ESTs, Highly similar to A35661 DNA excis	5.21
	415245	N59650	Hs.27252 ESTs	5.20
	436016	AA806465	Hs.121536 Human DNA sequence from clone RP11-472E5	5.20
	431242	AA987742	Hs.251278 KIAA1201 protein	5.20
	439818	AL360137	Hs.19934 Homo sapiens mRNA full length insert cDN	5.20
25	424281	AA766243	gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	5.20
	449138	AW294215	Hs.195631 ESTs	5.20
	449416	AI651016	Hs.246311 ESTs	5.20
	430092	AI821399	Hs.16514 ESTs	5.20
	436574	AW293527	Hs.126465 ESTs	5.18
30	433377	AI752713	Hs.43845 ESTs	5.18
	440987	AA911705	Hs.130229 ESTs	5.18
	426116	AA868729	Hs.144694 ESTs	5.18
	441928	AI370188	Hs.211454 ESTs	5.17
	432657	AA831815	Hs.270940 ESTs, Weakly similar to I78885 serine/th	5.17
35	438011	BE466173	Hs.145696 splicing factor (CC1.3)	5.16
	437257	AI283085	Hs.290931 ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.16
	423926	X03833	Hs.1722 interleukin 1, alpha	5.16
	433393	AF038564	Hs.98074 itchy (mouse homolog) E3 ubiquitin prote	5.15
	415757	AA830854	Hs.187810 ESTs	5.14
40	420170	U43374	Hs.95631 Human normal keratinocyte mRNA	5.14
	420493	AI635113	Hs.270366 ESTs, Weakly similar to I78885 serine/th	5.12
	425739	T19016	Hs.159410 molybdopterin synthase sulfurylase	5.12
	440652	AI216751	Hs.143977 ESTs	5.12
	419706	C04649	Hs.77899 tropomyosin 1 (alpha)	5.12
45	427728	AJ245600	Hs.180545 Homo sapiens mRNA for hypothetical prote	5.12
	416113	AA173525	Hs.118758 ESTs, Weakly similar to RLF [H.sapiens]	5.12
	446223	BE300091	Hs.119699 hypothetical protein FLJ12969	5.11
	407624	AW157431	Hs.248941 ESTs	5.11
	447197	R36075	gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.11
50	452465	AA610211	Hs.34244 ESTs	5.10
	442833	AA328153	Hs.88201 ESTs, Weakly similar to A Chain A, Cryst	5.10
	448952	AI609595	Hs.208038 ESTs	5.10
	408170	AW204516	Hs.31835 ESTs	5.08
	424238	AA337401	Hs.137635 ESTs	5.07
55	421072	AI215069	Hs.89113 ESTs	5.06
	424717	H03754	Hs.152213 wingless-type MMTV integration site fami	5.06
	423654	AI674253	Hs.35828 ESTs	5.06
	436862	AI821940	Hs.264622 ESTs, Moderately similar to ALU8_HUMAN A	5.06
	436554	AI985810	Hs.301173 ESTs	5.05
60	433264	D85782	Hs.3229 cysteine dioxygenase, type I	5.04
	452387	AI680772	Hs.306094 trinucleotide repeat containing 12	5.04
	412666	AL080116	Hs.74420 origin recognition complex, subunit 3 (y	5.03
	430287	AW182459	Hs.125759 ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.03
	413293	AL047483	Hs.302498 GTP-binding protein homologous to Saccha	5.00
65	418217	AI910647	Hs.13442 ESTs	5.00
	401480	NA	NA	5.00
	456179	H75490	Hs.271930 ESTs	5.00

TABLE 7B

70	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
<hr/>			
75	Pkey	CAT number	Accession
	408432	1058667_1	AW195262 R27868 AW811262
	408690	107490_1	AW864542 AA056567 AW882724
	411765	125700_1	H43346 AA248302 AA095182
	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
80	424281	237742_1	AA766243 AA338252 AA338213

5	424492	240008_1	AI133482 AI207619 AA341626
	428679	294049_1	AA431765 AA432015
	430848	324621_1	AW021726 AA487752 AA488085
	432340	345248_1	AA534222 AA632632 T81234
	432363	345469_1	AA534489 AW970240 AW970323
	432639	351744_1	AW973785 H60163 AA557608
	434609	38950_1	R76593 AF147390 R76594
	439518	47334_1	W76326 AF086341 W72300
10	443613	575391_1	AI079356 W23287
	447197	711623_1	R36075 AI366546 R36167
	447974	745643_1	R76886 AI453674 R77049
	452712	928309_1	AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784
	454653	1228081_1	AW812227 AW812294 AW812092
15	458311	543550_1	AF069478 AF069479 AF069480

TABLE 7C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

25	Pkey	Ref	Strand	Nt_position
	400534	6981826	Minus	278637-279292
	401352	9931258	Minus	26064-26208
30	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401714	6715702	Plus	96484-96681
	401742	2911728	Plus	64003-64147
	403432	9719611	Minus	68204-68392
	403776	7770611	Minus	1414-1513,1624-1756
	404227	7838233	Minus	93110-93259
35	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	406360	9256107	Minus	7513-7673

40 Table 8A shows 538 genes significantly down-regulated in colon cancer compared to normal colon. These were selected as for Table 7A and the ratio was equal to or less than than 0.33.

TABLE 8A: 538 GENES SIGNIFICANTLY DOWN-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

45	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title
50	R1:	Ratio of tumor to normal colon

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
55	421996	AW583807	Hs.1460	glucagon	0.0233
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	0.0307
	457407	AA505035	Hs.195651	ESTs	0.0416
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	0.0564
	426651	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.0567
60	425920	AL049977	Hs.162209	claudin 8	0.0601
	431436	AA505035	Hs.195651	ESTs	0.0607
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.0629
	442009	AI733281	Hs.128320	ESTs	0.0634
	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	0.0707
65	429050	X81333	Hs.194777	meprin A, beta	0.0714
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.0735
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	0.0739
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei	0.0769
	443506	H10661	Hs.192124	ESTs, Weakly similar to I38022 hypotheti	0.0838
70	415314	N88802	Hs.5422	glycoprotein M6B	0.0853
	451181	AI796330	Hs.207461	ESTs	0.0873
	429001	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	0.0888
	426635	BE395109	Hs.129327	hypothetical protein MGC13057	0.0900
	429350	AI754634	Hs.131987	ESTs	0.0927
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	0.0931

5	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	0.0951
	441066	AW205427	Hs.190726	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.0957
	431252	NM_005478	Hs.251380	insulin-like 5	0.0985
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	0.0987
	433546	AI075877	Hs.125461	hypothetical protein FLJ11539	0.1007
10	415154	D63175		gb:HUM501B09B Clontech human placenta po	0.1032
	409921	AW600239		gb:EST00009 pGEM-T library Homo sapiens	0.1067
	432440	X63597	Hs.2996	sucrase-isomaltase	0.1107
	430468	NM_004673	Hs.241519	angiopoietin-like 1	0.1114
	427167	AI239607	Hs.99196	hypothetical protein MGC11324	0.1147
15	441212	AW242447	Hs.146182	cytosolic beta-glucosidase	0.1167
	423605	AF047826	Hs.129887	cadherin 19, type 2	0.1190
	411381	AW841862	Hs.306831	Homo sapiens cDNA: FLJ22549 fis, clone H	0.1211
	412639	AW961284	Hs.296235	ESTs	0.1239
	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.1240
20	403548				0.1248
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	0.1274
	457982	AW856093	Hs.183617	ESTs	0.1277
	448835	BE277929	Hs.11081	UBX domain-containing 2	0.1277
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	0.1291
25	441805	AA285136	Hs.301914	neuronal specific transcription factor D	0.1309
	407639	AW205369	Hs.312830	ESTs	0.1315
	421741	AK001879	Hs.107527	hypothetical protein FLJ11017	0.1325
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	0.1328
	451742	T77609	Hs.117970	ankyrin 2, neuronal	0.1335
30	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	0.1379
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	0.1393
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	0.1395
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	0.1456
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	0.1459
35	404767				0.1460
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	0.1462
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	0.1463
	452768	AW069459	Hs.61539	ESTs	0.1466
	418692	AK000268	Hs.87383	hypothetical protein	0.1471
40	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	0.1471
	407551	Y10516		gb:H.sapiens mRNA for CD58 T3 protein.	0.1486
	402076				0.1487
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	0.1500
	442080	AW444761	Hs.44565	ESTs	0.1500
45	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	0.1513
	429545	AI824164	Hs.77667	lymphocyte antigen 6 complex, locus E	0.1523
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	0.1529
	435056	AW023337	Hs.5422	glycoprotein M6B	0.1532
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	0.1538
50	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	0.1542
	408221	AA912183	Hs.47447	ESTs	0.1552
	425220	AW975317	Hs.162987	ESTs	0.1558
	445200	AA084460	Hs.12409	somatostatin	0.1558
	443238	T78886	Hs.284450	ESTs	0.1563
55	456064	AA256213	Hs.72010	ESTs	0.1582
	428133	AW167727	Hs.11873	ESTs	0.1605
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.1615
	437734	AA693951	Hs.180284	ESTs	0.1637
	414290	AI568801	Hs.71721	ESTs	0.1638
60	418935	T28499	Hs.89485	carbonic anhydrase IV	0.1656
	411939	AI365585	Hs.146246	ESTs	0.1660
	442496	R55073	Hs.124130	ESTs	0.1676
	450693	AW450461	Hs.203965	ESTs	0.1698
	420736	AI263022	Hs.82204	ESTs	0.1718
65	405385				0.1745
	404638				0.1751
	427333	AF067797	Hs.176658	aquaporin 8	0.1757
	404246				0.1763
	433785	BE044593	Hs.112704	ESTs	0.1767
70	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	0.1769
	406980	S69265		(NONE)	0.1781
	421666	AL035250	Hs.1408	endothelin 3	0.1784
	452854	AA437061	Hs.14060	prokineticin 1 precursor	0.1795
	400514				0.1805
75	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	0.1808
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	0.1812
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	0.1812
	412474	AI791451		gb:ni50c09.y5 NCI_CGAP_Ov2 Homo sapiens	0.1812
	436008	AI078428	Hs.58785	ESTs	0.1820
80	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	0.1828
	431728	NM_007351	Hs.268107	multimerin	0.1832
	419746	AW867943	Hs.127216	hypothetical protein FLJ13465	0.1835
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	0.1838
	415672	N53097	Hs.193579	ESTs	0.1838
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	0.1838
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	0.1842
	413714	AI560944	Hs.71428	ESTs	0.1845



	427061	AB032971	Hs.173392	KIAA1145 protein	0.1847
	405282				0.1848
	400163				0.1855
5	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.1863
	447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	0.1876
	407891	AA486620	Hs.41135	endomucin-2	0.1895
	437140	AA312799	Hs.283689	activator of CREM in testis	0.1901
	431544	AK000770	Hs.299329	Homo sapiens cDNA FLJ20763 fis, clone CO	0.1904
10	436659	AI217900	Hs.144464	ESTs	0.1905
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	0.1926
	453698	AA037615	Hs.42746	ESTs	0.1928
	423743	AB023148	Hs.173373	KIAA0931 protein	0.1941
	428412	AA428240	Hs.126083	ESTs	0.1942
15	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	0.1944
	434683	AW298724	Hs.202639	ESTs	0.1957
	421865	AA609911	Hs.109012	MAX dimerization protein	0.1957
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	0.1969
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	0.1981
20	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	0.2004
	437740	AA810265	Hs.122915	ESTs	0.2016
	405610				0.2017
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	0.2025
	416961	BE391476	Hs.80617	ribosomal protein S16	0.2041
25	401465				0.2045
	437425	AW183714	Hs.20981	hypothetical protein DKFZp547M236	0.2049
	416231	H30333	Hs.165062	ESTs	0.2049
	401753				0.2050
	433430	AI863735	Hs.186755	ESTs	0.2051
30	432150	AK000224	Hs.272789	hypothetical protein FLJ20217	0.2052
	411644	H92064	Hs.278626	Arg/Abi-interacting protein ArgBP2	0.2059
	403957				0.2063
	435900	AI243036	Hs.16094	ESTs	0.2070
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.2075
35	445500	AW451938	Hs.257512	ESTs	0.2075
	419956	AL137939	Hs.40096	ESTs	0.2090
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	0.2093
	423655	AA722425	Hs.182785	ESTs, Moderately similar to 1207289A rev	0.2118
	401381				0.2120
40	426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014 8 simil	0.2122
	433476	AA594394	Hs.152616	ESTs	0.2125
	423405	NM_014151	Hs.128155	HSPC053 protein	0.2130
	442826	AI018777	Hs.131241	ESTs	0.2132
	427060	AW378993	Hs.90286	ESTs	0.2137
45	437354	AA749215	Hs.291886	ESTs	0.2137
	447734	AI421412	Hs.163659	ESTs	0.2144
	424585	AA464840	Hs.131987	ESTs	0.2146
	458016	AW188099	Hs.131813	ESTs	0.2151
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	0.2151
50	401521				0.2157
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	0.2165
	401024				0.2171
	414802	AI793107	Hs.27018	Ris	0.2179
55	441083	BE562611		gb:601336446F1 NIH_MGC_44 Homo sapiens c	0.2185
	417355	D13168	Hs.82002	endothelin receptor type B	0.2186
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	0.2188
	442930	AW881975	Hs.213923	ESTs	0.2193
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	0.2209
	444567	AV654020	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	0.2212
60	405654				0.2217
	415471	F09747	Hs.268707	ESTs	0.2222
	449243	AW295031	Hs.198671	ESTs	0.2229
	436088	AA704687	Hs.191294	ESTs	0.2232
	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapi	0.2242
65	427552	NM_005771	Hs.179608	retinol dehydrogenase homolog	0.2243
	416439	AA180363	Hs.118769	ESTs	0.2244
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	0.2254
	459395	Z30300	Hs.281935	ESTs	0.2257
	439039	AI656707	Hs.48713	ESTs	0.2268
70	433575	AA600175	Hs.39720	ESTs	0.2268
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	0.2273
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	0.2283
	441899	AI372588	Hs.8022	TU3A protein	0.2283
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	0.2290
75	434839	AI743069	Hs.134736	ESTs	0.2294
	435731	AA699581	Hs.186811	ESTs	0.2299
	400865				0.2304
	446294	AI284935		gb:qk55g09.x1 NCI_CGAP_Co8 Homo sapiens	0.2305
	414193	BE260069		gb:601150964F1 NIH_MGC_19 Homo sapiens c	0.2309
80	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	0.2315
	453098	Z25935	Hs.86379	ESTs	0.2315
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	0.2319
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	0.2320
	443482	AW188093	Hs.250385	ESTs	0.2326

5	432134	AI816782	Hs.122583	hypothetical protein FLJ21934	0.2329
	421539	AA292747	Hs.97296	ESTs	0.2330
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	0.2344
	408001	AA046458	Hs.95296	ESTs	0.2347
	409331	M36634	Hs.53973	vasoactive intestinal peptide	0.2351
10	431094	AW972276	Hs.116195	ESTs	0.2354
	429575	AA706003	Hs.99387	ESTs	0.2358
	404958				0.2361
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	0.2364
	452742	AW589945	Hs.97876	hypothetical protein DKFZp564K0322	0.2380
15	417511	AL049176	Hs.82223	chordin-like	0.2381
	404927				0.2387
	430297	AW243166	Hs.129806	ESTs	0.2412
	447482	AB033059	Hs.18705	KIAA1233 protein	0.2415
	418332	R34976	Hs.78293	ESTs	0.2416
20	454145	AA046872	Hs.62798	ESTs	0.2421
	422472	R59096	Hs.279939	mitochondrial carrier homolog 1	0.2424
	404070				0.2427
	421232	AA989220	Hs.292100	ESTs	0.2427
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	0.2432
25	412622	AW664708	Hs.171959	ESTs	0.2433
	454430	AI082777	Hs.61384	sema domain, seven thrombospondin repeat	0.2437
	416694	AW161284	Hs.79564	neuronal PAS domain protein 1	0.2443
	426724	AA383623	Hs.293616	ESTs	0.2444
	405073				0.2445
30	401236	H24185	Hs.92918	hypothetical protein	0.2445
	414203	BE262170	Hs.78629	ATPase, Na+/K+ transporting, beta 1 poly	0.2451
	401776				0.2452
	404696				0.2462
	426666	AW500131	Hs.171763	CD22 antigen	0.2471
35	427078	AI676062	Hs.111902	ESTs	0.2474
	424682	AW604804	Hs.151717	KIAA0437 protein	0.2478
	440383	AA884208	Hs.30484	ESTs	0.2481
	419118	AA234223	Hs.139204	ESTs	0.2494
	443515	AV657547	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	0.2495
40	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	0.2499
	404605				0.2500
	446066	AI343931	Hs.149383	ESTs	0.2505
	408345	R93851	Hs.63063	ESTs	0.2506
	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-re	0.2508
45	416950	AL049798	Hs.80552	dermatopontin	0.2510
	423555	AW958201	Hs.178589	hepatocellular carcinoma antigen gene 52	0.2513
	449833	R82252	Hs.106106	protein kinase (cAMP-dependent, catalytic)	0.2515
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	0.2519
	408897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	0.2523
50	422743	BE304678	Hs.119598	ribosomal protein L3	0.2526
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telen	0.2532
	450880	AK002183	Hs.285885	Homo sapiens cDNA FLJ11321 fis, clone PL	0.2536
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	0.2536
	451979	F06972	Hs.27372	BMX non-receptor tyrosine kinase	0.2549
55	440274	R24595	Hs.7122	scrapie responsive protein 1	0.2553
	430097	AI523245	Hs.127638	ESTs	0.2558
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	0.2564
	402695				0.2565
	453992	AW014995	Hs.281080	ESTs	0.2569
60	453888	AW450670	Hs.252819	ESTs	0.2569
	401371				0.2574
	456145	BE299427	Hs.21446	KIAA1716 protein	0.2579
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiesterase	0.2580
	422591	L07648	Hs.118630	MAX-interacting protein 1	0.2582
65	452359	BE167229	Hs.29206	hypothetical protein MGC14376	0.2584
	447569	AI393202	Hs.147554	hypothetical protein FLJ23392	0.2586
	405880				0.2588
	420321	D78761	Hs.96657	hypothetical protein	0.2595
	454415	AK000846	Hs.58679	solute carrier family 7, (cationic amino	0.2602
70	437032	AW867372	Hs.302063	immunoglobulin heavy constant mu	0.2604
	448025	BE502965	Hs.170426	ESTs	0.2605
	444304	AW628433	Hs.271296	ESTs, Weakly similar to I54374 gene NF2	0.2605
	424885	AI333771	Hs.82204	ESTs	0.2608
	425381	D84371	Hs.1898	paraoxonase 1	0.2611
75	457413	AA743462	Hs.165337	ESTs	0.2618
	452078	AA022620	Hs.52170	ESTs	0.2624
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	0.2628
	401974				0.2639
	411319	BE537094		gb:601063333F1 NIH_MGC_10 Homo sapiens c	0.2646
80	417761	R13727	Hs.21435	ESTs	0.2648
	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	0.2653
	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	0.2653
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	0.2660
	402182				0.2660
	402610				0.2661
	444814	BE010749	Hs.255097	ESTs	0.2663
	450017	W56434	Hs.201608	ESTs	0.2663

5	408684	R61377	Hs.12727	hypothetical protein FLJ21610	0.2667
	444209	AI753134	Hs.146494	ESTs	0.2668
	415022	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid	0.2677
	416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	0.2681
	422909	AA533356		gb:nj67f10.s1 NCI_CGAP_Pr10 Homo sapiens	0.2681
10	412047	AA934589	Hs.49696	ESTs	0.2693
	426356	BE536836	Hs.98682	hypothetical protein FKSG32	0.2703
	442238	AW135374	Hs.270949	ESTs, Moderately similar to F41925 hypot	0.2709
	402425				0.2710
	450545	AW135582	Hs.201767	ESTs	0.2710
15	417118	U38654	Hs.50477	RAB27A, member RAS oncogene family	0.2725
	419850	F06844		gb:HSC1ME091 normalized infant brain cDN	0.2727
	428020	L19058	Hs.181581	glutamate receptor, ionotropic, kainate	0.2730
	441493	AW070446	Hs.127037	ESTs	0.2733
	413541	BE147036		gb:QV4-HT0222-091199-024-e10 HT0222 Homo	0.2733
20	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.2734
	455597	BE008545	Hs.156110	immunoglobulin kappa constant	0.2740
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	0.2740
	444195	AB002351	Hs.10587	KIAA0353 protein	0.2743
	415160	T82802		gb:yd38a04.r1 Soares fetal liver spleen	0.2747
25	421823	N40850	Hs.28625	ESTs	0.2755
	434464	BE063921	Hs.295971	ESTs	0.2755
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [	0.2756
	430073	U86136	Hs.232070	telomerase-associated protein 1	0.2762
	432018	AA524447	Hs.152377	ESTs	0.2763
30	422954	AW998605		gb:PM0-BN0065-100300-001-b10 BN0065 Homo	0.2768
	416397	H53035	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	0.2775
	442420	AI024834	Hs.131729	ESTs	0.2775
	410950	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	0.2778
	427114	AI219896	Hs.97592	ESTs	0.2778
35	448466	AI522109	Hs.171066	ESTs	0.2778
	434445	AI349306	Hs.11782	ESTs	0.2784
	457115	AA420712		gb:nc63c07.s1 NCI_CGAP_Pr1 Homo sapiens	0.2785
	459511	AI142379		gb:qg64c01.r1 Soares_testis_NHT Homo sap	0.2786
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase (alanine	0.2794
40	433633	AI880516	Hs.84630	ESTs, Weakly similar to 2004399A chromos	0.2799
	440236	AW996722	Hs.125297	ESTs	0.2799
	405691				0.2804
	405334				0.2804
	403047				0.2809
45	412506	AW957159		gb:EST369229 MAGE resequences, MAGD Homo	0.2809
	441042	AA077736		gb:7B48A07 Chromosome 7 Fetal Brain cDNA	0.2815
	434660	AA764768	Hs.121158	hypothetical protein DKFZp434J0113	0.2816
	444453	AW379394	Hs.145126	ESTs	0.2817
	457736	AK000390	Hs.4205	hypothetical protein FLJ20124	0.2820
50	454012	M76424	Hs.37014	carbonic anhydrase VII	0.2821
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombo	0.2822
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	0.2827
	435021	AA922192	Hs.54709	ESTs	0.2828
	413344	U46024	Hs.75302	myotubular myopathy 1	0.2837
55	447787	BE620108		gb:601483015F1 NIH_MGC_69 Homo sapiens c	0.2840
	457290	AA465293	Hs.105069	ESTs	0.2841
	458244	AI929453	Hs.122489	Homo sapiens cDNA FLJ13289 fis, clone OV	0.2841
	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	0.2842
	407938	AA905097	Hs.85050	phospholamban	0.2845
60	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	0.2846
	428212	AW444451	Hs.134812	ESTs	0.2853
	424433	H04607	Hs.9218	ESTs	0.2857
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	0.2857
	404769				0.2863
65	411620	AW854536		gb:RC3-CT0255-200100-024-a08 CT0255 Homo	0.2868
	428746	AW503820	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	0.2870
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens	0.2872
	441290	W27501	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.2874
	422033	AW245905	Hs.110903	claudin 5 (transmembrane protein deleted	0.2877
70	421935	AA131632	Hs.109672	CMP-NeuAC;(beta)-N-acetylgalactosaminide	0.2878
	447955	BE544271	Hs.288390	hypothetical protein FLJ22795	0.2880
	405364				0.2881
	422165	AL041199	Hs.1481	histidine decarboxylase	0.2882
	431087	H12723	Hs.290791	ESTs	0.2882
75	450610	AA010370	Hs.60386	nuclear RNA export factor 3	0.2882
	445627	AW818475	Hs.7363	ESTs	0.2883
	436144	AW881250	Hs.148367	ESTs	0.2886
	445152	AI214667	Hs.283597	ESTs	0.2891
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.2891
80	455614	AI693369	Hs.202274	ESTs	0.2899
	419683	AA248897	Hs.48784	ESTs	0.2900
	411886	AL046810	Hs.20021	vesicle-associated membrane protein 1 (s	0.2904
	430770	AA765694	Hs.123296	ESTs	0.2913
	444459	AI680624	Hs.148676	ESTs	0.2913
	444918	AI202262	Hs.283362	ESTs	0.2915
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	0.2915
	435598	AA689470	Hs.163026	ESTs	0.2921

	413056	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	0.2922
	443998	AI620661	Hs.296276	ESTs	0.2924
	424412	H15512	Hs.10043	hypothetical protein FLJ13074	0.2925
5	421204	AW081587	Hs.165051	ESTs	0.2928
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	0.2938
	440507	H06994		gb:yl81b07.r1 Soares infant brain 1NIB H	0.2943
	445555	AW974013	Hs.260809	ESTs	0.2945
	438570	AW888554	Hs.84298	CD74 antigen (invariant polypeptide of m	0.2948
10	447195	T73745	Hs.279870	ESTs, Weakly similar to A46010 X-linked	0.2950
	423267	AL137416	Hs.126177	Homo sapiens mRNA; cDNA DKFZp434O192 (fr	0.2956
	421920	BE551245	Hs.1438	gamma-aminobutyric acid (GABA) receptor,	0.2956
	412177	Z23091	Hs.73734	glycoprotein V (platelet)	0.2959
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	0.2959
15	433745	AF075320	Hs.28980	hypothetical protein FLJ14540	0.2969
	417935	R53697	Hs.170044	ESTs	0.2970
	420674	NM_000055	Hs.1327	butyrylcholinesterase	0.2973
	413537	BE146866		gb:QV4-HT0222-211099-014-f06 HT0222 Homo	0.2973
	445194	AI215667	Hs.175044	ESTs	0.2974
20	454135	AW135965	Hs.246783	ESTs	0.2976
	403418				0.2986
	457605	AV657778	Hs.3314	selenoprotein P, plasma, 1	0.2989
	408896	AI610447	Hs.48778	niban protein	0.2993
	448542	BE256176	Hs.278712	eukaryotic translation initiation factor	0.2994
25	417945	R29072		gb:F1-101D 22 week old human fetal liver	0.2994
	412518	BE047637	Hs.173739	hypothetical protein FLJ10297	0.2996
	424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	0.2997
	430778	D90337	Hs.247916	natriuretic peptide precursor C	0.3000
	451531	AA018311	Hs.114762	ESTs	0.3003
30	444926	AI202492	Hs.212933	ESTs, Weakly similar to CLD4_HUMAN CLAUD	0.3003
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	0.3012
	459456	AA486036	Hs.190124	ESTs	0.3012
	417111	AW016321	Hs.82306	destrin (actin depolymerizing factor)	0.3012
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	0.3012
35	451959	AA056203	Hs.27337	hypothetical protein FLJ20623	0.3012
	410482	AW772187	Hs.191859	ESTs	0.3013
	417700	M36542	Hs.1101	POU domain, class 2, transcription facto	0.3018
	404414				0.3019
	432247	AA531287	Hs.105805	ESTs	0.3023
40	453471	AL037887	Hs.208179	ESTs	0.3028
	417481	AA203281	Hs.21798	ESTs	0.3029
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	0.3032
	448744	AL135424	Hs.9469	pleckstrin homology domain-containing, f	0.3033
	429223	BE264152	Hs.221994	ESTs	0.3034
45	404501	AW247252	Hs.75514	nucleoside phosphorylase	0.3037
	406829	AW419128	Hs.84298	CD74 antigen (invariant polypeptide of m	0.3039
	438839	AW297945	Hs.128490	ESTs	0.3039
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.3042
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	0.3045
50	458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	0.3048
	443294	AI733625	Hs.133053	ESTs	0.3050
	447023	AA356764	Hs.17109	integral membrane protein 2A	0.3052
	458583	AI479646	Hs.157081	hypothetical protein MGC4170	0.3056
	414567	BE281057	Hs.184519	hypothetical protein FLJ12949	0.3057
55	445123	AI762911	Hs.145369	ESTs	0.3064
	412682	AW983772		gb:RC3-HN0002-060400-012-h09 HN0002 Homo	0.3065
	434361	AF129755	Hs.117772	ESTs	0.3071
	414026	BE241713		gb:TCAAP1E0472 Pediatric acute myelogeno	0.3072
	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	0.3073
60	408350	AW183350	Hs.250127	ESTs	0.3074
	401042				0.3077
	422586	AA312704	Hs.59457	hypothetical protein FLJ22127	0.3077
	438692	AB007950	Hs.6360	KIAA0481 gene product	0.3077
	447452	BE618258	Hs.102480	Homo sapiens, clone IMAGE:3869590, mRNA,	0.3083
65	444414	AW293214	Hs.8752	transmembrane protein 4	0.3085
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	0.3088
	430410	AF099144	Hs.250700	tryptase beta 1	0.3090
	419299	AI311085	Hs.62406	hypothetical protein FLJ22573	0.3091
	400672				0.3094
70	444010	AW976457	Hs.282887	ESTs	0.3096
	451699	AL118571	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPO	0.3096
	432471	BE244667	Hs.296155	CGI-100 protein	0.3105
	405277				0.3106
	456765	AI497900	Hs.33067	ESTs	0.3106
75	452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	0.3106
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	0.3106
	406592				0.3106
	423621	BE002904		gb:QV4-BN0090-070400-163-c07 BN0090 Homo	0.3107
	417919	AI928203	Hs.86379	ESTs	0.3110
80	414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	0.3110
	457439	AW410408	Hs.271167	L-pipecolic acid oxidase	0.3116
	426449	AL134009	Hs.169936	Homo sapiens mRNA; cDNA DKFZp586N1918 (f	0.3116
	419942	U25138	Hs.93841	potassium large conductance calcium-acti	0.3119
	458544	AI631036	Hs.196843	ESTs	0.3119

	447778	BE620592	Hs.71190	ESTs, Weakly similar to S16506 hypotheti	0.3121
	449097	BE271708	Hs.95110	ESTs, Weakly similar to A55943 1-phospha	0.3125
	429338	AW170591	Hs.13967	ESTs, Weakly similar to PSM_HUMAN PROSTA	0.3125
5	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	0.3125
	446404	AA019961	Hs.26216	LOC50627	0.3130
	446616	R65964	Hs.241569	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.3132
	409404	BE220053	Hs.129056	ESTs	0.3135
	417318	AW953937	Hs.12891	ESTs	0.3139
10	443980	AI459140	Hs.299087	ESTs	0.3140
	459138	AI903291		gb:RC-BT029-080199-047 BT029 Homo sapien	0.3142
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.3143
	434704	AW135276	Hs.192311	ESTs	0.3143
	414214	D49958	Hs.75819	glycoprotein M6A	0.3145
15	446378	AI905699	Hs.239760	citrate synthase	0.3145
	459233	AI939966		gb:MR0-CT0015-160799-002-b06 CT0015 Homo	0.3146
	428193	NM_004235	Hs.7934	Kruppel-like factor 4 (gut)	0.3148
	426515	BE394222	Hs.231444	Homo sapiens, Similar to hypothetical pr	0.3150
	426597	AA382250	Hs.145601	ESTs	0.3153
20	459729	AL037285	Hs.289848	EST, Weakly similar to ALU4_HUMAN ALU SU	0.3157
	405071				0.3160
	407457	AJ242724		gb:Homo sapiens mRNA for partial putativ	0.3162
	409922	AW505582	Hs.130732	KIAA1575 protein	0.3172
	438219	AI916151	Hs.257194	ESTs	0.3173
25	412944	AA384110	Hs.197143	ESTs	0.3175
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	0.3178
	426662	AA879474	Hs.122710	ESTs	0.3178
	444391	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	0.3179
30	432168	AK000563	Hs.272805	hypothetical protein FLJ20556	0.3181
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	0.3183
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	0.3185
	448812	H30775	Hs.22140	BM88 antigen	0.3188
	411288	AW835511		gb:QV0-LT0015-180200-127-d02 LT0015 Homo	0.3189
35	422884	AW860975	Hs.13256	ESTs	0.3190
	405535				0.3195
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	0.3195
	455353	W26786		gb:15d7 Human retina cDNA randomly prime	0.3195
	414540	BE379050	Hs.306969	Homo sapiens, clone MGC:10782, mRNA, com	0.3195
	428568	AC004755	Hs.184922	Homo sapiens chromosome 19, fosmid 37502	0.3195
40	428106	BE620016	Hs.182470	PTD010 protein	0.3198
	411856	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	0.3202
	445682	AW378397		gb:RC3-HT0220-031299-012-g06 HT0220 Homo	0.3205
	437568	AI954795	Hs.156135	ESTs	0.3205
	448943	AI608810	Hs.193288	ESTs	0.3205
45	431999	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	0.3207
	419279	AA235900	Hs.87500	ESTs	0.3208
	405913				0.3209
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	0.3212
50	424729	AF063012	Hs.152531	heart and neural crest derivatives expre	0.3212
	440020	AI480204	Hs.177131	ESTs	0.3213
	429082	AL135682	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	0.3215
	433663	AF083131	Hs.229535	CATX-15 protein	0.3215
	400641				0.3216
	406140				0.3216
55	415280	R56473	Hs.268715	ESTs	0.3217
	447635	AI669669	Hs.195362	ESTs	0.3217
	401887				0.3217
	400767				0.3221
	457713	H47495	Hs.13810	hypothetical protein MGC15504	0.3221
60	448758	AB018311	Hs.21917	KIAA0768 protein	0.3222
	444750	AW242684	Hs.243623	ESTs	0.3223
	411466	AW847669		gb:IL3-CT0213-280100-056-G10 CT0213 Homo	0.3226
	432749	NM_014438	Hs.278909	interleukin 1, eta	0.3231
	408112	AW451982	Hs.248613	ESTs	0.3231
65	433234	AB040928	Hs.65366	KIAA1495 protein	0.3231
	422831	R02504	Hs.332943	ESTs	0.3234
	403215				0.3236
	451868	R85962	Hs.221926	ESTs, Weakly similar to I38022 hypotheti	0.3236
70	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	0.3242
	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	0.3254
	445848	AA774824	Hs.13377	Homo sapiens clone 23649 and 23755 unkno	0.3257
	441143	AI027604	Hs.159650	ESTs	0.3257
	405138				0.3262
	412888	M86151		gb:EST02679 Hippocampus, Stratagene (cat	0.3262
75	409662	AW452320	Hs.279726	ESTs	0.3262
	425438	T62216	Hs.270840	ESTs	0.3263
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	0.3263
	423512	AW844694	Hs.306752	Homo sapiens cDNA: FLJ21391 fis, clone C	0.3264
	436777	AA731199	Hs.293130	ESTs	0.3267
	431651	BE250915	Hs.266914	hypothetical protein FLJ10355	0.3267
80	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	0.3268
	426048	AI768853	Hs.134478	ESTs	0.3269
	451096	BE383234	Hs.25925	Homo sapiens, clone MGC:15393, mRNA, com	0.3270
	426942	AA393551	Hs.97450	ESTs	0.3271

	454947	AW846590	gb:QV0-CT0180-011099-025-d07 CT0180 Homo	0.3275
	413814	BE169692	gb:PM1-HT0527-290200-006-a05 HT0527 Homo	0.3275
	422818	AA404290	Hs.97848 ESTs	0.3277
5	423634	AW959908	Hs.1690 heparin-binding growth factor binding pr	0.3278
	414002	NM_006732	Hs.75678 FBj murine osteosarcoma viral oncogene h	0.3278
	452164	AI863171	gb:tz44b02.x1 NCI_CGAP_Brn52 Homo sapien	0.3279
	458477	NM_000314	Hs.10712 phosphatase and tensin homolog (mutated	0.3279
	433197	AB040889	Hs.281022 KIAA1456 protein	0.3280
	405701			0.3282
10	437782	AI370876	Hs.79090 exportin 1 (CRM1, yeast, homolog)	0.3284
	459001	AI761313	Hs.204605 ESTs	0.3286
	422783	AA598956	Hs.120439 ethanolamine kinase	0.3289
	417036	AF039918	Hs.80975 ectonucleoside triphosphate diphosphohyd	0.3290
15	456041	BE270795	Hs.268864 ESTs	0.3295
	423310	AA325225	Hs.124023 Homo sapiens cDNA FLJ14218 fis, clone NT	0.3296
	427530	AA405093	Hs.126519 ESTs	0.3296
	420172	AA601122	Hs.95655 secreted and transmembrane 1	0.3297
	445610	AI831648	Hs.143993 ESTs	0.3297
20	411328	AW837063	gb:QV1-LT0037-150200-069-g08 LT0037 Homo	0.3300

Table 8B

	Pkey:	Unique Eos probeset identifier number
25	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
Pkey	CAT number	Accession
30	409921	1159516_1 AW600239 AW600255 AW505332
	410626	1212621_1 BE407727
	410845	1223881_1 AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280 AW807283
	410950	1227728_1 AW811633 AW811652 AW811898
35	411288	1237709_1 AW835511 AW835517 AW835513
	411319	1238595_1 BE537094 AW836542
	411328	1238987_1 AW837063 AW935882 AW935957
	411466	1246771_1 AW847669 AW847667 BE145799
	411514	1248638_1 AW850178 AW850233 AW850445 AW850446
40	411620	1252014_1 AW854536 AW854417 AW854495 AW854355
	411880	1263110_1 AW872477 BE088101 T05990
	412474	129869_1 AI791451 AI791288 BE019234 BE296601 AA111939
	412506	1301336_1 AW957159 H09937 T75143
	412682	1321572_1 AW983772 AW983730 AW983769 AW983836 AW983835 AW983837
45	412888	1334784_1 M86151 BE061884 BE061883 BE061898 BE061882 BE061887 BE061891 BE061890 BE061896 BE061893 BE061895 BE061894 BE061885 BE007474
		BE007481 BE007553
	413056	1347545_1 BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072
	413537	1375441_1 BE146866 BE146865 BE146867
	413541	1375499_1 BE147036 BE146951 BE146958 BE146966 BE146976 BE146955
50	413814	1391574_1 BE169692 BE169421
	414026	1411109_1 BE241713 BE241912
	414193	1424706_2 BE260069
	414349	1437515_1 BE512968
	414484	1452830_1 BE314385
55	414539	1460320_1 BE379046 BE395459
	415154	1525577_1 D63175 D78984 D63269
	415160	1525766_1 T82802 D78670 R08505
	416035	1567254_1 H42314 H43080 H45217 H15384
	417945	1711126_1 R29072 R29717 R29699 R29709 R29751 R29609 R29060 R29718 R29057 R29591 R29683 R29575 R28913 R28910
60	419850	188485_1 F06844 F06845 Z45488 AW748501 AW748591 AW75021 AW748545 AW853362 AW853363 AW853427 AA251253
	422909	222858_1 AA533356 AW468427 R67736 AA779031 AA614088 AI823404 AA318991 AA720986
	422954	223239_1 AW998605 AW993131 BE514709 AA319445
	423621	230314_1 BE002904 H64880 AA328679
	424648	241947_1 AA344576 AA732430 AA344601
65	426132	261431_1 AA370501 AW962784 AA370727
	426497	268121_1 AA379913 AA379981 AW963523
	430553	319868_1 AW392821 AW392809 AW843258 AW843049 AW603156 BE165656 AW821728
	431822	338082_1 AA516049 AW004922
	434098	380006_1 AA625499 AA625269 AA625184
	437483	43756_1 AL390174 AW898817
70	440507	495677_1 H06994 BE147898
	441042	50823_1 AA077736 AA078505 BE562497 Z17859
	441083	50904_1 BE562611 AA436054
	445682	647580_1 AW378397 AW378390 AW378358 AI247957
75	446294	670076_1 AI284935 AW409822 BE408182
	446901	697809_1 AI347274 AW844024
	447787	73719_1 BE620108 BE312062 AW896316 BE262546
	451385	86787_1 AA017656 AA017374 AA019761
	452164	902091_1 AI863171 BE047919
80	454186	1049791_1 BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581
		BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460
		BE141749 AW177598

454790 1234752\_1 AW820852 AW820773 AW821088  
 454947 1245953\_1 AW846590 AW846615 AW846584 AW846592 AW846621 AW846610  
 455353 1284289\_1 W26786 AW998612 AW902272  
 457115 286601\_1 AA420712 AA469165 AA420737  
 459138 918860\_1 AI903291 AI903455 AI903367 AI903403 AI903447 AI903405 AI903364 AI903229 AI903240 AI903346  
 459233 944881\_1 AI939966 AI939988 AI939951 AI939981 AI939976 AI939959

Table 8C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
400641	8117693	Plus	4786-4992
400672	8118724	Minus	148067-148503
400767	8131627	Minus	80531-80629,82169-82278
400865	1945037	Minus	44482-45526
401024	8117489	Plus	60551-60802
401042	8117611	Plus	151364-151606
401371	9650602	Plus	80901-81283
401381	8570226	Minus	118629-119146,119392-119657
401465	6682292	Plus	25676-25800
401521	7705251	Plus	9127-9234
401753	9838183	Minus	155287-155529,159719-159997
401776	9966323	Plus	115535-115743,117746-117839,120290-120455
401887	7229981	Plus	93973-94120
401974	3126777	Plus	85330-85683
402076	8117410	Plus	128316-128627
402182	8575917	Minus	98298-98439
402425	9796347	Minus	50224-50395
402610	9926549	Minus	22955-23124
402695	8569871	Minus	159927-160055
403047	3540153	Minus	59793-59968
403215	7630945	Minus	177270-177971
403418	6862692	Minus	176202-176395
403548	8081591	Minus	38760-39352
403957	8076835	Minus	81649-81754
404070	2996642	Plus	7210-7414,10043-10195
404246	7406725	Plus	82477-82628,82721-82817,82910-83071,83149-83387
404414	7382165	Plus	143127-143398
404605	9212566	Plus	125032-125291
404638	9796751	Minus	99433-99528,100035-100161
404696	9800109	Minus	60037-60144,62675-63081
404767	7882827	Minus	23244-23759
404769	8099713	Minus	175801-176823
404927	7342002	Plus	68690-69563
404958	7407941	Minus	2731-4531
405071	7708797	Minus	11115-11552
405073	7769921	Plus	31419-31774
405138	8576241	Plus	90303-90516
405277	3980473	Plus	23471-23572
405282	3810573	Minus	10482-10689
405334	3135285	Plus	139386-139856
405364	2281075	Minus	48325-48491,49136-49252
405385	6552772	Plus	48332-48454
405535	9795658	Plus	63384-63545
405610	5757553	Minus	71907-72080
405654	4895155	Minus	53624-53759
405691	4508112	Plus	171350-171739
405701	4263751	Plus	93243-93364
405880	6758747	Minus	55673-56287
405913	7712139	Minus	7484-7678
406140	9168231	Minus	49887-50219
406592	4567182	Plus	352560-352963

Table 9A lists about 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). In order to remove gene-specific

background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: 90<sup>th</sup> percentile of tumor samples divided by the 70<sup>th</sup> percentile of normal body tissue samples, where the 15<sup>th</sup> percentile of normal body tissues was subtracted from the numerator and denominator

Pkey	ExAccn	UnigeneID	Unigene Title	R1
436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	29.34
406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	25.56
406667	M12523			20.28
414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	18.84
428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	17.38
416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	16.99
446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	16.61
431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S384_H	16.42
437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	15.92
407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	15.84
423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease i	15.59
441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	14.54
422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	13.68
432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.23
421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	13.21
453863	X02544	Hs.572	Hs.572:orosomucoid 1	13.06
421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	12.35
436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.11
422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	11.99
418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, LI c	11.87
407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	11.81
424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	11.27
414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	10.82
413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	10.73
450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	10.57
418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.10
423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	9.68
447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	9.44
421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	9.38
406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	9.34
427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (	9.18
422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	9.06
406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.02
409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	8.89
424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.53
422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	8.23
452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	8.10
430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	8.05
413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	7.96
406399				7.73
422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	7.71
428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	7.43
417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 1	7.40
435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	7.29
430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.25
451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	7.19
452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	7.18
452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	7.03
424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	7.00
443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	6.92
452194	AI694413	Hs.373599	Hs.373599:EST	6.88
411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.59
422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	6.55
431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	6.49
422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	6.33
412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	6.31
451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I isof	6.30
428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.29
430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	6.28
422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	6.27
444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	6.26
409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	6.23



5	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.23
	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cyste	6.23
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	6.17
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	6.17
	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.17
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.16
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	6.14
10	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	6.13
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis,	6.09
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	6.02
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	5.95
	403220				5.90
15	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	5.88
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	5.87
	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	5.79
	414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	5.79
	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	5.77
20	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	5.77
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
	431301	AA502384	Hs.151529	Hs.151529:ESTs	5.71
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	5.71
	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	5.68
25	436972	AA284679	Hs.25640	Hs.25640:claudin 3	5.66
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	5.61
	431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine deficie	5.57
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	5.55
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.54
30	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.50
	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	5.38
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	5.33
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	5.32
35	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	5.32
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	5.28
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.28
	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	5.27
40	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.26
	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	5.25
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	5.25
	436251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	5.25
	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.23
45	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	5.22
	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	5.20
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	5.18
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.13
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	5.12
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	5.11
50	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	5.08
	426174	AA547959	Hs.115838	Hs.115838:ESTs	5.07
	403218				5.07
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	5.00
55	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	4.98
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	4.96
	431779	AW971178	Hs.268571	(locuslink)NM_001645:Homo sapiens apolip	4.92
	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif	4.91
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	4.91
	422667	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix prot	4.90
60	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
	424010	AI080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	4.86
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	4.86
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	4.83
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	4.81
65	428289	M26301	Hs.2253	Hs.2253:complement component 2	4.79
	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	4.78
	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.77
	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
70	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	4.72
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	4.72
	430680	AW138724	Hs.168974	Hs.168974:ESTs	4.69
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.69
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	4.67
	403221				4.65
75	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	4.65
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	4.64
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	4.64
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.64
	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	4.60
80	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.60
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	4.60
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	4.59
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	4.57
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.56

5	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	4.56
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	4.55
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.55
	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	4.55
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	4.54
10	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.53
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.53
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	4.53
	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
15	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.49
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	4.48
	432378	AI493046	Hs.146133	Hs.146133:ESTs	4.48
	431958	X63629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	4.47
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.47
20	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.47
	422511	AI076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	4.46
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.46
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	4.44
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.44
25	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.43
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	4.43
	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	4.40
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	4.38
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.37
30	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	4.36
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	4.36
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.35
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	4.33
	432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	4.33
35	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	4.33
	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.32
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.32
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.30
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.30
40	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.30
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.29
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	4.28
45	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	4.28
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.27
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.27
	414361	AI086138	Hs.204044	Hs.204044:ESTs	4.26
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.26
50	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	4.24
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.22
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	4.19
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.18
55	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.18
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	4.18
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	4.18
	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	4.17
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	4.17
60	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.16
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.15
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.15
	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3-)glycoprote	4.14
	403219				4.14
65	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.14
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.14
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (	4.12
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.12
70	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	4.12
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (	4.11
	428698	AA852773	Hs.334838	Hs.334838:KIAA1866 protein	4.10
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	4.09
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.07
75	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.07
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.06
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.05
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (	4.04
80	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	4.03
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.03
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.03
	452721	AI269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.02
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.01
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.01
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.01
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.01

	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	3.99
	403739				3.99
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.98
	405484				3.98
5	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.98
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	3.97
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.97
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.97
10	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.96
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.96
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.96
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.95
	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	3.95
15	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	3.93
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.93
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	3.93
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	3.92
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.92
20	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.91
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	3.90
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	3.89
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutas	3.89
	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	3.88
25	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.88
	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis,	3.88
	409453	AI885516	Hs.95612	Hs.95612:ESTs	3.87
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.86
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	3.86
30	434263	N34895	Hs.79187	Hs.79187:coxsaekie virus and adenovirus	3.85
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	3.85
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	3.84
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	3.84
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	3.84
35	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.83
	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.83
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.83
	426514	BE616633	Hs.170195	Hs.170195:bone morphogenetic protein 7 (	3.82
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	3.82
40	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	3.81
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	3.81
	409636	AA305729	Hs.18272	(locuslink)NM_030574:Homo sapiens solute	3.81
	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	3.80
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	3.79
45	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	3.79
	405556				3.79
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.79
	400529				3.79
50	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.78
	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	3.78
	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	3.77
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	3.77
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.77
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	3.76
55	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.76
	431350	AI192528	Hs.164537	Hs.164537:ESTs	3.76
	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.75
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	3.75
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	3.74
60	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.74
	413063	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.72
65	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	3.72
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.72
	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypoth	3.72
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.71
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	3.71
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	3.71
70	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.70
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.70
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.70
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	3.69
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.69
75	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	3.69
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	3.69
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	3.69
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.68
80	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.68
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	3.67
	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	3.67
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	3.67
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	3.67
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	3.67

5	452679	Z42387	Hs.83883	(locuslink)NM_020182:Homo sapiens transmembrane protein 7 (CLDN7)	3.66
	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	3.66
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical protein	3.66
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap)	3.66
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.66
10	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.65
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	3.64
	404826				3.63
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	3.63
	409964	AW368226	Hs.67928	Hs.67928:ESTs	3.63
15	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.63
	452098	AI858183		BF755039:QV0-CT0583-181000-428-f07 CT058	3.62
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protein	3.61
	439223	AW238299	Hs.250618	NM_025217:Homo sapiens UL16 binding protein	3.60
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	3.59
20	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	3.59
	436856	AI469355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	3.59
	449667	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.59
	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcinoma	3.58
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	3.58
25	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cisplatin	3.58
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.57
	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolinate phosphatase	3.57
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	3.57
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility complex	3.56
30	413880	AI680842	Hs.110915	NM_021258:Homo sapiens interleukin 22 receptor	3.55
	421357	AK000609	Hs.103808	NM_017896:Homo sapiens chromosome 20 open reading frame	3.55
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guaranine	3.55
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	3.55
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent kinase	3.55
35	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.55
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	3.55
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine monophosphate)	3.54
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.54
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphatase	3.54
40	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2	3.54
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger protein	3.53
	414812	X72755	Hs.77367	NM_002416:Homo sapiens monokine induced by	3.53
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, renal	3.53
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN12)	3.53
45	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation factor	3.53
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	3.52
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromosome	3.52
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.51
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (inosine monophosphate)	3.51
50	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyrosine kinase	3.51
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell death	3.51
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373	3.51
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF receptor	3.51
	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	3.51
55	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisiae	3.51
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	3.51
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976	3.51
	419693	AA133749	Hs.301350	Hs.301350:FXD domain-containing ion transport	3.51
	407971	AI469117	Hs.62918	Hs.62918:CDCC91 cell division cycle 91-like	3.50
60	424865	AF011333	Hs.153563	NM_002349:Homo sapiens lymphocyte antigen	3.50
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.50
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.50
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	3.50
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger protein	3.50
65	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lymphoma	3.50
	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell death	3.50
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyridoxal)	3.49
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptide	3.49
	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical protein	3.48
70	407137	T97307			3.48
	454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypothetical	3.48
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433	3.48
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN2)	3.47
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DNA)	3.47
75	413380	AI904232	Hs.75323	Hs.75323:prohibitin	3.46
	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.46
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 open	3.45
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN15)	3.45
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.44
80	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.44
	420319	AW406289	Hs.96593	NM_019034:Homo sapiens ras homolog gene	3.44
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	3.44
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.43
	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inactive)	3.43
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically defined	3.43
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens melanoma transforming	3.43
	428093	AW594506	Hs.104830	Hs.104830:ESTs	3.43

	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	3.43
	400750				3.42
5	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	3.41
	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	3.40
	453857	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.40
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	3.39
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.39
	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	3.39
10	450506	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.39
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	3.38
	440676	NM_004987	Hs.112378	(locuslink)NM_004987:Homo sapiens LIM an	3.38
	400847				3.37
	431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	3.37
15	410199	AW377424	Hs.205126	Hs.205126:Homo sapiens cDNA: FLJ22667 fi	3.37
	432633	AI796390	Hs.210667	Hs.210667:ESTs	3.36
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (	3.36
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.36
	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	3.35
20	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	3.35
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.35
	400448				3.35
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.35
25	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	3.35
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.35
	429824	AA296363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.35
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.34
	451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.34
30	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.34
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	3.34
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	3.34
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	3.34
35	421190	U95031	Hs.102482	Hs.102482:mucin 5, subtype B, tracheobro	3.34
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.33
	435975	AL118990	Hs.373554	(locuslink)NM_130786:Homo sapiens alpha-	3.33
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	3.33
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	3.33
40	441128	AA570256	Hs.348504	Hs.348504:hypothetical protein BC014072	3.33
	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	3.33
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens interf	3.32
	410219	T98226	Hs.171952	Hs.171952:occludin	3.32
45	410663	AA194952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.32
	402829				3.32
	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	3.32
	414198	AW505308	Hs.75812	NM_004563:Homo sapiens phosphoenolpyruva	3.32
	443425	AI056776	Hs.133397	Hs.133397:ESTs	3.32
50	436485	X59135	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.31
	410268	AA316181	Hs.61635	NM_012449:Homo sapiens six transmembrane	3.30
	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	3.30
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.30
	421814	L12350	Hs.108623	NM_003247:Homo sapiens thrombospondin 2	3.30
55	432215	AU076609	Hs.2934	NM_001033:Homo sapiens ribonucleotide re	3.30
	409402	AF208234	Hs.695	Hs.695:cystatin B (stefin B)	3.30
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.29
	424408	AI754813	Hs.146428	Hs.146428:collagen, type V, alpha 1	3.29
	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	3.29
60	442821	BE391929	Hs.8752	Hs.8752:transmembrane protein 4	3.29
	459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	3.28
	400846				3.28
	422256	M64673	Hs.1499	NM_005526:Homo sapiens heat shock transc	3.28
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	3.28
65	432078	BE314877	Hs.24553	(locuslink)NM_022369:Homo sapiens hypoth	3.27
	435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.27
	456534	X91195	Hs.100623	NM_138689:Homo sapiens protein phosphata	3.27
	447335	BE617695	Hs.286192	NM_032192:Homo sapiens protein phosphata	3.27
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	3.27
70	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	3.26
	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	3.26
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	3.26
	457635	AV660976	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.26
	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.25
75	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	3.25
	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-ral simian leuk	3.25
	401179				3.25
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	3.25
80	453323	AF034102	Hs.32951	NM_001532:Homo sapiens solute carrier fa	3.25
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.25
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	3.25
	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.24
	428390	AI640377	Hs.350077	NM_000982:Homo sapiens ribosomal protein	3.24
	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.24

5	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.24
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.24
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.23
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.23
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.23
10	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.23
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltg	3.23
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-li	3.23
	409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multid	3.23
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.23
15	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.22
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.22
	413835	AI272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	3.22
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.22
	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	3.21
20	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.21
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.21
	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.21
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.21
	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.21
25	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.21
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diffe	3.20
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.20
	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.20
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.20
30	413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjuga	3.19
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.19
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.19
	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfet 4 (SURF4)	3.19
	430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripar	3.19
35	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutat	3.18
	434224	AA380731	Hs.84	NM_000206:Homo sapiens interleukin 2 rec	3.18
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	3.18
	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.18
	420531	AI652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.18
40	417389	BE260964	Hs.82045	Hs.82045:midkine (neurite growth-promoti	3.18
	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.18
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.18
	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.18
	414883	AA926960	Hs.348669	Hs.348669:CDK28 protein kinase 1	3.18
45	421743	T35958	Hs.107614	Hs.107614:DKFZP56411171 protein	3.18
	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.17
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2-I	3.17
	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.17
50	449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhtek	3.17
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
	428484	AF104032	Hs.184601	(locuslink)NM_003486:Homo sapiens solute	3.16
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.16
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.15
55	447151	AI022813	Hs.92679	(locuslink)NM_145754:Homo sapiens kinesi	3.15
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.15
	410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.15
	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.15
	435886	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.15
60	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (	3.14
	420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.14
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.14
	450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXD d	3.14
	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
65	406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.13
	426841	AI052358	Hs.131741	Hs.131741:ESTs	3.13
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.12
70	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.12
	438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
	439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.12
	412326	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.12
75	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.11
	421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.11
	400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.11
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.11
	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.11
80	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.11
	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.11
	433179	AW362945	Hs.162459	Hs.162459:ESTs	3.11
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.11
	418641	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.10
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	3.10
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.10
	457670	AF119666	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.10

5	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.10
	428293	BE250944	Hs.183556	Hs.183556:solute carrier family 1 (neur	3.10
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.10
10	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.09
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.09
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.08
	404240				3.08
	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	3.08
15	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.08
	446506	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.08
	402260				3.08
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.08
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.08
20	445937	AI452943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.07
	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.07
	422611	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosy	3.07
	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.07
	449644	AW960707	Hs.148324	Hs.148324:ESTs	3.07
25	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.07
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.07
	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.07
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.07
30	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.06
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.06
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.06
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.06
	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.06
35	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	3.06
	430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.06
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.06
	412525	AA581439	Hs.152328	Hs.152328:ESTs	3.06
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.05
40	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.05
	408806	AW847814	Hs.75608	Hs.75608:tight junction protein 2 (zona	3.05
	435730	AB020635	Hs.4984	Hs.4984:KIAA0828 protein	3.05
	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.05
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.05
45	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.05
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.05
	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.05
	406363				3.05
	439841	AF038961	Hs.6710	NM_004870:Homo sapiens mannose-P-dolicho	3.05
50	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-fl	3.04
	447966	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	3.04
	439246	AI498072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.04
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.04
	427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.04
55	430281	AI878842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.04
	446620	AA128808	Hs.179902	(locuslink)NM_022109:Homo sapiens CDw92	3.04
	452865	AI924046	Hs.119567	Hs.119567:ESTs, Weakly similar to ALU1_H	3.04
	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.04
	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.04
60	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antimicr	3.03
	417777	AI823763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis,	3.03
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.03
	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
65	409430	R21945	Hs.346735	Hs.346735:Homo sapiens, clone IMAGE:3881	3.03
	440659	AF134160	Hs.7327	NM_021101:Homo sapiens claudin 1 (CLDN1)	3.03
	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.03
	438930	AW843633	Hs.343261	Hs.343261.histocompatibility (minor) 13	3.02
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.02
70	426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.02
	425966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.02
	448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.02
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	3.02
	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.02
75	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	3.02
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.01
	442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.01
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.01
	410293	AK000047	Hs.61960	NM_018992:Homo sapiens hypothetical prot	3.01
80	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.01
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.00
	447032	AK000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.00
	414249	AI797994	Hs.279929	(locuslink)NM_017510:Homo sapiens gp25L2	3.00
	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.00
	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.00
	419452	U33635	Hs.90572	Hs.90572:PTK7 protein tyrosine kinase 7	3.00
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.00

5	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.00
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.00
	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.00
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	2.99
	437763	AA469369	Hs.5831	Hs.5831:tissue inhibitor of metalloprote	2.99
10	406865	AI025931	Hs.181357	Hs.181357: laminin receptor 1 (67kD, ribo	2.99
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.99
	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca	2.98
	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	2.98
	432396	AW295956	Hs.11900	(locuslink)NM_032527:Homo sapiens hypoth	2.98
15	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	2.98
	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	2.98
	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.98
	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	2.98
	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	2.98
20	452124	AA454220	Hs.61170	Hs.61170:ESTs	2.98
	416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	2.98
	419092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transmem	2.97
	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	2.97
	437296	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	2.97
25	407736	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	2.97
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.97
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	2.97
	430354	AA954810	Hs.239784	Hs.239784:scribble	2.97
	417079	U65590	Hs.81134	(locuslink)NM_000577:Homo sapiens interl	2.97
30	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.97
	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prostasin)	2.97
	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	2.96
	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kinesi	2.96
	412429	AV650262	Hs.75765	NM_002089:Homo sapiens GRO2 oncogene (GR	2.96
35	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	2.96
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	2.96
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.96
	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.96
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	2.96
40	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	2.96
	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	2.96
	429597	NM_003816	Hs.2442	Hs.2442:a disintegrin and metalloprotein	2.95
	421179	U72664	Hs.148495	NM_002810:Homo sapiens proteasome (proso	2.95
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.95
45	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	2.95
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alpha	2.95
	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	2.95
	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	2.95
	445720	AL040482	Hs.286173	Hs.286173:KIAA1595 protein	2.95
50	429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	2.95
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif	2.94
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.94
	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	2.94
	444824	AA843575	Hs.12056	NM_001671:Homo sapiens asialoglycoprotei	2.94
55	431629	AU077025	Hs.265827	NM_022873:Homo sapiens interferon, alpha	2.94
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	2.94
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.93
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.93
	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	2.93
60	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	2.93
	412088	AI689496	Hs.108932	Hs.108932:ESTs	2.93
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.92
	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	2.92
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.92
65	417944	AU077196	Hs.82985	NM_000393:Homo sapiens collagen, type V,	2.92
	428343	AL043021	Hs.12705	(locuslink)NM_145294:Homo sapiens simila	2.92
	435640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	2.92
	451608	AA384525	Hs.26745	NM_016499:Homo sapiens HSPC244 (MGC:1337	2.92
	434608	AA805443	Hs.179909	NM_024831:Homo sapiens nuclear receptor	2.92
70	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	2.91
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	2.91
	438549	BE386801	Hs.21858	Hs.21858:serine (or cysteine) proteinase	2.91
	440246	W52010	Hs.191379	Hs.191379:ESTs	2.91
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	2.91
75	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	2.91
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	2.91
	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	2.91
	450167	AA446404	Hs.24563	NM_013248:Homo sapiens NTF2-like export	2.91
	408815	AW957974	Hs.25485	(locuslink)NM_024599:Homo sapiens hypoth	2.91
80	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	2.91
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	2.91
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	2.91
	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	2.90
	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	2.90
	405203				2.90
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	2.90
	412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	2.90



	455967	L12535	Hs.75551	(locuslink)NM_012425:Homo sapiens Ras su	2.90
	402104				2.90
	414814	D14697	Hs.77393	(locuslink)NM_002004:Homo sapiens farnes	2.90
5	442739	NM_007274	Hs.8679	(locuslink)NM_007274:Homo sapiens cyto	2.90
	456157	AW979153	Hs.336881	Hs.336881:ESTs	2.90
	429505	AW820035	Hs.278679	NM_033274:Homo sapiens a disintegrin and	2.89
	430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	2.89
	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	2.89
10	438543	AA810141	Hs.192182	Hs.192182:ESTs	2.89
	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	2.89
	441455	AJ271671	Hs.7854	NM_014437:Homo sapiens solute carrier fa	2.89
	420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	2.89
	415674	BE394784	Hs.78596	NM_002797:Homo sapiens proteasome (proso	2.89
15	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.89
	418062	AW630656	Hs.83383	NM_006406:Homo sapiens peroxiredoxin 4 (	2.89
	436540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	2.89
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	2.89
	417018	M16038	Hs.80887	Hs.80887:v-yes-1 Yamaguchi sarcoma viral	2.89
20	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	2.88
	429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylation	2.88
	411030	BE387193	Hs.67896	(locuslink)NM_007346:Homo sapiens opioid	2.88
	413822	R08950	Hs.272044	Hs.272044:ESTs, Weakly similar to hypoth	2.88
	438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	2.88
25	409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	2.88
	440490	AW513684	Hs.7218	Hs.7218:acetyl-Coenzyme A synthetase 2 (	2.87
	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	2.87
	423570	AW838306	Hs.129819	NM_018344:Homo sapiens hypothetical prot	2.87
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	2.87
30	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	2.87
	442643	U82756	Hs.374973	(locuslink)NM_004697:Homo sapiens PRP4 p	2.87
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	2.87
	421178	BE267994	Hs.102419	Hs.102419:zinc finger protein	2.87
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	2.87
35	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	2.87
	453145	R63438	Hs.183454	Hs.183454:Homo sapiens cDNA FLJ14883 fis	2.86
	427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	2.86
	424732	D80001	Hs.152629	Hs.152629:KIAA0179 protein	2.86
	426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	2.86
40	450273	AW296454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	2.86
	407082	Z47055			2.86
	450038	AA005159	Hs.188489	Hs.188489:ESTs	2.86
	457274	AW674193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.85
	417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rh-related antige	2.85
45	417824	AA084798	Hs.82646	NM_006145:Homo sapiens DnaJ (Hsp40) homo	2.85
	426989	A1815206	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (	2.85
	434916	AF161383	Hs.284207	Hs.284207:hypothetical protein BC003515	2.85
	412664	AA421404	Hs.346868	NM_006824:Homo sapiens EBNA1 binding pro	2.85
	414172	AW954324	Hs.75790	(locuslink)NM_002642:Homo sapiens phosph	2.85
50	409504	AA304961	Hs.699	Hs.699:peptidylprolyl isomerase B (cyclo	2.84
	439920	H05430	Hs.288433	NM_016522:Homo sapiens neurotrimin (HNT)	2.84
	418462	BE001596	Hs.85266	Hs.85266:integrin, beta 4	2.84
	442199	BE277633	Hs.372542	NM_004879:Homo sapiens etoposide-induced	2.84
	406710	A1708347	Hs.184014	Hs.184014:ribosomal protein L31	2.84
55	433435	BE545277	Hs.340959	NM_005726:Homo sapiens Ts translation el	2.84
	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3)-glycopro	2.84
	448730	AB032983	Hs.21894	Hs.21894:KIAA1157 protein	2.84
	433027	AF191018	Hs.279923	(locuslink)NM_014366:Homo sapiens putati	2.84
	449090	AK001735	Hs.22983	NM_020121:Homo sapiens UDP-glucose ceram	2.84
60	439737	AI751438	Hs.41271	Hs.41271:Homo sapiens mRNA full length i	2.84
	403912				2.84
	423225	AA852604	Hs.125359	NM_006288:Homo sapiens Thy-1 cell surfac	2.84
	458376	AB023179	Hs.9059	Hs.9059:KIAA0962 protein	2.84
	429211	AF052693	Hs.198249	NM_005268:Homo sapiens gap junction prot	2.84
65	452518	AA280722	Hs.24758	Hs.24758:Homo sapiens cDNA FLJ32068 fis,	2.84
	418127	BE243982	Hs.83532	(locuslink)NM_002389:Homo sapiens membra	2.83
	448489	AI523875		R45782:Ha616-f Adult heart, Clontech Hom	2.83
	426194	T50872	Hs.2001	NM_001061:Homo sapiens thromboxane A syn	2.83
	422129	AU076635	Hs.1478	NM_000185:Homo sapiens serine (or cystei	2.83
70	437651	BE560672	Hs.13543	(locuslink)NM_145214:Homo sapiens tripar	2.83
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	2.83
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	2.83
	444758	AI044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methy	2.83
	423323	AI951628	Hs.127007	NM_003740:Homo sapiens potassium channel	2.83
75	439720	AI935202	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.83
	435550	AI224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	2.83
	425907	AA365752	Hs.155965	Hs.155965:ESTs	2.83
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	2.82
	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	2.82
	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	2.82
80	415697	AI365603	Hs.279696	Hs.279696:DKFZP5661024 protein	2.82
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	2.82
	430040	AW503115	Hs.227823	NM_014287:Homo sapiens pM5 protein (PM5)	2.82
	449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	2.82

	427022	AW245839	Hs.173255	NM_004596:Homo sapiens small nuclear rib	2.82
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	2.82
	400845				2.81
5	419501	AW843822	Hs.199961	Hs.199961:ESTs, Weakly similar to hypoth	2.81
	418140	BE613836	Hs.83551	(locuslink)NM_002403:Homo sapiens microf	2.81
	422032	AA476966	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	2.81
	419768	T72104	Hs.93194	Hs.93194:apolipoprotein A-I	2.81
	436673	AF201931	Hs.5268	Hs.5268:zinc finger, DHHC domain contain	2.81
10	421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	2.81
	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	2.81
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	2.81
	433061	AW068033	Hs.296422	(locuslink)NM_025233:Homo sapiens nucleo	2.81
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.81
15	407338	AA773213	Hs.91202	Hs.91202:Homo sapiens cDNA FLJ25946 fis,	2.81
	410240	AL157424	Hs.61289	Hs.61289:synaptojanin 2	2.80
	423880	BE278111	Hs.134200	Hs.134200:DKFZP564C186 protein	2.80
	422098	H03117	Hs.111497	Hs.111497:neuronal protein 17.3	2.80
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	2.80
20	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	2.80
	456602	AA411607	Hs.118964	NM_017660:Homo sapiens hypothetical prot	2.80
	457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	2.80
	426437	BE076537	Hs.169895	Hs.169895:ubiquitin-conjugating enzyme E	2.79
	412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	2.79
25	452695	AW780199	Hs.30327	NM_003668:Homo sapiens mitogen-activated	2.79
	409531	BE384319	Hs.54702	(locuslink)NM_007255:Homo sapiens xylosy	2.79
	448988	Y09763	Hs.22785	NM_021987:Homo sapiens gamma-aminobutyri	2.79
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	2.79
	419846	NM_015977	Hs.285681	NM_032951:Homo sapiens Williams Beuren s	2.79
30	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	2.79
	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Not56 (D. melanog	2.79
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	2.79
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	2.79
	407844	AW073716	Hs.8037	(locuslink)NM_005723:Homo sapiens tetras	2.79
35	448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	2.79
	419235	AW470411	Hs.288433	NM_016522:Homo sapiens neurotrimin (HNT)	2.78
	407754	AA527348	Hs.288967	Hs.288967:Homo sapiens, similar to RIKEN	2.78
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	2.78
	414181	AK000476	Hs.75798	NM_016470:Homo sapiens chromosome 20 ope	2.78
40	418869	AW516565		AA229762:nc49f01.r1 NCL_CGAP_Pr3 Homo sa	2.78
	419444	NM_002496	Hs.90443	NM_002496:Homo sapiens NADH dehydrogenas	2.78
	430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	2.78
	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.78
	423013	AW875443	Hs.22209	Hs.22209:secreted modular calcium-bindin	2.78
45	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.78
	447402	H54520	Hs.351327	(locuslink)NM_017828:Homo sapiens hypoth	2.78
	417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	2.78
	422051	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	2.78
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	2.78
50	419757	AA773820	Hs.63970	Hs.63970:ESTs	2.77
	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	2.77
	408044	BE206939	Hs.42287	NM_001952:Homo sapiens E2F transcription	2.77
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	2.77
	451690	AW451469	Hs.209990	Hs.209990:ESTs	2.77
55	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	2.77
	444207	AI565004	Hs.374415	Hs.374415:ESTs	2.77
	417089	H52280	Hs.18612	Hs.18612:Homo sapiens cDNA: FLJ21909 fis	2.77
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	2.77
	425978	BE253927	Hs.24983	Hs.24983:hypothetical protein from EUROI	2.77
60	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	2.77
	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	2.77
	450701	H39960	Hs.288467	Hs.288467:Homo sapiens cDNA FLJ12280 fis	2.77
	412890	T85247	Hs.351875	NM_004374:Homo sapiens cytochrome c oxid	2.77
	415752	BE314524	Hs.78776	NM_012342:Homo sapiens putative transmem	2.76
65	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	2.76
	450770	AA019924	Hs.28803	Hs.28803:ESTs	2.76
	419594	AA013051	Hs.91417	(locuslink)NM_007027:Homo sapiens topois	2.76
	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 I	2.76
	417767	BE242241	Hs.82542	NM_001637:Homo sapiens acyloxyacyl hydro	2.76
70	439968	AA224760	Hs.153	NM_000971:Homo sapiens ribosomal protein	2.76
	426520	BE545684	Hs.343566	Hs.343566:KIAA0251 protein	2.75
	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.75
	445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	2.75
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.75
75	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	2.75
	416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	2.75
	435025	T08990	Hs.4742	Hs.4742:GPAA1P anchor attachment protein	2.75
	421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.75
	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	2.75
80	408196	AL034548	Hs.43627	NM_006943:Homo sapiens SRY (sex determin	2.75
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	2.75
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.75
	451356	AA748418	Hs.33368	Hs.33368:hypothetical protein FLJ11175	2.75
	421643	BE281170	Hs.106357	NM_007126:Homo sapiens valosin-containin	2.74

	423527	AI206965	Hs.105861	(locustlink)NM_024712:Homo sapiens engulf	2.74
	428000	R35145	Hs.291904	Hs.291904:accessory protein BAP31	2.74
	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	2.74
5	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	2.74
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	2.74
	440457	BE387593	Hs.21321	(locuslink)NM_145808:Homo sapiens granul	2.74
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	2.74
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	2.73
10	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	2.73
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	2.73
	421921	H83363	Hs.355993	NM_012456:Homo sapiens translocase of in	2.73
	403217				2.73
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to choli	2.73
15	418733	AA227714	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.73
	400275		Hs.4888	NM_006513:Homo sapiens seryl-tRNA synthe	2.73
	445084	H38914	Hs.250848	Hs.250848:Homo sapiens cDNA FLJ14761 fis	2.73
	411872	AW327356	Hs.90918	Hs.90918:chromosome 11 open reading fram	2.73
	403483				2.73
20	438119	AW963217	Hs.203961	Hs.203961:ESTs, Weakly similar to hypoth	2.73
	422009	AI742845	Hs.110713	NM_003472:Homo sapiens DEK oncogene (DNA	2.73
	436995	AI160015	Hs.125489	Hs.125489:KIAA1961 protein	2.73
	400509				2.73
	429305	AF095727	Hs.287832	Hs.287832:myelin protein zero-like 1	2.73
25	445899	AI263736	Hs.145626	Hs.145626:Homo sapiens, Similar to hypot	2.72
	453557	AA522464	Hs.285996	NM_024956:Homo sapiens hypothetical prot	2.72
	446859	AI494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.72
	424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	2.72
	437809	AL137723	Hs.5855	Hs.5855:Homo sapiens mRNA; cDNA DKFZp434	2.72
30	428466	AF151063	Hs.184456	NM_016486:Homo sapiens hypothetical prot	2.71
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic I	2.71
	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protei	2.71
	429359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metallopro	2.71
	427782	AI956052	Hs.115960	NM_024036:Homo sapiens hypothetical prot	2.71
35	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.71
	400277		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.71
	426263	AI908774	Hs.259785	Hs.259785:carnitine palmitoyltransferase	2.71
	445515	BE388665	Hs.179999	Hs.179999:Homo sapiens, clone IMAGE:3457	2.71
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	2.71
40	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	2.71
	420511	AF052692	Hs.98485	NM_024009:Homo sapiens gap junction prot	2.71
	424965	AW956282	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.71
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	2.71
	412973	L37368	Hs.75104	Hs.75104:RNA binding protein S1, serine-	2.70
45	410113	AW996564	Hs.250824	Hs.250824:Homo sapiens cDNA: FLJ23435 fi	2.70
	413092	AA126856	Hs.118665	Hs.118665:ESTs	2.70
	447096	BE539199	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	2.70
	450493	M93718	Hs.166373	Hs.166373:nitric oxide synthase 3 (endot	2.70
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	2.70
50	450747	AI064821	Hs.129953	Hs.129953:Ewing sarcoma breakpoint regio	2.70
	436042	AF284422	Hs.119178	(locuslink)NM_020246:Homo sapiens cation	2.70
	432981	NM_002733	Hs.3136	Hs.3136:protein kinase, AMP-activated, g	2.70
	431341	AA307211	Hs.251531	NM_002789:Homo sapiens proteasome (proso	2.70
	408204	AA454501	Hs.43666	NM_007079:Homo sapiens protein tyrosine	2.70
55	416770	AW163570	Hs.79768	NM_014740:Homo sapiens KIAA0111 gene pro	2.70
	447507	H59696	Hs.18747	NM_005837:Homo sapiens POP7 (processing	2.70
	424500	AF040704	Hs.149443	(locuslink)NM_007022:Homo sapiens putati	2.69
	414237	BE536554	Hs.278270	Hs.278270:inactive progesterone receptor	2.69
	400231		Hs.169476	NM_002046:Homo sapiens glyceraldehyde-3-	2.69
60	431209	NM_001533	Hs.2730	Hs.2730:heterogeneous nuclear ribonucleo	2.69
	444118	AA458542	Hs.10326	NM_007263:Homo sapiens coatomer protein	2.69
	424608	X80695	Hs.151134	Hs.151134:oxidase (cytochrome c) assembl	2.69
	418546	AA224827		AA224827:nc32g04.s1 NCL_CGAP_Pr2 Homo sa	2.69
	440002	AW769844	Hs.111222	Hs.111222:hypothetical protein FLJ22875	2.69
65	449957	D31365	Hs.24220	(locuslink)NM_016479:Homo sapiens scotin	2.69
	432920	U37689	Hs.3128	NM_006232:Homo sapiens polymerase (RNA)	2.69
	450306	AL080080	Hs.24766	NM_030755:Homo sapiens thioredoxin domai	2.69
	429544	BE299343	Hs.2430	NM_005997:Homo sapiens transcription fac	2.68
	428582	BE336699	Hs.185055	Hs.185055:BENE protein	2.68
70	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XIII	2.68
	453905	NM_002314	Hs.36566	NM_016735:Homo sapiens LIM domain kinase	2.68
	418883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	2.68
	420957	X98743	Hs.100555	Hs.100555:DEAD/H (Asp-Glu-Ala-Asp/His) b	2.68
	418187	NM_004604	Hs.83734	NM_004604:Homo sapiens syntaxin 4A (plac	2.68
75	409533	AW969543	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.68
	433184	AA147979	Hs.285005	NM_020243:Homo sapiens translocase of ou	2.68
	455303	AW892049		BE066891:PM3-BT0338-211299-002-e12 BT033	2.68
	452600	AI910842	Hs.103381	Hs.103381:ESTs, Weakly similar to hypoth	2.68
80	415410	AF037332	Hs.278569	NM_014748:Homo sapiens KIAA0064 gene pro	2.67
	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paraoxonase 2 (PO	2.67
	435049	AL122067	Hs.4746	NM_021941:Homo sapiens hypothetical prot	2.67
	450528	NM_014072	Hs.25063	NM_031268:Homo sapiens PRO0461 protein (	2.67
	433339	AF019226	Hs.8036	NM_004283:Homo sapiens RAB3D, member RAS	2.67
	408783	AF192522	Hs.47701	NM_013389:Homo sapiens NPC1 (Niemann-Pic	2.67

	451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	2.67
	427716	L38951	Hs.180446	Hs.180446:karyopherin (importin) beta 1	2.67
	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	2.67
5	415116	AA160363	Hs.269956	Hs.269956:ESTs	2.67
	425838	NM_014071	Hs.159613	NM_014071:Homo sapiens nuclear receptor	2.66
	418706	U73524	Hs.87465	NM_006831:Homo sapiens ATP/GTP-binding p	2.66
	410165	BE560228	Hs.71869	NM_013258:Homo sapiens apoptosis-associa	2.66
	410134	U68140	Hs.58927	(locuslink)NM_002533:Homo sapiens nuclea	2.66
10	430066	AI929659	Hs.237825	Hs.237825:signal recognition particle 72	2.66
	425910	AA830797	Hs.184760	NM_005760:Homo sapiens CCAAT-box-binding	2.66
	427954	J03060	Hs.247551	NM_002455:Homo sapiens metaxin 1 (MTX1),	2.66
	439971	W32474	Hs.301746	Hs.301746:Homo sapiens cDNA FLJ37267 fis	2.66
	438449	AK001333	Hs.6216	Hs.6216:DnaJ (Hsp40) homolog, subfamily	2.66
	435906	AI686379	Hs.110796	(locuslink)NM_020150:Homo sapiens SAR1 p	2.66
15	433387	L76528	Hs.3260	NM_000021:Homo sapiens presenilin 1 (Alz	2.66
	447191	NM_014521	Hs.17667	(locuslink)NM_014521:Homo sapiens SH3-do	2.66
	444099	D87432	Hs.10315	NM_003983:Homo sapiens solute carrier fa	2.66
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	2.66
	418529	AW005695	Hs.250897	Hs.250897:TRK-fused gene	2.65
20	426025	AW138330	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.65
	420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	2.65
	408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	2.65
	444395	N66148	Hs.11125	(locuslink)NM_014041:Homo sapiens signal	2.65
25	431222	X56777	Hs.273790	NM_007155:Homo sapiens zona pellucida gl	2.65
	406790	AA293303	Hs.356342	Hs.356342:ESTs, Highly similar to 211320	2.65
	440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	2.65
	416526	H61082	Hs.14743	Hs.14743:ESTs	2.65
	413995	BE048146	Hs.75671	NM_004603:Homo sapiens syntaxin 1A (brai	2.65
30	424908	AW513963	Hs.39143	Hs.39143:hypothetical protein MGC13125	2.65
	442110	AF113008	Hs.8102	NM_001023:Homo sapiens ribosomal protein	2.65
	452882	AW972990	Hs.196270	NM_030780:Homo sapiens folate transporte	2.65
	406862	AW150807	Hs.356262	Hs.356262:ESTs, Highly similar to A31233	2.64
	451295	AI557212	Hs.17132	Hs.17132:ESTs	2.64
35	448428	AF282874	Hs.21201	NM_015480:Homo sapiens necln 3 (DKFZP56	2.64
	426611	BE178050	Hs.171271	NM_001904:Homo sapiens catenin (cadherin	2.64
	426216	N77630	Hs.13895	Hs.13895:Homo sapiens cDNA FLJ11654 fis,	2.64
	407223	H96850		H96850:yo03b12.s1 Soares melanocyte 2NbH	2.64
	427725	U66839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	2.64
40	420157	AA857991	Hs.123106	Hs.123106:ESTs	2.64
	428471	X57348	Hs.184510	Hs.184510:stratifin	2.64
	451544	AK000429	Hs.26570	NM_017814:Homo sapiens hypothetical prot	2.64
	413245	BE244334	Hs.75249	Hs.75249:ADP-ribosylation factor-like G	2.64
	415020	BE249915	Hs.293533	Hs.293533:Homo sapiens cDNA FLJ37093 fis	2.64
45	437193	BE259190	Hs.289721	Hs.289721:growth arrest-specific 5	2.64
	418684	U82987	Hs.87246	NM_014417:Homo sapiens BCL2 binding comp	2.64
	410668	BE379794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	2.64
	436183	AI146327	Hs.334802	(locuslink)NM_024718:Homo sapiens hypoth	2.64
	441226	BE563042	Hs.118820	Hs.118820:hypothetical protein BC007882	2.64
50	432788	AA521091	Hs.178499	Hs.178499:HSPC063 protein	2.64
	432746	AA564512	Hs.372775	Hs.372775:Homo sapiens, clone IMAGE:3946	2.64
	450377	AB033091	Hs.355925	Hs.355925:KIAA1265 protein	2.64
	434633	AI189587	Hs.120915	Hs.120915:ESTs	2.64
	424707	BE061914	Hs.10844	Hs.10844:leucine-rich alpha-2-glycoprote	2.64
55	427600	AW630918	Hs.179774	Hs.179774:proteasome (prosome, macropain	2.63
	446522	NM_003876	Hs.15196	NM_003876:Homo sapiens putative receptor	2.63
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	2.63
	410701	AF198620	Hs.10283	NM_005105:Homo sapiens RNA binding motif	2.63
	410182	NM_001983	Hs.59544	NM_001983:Homo sapiens excision repair c	2.63
60	406716	AW148546	Hs.169476	Hs.169476:glyceraldehyde-3-phosphate deh	2.63
	430308	BE540865	Hs.238990	NM_004064:Homo sapiens cyclin-dependent	2.63
	431074	BE072772	Hs.8997	Hs.8997:Sad1 unc-84 domain protein 1	2.63
	412867	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	2.63
	440524	R71264	Hs.16798	Hs.16798:Homo sapiens mRNA; cDNA DKFZp56	2.63
65	435968	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens integr	2.63
	422672	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	2.63
	447528	AI612027	Hs.76277	NM_138393:Homo sapiens hypothetical prot	2.63
	406774	AW518383	Hs.177592	Hs.177592:ribosomal protein, large, P1	2.63
	439755	AW748482	Hs.77873	Hs.77873:B7 homolog 3	2.63
70	435311	W86610	Hs.185736	Hs.185736:ESTs	2.63
	428699	AW578252	Hs.190161	Hs.190161:LR8 protein	2.62
	410678	BE540516	Hs.378825	Hs.378825:Homo sapiens cDNA FLJ37850 fis	2.62
	414839	X63692	Hs.77462	(locuslink)NM_001379:Homo sapiens DNA (c	2.62
	443217	NM_001545	Hs.9078	Hs.9078:immature colon carcinoma transcr	2.62
75	448749	AW859679	Hs.21902	Hs.21902:Homo sapiens clone 25237 mRNA s	2.62
	450009	AI399947	Hs.166486	Hs.166486:Homo sapiens cDNA FLJ11432 fis	2.62
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	2.62
	442232	AI357813	Hs.337460	Hs.337460:ESTs, Highly similar to HYEP_H	2.62
	419625	U91616	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.62
80	416114	AI695549	Hs.183868	Hs.183868:glucuronidase, beta	2.62
	439437	AI207788	Hs.343628	Hs.343628:sialyltransferase 4B (beta-gal	2.61
	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	2.61
	443142	AI696513	Hs.108705	Hs.108705:protein phosphatase 2 (formerl	2.61
	426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.61

	419667	AU077005	Hs.92208	NM_003815:Homo sapiens a disintegrin and	2.61
	415072	BE253687	Hs.77876	Hs.77876:hypothetical gene MGC19595	2.61
	406670	W79632	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.61
	403399				2.61
5	419579	W49529	Hs.296200	NM_023948:Homo sapiens hypothetical prot	2.61
	437202	AA326110	Hs.374481	Hs.374481:ESTs, Weakly similar to T34549	2.61
	414020	NM_002984	Hs.75703	NM_002984:Homo sapiens small inducible c	2.61
	421295	AW081061	Hs.103180	Hs.103180:DC2 protein	2.61
	446488	AB037782	Hs.15119	Hs.15119:KIAA1361 protein	2.61
10	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	2.60
	448204	AI475124	Hs.170561	Hs.170561:ESTs	2.60
	449175	AJ005892	Hs.23170	(locuslink)NM_012280:Homo sapiens FlsJ h	2.60
	411201	T74588	Hs.8509	Hs.8509:ESTs, Weakly similar to C3HU com	2.60
15	424805	AF230904	Hs.153260	NM_031892:Homo sapiens SH3-domain kinase	2.60
	425421	L11669	Hs.157145	Hs.157145:tetracycline transporter-like	2.60
	422739	H20106	Hs.119591	(locuslink)NM_004069:Homo sapiens adapt	2.60
	450858	C18458	Hs.25597	Hs.25597:elongation of very long chain f	2.59
	443195	BE148235	Hs.193063	Hs.193063:Homo sapiens cDNA FLJ14201 fis	2.59
20	430504	H52761	Hs.44095	Hs.44095:cyclin M3	2.59
	439578	AW263124	Hs.350547	NM_024665:Homo sapiens nuclear receptor	2.59
	416041	AA345547	Hs.53263	(locuslink)NM_024647:Homo sapiens nucleo	2.59
	451920	AA224483	Hs.27239	Hs.27239:zinc finger, DHHC domain contai	2.59
	414163	BE262310	Hs.75782	NM_001521:Homo sapiens general transcrip	2.59
	422140	BE295918	Hs.112193	(locuslink)NM_025259:Homo sapiens chromo	2.59
25	452817	AA322859	Hs.284275	Hs.284275:p21 (CDKN1A)-activated kinase	2.59
	413353	AW293542	Hs.75309	Hs.75309:eukaryotic translation elongati	2.59
	421700	BE515018	Hs.107014	NM_016641:Homo sapiens membrane interact	2.59
	410801	BE275469	Hs.66493	NM_016430:Homo sapiens Down syndrome cri	2.59
30	440511	AF132959	Hs.7236	NM_015953:Homo sapiens eNOS interacting	2.59
	407887	AA579668	Hs.41072	(locuslink)NM_004568:Homo sapiens serine	2.59
	425356	BE244879	Hs.155939	NM_005541:Homo sapiens inositol polyphos	2.59
	408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	2.59
	417952	AI192838	Hs.173135	Hs.173135:dual-specificity tyrosine-(Y)-	2.59
35	433053	BE301909	Hs.279952	NM_015917:Homo sapiens glutathione S-tra	2.59
	450935	BE514743	Hs.379039	NM_005851:Homo sapiens tumor suppressor	2.59
	417891	W79410	Hs.82887	(locuslink)NM_021959:Homo sapiens protei	2.59
	438364	AK000860	Hs.6191	NM_020441:Homo sapiens coronin, actin-bi	2.59
	430976	AA505112	Hs.282990	NM_033550:Homo sapiens chromosome 20 ope	2.58
40	444838	AV651680	Hs.208558	Hs.208558:ESTs	2.58
	416435	AI431301	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.58
	415444	BE247295	Hs.78452	Hs.78452:solute carrier family 20 (phosp	2.58
	452222	AW806287	Hs.21432	Hs.21432:SEX gene	2.58
	400541				2.58
45	444309	U83236	Hs.10803	Hs.10803:calcium and integrin binding 1	2.58
	416116	H51847	Hs.99858	Hs.99858:ribosomal protein L7a	2.58
	418629	BE247550	Hs.86859	(locuslink)NM_005310:Homo sapiens growth	2.58
	432996	AF105025	Hs.279901	Hs.279901:PTD009 protein	2.57
	426781	AL048967	Hs.172207	(locuslink)NM_007363:Homo sapiens non-PO	2.57
50	452636	BE615074	Hs.145279	Hs.145279:SET translocation (myeloid leu	2.57
	406851	AA609784	Hs.352392	Hs.352392:major histocompatibility compl	2.57
	447674	BE270640	Hs.19192	NM_001798:Homo sapiens cyclin-dependent	2.57
	445647	AV654627	Hs.271808	Hs.271808:Homo sapiens cDNA FLJ38018 fis	2.57
	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	2.57
	402861				2.57
55	450069	AI698139	Hs.202093	Hs.202093:ESTs	2.57
	414029	BE297731	Hs.75709	NM_002355:Homo sapiens mannose-6-phospha	2.57
	427700	AA262294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.57
	449961	AW265634	Hs.133100	Hs.133100:ESTs	2.56
60	449378	AW664026	Hs.59892	Hs.59892:ESTs, Weakly similar to alpha 5	2.56
	442599	AF078037	Hs.324051	(locuslink)NM_006663:Homo sapiens RelA-a	2.56
	448633	AA311426	Hs.21635	NM_001070:Homo sapiens tubulin, gamma 1	2.56
	416078	AL034349	Hs.79005	NM_002844:Homo sapiens protein tyrosine	2.56
	428044	AA093322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	2.56
65	451564	AU076698	Hs.132760	(locuslink)NM_001467:Homo sapiens glucos	2.56
	457601	AF041429	Hs.284265	(locuslink)NM_145169:Homo sapiens simila	2.56
	439630	AA313607	Hs.58633	Hs.58633:Homo sapiens cDNA: FLJ22145 fis	2.55
	419587	S62907	Hs.91343	NM_000807:Homo sapiens gamma-aminobutyri	2.55
	448279	BE250564	Hs.283655	Hs.283655:lysophospholipase II	2.55
70	453350	AI917771	Hs.61790	(locuslink)NM_024658:Homo sapiens import	2.55
	423720	AL044191	Hs.23388	NM_030817:Homo sapiens hypothetical prot	2.55
	400237		Hs.83347	NM_001087:Homo sapiens angio-associated,	2.55
	420856	BE513294	Hs.205736	Hs.205736:KIAA1978 protein	2.55
	421541	NM_003942	Hs.105584	Hs.105584:ribosomal protein S6 kinase, 9	2.55
75	434848	BE256304	Hs.32148	NM_018445:Homo sapiens AD-015 protein (L	2.55
	424488	AK000413	Hs.149227	(locuslink)NM_017806:Homo sapiens hypo	2.55
	449089	D78850	Hs.250465	Hs.250465:Homo sapiens mRNA; cDNA DKFZp4	2.55
	430053	AF052155	Hs.227949	NM_030673:Homo sapiens SEC13-like 1 (S.	2.55
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	2.55
	407755	AI151353	Hs.29742	Hs.29742:Homo sapiens cDNA FLJ32147 fis,	2.55
80	446673	NM_016361	Hs.15871	NM_016361:Homo sapiens LPAP for lysophos	2.55
	411766	AA399871	Hs.71969	Hs.71969:Homo sapiens mRNA; cDNA DKFZp66	2.55
	415198	AW009480	Hs.943	Hs.943:natural killer cell transcript 4	2.55
	436495	BE258948	Hs.290874	Hs.290874:Homo sapiens, clone MGC:31984	2.55

5	417785	X59812	Hs.82568	NM_000784:Homo sapiens cytochrome P450,	2.55
	443358	H65417	Hs.17757	(locuslink)NM_021622:Homo sapiens plecks	2.55
	452349	AB028944	Hs.29189	Hs.29189:ATPase, Class VI, type 11A	2.55
	427721	AI582843	Hs.180455	NM_005053:Homo sapiens RAD23 homolog A (	2.54
	407559	AA313352	Hs.280858	Hs.280858:Homo sapiens cDNA FLJ32370 fis	2.54
10	413426	U88837	Hs.75354	Hs.75354:GCN1 general control of amino-a	2.54
	425465	L18964	Hs.1904	Hs.1904:protein kinase C, iota	2.54
	444152	AI125694	Hs.149305	Hs.149305:hypothetical protein MGC2603	2.54
	451820	AW058357	Hs.199248	NM_000958:Homo sapiens prostaglandin E r	2.54
	441356	BE384361	Hs.182885	(locuslink)NM_004556:Homo sapiens nuclea	2.54
15	444410	BE387360	Hs.33719	Hs.33719:Homo sapiens, similar to data s	2.54
	415200	AL040328	Hs.78202	NM_003072:Homo sapiens SWI/SNF related,	2.54
	403955				2.54
	430361	AI033965	Hs.239926	Hs.239926:sterol-C4-methyl oxidase-like	2.54
	432401	NM_013330	Hs.274479	NM_013330:Homo sapiens NME7 (NME7), mRNA	2.54
20	446719	W39500	Hs.301872	Hs.301872:hypothetical protein MGC4840	2.54
	439941	AI392640	Hs.18272	NM_030674:Homo sapiens solute carrier fa	2.54
	436685	W28661	Hs.5288	Hs.5288:Homo sapiens mRNA; cDNA DKFZp434	2.54
	424522	AL134847	Hs.149957	Hs.149957:ribosomal protein S6 kinase, 9	2.54
	442904	AW575008	Hs.11355	Hs.11355:thymopoietin	2.54
25	422605	H16646	Hs.118666	Hs.118666:hypothetical protein PP591	2.54
	442069	AW664144	Hs.297007	Hs.297007:Homo sapiens cDNA FLJ32174 fis	2.54
	447362	AW176120	Hs.9061	NM_024099:Homo sapiens hypothetical prot	2.53
	416305	AU076628	Hs.79187	NM_001338:Homo sapiens coxsackie virus a	2.53
	422624	BE616678	Hs.76152	NM_006854:Homo sapiens KDEL (Lys-Asp-Glu	2.53
30	447298	BE617527	Hs.239818	NM_006219:Homo sapiens phosphoinositide-	2.53
	412833	AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.53
	404854				2.53
	415761	AA132666	Hs.78802	(locuslink)NM_002093:Homo sapiens glycog	2.53
	431104	AW970859	Hs.313503	Hs.313503:ESTs	2.53
35	439180	AI393742	Hs.199067	Hs.199067:v-erb-b2 erythroblastic leukem	2.53
	424250	AF073310	Hs.143648	NM_003749:Homo sapiens insulin receptor	2.53
	452878	AW081128	Hs.246374	Hs.246374:Homo sapiens cDNA FLJ31250 fis	2.53
	415742	BE410243	Hs.78769	NM_003249:Homo sapiens thimet oligopepti	2.53
	404140				2.53
40	407255	AA012992	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.53
	422509	AA258513	Hs.117865	Hs.117865:solute carrier family 17 (anio	2.53
	434866	AW002565	Hs.355460	Hs.355460:Homo sapiens cDNA: FLJ21763 fi	2.53
	429743	AA804398	Hs.288995	(locuslink)NM_017961:Homo sapiens hypoth	2.53
	433047	M86135	Hs.279946	NM_004990:Homo sapiens methionine-tRNA s	2.53
45	418945	BE246762	Hs.89499	Hs.89499:arachidonate 5-lipoxygenase	2.52
	445926	AF054284	Hs.334826	NM_012433:Homo sapiens splicing factor 3	2.52
	411353	BE383533	Hs.279784	Hs.279784:prolactin regulatory element b	2.52
	448252	BE622791	Hs.12199	NM_030577:Homo sapiens hypothetical prot	2.52
	447365	BE383676	Hs.334	(locuslink)NM_005435:Homo sapiens Rho gu	2.52
50	414844	AA296874	Hs.77494	NM_080916:Homo sapiens deoxyguanosine ki	2.52
	444025	AA578364	Hs.349093	NM_015945:Homo sapiens ovarian cancer ov	2.52
	416149	AA311965	Hs.79058	NM_003168:Homo sapiens suppressor of Ty	2.52
	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis,	2.52
	437952	D63209	Hs.5944	NM_014585:Homo sapiens solute carrier fa	2.52
55	445625	BE246743	Hs.353181	(locuslink)NM_025092:Homo sapiens hypoth	2.52
	431565	AF161470	Hs.260622	Hs.260622:butyrate-induced transcript 1	2.52
	410179	W27723	Hs.59498	(locuslink)NM_003718:Homo sapiens cell d	2.52
	431476	BE612705	Hs.256697	(locuslink)NM_005340:Homo sapiens histid	2.52
	406672	M26041	Hs.198253	(locuslink)NM_002122:Homo sapiens major	2.52
60	418180	BE618087	Hs.83724	Hs.83724:hypothetical protein MGC5466	2.52
	428248	AI126772	Hs.40479	Hs.40479:Homo sapiens cDNA FLJ25802 fis,	2.52
	419935	AB020980	Hs.93832	Hs.93832:putative membrane protein	2.52
	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.52
	426691	NM_006201	Hs.171834	(locuslink)NM_006201:Homo sapiens PCTAIR	2.51
65	408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	2.51
	456266	L29073	Hs.198726	NM_003651:Homo sapiens cold shock domain	2.51
	428921	Z43809	Hs.194638	Hs.194638:polymerase (RNA) II (DNA direc	2.51
	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxyribonuclease	2.51
	422607	Z45471	Hs.118684	NM_006923:Homo sapiens stromal cell-deri	2.51
70	421846	AA017707	Hs.1432	NM_002743:Homo sapiens protein kinase C	2.51
	414874	D26351	Hs.77515	NM_002224:Homo sapiens inositol 1,4,5-tr	2.51
	432956	AL037895	Hs.279861	NM_015959:Homo sapiens CGI-31 protein (L	2.51
	438393	AA351815	Hs.50740	Hs.50740:Homo sapiens mRNA; cDNA DKFZp76	2.51
	418360	AW296974	Hs.84264	NM_006401:Homo sapiens acidic (leucine-r	2.50
75	401061				2.50
	426559	AB001914	Hs.170414	Hs.170414:paired basic amino acid cleavi	2.50
	412204	AI125507	Hs.24937	Hs.24937:transformer-2 alpha (htra-2 alp	2.50
	448950	AF288687	Hs.9275	NM_020410:Homo sapiens CGI-152 protein (	2.50
	409936	AK001691	Hs.57655	(locuslink)NM_018234:Homo sapiens duduli	2.50
80	414675	R79015	Hs.288968	Hs.288968:RAB22A, member RAS oncogene fa	2.50
	409983	D50922	Hs.57729	(locuslink)NM_012289:Homo sapiens Kelch-	2.50
	450914	AI743761	Hs.142528	Hs.142528:ESTs	2.50
	444630	AI753230	Hs.323562	(locuslink)NM_032121:Homo sapiens hypoth	2.50
	401353				2.50
85	441680	AW444598	Hs.7940	(locuslink)NM_021159:Homo sapiens RAP1,	2.50
	406860	AA876469		AA876469:oe48b04.s1 NCL_CGAP_Pr25 Homo s	2.50
	449163	AW161356	Hs.23119	NM_003492:Homo sapiens chromosome X open	2.50

432975	AA331517	Hs.286055	Hs.286055:chimerin (chimaerin) 2	2.50
430600	AW950967	Hs.274348	NM_004639:Homo sapiens HLA-B associated	2.50
407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	2.50

## 5 TABLE 9B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

10

Pkey	CAT Number	Accession
406685	0_0	M18728
452098	161393_1	BC028348 BF772844 H83066 AW817969 H90985 BF755039 AI858183
451129	1495511_1	BE072881 AI762181 BE072946
15 459306	223120_-4	AW578452
448489	2189115_1	R45782 R45781
418869	12789_14	AA229762 AA230035
418546	242836_1	T59708 AA224827 T59843 BE156903
20 455303	1152492_1	BE066891 BE066895 AW892049 BE066897 BE903884
406860	0_0	AA876469

## TABLE 9C

25 Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

30

Pkey	Ref	Strand	Nt_position
406399	9256288	Minus	63448-63554
403220	7630969	Plus	64338-64517
403218	7630969	Plus	58039-58149
35 403221	7630969	Plus	66294-66438,66936-67124
403219	7630969	Plus	61858-61995
403739	7630882	Plus	44563-44766,48209-48483,52255-52495
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
40 405556	1552511	Plus	163497-163623,164715-164968,165369-16550
400529	9796988	Plus	138232-138423
404826	6572184	Plus	47726-48046
400750	8119067	Plus	198991-199168,199316-199548
400847	9188605	Plus	44643-44835
45 400448	9887687	Minus	177372-177674
402829	8918414	Plus	101532-101852,102006-102263
400846	9188605	Plus	39310-39474
401179	9438647	Plus	113477-113893
404240	5002624	Minus	116132-116407,116653-116922
50 402260	3399665	Minus	113765-113910,115653-115765,116808-11694
406363	9256114	Plus	14403-14602,17000-17147,17241-17368
405203	7230116	Plus	125295-125463
402104	8119072	Plus	122409-122600
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
55 400845	9188605	Plus	34428-34612
403217	7630969	Plus	54089-54163,55427-55623
403483	9966188	Minus	144546-144854
400509	9796539	Minus	157909-158430
403399	6684178	Plus	61841-62145,62367-62756
60 400541	7574902	Plus	126235-126380,126478-126597
402861	2814366	Minus	14933-15231,15387-15627
403955	7770475	Minus	54527-54740
404854	7143420	Plus	14260-14537
404140	9843520	Plus	37761-38147
65 401061	3242744	Minus	99468-99549,100707-100848,100918-101107,
401353	9931296	Minus	50831-51352

70 Table 10A lists about 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium). These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 85th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

75

TABLE 10A: 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

80

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of tumor to normal adult tissues

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
5	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	15.54
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	14.52
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	14.04
	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	14.02
	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease i	13.72
10	406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	13.44
	418406	X73501	Hs.84905	Hs.84905:cytokeratin 20	12.70
	406667	M12523			12.42
	416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	11.98
	437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	11.58
15	422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	11.50
	418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, LI c	10.16
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.11
	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	10.01
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	9.77
20	441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	9.69
	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	9.48
	453863	X02544	Hs.572	Hs.572:orosomuroid 1	9.20
	407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	9.18
	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	9.04
25	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	8.69
	430178	AW449612	Hs.152475	Hs.152475:ESTs	8.51
	423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	8.43
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	8.17
	409683	U33317	Hs.711	NM_001926:Homo sapiens defensin, alpha 6	8.12
30	431777	AA570296	Hs.307047	NM_032579:Homo sapiens colon and small i	8.08
	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	8.06
	427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (	7.95
	436624	T64297	Hs.351719	NM_001443:Homo sapiens fatty acid bindin	7.74
	410407	X66839	Hs.63287	NM_001216:Homo sapiens carbonic anhydras	7.46
35	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	7.41
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	7.40
	412374	X01388	Hs.73849	NM_000040:Homo sapiens apolipoprotein C-	7.34
	407244	M10014			7.31
	419741	NM_007019	Hs.93002	Hs.93002:ubiquitin-conjugating enzyme E2	7.31
40	406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	7.26
	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	7.21
	404519				7.18
	413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	7.13
	422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	7.10
45	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	7.02
	430828	AI763257	Hs.86327	Hs.86327:homeo box B9	6.83
	433927	AI557019	Hs.116467	NM_032391:Homo sapiens small nuclear pro	6.81
	406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	6.78
	423538	AW603823	Hs.146268	Hs.146268:ESTs, Weakly similar to C71400	6.53
50	434206	AW136973	Hs.362915	Hs.362915:Homo sapiens cDNA FLJ34876 fis	6.37
	409041	AB033025	Hs.50081	Hs.50081:KIAA1199 protein	6.33
	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	6.19
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.19
	436330	NM_004413	Hs.109	NM_004413:Homo sapiens dipeptidase 1 (re	6.01
55	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	6.00
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	5.97
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	5.94
	420923	AF097021	Hs.273321	NM_006418:Homo sapiens differentially ex	5.94
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	5.90
60	420802	U22376	Hs.1334	NM_005375:Homo sapiens v-myb myeloblasto	5.89
	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	5.89
	431727	AW293464	Hs.162031	Hs.162031:ESTs	5.85
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	5.84
	432023	AW273128	Hs.300268	Hs.300268:EST	5.75
65	447033	AI357412	Hs.157601	Hs.157601:ESTs	5.69
	411734	AW374954	Hs.71779	Hs.71779:ESTs, Weakly similar to S24C_AR	5.69
	406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	5.55
	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	5.48
	443247	BE614387	Hs.333893	Hs.333893:cell division cycle associated	5.45
70	409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	5.44
	449388	H53191	Hs.36723	Hs.36723:ESTs, Weakly similar to C05G5.5	5.38
	428046	AW812795	Hs.337534	Hs.337534:Homo sapiens cDNA FLJ25241 fis	5.38
	433013	AI697890	Hs.127337	(locuslink)NM_004655:Homo sapiens axin 2	5.38
	419079	AW014836	Hs.18844	Hs.18844:ESTs	5.37
75	428355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	5.35
	422956	BE545072	Hs.122579	(locuslink)NM_018098:Homo sapiens epithe	5.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	5.30
	450543	AI394037	Hs.170296	Hs.170296:Homo sapiens cDNA: FLJ22090 fi	5.30
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	5.30
80	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	5.28
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	5.28
	427722	AK000123	Hs.180479	NM_017671:Homo sapiens chromosome 20 ope	5.26
	430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	5.26
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	5.21
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	5.16



5	447208	BE315291	Hs.237971	NM_024096:Homo sapiens hypothetical prot	5.14
	430207	AW079559	Hs.152258	Hs.152258:ESTs	5.12
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	5.12
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.07
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	5.06
10	452194	AI694413	Hs.373599	Hs.373599:EST	5.01
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	4.99
	406399				4.98
	403220				4.94
	408380	AF123050	Hs.44532	NM_006398:Homo sapiens ubiquitin D (UBD)	4.92
15	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	4.92
	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	4.85
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	4.84
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	4.81
	441377	BE218239	Hs.202656	Hs.202656:ESTs	4.81
20	444666	BE293347	Hs.11638	(locuslink)NM_016234:Homo sapiens fatty-	4.80
	415701	NM_003878	Hs.78619	(locuslink)NM_003878:Homo sapiens gamma-	4.80
	419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	4.80
	455630	AV655701	Hs.75183	NM_000773:Homo sapiens cytochrome P450,	4.78
	422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	4.78
25	423337	NM_004655	Hs.127337	NM_004655:Homo sapiens axin 2 (conductin	4.75
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	4.73
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	4.70
	423936	U77629	Hs.135639	NM_005170:Homo sapiens achaete-scute com	4.70
	404661				4.68
30	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	4.67
	420005	AW271106	Hs.133294	Hs.133294:ESTs	4.66
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I iso	4.61
	427506	AK000134	Hs.179100	NM_017678:Homo sapiens hypothetical prot	4.60
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	4.59
35	453884	AA355925	Hs.36232	NM_021067:Homo sapiens KIAA0186 gene pro	4.55
	431301	AA502384	Hs.151529	Hs.151529:ESTs	4.54
	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	4.54
	449032	AA045573	Hs.22900	NM_004289:Homo sapiens nuclear factor (e	4.54
	434540	NM_016045	Hs.3945	NM_016045:Homo sapiens chromosome 20 ope	4.54
40	407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	4.53
	458748	AI381530	Hs.371132	Hs.371132:ESTs	4.53
	408298	AI745325	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.51
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	4.50
	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	4.49
45	425371	D49441	Hs.155591	NM_005823:Homo sapiens mesothelin (MSLN)	4.49
	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	4.46
	432867	AW016936	Hs.233364	Hs.233364:ESTs	4.44
	419559	Y07828	Hs.91096	NM_007028:Homo sapiens tripartite motif-	4.44
	430294	AI538226	Hs.32976	(locuslink)NM_004485:Homo sapiens guanin	4.42
50	411248	AA551538	Hs.69321	Hs.69321:KIAA1359 protein	4.39
	402496				4.38
	430937	X53463	Hs.2704	NM_002083:Homo sapiens glutathione perox	4.37
	434414	AI798376		AF134163:Homo sapiens Human endogenous r	4.36
	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	4.35
55	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.33
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	4.33
	450531	AW301032	Hs.203800	Hs.203800:ESTs	4.33
	403055				4.31
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	4.31
60	400965				4.30
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	4.29
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	4.29
	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:225881	4.28
	430832	AI073913	Hs.100686	Hs.100686:anterior gradient protein 3	4.28
65	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	4.28
	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	4.27
	414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	4.27
	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	4.27
	439211	AI890347	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.27
70	459299	BE094291	Hs.155651	NM_021784:Homo sapiens hepatocyte nuclea	4.25
	449720	AA311152	Hs.288708	(locuslink)NM_025113:Homo sapiens hypoth	4.24
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	4.24
	421777	BE562088	Hs.108196	NM_016095:Homo sapiens HSPC037 protein (	4.21
	419395	BE268326	Hs.90280	Hs.90280:5-aminoimidazole-4-carboxamide	4.20
75	443211	AI128388	Hs.143655	Hs.143655:ESTs	4.20
	403218				4.20
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	4.19
	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	4.19
	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	4.19
80	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif-	4.18
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	4.18
	440869	NM_014297	Hs.7486	NM_014297:Homo sapiens protein expressed	4.17
	414075	U11862	Hs.75741	NM_001091:Homo sapiens amiloride binding	4.17
	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	4.16
	440409	AW294316	Hs.125608	Hs.125608:ESTs	4.16
	445564	AB028957	Hs.12896	Hs.12896:KIAA1034 protein	4.16
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	4.12

	401866				4.11
	431611	U58766	Hs.264428	Hs.264428:tissue specific transplantatio	4.10
	430187	AI799909	Hs.158989	Hs.158989:Homo sapiens cDNA FLJ37936 fis	4.10
5	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	4.08
	449281	AI808699	Hs.162717	NM_032756:Homo sapiens hypothetical prot	4.08
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	4.08
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	4.06
	435066	BE261750	Hs.4747	NM_001363:Homo sapiens dyskeratosis cong	4.05
10	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	4.04
	403221				4.04
	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.03
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	4.03
	431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine deficie	4.01
15	439759	AL359055	Hs.67709	Hs.67709:Homo sapiens mRNA full length i	4.00
	441362	BE614410	Hs.23044	NM_080668:Homo sapiens similar to RIKEN	3.99
	417900	BE250127	Hs.82906	Hs.82906:CD20 cell division cycle 20 ho	3.99
	428987	NM_004751	Hs.194710	NM_004751:Homo sapiens glucosaminyl (N-a	3.99
	456977	AK000252	Hs.169758	NM_017723:Homo sapiens hypothetical prot	3.99
20	445919	T53519	Hs.334692	Hs.334692:hypothetical protein MGC14141	3.98
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	3.98
	422827	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	3.97
	422363	T55979	Hs.115474	NM_002915:Homo sapiens replication facto	3.97
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	3.97
25	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	3.96
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	3.96
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	3.95
	432407	AA221036		AF134164:Homo sapiens Human endogenous r	3.95
	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	3.94
30	408494	AA554714	Hs.187578	Hs.187578:Homo sapiens cDNA FLJ11639 fis	3.94
	412610	X90908	Hs.74126	NM_001445:Homo sapiens fatty acid bindin	3.94
	433323	AA805132	Hs.159142	Hs.159142:lunatic fringe homolog (Drosop	3.94
	422515	AW500470	Hs.117950	Hs.117950:phosphoribosylaminoimidazole c	3.92
	436543	NM_002212	Hs.5215	Hs.5215:integrin beta 4 binding protein	3.91
35	418113	AI272141	Hs.83484	Hs.83484:SRY (sex determining region Y)-	3.91
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	3.90
	431939	AW008061	Hs.231994	Hs.231994:Homo sapiens, clone IMAGE:4341	3.90
	453439	AI572438	Hs.32976	NM_004485:Homo sapiens guanine nucleotid	3.89
	441888	AI733306	Hs.128071	NM_022901:Homo sapiens hypothetical prot	3.89
40	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	3.89
	425234	AW152225	Hs.165909	Hs.165909:ESTs, Weakly similar to hypoth	3.89
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	3.87
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	3.85
45	436251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	3.85
	422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	3.84
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	3.84
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	3.84
	416209	AA236776	Hs.79078	NM_002358:Homo sapiens MAD2 mitotic arre	3.83
	430680	AW138724	Hs.168974	Hs.168974:ESTs	3.83
50	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	3.82
	436481	AA379597	Hs.5199	NM_014176:Homo sapiens HSPC150 protein s	3.82
	453700	AB009426	Hs.560	NM_001644:Homo sapiens apolipoprotein B	3.81
	410619	BE512730	Hs.65114	Hs.65114:keratin 18	3.81
	409420	Z15008	Hs.54451	NM_005562:Homo sapiens laminin, gamma 2	3.79
55	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	3.79
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPH3B), mR	3.78
	453967	AW009077	Hs.232947	Hs.232947:ESTs	3.78
	426106	AI678765	Hs.21812	Hs.21812:ESTs	3.78
	434170	AA626509	Hs.159642	(locuslink)NM_001490:Homo sapiens glucos	3.78
60	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	3.78
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	3.74
	419229	AI827237	Hs.362919	Hs.362919:ESTs	3.74
	437156	AI916600	Hs.121194	Hs.121194:Homo sapiens cDNA: FLJ21569 fi	3.74
	452833	BE559681	Hs.30736	(locuslink)NM_015201:Homo sapiens block	3.73
65	426831	BE296216	Hs.172673	NM_000687:Homo sapiens S-adenosylhomocys	3.73
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	3.72
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	3.71
	408832	AW085690	Hs.63428	Hs.63428:Homo sapiens cDNA FLJ34457 fis,	3.71
	440300	N39760	Hs.8859	NM_138793:Homo sapiens apyrase (SHAPY),	3.71
70	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	3.71
	432575	AA553722	Hs.194346	Hs.194346:Sp1-2 protein	3.71
	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	3.71
	417001	AU076648	Hs.80741	NM_000282:Homo sapiens propionyl Coenzym	3.69
	421225	AA463798	Hs.102696	Hs.102696:MCT-1 protein	3.69
75	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	3.69
	428330	L22524	Hs.2256	NM_002423:Homo sapiens matrix metallopro	3.67
	447472	AW207347	Hs.211101	Hs.211101:ESTs	3.67
	423349	AF010258	Hs.127428	NM_002142:Homo sapiens homeo box A9 (HOX	3.67
	422026	U80736	Hs.110826	Hs.110826:trinucleotide repeat containin	3.66
	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	3.66
80	417720	AA205625	Hs.208067	Hs.208067:ESTs	3.66
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	3.66
	421515	Y11339	Hs.105352	(locuslink)NM_018414:Homo sapiens GalNAc	3.65
	433675	AW977653	Hs.75319	Hs.75319:ribonucleotide reductase M2 pol	3.65

5	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	3.65
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis	3.64
	412140	AA219691	Hs.73625	NM_005733:Homo sapiens RAB6 interacting,	3.64
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	3.63
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	3.63
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	3.62
	428862	NM_000346	Hs.2316	Hs.2316:SRY (sex determining region Y)-b	3.62
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	3.62
10	412056	T28160	Hs.778	Hs.778:guanylate cyclase activator 2A (g	3.61
	401519				3.60
	428011	BE387514	Hs.181418	NM_014730:Homo sapiens KIAA0152 gene pro	3.60
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	3.60
	421903	AW079940	Hs.15951	(locuslink)NM_145202:Homo sapiens prolin	3.58
15	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	3.58
	424544	M88700	Hs.150403	NM_000790:Homo sapiens dopa decarboxylas	3.58
	431563	AI027643	Hs.120912	Hs.120912:ESTs	3.57
	435602	AF217515	Hs.283532	NM_018455:Homo sapiens uncharacterized b	3.57
	434369	AI650363	Hs.116462	Hs.116462:ESTs	3.57
20	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	3.56
	447334	AA515032	Hs.91109	Hs.91109:ESTs, Weakly similar to putativ	3.56
	422150	AI867118	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	3.56
	450663	H43540	Hs.25292	Hs.25292:ribonuclease H2, large subunit	3.56
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	3.56
25	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	3.55
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	3.55
	422532	AL008726	Hs.118126	(locuslink)NM_000308:Homo sapiens protec	3.55
	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	3.55
	442053	R35343	Hs.24968	Hs.24968:hypothetical protein BC016683	3.55
30	437386	W52452	Hs.356766	Hs.356766:Homo sapiens mRNA; cDNA DKFZp7	3.54
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	3.53
	446372	AB020644	Hs.14945	Hs.14945:fatty-acid-Coenzyme A ligase, I	3.53
	432378	AI493046	Hs.146133	Hs.146133:ESTs	3.53
	434171	BE247688	Hs.347349	(locuslink)NM_004749:Homo sapiens cell c	3.52
35	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	3.52
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	3.51
	414918	AI219207	Hs.72222	Hs.72222:fer-1-like 4 (C. elegans)	3.51
	440340	AW895503	Hs.125276	Hs.125276:Homo sapiens cDNA FLJ25833 fis	3.51
	418384	AW149266	Hs.25130	Hs.25130:Homo sapiens cDNA FLJ14923 fis	3.51
40	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	3.51
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	3.51
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	3.50
	431567	N51357	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (	3.50
	453883	AI638516	Hs.347524	Hs.347524:Homo sapiens, clone MGC:24665	3.50
45	442700	AA377618	Hs.103834	NM_024056:Homo sapiens hypothetical prot	3.50
	410237	AI750589	Hs.61258	Hs.61258:argininosuccinate lyase	3.50
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	3.49
	436213	AA325512	Hs.71472	NM_024662:Homo sapiens hypothetical prot	3.49
	442923	AW248322	Hs.95835		3.49
50	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	3.48
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	3.48
	448993	AI471630	Hs.355952	Hs.355952:ESTs, Weakly similar to 090320	3.48
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	3.48
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	3.47
55	420996	AK001927	Hs.100895	(locuslink)NM_018099:Homo sapiens hypoth	3.47
	439580	AF086401	Hs.293847	Hs.293847:ESTs	3.46
	422158	L10343	Hs.112341	NM_002638:Homo sapiens protease inhibito	3.46
	418256	AW845318	Hs.12271	(locuslink)NM_012162:Homo sapiens F-box	3.46
	400157		Hs.356473	NM_006713:Homo sapiens activated RNA pol	3.46
60	406709	AI355761	Hs.242463	Hs.242463:keratin 8	3.46
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.46
	421526	AL080121	Hs.105460	NM_015393:Homo sapiens DKFZP564O0823 pro	3.45
	415164	AW084352	Hs.157123	Hs.157123:ESTs	3.45
	405451				3.44
65	414361	AI086138	Hs.204044	Hs.204044:ESTs	3.44
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	3.44
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.44
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	3.43
	450983	AA305384	Hs.25740	NM_014584:Homo sapiens ERO1-like (S. cer	3.43
70	421828	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.42
	418588	BE387040	Hs.182476	NM_031295:Homo sapiens Williams Beuren s	3.42
	417348	AI940507	Hs.318526	NM_025138:Homo sapiens hypothetical prot	3.42
	423554	M90516	Hs.1674	NM_002056:Homo sapiens glutamine-fructos	3.42
	451310	AW250651	Hs.26213	NM_052951:Homo sapiens chromosome 20 ope	3.41
75	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	3.41
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	3.40
	437575	AW954355	Hs.36529	NM_024320:Homo sapiens hypothetical prot	3.40
	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alph	3.40
	439955	AW203959	Hs.149532	Hs.149532:ESTs	3.40
80	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	3.40
	435745	AW967059	Hs.374342	Hs.374342:Homo sapiens clone 24711 mRNA	3.40
	403532				3.39
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	3.39
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	3.39

	424996	AF006005	Hs.154104	NM_002657:Homo sapiens pleiomorphic aden	3.38
	402944				3.37
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.37
5	427528	AU077143	Hs.179565	NM_002388:Homo sapiens MCM3 minichromoso	3.37
	426711	AA383471	Hs.343800	(locuslink)NM_033255:Homo sapiens epithe	3.37
	439186	AI697274	Hs.105435	Hs.105435:GDP-mannose 4,6-dehydratase	3.36
	444783	AK001468	Hs.62180	NM_018685:Homo sapiens anillin, actin bi	3.36
	426174	AA547959	Hs.115838	Hs.115838:ESTs	3.36
10	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	3.36
	421605	BE440108	Hs.106127	NM_015972:Homo sapiens RNA polymerase I	3.36
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	3.36
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	3.36
	403219				3.36
15	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	3.34
	456946	T29678	Hs.166068	Hs.166068:villin 1	3.33
	425580	L11144	Hs.1907	Hs.1907:galarin	3.33
	412605	AW410734	Hs.74111	Hs.74111:RNA binding protein (autoantige	3.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	3.33
20	416782	L35035	Hs.79886	(locuslink)NM_144563:Homo sapiens ribose	3.33
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	3.33
	441633	AW958544	Hs.112242	NM_032413:Homo sapiens normal mucosa of	3.32
	416975	NM_004131	Hs.1051	NM_004131:Homo sapiens granzyme B (granz	3.31
	428874	W32133	Hs.194366	Hs.194366:transferrin (prealbumin, amy	3.31
25	431192	AI670056	Hs.137274	Hs.137274:ESTs, Weakly similar to hypoth	3.30
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	3.30
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	3.29
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	3.29
30	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.29
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	3.29
	437810	BE246399	Hs.367646	NM_016617:Homo sapiens hypothetical prot	3.29
	403381				3.28
	434031	BE384165	Hs.23723	(locuslink)NM_025215:Homo sapiens pseudo	3.28
35	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.28
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.28
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	3.28
	412994	D32257	Hs.75113	Hs.75113:general transcription factor II	3.28
	443162	T49951	Hs.9029	(locuslink)NM_015515:Homo sapiens type I	3.28
40	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	3.28
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	3.28
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	3.27
	419359	AL043202	Hs.90073	Hs.90073:CSE1 chromosome segregation 1-I	3.27
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.27
45	444371	BE540274	Hs.239	Hs.239:forkhead box M1	3.27
	450221	AA328102	Hs.24641	NM_018204:Homo sapiens cytoskeleton asso	3.27
	449207	AL044222	Hs.23255	NM_004298:Homo sapiens nucleoporin 155kD	3.27
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	3.27
	403485				3.27
50	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	3.26
	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.26
	405484				3.26
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	3.26
	449139	BE268315	Hs.23111	NM_004461:Homo sapiens phenylalanine-tRN	3.26
	404684				3.25
55	447188	H65423	Hs.17631	NM_030804:Homo sapiens hypothetical prot	3.25
	423226	AA323414	Hs.146109	Hs.146109:ESTs, Weakly similar to T28937	3.24
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.24
	424243	AI949359	Hs.143600	Hs.143600:golgi phosphoprotein 4	3.24
60	435014	BE560898	Hs.10026	NM_022061:Homo sapiens ribosomal protein	3.24
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis	3.24
	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	3.23
	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.23
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	3.23
65	432035	AA524725	Hs.162108	Hs.162108:ESTs	3.23
	408868	AW292286	Hs.255058	Hs.255058:ESTs	3.23
	429504	X99133	Hs.204238	Hs.204238:lipocalin 2 (oncogene 24p3)	3.22
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	3.22
	426991	AK001536	Hs.214410	Hs.214410:Homo sapiens cDNA FLJ31573 fis	3.22
70	408901	AK001330	Hs.48855	(locuslink)NM_018101:Homo sapiens hypoth	3.22
	439979	AW600291	Hs.6823	NM_018092:Homo sapiens neuropilin (NRP)	3.22
	453968	AA847843	Hs.62711	Hs.62711:Homo sapiens, clone IMAGE:33512	3.22
	457465	AW301344	Hs.122908	NM_030928:Homo sapiens DNA replication f	3.22
	426317	AA312350	Hs.169294	NM_003202:Homo sapiens transcription fac	3.21
75	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	3.21
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	3.20
	444261	AA298958	Hs.10724	Hs.10724:mitochondrial ribosomal protein	3.20
	454033	AF107457	Hs.37035	NM_005515:Homo sapiens homeo box HB9 (HL	3.20
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	3.20
80	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	3.20
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	3.19
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	3.19
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	3.19
	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.18

5	419239	AA468183	Hs.335798	(locuslink)NM_033103:Homo sapiens rhophi	3.18
	426215	AW963419	Hs.155223	NM_003714:Homo sapiens stanniocalcin 2 (	3.18
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	3.17
	413313	NM_002047	Hs.293885	NM_002047:Homo sapiens glycyL-tRNA synth	3.17
	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	3.17
	408353	BE439838	Hs.44298	NM_015969:Homo sapiens mitochondrial rib	3.17
	400203		Hs.1390	NM_002794:Homo sapiens proteasome (proso	3.16
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.16
10	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	3.16
	416984	H38765	Hs.80706	NM_000903:Homo sapiens NAD(P)H dehydroge	3.16
	450635	AW403954	Hs.25237	NM_016647:Homo sapiens mesenchymal stem	3.16
	406708	AI282759		AI282759:qt84a01.x1 NCI_CGAP_Co14 Homo s	3.16
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.16
15	430127	AA219498	Hs.233952	Hs.233952:proteasome (prosome, macropain	3.16
	417308	H60720	Hs.81892	NM_014736:Homo sapiens KIAA0101 gene pro	3.15
	408116	AA251393	Hs.289052	NM_052842:Homo sapiens BCL2-like 12 (pro	3.15
	402474				3.15
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	3.15
20	446595	T57448	Hs.15467	NM_017943:Homo sapiens hypothetical prot	3.15
	444954	AW247076	Hs.12163	NM_003908:Homo sapiens eukaryotic transl	3.15
	434263	N34895	Hs.79187	Hs.79187:cox sackie virus and adenovirus	3.15
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.15
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.15
25	436391	AJ227892	Hs.146274	Hs.146274:ESTs	3.15
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	3.14
	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.14
	432370	AA308334	Hs.274424	NM_018946:Homo sapiens N-acetylneuramini	3.14
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	3.14
30	417791	AW965339	Hs.44269	Hs.44269:Homo sapiens cDNA FLJ37972 fis,	3.14
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	3.13
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	3.13
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	3.13
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutas	3.13
35	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.13
	446386	AI032108	Hs.54424	Hs.54424:hepatocyte nuclear factor 4, al	3.12
	407804	AF228603	Hs.39957	NM_016445:Homo sapiens pleckstrin 2 (mou	3.12
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	3.12
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.11
40	407168	R45175	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	3.11
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	3.11
	426427	M86699	Hs.169840	Hs.169840:TTK protein kinase	3.11
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.10
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (	3.10
45	434861	AA206153	Hs.4209	NM_016491:Homo sapiens mitochondrial rib	3.10
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	3.10
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.09
	454464	AW811606	Hs.271819	Hs.271819:mucin 17	3.09
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	3.09
50	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.09
	421470	R27496	Hs.1378	NM_005139:Homo sapiens annexin A3 (ANXA3	3.09
	419551	AW582256	Hs.91011	NM_006408:Homo sapiens anterior gradient	3.09
	418691	AW752389	Hs.87296	Hs.87296:Homo sapiens cDNA FLJ20269 fis,	3.08
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	3.08
55	447760	AI431328	Hs.348605	NM_052963:Homo sapiens mitochondrial top	3.08
	405506				3.08
	429957	AW204530	Hs.99500	Hs.99500:ESTs	3.08
	410166	AK001376	Hs.59346	NM_018122:Homo sapiens hypothetical prot	3.08
	422880	AF228704	Hs.193974	Hs.193974:glutathione reductase	3.08
60	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	3.08
	431722	AF161528	Hs.268049	(locuslink)NM_016101:Homo sapiens hypoth	3.08
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	3.08
	433659	AK001301	Hs.3487	NM_018093:Homo sapiens hypothetical prot	3.07
	439492	AF086310	Hs.103159	Hs.103159:ESTs, Weakly similar to TC6291	3.07
65	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	3.07
	412530	AA766268	Hs.266273	(locuslink)NM_024918:Homo sapiens chromo	3.07
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.06
	453132	AW951952	Hs.293724	Hs.293724:Homo sapiens cDNA FLJ12683 fis	3.06
	424971	AA479005	Hs.154036	NM_003311:Homo sapiens tumor suppressing	3.06
70	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	3.05
	439273	AW139099	Hs.367692	Hs.367692:Homo sapiens cDNA FLJ25668 fis	3.05
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	3.05
	435703	AW630133	Hs.83313	(locuslink)NM_020192:Homo sapiens GK003	3.05
	407289	AA135159	Hs.203349	Hs.203349:Homo sapiens cDNA FLJ12149 fis	3.04
	403739				3.04
75	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	3.04
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	3.04
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.04
	406545				3.03
80	450553	AW850613	Hs.8715	Hs.8715:hypothetical protein MGC3232	3.03
	418867	D31771	Hs.89404	NM_002449:Homo sapiens msh homeo box hom	3.03
	422976	AU076657	Hs.1600	Hs.1600:chaperonin containing TCP1, subu	3.03
	434523	AA703709	Hs.23410	(locuslink)NM_016539:Homo sapiens sirtui	3.03
	440088	BE559877	Hs.183232	NM_024839:Homo sapiens hypothetical prot	3.02

5	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.02
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	3.02
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.02
	422283	AW411307	Hs.114311	NM_003504:Homo sapiens CDC45 cell divisi	3.02
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.02
10	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.02
	417975	AA641836	Hs.30085	NM_024616:Homo sapiens hypothetical prot	3.02
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.01
	436561	BE560135	Hs.5232	NM_014165:Homo sapiens HSPC125 protein (	3.01
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cispla	3.01
15	417678	X06560	Hs.82396	(locuslink)NM_002534:Homo sapiens 2',5'-	3.01
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.00
	429983	W92620	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (	3.00
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.00
	414732	AW410976	Hs.77152	Hs.77152:MCM7 minichromosome maintenance	3.00
20	409614	BE297412	Hs.55189	NM_016489:Homo sapiens 5'-nucleotidase,	3.00
	439053	BE244588	Hs.6456	Hs.6456:chaperonin containing TCP1, subu	3.00
	411096	U80034	Hs.68583	NM_005932:Homo sapiens mitochondrial int	2.99
	433312	AI241331	Hs.131765	Hs.131765:ESTs, Moderately similar to l3	2.99
	420767	AF072711	Hs.99918	Hs.99918:carboxyl ester lipase (bile sal	2.99
25	429523	AK000788	Hs.205280	Hs.205280:Homo sapiens cDNA FLJ20781 fis	2.99
	423242	AL039402	Hs.125783	Hs.125783:chromosome 1 open reading fram	2.99
	420552	AK000492	Hs.98806	Hs.98806:hypothetical protein FLJ20485	2.99
	413380	AI904232	Hs.75323	Hs.75323:prohibitin	2.99
	421533	N71826	Hs.105465	NM_003095:Homo sapiens small nuclear rib	2.99
30	439352	BE614347	Hs.169615	NM_023080:Homo sapiens hypothetical prot	2.98
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	2.98
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.98
	457211	AW972565	Hs.32399	(locuslink)NM_145240:Homo sapiens simila	2.98
	410467	AF102546	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.97
35	422066	AW249275	Hs.343521	Hs.343521:malate dehydrogenase 2, NAD (m	2.97
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	2.97
	453012	T95804	Hs.31334	NM_012469:Homo sapiens chromosome 20 ope	2.97
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	2.97
	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	2.97
40	418362	AL031714	Hs.84285	NM_003345:Homo sapiens ubiquitin-conjuga	2.97
	431350	AI192528	Hs.164537	Hs.164537:ESTs	2.96
	417911	AA333387	Hs.82916	Hs.82916:chaperonin containing TCP1, sub	2.96
	413597	AW302885	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	2.96
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (	2.96
45	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	2.96
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	2.96
	408194	AA601038	Hs.191797	Hs.191797:ESTs	2.96
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	2.96
	459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	2.96
50	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	2.96
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	2.95
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	2.95
	432843	BE250865	Hs.279529	NM_013237:Homo sapiens px19-like protein	2.95
	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	2.95
55	410006	AW732308	Hs.57783	NM_003751:Homo sapiens eukaryotic transl	2.94
	442577	AA292998	Hs.163900	Hs.163900:ESTs, Highly similar to winged	2.94
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	2.94
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	2.94
	427779	AA906997	Hs.180780	NM_021238:Homo sapiens TERA protein (TER	2.94
60	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	2.94
	414549	BE393069	Hs.183506	NM_024841:Homo sapiens hypothetical prot	2.93
	410817	AI262789	Hs.93659	(locuslink)NM_004911:Homo sapiens protei	2.93
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	2.93
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	2.93
65	414416	AW409985	Hs.76084	(locuslink)NM_032737:Homo sapiens hypoth	2.93
	434094	AA305599	Hs.238205	Hs.238205:hypothetical protein PRO2013	2.93
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.93
	429048	AI372949	Hs.44241	Hs.44241:Homo sapiens cDNA: FLJ21447 fis	2.93
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	2.92
70	422397	AJ223366	Hs.116051	(locuslink)NM_138768:Homo sapiens myelom	2.92
	426715	AB037855	Hs.171917	Hs.171917:hypothetical protein FLJ11085	2.92
	429539	AK001839	Hs.206501	(locuslink)NM_020467:Homo sapiens hypoth	2.92
	443715	AI583187	Hs.9700	NM_001238:Homo sapiens cyclin E1 (CCNE1)	2.92
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	2.92
75	433888	BE176078	Hs.30819	Hs.30819:hypothetical protein C40	2.92
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	2.92
	422558	NM_006420	Hs.118249	Hs.118249:ADP-ribosylation factor guanin	2.92
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	2.92
	429626	U36787	Hs.211571	NM_005333:Homo sapiens holocytochrome c	2.92
80	413374	NM_001034	Hs.75319	NM_001034:Homo sapiens ribonucleotide re	2.92
	442159	AW163390	Hs.278554	NM_007276:Homo sapiens chromobox homolog	2.92
	400133		Hs.184693	NM_005648:Homo sapiens transcription elo	2.91
	419381	AB023420	Hs.90093	Hs.90093:heat shock 70kD protein 4	2.91
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	2.91
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	2.91
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	2.91
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	2.91

5	433487	U31814	Hs.3352	NM_001527:Homo sapiens histone deacetyla	2.91
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	2.90
	430287	AW182459	Hs.125759	Hs.125759:likely ortholog of mouse RING	2.90
	434026	R15486	Hs.285218	(locuslink)NM_021213:Homo sapiens phosph	2.90
	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	2.90
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	2.90
	432754	BE241691	Hs.3100	Hs.3100:lysyl-tRNA synthetase	2.90
	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	2.90
10	446228	NM_016046	Hs.14415	NM_016046:Homo sapiens exosomal core pro	2.90
	420421	AF281133	Hs.343589	Hs.343589:exosome component Rrp41	2.89
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	2.89
	414420	AA043424	Hs.76095	NM_052815:Homo sapiens immediate early r	2.89
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	2.89
	401405				2.89
15	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	2.89
	400247		Hs.356473	NM_006713:Homo sapiens activated RNA pol	2.89
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	2.89
	413610	AL117554	Hs.119908	NM_015934:Homo sapiens nucleolar protein	2.89
20	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	2.89
	418661	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription	2.88
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	2.88
	417634	W27202	Hs.82327	NM_000178:Homo sapiens glutathione synth	2.88
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	2.88
25	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	2.88
	446849	AU076617	Hs.16251	(locuslink)NM_016207:Homo sapiens cleava	2.88
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	2.88
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	2.88
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	2.88
30	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	2.87
	448250	NM_016034	Hs.20776	(locuslink)NM_016034:Homo sapiens mitoch	2.87
	428810	AF068236	Hs.193788	NM_000625:Homo sapiens nitric oxide synt	2.87
	427505	AA361562	Hs.178761	Hs.178761:26S proteasome-associated pad1	2.87
	418443	NM_005239	Hs.85146	Hs.85146:v-ets erythroblastosis virus E2	2.87
35	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	2.87
	409262	AK000631	Hs.52256	Hs.52256:hypothetical protein FLJ20624	2.87
	443323	BE560621	Hs.9222	Hs.9222:estrogen receptor binding site a	2.87
	450378	AW249181	Hs.154796	Hs.154796:Homo sapiens cDNA FLJ37976 fis	2.86
	411761	AI733848	Hs.71935	NM_021220:Homo sapiens zinc finger prote	2.86
40	415691	AW963979	Hs.24723	Hs.24723:ESTs	2.86
	417715	AW969587	Hs.86366	Hs.86366:ESTs	2.86
	452099	BE612992	Hs.27931	Hs.27931:hypothetical protein FLJ10607 s	2.86
	436138	H53323	Hs.25717	Hs.25717:Homo sapiens cDNA: FLJ23454 fis	2.86
45	432858	BE618609	Hs.279591	Hs.279591:Homo sapiens, Similar to RNA p	2.86
	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	2.86
	444237	AA336878	Hs.9842	Hs.9842:ESTs	2.85
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	2.85
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	2.85
50	424270	AK001818	Hs.144407	NM_018283:Homo sapiens hypothetical prot	2.85
	414396	BE548266	Hs.76057	(locuslink)NM_000403:Homo sapiens galact	2.85
	426120	AA325243	Hs.166887	Hs.166887:copine I	2.85
	448663	BE614599	Hs.356501	(locuslink)NM_032335:Homo sapiens hypoth	2.85
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	2.85
55	445863	R12234	Hs.13396	Hs.13396:Homo sapiens clone 25028 mRNA s	2.85
	434808	AF155108	Hs.256150	Hs.256150:NY-REN-41 antigen	2.85
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	2.85
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	2.85
	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens interf	2.84
60	446421	BE297434	Hs.15071	Hs.15071:chaperonin containing TCP1, sub	2.84
	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	2.84
	425649	U30930	Hs.158540	(locuslink)NM_003360:Homo sapiens UDP gl	2.84
	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	2.84
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	2.84
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	2.84
65	407833	AW955632	Hs.66666	Hs.66666:chromosome 7 open reading frame	2.84
	415083	AI632683	Hs.27179	Hs.27179:Homo sapiens cDNA FLJ12933 fis	2.83
	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	2.83
	443572	AA025610	Hs.9605	Hs.9605:cleavage and polyadenylation spe	2.83
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	2.83
70	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (	2.83
	453028	AB006532	Hs.31442	NM_004260:Homo sapiens RecQ protein-like	2.83
	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	2.83
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	2.83
	410197	NM_005518	Hs.59889	(locuslink)NM_005518:Homo sapiens 3-hydr	2.83
75	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	2.83
	417677	NM_016055	Hs.82389	NM_016055:Homo sapiens mitochondrial rib	2.83
	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	2.82
	437430	W44671	Hs.124	NM_014628:Homo sapiens gene predicted fr	2.82
	428289	M26301	Hs.2253	Hs.2253:complement component 2	2.82
80	407137	T97307			2.82
	400750				2.82
	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	2.82
	432633	AI796390	Hs.210667	Hs.210667:ESTs	2.82
	432816	N38913	Hs.221575	Hs.221575:ESTs	2.82

	410045	AA806930	Hs.58189	Hs.58189:eukaryotic translation initiati	2.82
	454144	BE280478	Hs.182695	NM_024026:Homo sapiens mitochondrial rib	2.82
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	2.81
5	434583	AA095761	Hs.349092	Hs.349092:ESTs, Weakly similar to A42442	2.81
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	2.81
	428093	AW594506	Hs.104830	Hs.104830:ESTs	2.81
	416047	BE439894	Hs.78991	NM_012080:Homo sapiens DNA segment, nume	2.81
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	2.81
10	452199	BE255643	Hs.110695	Hs.110695:hypothetical protein MGC3133	2.81
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	2.80
	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	2.80
	422809	AK001379	Hs.121028	NM_018136:Homo sapiens hypothetical prot	2.80
	417869	BE076254	Hs.82793	Hs.82793:proteasome (prosome, macropain)	2.80
15	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	2.80
	418731	AI264688	Hs.1197	NM_002157:Homo sapiens heat shock 10kD p	2.80
	432840	AK001403	Hs.279521	Hs.279521:hypothetical protein FLJ20530	2.80
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	2.80
	441181	AA416925	Hs.374811	Hs.374811:Homo sapiens, similar to 4-1BB	2.80
20	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	2.79
	450010	AW293801	Hs.255052	Hs.255052:ESTs	2.79
	418960	NM_004494	Hs.89525	(locuslink)NM_004494:Homo sapiens hepato	2.79
	401179				2.79
	419252	AW138434	Hs.129805	Hs.129805:ESTs	2.79
25	434750	BE019254	Hs.4112	Hs.4112:t-complex 1	2.79
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	2.79
	400529				2.79
	436414	BE264633	Hs.143638	NM_033661:Homo sapiens WD repeat domain	2.79
	436291	BE568452	Hs.344037	(locuslink)NM_003981:Homo sapiens protei	2.79
30	427963	AI042582	Hs.181271	NM_016057:Homo sapiens CGI-120 protein (	2.79
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	2.79
	413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	2.79
	442468	N77737	Hs.8349	NM_138933:Homo sapiens apobec-1 compleme	2.79
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	2.79
35	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	2.79
	430120	AW675298	Hs.233694	(locuslink)NM_018396:Homo sapiens putati	2.79
	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	2.79
	417164	AA338283	Hs.81361	Hs.81361:heterogeneous nuclear ribonucle	2.79
40	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	2.79
	409636	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	2.78
	447619	AI174800	Hs.19054	(locuslink)NM_018530:Homo sapiens hypoth	2.78
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	2.78
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	2.78
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	2.78
45	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	2.78
	430512	AF182294	Hs.241578	NM_016200:Homo sapiens U6 snRNA-associa	2.78
	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	2.78
	414697	BE266134	Hs.76927	Hs.76927:translocase of outer mitochondr	2.78
	420665	AW469240	Hs.371581	Hs.371581:ESTs	2.78
50	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	2.78
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	2.77
	443343	BE409809	Hs.301005	Hs.301005:histone H2A.F/Z variant	2.77
	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	2.77
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	2.77
55	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	2.77
	432543	AA552690	Hs.152423	Hs.152423:Homo sapiens cDNA: FLJ21274 fi	2.77
	423271	W47225	Hs.126256	NM_000576:Homo sapiens interleukin 1, be	2.77
	410595	AW629223	Hs.64794	NM_006978:Homo sapiens zinc finger prote	2.77
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	2.77
60	457757	AA434109	Hs.12271	NM_012162:Homo sapiens F-box and leucine	2.77
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	2.77
	410094	BE147897	Hs.58593	NM_004128:Homo sapiens general transcrip	2.77
	403817				2.77
	459125	AA811363	Hs.29464	Hs.29464:Homo sapiens cDNA: FLJ23460 fis	2.77
65	432705	AI879473	Hs.157123	Hs.157123:ESTs	2.77
	446658	AI440137	Hs.164989	NM_138492:Homo sapiens hypothetical prot	2.76
	419485	AA489023	Hs.99807	Hs.99807:Homo sapiens mRNA; cDNA DKFZp31	2.76
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	2.76
	428438	NM_001955	Hs.2271	NM_001955:Homo sapiens endothelin 1 (EDN	2.76
70	414767	BE541381	Hs.178705	NM_033515:Homo sapiens MacGAP protein (M	2.76
	406830	AI829848	Hs.342389	Hs.342389:peptidylprolyl isomerase A (cy	2.76
	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	2.76
	430450	R23553	Hs.241489	(locuslink)NM_015913:Homo sapiens hypoth	2.76
	433808	NM_014062	Hs.3566	Hs.3566:ART-4 protein	2.75
75	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	2.75
	433369	Z49254	Hs.3254	NM_021134:Homo sapiens mitochondrial rib	2.75
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	2.75
	432204	AI916132	Hs.121593	Hs.121593:Homo sapiens cDNA FLJ13123 fis	2.75
	424438	AA340724	Hs.271912	Hs.271912:Homo sapiens cDNA FLJ38690 fis	2.75
80	433862	D86960	Hs.3610	NM_014873:Homo sapiens KIAA0205 gene pro	2.75
	417080	BE392846	Hs.1063	Hs.1063:small nuclear ribonucleoprotein	2.75
	428242	H55709	Hs.2250	Hs.2250:leukemia inhibitory factor (chol	2.75
	416188	BE157260	Hs.79070	NM_002467:Homo sapiens v-myc myelocytoma	2.75
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	2.75



5	419489	AW411280	Hs.90693	NM_013400:Homo sapiens replication initi	2.75
	407971	AI469117	Hs.62918	Hs.62918: CDC91 cell division cycle 91-li	2.75
	432403	AA550815	Hs.124840	(locuslink)NM_138456:Homo sapiens hypoth	2.75
	410775	AB014460	Hs.66196	NM_002528:Homo sapiens nth endonuclease	2.75
	444197	BE266947	Hs.10590	NM_018683:Homo sapiens zinc finger prote	2.75
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	2.75
	406806	AW088535	Hs.350108	Hs.350108:ribosomal protein, large, P0	2.75
	411580	AL080088	Hs.70877	NM_015421:Homo sapiens DKFZP564K2062 pro	2.75
10	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	2.74
	426235	AI631964	Hs.34447	Hs.34447:Homo sapiens cDNA FLJ38512 fis,	2.74
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	2.74
	419713	AW968058	Hs.92381	NM_019094:Homo sapiens nudix (nucleoside	2.74
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	2.74
	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	2.74
15	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	2.74
	452767	AW014195	Hs.61472	Hs.61472:Homo sapiens, clone IMAGE:51841	2.74
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	2.73
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	2.73
20	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	2.73
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	2.73
	423908	AJ006422	Hs.135183	NM_006869:Homo sapiens centaurin, alpha	2.73
	433412	AV653729	Hs.8185	NM_021199:Homo sapiens sulfide dehydroge	2.73
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	2.73
25	452461	N78223	Hs.108106	Hs.108106:ubiquitin-like, containing PHD	2.73
	407699	AA825974	Hs.32646	NM_024622:Homo sapiens hypothetical prot	2.73
	412258	AA376768	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.73
	450256	AA286887	Hs.24724	Hs.24724:Homo sapiens cDNA FLJ39185 fis,	2.72
	443905	AI215948	Hs.143969	Hs.143969:ESTs	2.72
30	413274	NM_004893	Hs.75258	NM_004893:Homo sapiens H2A histone famil	2.72
	408885	C02741	Hs.48712	NM_017948:Homo sapiens hypothetical prot	2.72
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	2.72
	424692	AA429834	Hs.151791	NM_014679:Homo sapiens KIAA0092 gene pro	2.72
	413762	AW411479	Hs.848	NM_002014:Homo sapiens FK506 binding pro	2.72
35	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	2.72
	450164	AI239923	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.71
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	2.71
	450897	W16741	Hs.351629	NM_014017:Homo sapiens HSPC003 protein (	2.71
	447349	AI375546		BE743847:601577765F1 NIH_MGC_9 Homo sapi	2.71
40	445413	AA151342	Hs.12677	(locuslink)NM_016077:Homo sapiens CGI-14	2.71
	448826	AI580252	Hs.255565	Hs.255565:Homo sapiens cDNA FLJ33892 fis	2.71
	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	2.71
	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	2.71
	441020	W79283	Hs.35962	Hs.35962:Homo sapiens mRNA; cDNA DKFZp68	2.70
45	458933	AI638429	Hs.24763	NM_002882:Homo sapiens RAN binding prote	2.70
	423787	AJ295745	Hs.236204	Hs.236204:nuclear pore complex protein	2.70
	430462	AI584156	Hs.105640	Hs.105640:hypothetical protein BC007772	2.70
	439656	AW138241	Hs.160602	Hs.160602:Homo sapiens cDNA FLJ36008 fis	2.70
	425236	AW067800	Hs.155223	NM_003714:Homo sapiens stannocalcin 2 (	2.70
50	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	2.70
	448296	BE622756	Hs.10949	Hs.10949:Homo sapiens cDNA FLJ14162 fis,	2.70
	430200	BE613337	Hs.234896	Hs.234896:geminin	2.70
	424308	AW975531	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.70
	423453	AW450737	Hs.128791	NM_015939:Homo sapiens CGI-09 protein (L	2.70
55	421344	AW631030	Hs.103665	(locuslink)NM_015873:Homo sapiens villin	2.70
	446607	AI691065	Hs.155780	Hs.155780:ESTs	2.70
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	2.70
	443835	AF016371	Hs.9880	NM_006347:Homo sapiens peptidyl prolyl i	2.70
	413794	AF234532	Hs.61638	NM_012334:Homo sapiens myosin X (MYO10),	2.70
60	451481	AA300228	Hs.295866	(locuslink)NM_030974:Homo sapiens hypoth	2.70
	458820	BE552151	Hs.108118	Hs.108118:hypothetical protein FLJ22474	2.70
	425905	AB032959	Hs.318584	NM_032173:Homo sapiens hypothetical prot	2.69
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	2.69
	431201	AA678405	Hs.8854	Hs.8854:Pvt1 oncogene homolog, MYC activ	2.69
65	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	2.69
	441703	AW390054	Hs.192843	NM_022145:Homo sapiens leucine zipper pr	2.69
	433916	AW732839	Hs.3631	NM_001551:Homo sapiens immunoglobulin (C	2.69
	422516	BE258862	Hs.117950	NM_006452:Homo sapiens phosphoribosylami	2.69
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	2.69
70	427464	BE262956	Hs.178292	Hs.178292:protein O-fucosyltransferase 1	2.69
	453876	AW021748	Hs.110406	Hs.110406:ESTs	2.69
	424373	AJ133798	Hs.146219	NM_014427:Homo sapiens copine VII (CPNE7	2.69
	411619	AI418609	Hs.71040	NM_017816:Homo sapiens hypothetical prot	2.69
	413004	T35901	Hs.75117	Hs.75117:interleukin enhancer binding fa	2.69
75	420062	AW411096	Hs.94785	(locuslink)NM_021809:Homo sapiens TGF-beta	2.69
	446077	BE251048	Hs.22579	Hs.22579:Homo sapiens clone CDABP0036 mR	2.68
	446269	AW263155	Hs.14559	NM_018131:Homo sapiens hypothetical prot	2.68
	428728	NM_016625	Hs.191381	Hs.191381:hypothetical protein LOC51319	2.68
80	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	2.68
	421933	R98881	Hs.109655	NM_006746:Homo sapiens sex comb on midle	2.68
	417750	AI267720	Hs.260523	Hs.260523:neuroblastoma RAS viral (v-ras	2.68
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	2.68
	421720	AF155096	Hs.107213	Hs.107213:formin binding protein 3	2.68
	425601	AW629485	Hs.140720	NM_012083:Homo sapiens frequently rearra	2.68

	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	2.68
	433159	AB035898	Hs.150587	NM_020242:Homo sapiens kinesin-like 7 (K	2.68
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	2.68
5	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	2.68
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (	2.68
	427719	AI393122	Hs.134726	(locuslink)NM_145060:Homo sapiens hypoth	2.68
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	2.68
	457313	AF047002	Hs.241520	NM_005782:Homo sapiens transcriptional c	2.67
10	413142	M81740	Hs.75212	(locuslink)NM_002539:Homo sapiens ornith	2.67
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	2.67
	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	2.67
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	2.67
	447913	AW438602	Hs.191179	Hs.191179:ESTs	2.67
15	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	2.67
	439586	AA922936	Hs.110039	Hs.110039:ESTs	2.67
	427477	AW973119	Hs.178391	NM_021029:Homo sapiens ribosomal protein	2.67
	421839	BE258778	Hs.108809	NM_006429:Homo sapiens chaperonin contai	2.67
	400448				2.67
20	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	2.67
	445304	BE613206	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	2.67
	417601	NM_014735	Hs.82292	NM_014735:Homo sapiens KIAA0215 gene pro	2.66
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	2.66
	431021	AI869664	Hs.351863	(locuslink)NM_003312:Homo sapiens thiosu	2.66
25	453157	AF077036	Hs.31989	NM_015449:Homo sapiens NICE-3 protein (N	2.66
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	2.66
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	2.66
	456248	AL035786	Hs.82425	NM_005717:Homo sapiens actin related pro	2.66
	427691	AW194426	Hs.20726	Hs.20726:ESTs, Moderately similar to hyp	2.66
30	419705	AW368634	Hs.154331	Hs.154331:ESTs	2.66
	421254	AK001724	Hs.102950	NM_016128:Homo sapiens coat protein gamm	2.66
	422719	BE017985	Hs.102558	Hs.102558:Homo sapiens cDNA FLJ40369 fis	2.66
	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	2.66
	432435	BE218886	Hs.282070	Hs.282070:ESTs	2.66
35	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.65
	436106	AI050715	Hs.2331	Hs.2331:E2F transcription factor 5, p130	2.65
	431127	U66618	Hs.250581	Hs.250581:SWI/SNF related, matrix associ	2.65
	425568	AW963118	Hs.161784	Hs.161784:ESTs	2.65
	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	2.65
40	414761	AU077228	Hs.77256	NM_004456:Homo sapiens enhancer of zeste	2.65
	412738	N34731	Hs.74562	NM_078480:Homo sapiens fuse-binding prot	2.65
	408993	AW247090	Hs.57101	Hs.57101:MCM2 minichromosome maintenanc	2.65
	421743	T35958	Hs.107614	Hs.107614:DKFZP56411171 protein	2.64
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protei	2.64
45	417957	H53497	Hs.83006	NM_016071:Homo sapiens mitochondrial rib	2.64
	409119	AA531133	Hs.4253	Hs.4253:hypothetical protein MGC2574	2.64
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	2.64
	409214	AW405967	Hs.333388	Hs.333388:similar to CG3714 gene product	2.64
	414883	AA926960	Hs.348669	Hs.348669:CDC28 protein kinase 1	2.64
50	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	2.64
	408633	AW963372	Hs.222088	NM_014109:Homo sapiens PRO2000 protein (	2.64
	447769	AW873704	Hs.320831	Hs.320831:chromosome 20 open reading fra	2.64
	432964	AF118395	Hs.279865	NM_014317:Homo sapiens trans-prenyltrans	2.63
	444855	BE409261	Hs.12084	Hs.12084:Tu translation elongation facto	2.63
55	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	2.63
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	2.63
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	2.63
	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	2.63
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	2.63
60	406122				2.63
	420988	AW006352	Hs.159643	Hs.159643:ESTs, Weakly similar to putati	2.63
	436433	AW631437	Hs.5184	(locuslink)NM_016397:Homo sapiens TH1-li	2.63
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	2.63
	410397	AF217517	Hs.63042	NM_018457:Homo sapiens DKFZp564J157 prot	2.63
65	419420	AA355435	Hs.30724	(locuslink)NM_001516:Homo sapiens genera	2.63
	400298	AA032279	Hs.61635	Hs.61635:six transmembrane epithelial an	2.63
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	2.63
	436199	R38946	Hs.127951	Hs.127951:Homo sapiens cDNA FLJ14503 fis	2.63
	425081	X74794	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.63
70	442025	AW887434	Hs.11810	NM_032026:Homo sapiens CDA11 protein (CD	2.62
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endoropeptidase-	2.62
	409703	NM_006187	Hs.56009	Hs.56009:2'-5'-oligoadenylate synthetase	2.62
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	2.62
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	2.62
75	451926	AW134519	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.62
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	2.62
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	2.62
	421405	AA251944	Hs.104058	NM_015957:Homo sapiens CGI-29 protein (L	2.62
	429491	NM_012111	Hs.204041	NM_012111:Homo sapiens chromosome 14 ope	2.62
80	453335	AW857376	Hs.169238	NM_000149:Homo sapiens fucosyltransferas	2.62
	441126	NM_000429	Hs.323715	(locuslink)NM_000429:Homo sapiens methio	2.62
	417404	NM_007350	Hs.82101	(locuslink)NM_007350:Homo sapiens plecks	2.62
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	2.62
	446766	AF083208	Hs.16178	NM_012138:Homo sapiens apoptosis antagon	2.62

	437033	AW248364	Hs.5409	(locuslink)NM_004875:Homo sapiens RNA po	2.62
	412123	BE251328	Hs.73291	NM_018256:Homo sapiens WD repeat domain	2.62
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	2.61
5	433037	NM_014158	Hs.279938	NM_014158:Homo sapiens HSPC067 protein (	2.61
	414438	AI879277	Hs.76136	(locuslink)NM_003329:Homo sapiens thiore	2.61
	416221	BE513171	Hs.79086	(locuslink)NM_007208:Homo sapiens mitoch	2.61
	443898	AW804296	Hs.9950	NM_014302:Homo sapiens Sec61 gamma (SEC6	2.61
	410007	AW950887	Hs.57813	NM_014596:Homo sapiens zinc ribbon domai	2.61
10	412715	NM_000947	Hs.74519	NM_000947:Homo sapiens primase, polypept	2.61
	449864	BE276386	Hs.111429	NM_032486:Homo sapiens dynactin 4 (MGC32	2.61
	448625	AW970786	Hs.178470	NM_024829:Homo sapiens hypothetical prot	2.61
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	2.61
	410686	AI733735	Hs.114905	NM_033266:Homo sapiens ER to nucleus sig	2.60
	411400	AA311919	Hs.69851	NM_018983:Homo sapiens nucleolar protein	2.60
15	429770	AI766047	Hs.99736	Hs.99736: hypothetical protein MGC39350	2.60
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	2.60
	420237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	2.60
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	2.60
20	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	2.60
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	2.60
	457234	AW968360	Hs.14355	Hs.14355:Homo sapiens cDNA FLJ13207 fis,	2.60
	420911	U77413	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (	2.60
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.60
25	438533	AI440266	Hs.170673	NM_138969:Homo sapiens retinal short cha	2.60
	421699	AL161994	Hs.107003	NM_021178:Homo sapiens enhancer of invas	2.60
	452220	BE158006	Hs.212296	Hs.212296:ESTs	2.60
	439148	AA372280	Hs.178576	(locuslink)NM_030877:Homo sapiens cateni	2.60
	453949	AU077146	Hs.36927	(locuslink)NM_006644:Homo sapiens heat s	2.59
	451110	AI955040	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.59
30	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	2.59
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	2.59
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	2.59
	424290	AA197226	Hs.19347	NM_032351:Homo sapiens mitochondrial rib	2.59
35	424197	AF096834	Hs.142989	NM_015982:Homo sapiens germ cell specifi	2.59
	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	2.59
	410219	T98226	Hs.171952	Hs.171952:occludin	2.59
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	2.59
	441153	BE562826		BE562826:601336534F1 NIH_MGC_44 Homo sap	2.59
40	410570	AI133096	Hs.64593	NM_006356:Homo sapiens ATP synthase, H+	2.58
	430594	AK000790	Hs.246885	NM_017958:Homo sapiens hypothetical prot	2.58
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	2.58
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.58
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.58
45	449019	AI949095	Hs.67776	Hs.67776:Homo sapiens, clone IMAGE:54556	2.58
	410442	X73424	Hs.63788	Hs.63788:propionyl Coenzyme A carboxylas	2.58
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	2.58
	454417	AI244459	Hs.110826	Hs.110826:trinucleotide repeat containin	2.58
	416330	AU077101	Hs.79222	Hs.79222:galactosidase, beta 1	2.58
50	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	2.58
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	2.58
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	2.58
	406180				2.58
	416297	AA157634	Hs.79172	Hs.79172:solute carrier family 25 (mitoc	2.58
55	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	2.58
	447532	AK000614	Hs.18791	NM_017899:Homo sapiens hypothetical prot	2.57
	420309	AW043637	Hs.21766	Hs.21766:ESTs, Weakly similar to hypothe	2.57
	447418	AA063074	Hs.18552	Hs.18552:E2IG2 protein	2.57
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	2.57
60	428342	AI739168	Hs.349283	Hs.349283:Homo sapiens cDNA FLJ31753 fis	2.57
	427254	AL121523	Hs.97774	Hs.97774:ESTs	2.57
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (	2.57
	425689	W16480	Hs.24283	Hs.24283:Homo sapiens cDNA FLJ25952 fis,	2.57
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	2.57
65	427678	BE267756	Hs.180312	NM_016065:Homo sapiens mitochondrial rib	2.57
	444656	AI277924	Hs.145199	Hs.145199:ESTs, Weakly similar to hypothe	2.57
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	2.57
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	2.56
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	2.56
70	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.56
	409964	AW368226	Hs.67928	Hs.67928:ESTs	2.56
	431910	AK000142	Hs.101774	Hs.101774: hypothetical protein FLJ23045	2.56
	413010	AA393273	Hs.75133	NM_003201:Homo sapiens transcription fac	2.56
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	2.56
75	419423	D26488	Hs.90315	Hs.90315:KIAA0007 protein	2.56
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.56
	437623	D63880	Hs.5719	NM_014865:Homo sapiens chromosome conden	2.56
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	2.56
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	2.56
80	425368	AB014595	Hs.155976	(locuslink)NM_003588:Homo sapiens cullin	2.56
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	2.56
	427876	AI494291	Hs.369171	Hs.369171:ESTs	2.56
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	2.56
	416432	BE391767	Hs.79322	(locuslink)NM_005051:Homo sapiens glutam	2.55

5	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	2.55
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	2.55
	454003	AA058944	Hs.116602	Hs.116602:hypothetical protein BC009115	2.55
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	2.55
	457400	AF032906	Hs.252549	NM_001336:Homo sapiens cathepsin Z (CTSZ	2.55
10	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	2.55
	402829				2.55
	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	2.55
	400995				2.55
	452945	AW978187	Hs.79103	NM_030579:Homo sapiens cytochrome b5 out	2.55
15	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	2.55
	422192	AA305159	Hs.113019	NM_015931:Homo sapiens fis485 (LOC51066)	2.55
	424755	AB033094	Hs.152925	Hs.152925:KIAA1268 protein	2.55
	410012	AW015832	Hs.57898	(locuslink)NM_017819:Homo sapiens hypoth	2.55
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	2.55
20	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	2.55
	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	2.55
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	2.55
	406629	AW277078	Hs.181165	Hs.181165:eukaryotic translation elongat	2.55
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	2.54
25	446715	AI337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	2.54
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	2.54
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	2.54
	427368	BE041451	Hs.177507	Hs.177507:hypothetical protein HSPC155	2.54
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	2.54
30	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	2.54
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCCTA00142	2.54
	456031	AA335996	Hs.355907	Hs.355907:ESTs, Weakly similar to protei	2.54
	442432	BE093589	Hs.38178	NM_024629:Homo sapiens hypothetical prot	2.54
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	2.54
35	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	2.54
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	2.54
	432876	AW248272	Hs.279652	NM_015956:Homo sapiens mitochondrial rib	2.53
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	2.53
	425994	AK000207	Hs.165803	NM_017708:Homo sapiens hypothetical prot	2.53
40	445982	BE410233	Hs.13501	(locuslink)NM_014303:Homo sapiens pescad	2.53
	444232	W56010	Hs.347297	(locuslink)NM_013397:Homo sapiens over-e	2.53
	435655	AW105663	Hs.6947	(locuslink)NM_014159:Homo sapiens Huntin	2.53
	417686	AA769155	Hs.235498	Hs.235498:hypothetical protein FLJ14075	2.53
	417933	X02308	Hs.82962	NM_001071:Homo sapiens thymidylate synth	2.53
45	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	2.53
	452313	Y00486	Hs.28914	Hs.28914:adenine phosphoribosyltransfera	2.53
	438317	AA826401	Hs.122393	Hs.122393:ESTs	2.53
	409299	AA045650	Hs.53125	NM_004597:Homo sapiens small nuclear rib	2.53
	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	2.53
50	412525	AA581439	Hs.152328	Hs.152328:ESTs	2.53
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.53
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif-	2.53
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	2.53
	434274	AA628539	Hs.57783	Hs.57783:eukaryotic translation initiati	2.53
55	400282		Hs.289101	NM_005313:Homo sapiens glucose regulated	2.53
	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	2.53
	453344	BE349075	Hs.44571	Hs.44571:ESTs	2.53
	449915	NM_004529	Hs.404	NM_004529:Homo sapiens myeloid/lymphoid	2.53
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.52
60	439012	BE383814	Hs.6455	NM_006666:Homo sapiens RuvB-like 2 (E. c	2.52
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.52
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidas	2.52
	442315	AA173992	Hs.7956	Hs.7956:ESTs	2.52
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.52
65	422385	BE549407	Hs.115823	(locuslink)NM_006638:Homo sapiens ribonu	2.52
	433517	AW022133	Hs.189838	Hs.189838:ESTs	2.52
	450230	AW016607	Hs.201582	Hs.201582:ESTs	2.52
	432866	BE395875	Hs.279609	NM_014342:Homo sapiens mitochondrial car	2.52
	433001	AF217513	Hs.279905	NM_016359:Homo sapiens nucleolar protein	2.52
70	440773	AA352702	Hs.37747	NM_022767:Homo sapiens hypothetical prot	2.52
	440587	AL138461	Hs.323084	(locuslink)NM_031209:Homo sapiens tRNA-g	2.52
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	2.52
	424259	AK001776	Hs.143954	(locuslink)NM_018270:Homo sapiens chromo	2.52
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.52
75	453204	R10799	Hs.191990	Hs.191990:ESTs	2.52
	453665	AA626250	Hs.326184	Hs.326184:Homo sapiens nuclear protein p	2.52
	432353	NM_016558	Hs.274411	NM_016558:Homo sapiens SCAN domain conta	2.52
	433271	BE621697	Hs.14317	NM_018648:Homo sapiens nucleolar protein	2.51
	431770	BE221880	Hs.268555	NM_012255:Homo sapiens 5'-3' exoribonuc	2.51
80	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	2.51
	428839	AI767756	Hs.82302	(locuslink)NM_147174:Homo sapiens hepara	2.51
	404826				2.51
	429669	BE185499	Hs.2471	NM_014878:Homo sapiens KIAA0020 gene pro	2.51
	434474	AL042936	Hs.211571	(locuslink)NM_005333:Homo sapiens holocy	2.51
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	2.51
	450422	AA743525	Hs.60300	NM_033414:Homo sapiens hypothetical prot	2.51
	440214	AA247118	Hs.7049	(locuslink)NM_018386:Homo sapiens hypoth	2.51

421168	AF182277	Hs.330780	Hs.330780:cytochrome P450, subfamily IIB	2.51
435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.51
452101	T60298	Hs.10844	NM_052972:Homo sapiens leucine-rich alph	2.51
436043	AW963838	Hs.168830	Hs.168830:Homo sapiens cDNA FLJ12136 fis	2.51
424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	2.51
435677	AA694142	Hs.6685	Hs.6685:thyroid hormone receptor interac	2.51
406363				2.51
452018	AW102941	Hs.211265	Hs.211265:ESTs	2.51
409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.51
421937	AI878857	Hs.109706	NM_016185:Homo sapiens hematological and	2.51
416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.51
421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	2.50
434584	D57341	Hs.188361	Hs.188361:Homo sapiens cDNA FLJ12807 fis	2.50
428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	2.50
426053	U68105	Hs.172182	NM_002568:Homo sapiens poly(A) binding p	2.50
432642	BE297635	Hs.3069	NM_004134:Homo sapiens heat shock 70kD p	2.50
452390	AI864142	Hs.29288	(locuslink)NM_022759:Homo sapiens endo-b	2.50
429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	2.50
400076				2.50
420596	NM_002692	Hs.99185	NM_002692:Homo sapiens polymerase (DNA d	2.50
422244	Y08890	Hs.113503	NM_002271:Homo sapiens karyopherin (impo	2.50
410723	AA100683	Hs.372108	Hs.372108:ESTs	2.50
435496	AW840171	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.50
425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	2.50
433626	AF078859	Hs.86347	NM_013341:Homo sapiens hypothetical prot	2.50
448391	H71025	Hs.21075	NM_016328:Homo sapiens GTF2I repeat doma	2.50

TABLE 10B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
406685	0_0	M18728
434414	35978_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175 BF854337
432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
406708	0_0	AI282759
459306	223120_4	AW578452
447349	1063443_1	BE743847 AW809603 BM469626 AI375546
441153	264480_3	BE562826 BE378727

TABLE 10C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404519	8152000	Plus	12817-13000
406399	9256288	Minus	63448-63554
403220	7630969	Plus	64338-64517
404661	9797073	Plus	33374-33675,33769-34008
402496	9797769	Minus	8615-9103
403055	8748904	Minus	109532-110225
400965	7770576	Minus	173043-173564
403218	7630969	Plus	58039-58149
401866	8018106	Plus	73126-73623
403221	7630969	Plus	66294-66438,66936-67124
401519	6649315	Plus	157315-157950
405451	7622517	Minus	145949-146227
403532	8076842	Minus	81750-81901
402944	9368423	Plus	110411-110716,111173-111640
403219	7630969	Plus	61858-61995
403381	9438267	Minus	26009-26178
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
404684	9797403	Minus	110881-111020
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
405506	6466489	Plus	80014-80401,80593-81125
403739	7630882	Plus	44563-44766,48209-48483,52255-52495

406545	7711510	Plus	145662-145781,147854-147984,148098-14824
401405	7768126	Minus	69276-69452,69548-69958
400750	8119067	Plus	198991-199168,199316-199548
401179	9438647	Plus	113477-113893
400529	9796988	Plus	138232-138423
403817	8962065	Plus	110297-111052
400448	9887687	Minus	177372-177674
406122	9144087	Minus	30940-31386
406180	7283201	Minus	38923-39107
402829	8918414	Plus	101532-101852,102006-102263
400995	8099094	Plus	141186-141601
404826	6572184	Plus	47726-48046
406363	9256114	Plus	14403-14602,17000-17147,17241-17368

Table 11A lists about 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium) that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 3.0, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 11A: 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigenelD	Unigene Title	R1
436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	37.18
406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	31.24
407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	24.81
406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	20.54
431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	20.38
428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	20.13
406667	M12523			19.89
437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	19.68
446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	19.55
423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease i	18.33
421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	17.47
414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	17.37
416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	16.99
422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	15.15
441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefol factor 1	14.23
407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	14.12
422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	13.64
432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.48
424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	13.43
418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, LI c	13.20
453863	X02544	Hs.572	Hs.572:orosomucoid 1	13.06
413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	12.58
436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.34
421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	11.72
409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	11.72
452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	11.49
406399				11.25
414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	11.12
407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	11.01
423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.70
447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	10.69
450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	10.57
427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (	10.48
418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	10.20
422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	10.19
423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	9.72
422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	9.70
430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	9.65
406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.52
428355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	9.47
422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	9.41
413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	9.39
422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	9.31
417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 I	9.30

5	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	9.01
	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	8.99
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.80
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	8.71
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	8.67
10	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	8.47
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	8.47
	422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	8.43
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	8.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	8.12
15	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	8.09
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	7.96
	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	7.92
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	7.89
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	7.87
20	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	7.71
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	7.58
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.48
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I isof	7.31
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	7.31
25	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	7.29
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	7.23
	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	7.12
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	7.12
30	414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	7.10
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	7.06
	452194	AI694413	Hs.373599	Hs.373599:EST	7.02
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.97
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.96
35	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	6.96
	403220				6.95
	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	6.87
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	6.87
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	6.80
40	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.78
	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
	422511	AU076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	6.66
	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	6.65
	431301	AA502384	Hs.151529	Hs.151529:ESTs	6.62
45	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	6.59
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	6.56
	431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine deficie	6.54
	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	6.50
50	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.47
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	6.46
	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	6.45
	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.41
	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	6.41
55	419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	6.27
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	6.20
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19
	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	6.19
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	6.18
60	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	6.16
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	6.16
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	6.15
	426174	AA547959	Hs.115838	Hs.115838:ESTs	6.10
	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	6.07
65	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	6.06
	409453	AI885516	Hs.95612	Hs.95612:ESTs	6.06
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	6.03
	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	5.99
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	5.97
70	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif	5.95
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.92
	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	5.90
	428874	W32133	Hs.194366	Hs.194366:transthyretin (prealbumin, amy	5.88
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	5.88
75	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:beta-Ga	5.86
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis,	5.82
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	5.77
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	5.75
80	403218				5.74
	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	5.72
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	5.72
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	5.72
	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.72
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	5.71
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	5.70
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	5.70

5	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	5.67
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	5.67
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.63
	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	5.62
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	5.60
10	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	5.59
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.58
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.56
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	5.56
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	5.54
15	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	5.53
	403221				5.52
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	5.52
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.48
20	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	5.44
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.42
	436251	BE515085	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	5.41
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	5.36
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	5.34
25	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	5.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	5.32
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.31
	430680	AW138724	Hs.168974	Hs.168974:ESTs	5.25
	432378	AI493046	Hs.146133	Hs.146133:ESTs	5.25
30	419693	AA133749	Hs.301350	Hs.301350:FXD domain-containing ion tra	5.24
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	5.21
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	5.21
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	5.21
	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	5.20
35	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	5.20
	428289	M26301	Hs.2253	Hs.2253:complement component 2	5.19
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	5.19
	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	5.15
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	5.13
40	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	5.11
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	5.09
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	5.08
	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	5.08
	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	5.07
45	432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	5.07
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	5.07
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	5.06
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	5.06
	414361	AI086138	Hs.204044	Hs.204044:ESTs	5.04
50	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	5.03
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	5.03
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	5.01
	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	5.00
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.99
55	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	4.99
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.98
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	4.98
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.98
	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.97
60	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	4.97
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.95
	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	4.95
	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.93
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.93
65	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	4.93
	431779	AW971178	Hs.268571	(locuslink)NM_001645:Homo sapiens apolip	4.92
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.91
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.91
	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
70	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.89
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.89
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.88
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	4.88
	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	4.87
75	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (	4.87
	405484				4.87
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	4.87
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	4.86
	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	4.83
80	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	4.81
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.79
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.79
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.79
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	4.78
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.77
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.76
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	4.76



	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	4.75
	400529				4.75
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carc	4.75
5	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
	447966	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	4.72
	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.72
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.70
	405556				4.70
10	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.70
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	4.70
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.70
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.70
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, ren	4.65
15	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.64
	403739				4.61
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	4.61
	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	4.61
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	4.60
20	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.60
	447335	BE617695	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.59
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	4.59
	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	4.59
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	4.59
25	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.58
	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	4.57
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.57
	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	4.55
	409964	AW368226	Hs.67928	Hs.67928:ESTs	4.54
30	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	4.54
	432407	AA221036		AF134164:Homo sapiens Human endogenous r	4.54
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.53
	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyro	4.53
	403219				4.53
35	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.52
	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	4.51
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.51
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutas	4.51
40	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.50
	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carc	4.50
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.49
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.48
45	434263	N34895	Hs.79187	Hs.79187:cox sackie virus and adenovirus	4.47
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	4.47
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	4.46
	452299	AW206330	Hs.355663	Hs.355663:ESTs	4.46
50	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.46
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	4.46
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.46
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	4.45
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	4.44
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	4.44
55	419559	Y07828	Hs.91096	NM_007028:Homo sapiens tripartite motif	4.44
	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	4.43
	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.43
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	4.43
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.42
60	422867	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix prot	4.41
	431350	AI192528	Hs.164537	Hs.164537:ESTs	4.39
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	4.39
	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	4.39
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	4.38
65	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	4.38
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	4.38
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	4.38
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	4.37
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	4.36
70	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alph	4.36
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.35
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.34
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (	4.34
	424865	AF011333	Hs.153563	NM_002349:Homo sapiens lymphocyte antige	4.34
75	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	4.33
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	4.32
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.32
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	4.32
80	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	4.31
	436391	AJ227892	Hs.146274	Hs.146274:ESTs	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.29
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.29
	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	4.29

5	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	4.29
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	4.29
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	4.28
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.27
	409636	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	4.27
10	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	4.27
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	4.27
	410199	AW377424	Hs.205126	Hs.205126:Homo sapiens cDNA: FLJ22667 fi	4.24
	431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	4.24
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (	4.24
15	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	4.23
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	4.23
	436856	AI469355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	4.23
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	4.23
	426862	AV660038	Hs.2056	Hs.2056:UDP glycosyltransferase 1 family	4.23
20	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	4.22
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	4.22
	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	4.21
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	4.21
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	4.21
25	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	4.20
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
	426427	M86699	Hs.169840	Hs.169840:TTK protein kinase	4.19
	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	4.19
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cispla	4.19
30	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.19
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	4.18
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	4.17
	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	4.17
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	4.17
35	404826				4.17
	414198	AW505308	Hs.75812	NM_004563:Homo sapiens phosphoenolpyruva	4.17
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	4.17
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	4.16
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	4.16
40	420319	AW406289	Hs.96593	NM_019034:Homo sapiens ras homolog gene	4.15
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	4.15
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	4.14
	431890	X17033	Hs.271996	NM_002203:Homo sapiens integrin, alpha 2	4.14
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	4.13
45	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	4.13
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	4.13
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	4.12
	428471	X57348	Hs.184510	Hs.184510:stratifin	4.12
50	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.11
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	4.10
	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	4.10
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	4.10
	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	4.10
55	413835	AI272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	4.09
	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	4.09
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	4.09
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	4.09
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	4.08
60	421190	U95031	Hs.102482	Hs.102482:mucin 5, subtype B, tracheobro	4.08
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	4.08
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	4.06
	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	4.06
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
65	443802	AW504924	Hs.9805	Hs.9805:exportin 5	4.04
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	4.04
	434808	AF155108	Hs.256150	Hs.256150:NY-REN-41 antigen	4.04
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	4.04
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	4.02
70	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	4.02
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	4.02
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.02
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	4.01
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	4.00
75	414812	X72755	Hs.77367	NM_002416:Homo sapiens monokine induced	4.00
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	3.99
	431958	X63629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	3.98
	418661	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription	3.98
	419092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transm	3.98
80	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	3.98
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.97
	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.96
	436485	X59135	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.96
	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.95
	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	3.94
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.94
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	3.94

	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.94
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	3.93
	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	3.93
5	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	3.92
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	3.92
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	3.91
	428698	AA852773	Hs.334838	Hs.334838:KIAA1866 protein	3.90
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	3.89
10	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanine	3.89
	407971	AI469117	Hs.62918	Hs.62918:CDCC91 cell division cycle 91-li	3.89
	400750				3.89
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	3.89
	413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	3.89
15	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	3.89
	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	3.88
	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolinate phosph	3.88
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.88
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	3.87
20	410268	AA316181	Hs.61635	NM_012449:Homo sapiens six transmembrane	3.87
	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	3.87
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	3.86
	449667	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.86
	400298	AA032279	Hs.61635	Hs.61635:six transmembrane epithelial an	3.85
25	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	3.85
	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	3.85
	413380	AI904232	Hs.75323	Hs.75323:prohibitin	3.85
	452220	BE158006	Hs.212296	Hs.212296:ESTs	3.85
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	3.85
30	433658	L03678	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.84
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	3.84
	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.84
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	3.84
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens mel transforming	3.84
35	427318	AF186081	Hs.175783	NM_014579:Homo sapiens solute carrier fa	3.83
	459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	3.83
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.83
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	3.82
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.82
40	426514	BE616633	Hs.170195	Hs.170195:bone morphogenetic protein 7 (	3.82
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.82
	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	3.81
	421481	AW391972	Hs.104696	Hs.104696:KIAA1324 protein	3.81
45	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	3.80
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	3.80
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	3.80
	413813	M98956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.80
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diffe	3.80
	410219	T98226	Hs.171952	Hs.171952:occludin	3.80
50	407137	T97307			3.78
	430462	AI584156	Hs.105640	Hs.105640:hypothetical protein BC007772	3.78
	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens interf	3.78
	450010	AW293801	Hs.255052	Hs.255052:ESTs	3.78
55	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	3.78
	440676	NM_004987	Hs.112378	(locuslink)NM_004987:Homo sapiens LIM an	3.77
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protei	3.77
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrid	3.77
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	3.77
	443323	BE560621	Hs.9222	Hs.9222:estrogen receptor binding site a	3.76
60	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.76
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	3.76
	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	3.75
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.74
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	3.74
65	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.74
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.74
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.74
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	3.74
	435886	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.73
70	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutat	3.73
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	3.73
	400419	AF084545		AF084545:Homo sapiens versican Vint isof	3.73
	421357	AK000609	Hs.103808	NM_017896:Homo sapiens chromosome 20 ope	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
75	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.73
	452679	Z42387	Hs.83883	(locuslink)NM_020182:Homo sapiens transm	3.72
	419743	AW408762	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.72
	435730	AB020635	Hs.4984	Hs.4984:KIAA0828 protein	3.72
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.72
80	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypoth	3.72
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCTA00142	3.71
	413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjuga	3.71
	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis,	3.71
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	3.71

5	406722	H27498	Hs.293441	Hs.293441:Homo sapiens SNC73 protein (SN	3.71
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	3.71
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.70
	409327	L41162	Hs.53563	NM_001853:Homo sapiens collagen, type IX	3.70
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.70
10	400846				3.70
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.70
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	3.70
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.70
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	3.69
15	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	3.69
	432215	AU076609	Hs.2934	NM_001033:Homo sapiens ribonucleotide re	3.69
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.69
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (	3.69
	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.68
20	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.68
	401179				3.67
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.67
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.67
	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-ral simian leuk	3.66
25	409402	AF208234	Hs.695	Hs.695:cystatin B (stefin B)	3.66
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.66
	432633	AI796390	Hs.210667	Hs.210667:ESTs	3.66
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.66
	453857	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.65
30	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.65
	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	3.65
	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	3.64
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.64
	441128	AA570256	Hs.348504	Hs.348504:hypothetical protein BC014072	3.64
35	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.64
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	3.63
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.62
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.62
	452098	AI858183		BF755039:QV0-CT0583-181000-428-f07 CT058	3.62
40	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	3.62
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.61
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.61
	400847				3.60
	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	3.60
45	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.60
	404854				3.60
	400448				3.60
	453331	AI240665	Hs.352537	Hs.352537:Homo sapiens cDNA FLJ31066 fis	3.60
	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.60
50	417389	BE260964	Hs.82045	Hs.82045:midline (neurite growth-promoti	3.59
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.59
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	3.59
	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.59
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	3.59
55	426722	U53823	Hs.171952	NM_002538:Homo sapiens occludin (OCLN),	3.58
	420531	AI652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.58
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	3.57
	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.57
	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.57
60	424241	AW995948	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, i	3.57
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.57
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.56
	434224	AA380731	Hs.84	NM_000206:Homo sapiens interleukin 2 rec	3.56
	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.56
65	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.56
	413859	AW992356	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, i	3.56
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.55
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	3.55
	411704	AI499220	Hs.71573	(locuslink)NM_017988:Homo sapiens hypoth	3.55
70	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.54
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.54
	453323	AF034102	Hs.32951	NM_001532:Homo sapiens solute carrier fa	3.54
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.54
	452488	N74921	Hs.184389	Hs.184389:ESTs, Moderately similar to S1	3.54
75	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.54
	426811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.53
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.53
	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.53
	428582	BE336699	Hs.185055	Hs.185055:BENE protein	3.53
80	446147	AL133064	Hs.14051	(locuslink)NM_145698:Homo sapiens endoze	3.53
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.52
	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.52
	442007	AA301116	Hs.142838	NM_032390:Homo sapiens MKI67 (FHA domain	3.52
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.52
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	3.51
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.51
	421340	F07783	Hs.1369	NM_000574:Homo sapiens decay acceleratin	3.50

	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	3.50
	452862	AW378065	Hs.8687	Hs.8687:ESTs	3.50
	442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.50
5	404240				3.50
	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	3.50
	429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	3.50
	445937	AI452943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.49
10	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.49
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.49
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	3.49
	456534	X91195	Hs.100623	NM_138689:Homo sapiens protein phosphata	3.49
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.49
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.49
15	439841	AF038961	Hs.6710	NM_004870:Homo sapiens manncse-P-dolicho	3.49
	428390	AI640377	Hs.350077	NM_000982:Homo sapiens ribosomal protein	3.48
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alpha	3.48
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	3.48
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	3.48
20	457635	AV660976	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.48
	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.48
	454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypoth	3.48
	402829				3.47
	451707	AW051061	Hs.60973	Hs.60973:Homo sapiens cDNA FLJ40829 fis,	3.47
25	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.47
	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.47
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976 fis	3.47
	439223	AW238299	Hs.250618	NM_025217:Homo sapiens UL16 binding prot	3.46
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.46
30	450273	AW296454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	3.46
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	3.46
	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	3.46
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.45
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif	3.45
35	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfait 4 (SURF4)	3.45
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.45
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	3.45
	410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.45
	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	3.44
40	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.44
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.44
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.44
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (	3.44
	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	3.44
45	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	3.44
	448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.44
	420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	3.44
	412420	AL035668	Hs.73853	NM_001200:Homo sapiens bone morphogeneti	3.43
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	3.43
50	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prostatic)	3.43
	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	3.43
	426093	AW594506	Hs.104830	Hs.104830:ESTs	3.43
	428293	BE250944	Hs.183556	Hs.183556:solute carrier family 1 (neutr	3.42
55	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.42
	442821	BE391929	Hs.8752	Hs.8752:transmembrane protein 4	3.42
	427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.42
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.41
	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.41
	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	3.41
60	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	3.41
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	3.41
	423323	AI951628	Hs.127007	NM_003740:Homo sapiens potassium channel	3.41
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	3.41
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.40
65	422256	M64673	Hs.1499	NM_005526:Homo sapiens heat shock transc	3.40
	451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.40
	400205		Hs.81848	NM_006265:Homo sapiens RAD21 homolog (S.	3.40
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.39
	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.39
70	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.39
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.39
	406363				3.39
	444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methy	3.39
	423309	BE006775	Hs.126782	NM_014467:Homo sapiens sushi-repeat prot	3.38
75	426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	3.38
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.38
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.38
	457670	AF119666	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.38
	400125		Hs.125078	(locuslink)NM_004152:Homo sapiens ornith	3.38
80	429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylation	3.37
	410293	AK000047	Hs.61960	NM_018992:Homo sapiens hypothetical prot	3.37
	434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.37
	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.37
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	3.37

	446715	AI337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	3.36
	426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.36
	429747	M87507	Hs.2490	Hs.2490:caspase 1, apoptosis-related cys	3.36
5	406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.36
	439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.36
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.36
	421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	3.36
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.36
10	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	3.36
	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	3.36
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	3.35
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.35
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.35
15	457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	3.35
	432169	Y00971	Hs.2910	NM_002765:Homo sapiens phosphoribosyl py	3.35
	412525	AA581439	Hs.152328	Hs.152328:ESTs	3.35
	416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	3.35
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	3.35
20	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	3.34
	400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.34
	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	3.34
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	3.34
	450506	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.34
25	437296	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	3.34
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.34
	439246	AI498072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.34
30	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	3.34
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.34
	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	3.34
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.34
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	3.33
35	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.33
	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	3.33
	414271	AK000275	Hs.75871	(locuslink)NM_012408:Homo sapiens protei	3.33
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.33
	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	3.32
40	430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.32
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	3.32
	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	3.32
	430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripar	3.32
45	402104				3.32
	446620	AA128808	Hs.179902	(locuslink)NM_022109:Homo sapiens CDw92	3.32
	443425	AI056776	Hs.133397	Hs.133397:ESTs	3.32
	414883	AA926960	Hs.348669	Hs.348669:CDK28 protein kinase 1	3.31
50	413053	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.31
	451564	AU076698	Hs.132760	(locuslink)NM_001467:Homo sapiens glucos	3.31
	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	3.31
	441866	BE464341	Hs.21201	Hs.21201:nectin 3	3.31
	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.31
	422192	AA305159	Hs.113019	NM_015931:Homo sapiens fis485 (LOC51066)	3.31
55	446506	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.31
	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytosol	3.31
	449644	AW960707	Hs.148324	Hs.148324:ESTs	3.31
	422611	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosy	3.31
	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	3.30
60	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	3.30
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.30
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.30
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	3.30
	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	3.30
65	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.29
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	3.29
	442772	AW503680	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.29
	430281	AI878842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.29
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.29
70	420332	NM_001756	Hs.1305	NM_001756:Homo sapiens serine (or cystei	3.29
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	3.29
	412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	3.28
	427308	D26067	Hs.174905	Hs.174905:KIAA0033 protein	3.28
	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.28
75	449199	AI990122	Hs.196988	Hs.196988:ESTs	3.28
	442739	NM_007274	Hs.8679	(locuslink)NM_007274:Homo sapiens cytosol	3.28
	422051	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	3.28
	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	3.28
	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.28
80	402260				3.28
	409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multidi	3.28
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.28
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.27
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier ta	3.27

5	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.27
	434521	NM_002267	Hs.3886	Hs.3886:karyopherin alpha 3 (importin al	3.27
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.27
	445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	3.27
	448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	3.26
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	3.26
	440286	U29589	Hs.7138	NM_000740:Homo sapiens cholinergic recep	3.26
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	3.26
10	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	3.26
	426520	BE545684	Hs.343566	Hs.343566:KIAA0251 protein	3.26
	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.26
	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	3.26
	425966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.25
15	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	3.25
	449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.25
	424381	AA285249	Hs.146329	NM_007194:Homo sapiens CHK2 checkpoint h	3.25
	426784	U03749	Hs.172216	NM_001275:Homo sapiens chromogranin A (p	3.25
	420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.25
20	438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	3.24
	419216	AU076718	Hs.164021	NM_002993:Homo sapiens small inducible c	3.24
	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.24
	458376	AB023179	Hs.9059	Hs.9059:KIAA0962 protein	3.24
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	3.24
25	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.24
	435640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	3.23
	427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	3.23
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	3.23
	430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	3.23
30	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.23
	432731	R31178	Hs.287820	Hs.287820:fibronectin 1	3.23
	410340	AW182833	Hs.112188	(locuslink)NM_021826:Homo sapiens hypoth	3.23
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	3.23
	430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	3.23
35	425907	AA365752	Hs.155965	Hs.155965:ESTs	3.23
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	3.22
	403912				3.22
	429782	NM_005754	Hs.220689	Hs.220689:Ras-GTPase-activating protein	3.22
40	416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	3.22
	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.22
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	3.22
	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	3.22
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.22
	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	3.22
45	450770	AA019924	Hs.28803	Hs.28803:ESTs	3.22
	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	3.22
	414172	AW954324	Hs.75790	(locuslink)NM_002642:Homo sapiens phosph	3.21
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	3.21
	432078	BE314877	Hs.24553	(locuslink)NM_022369:Homo sapiens hypoth	3.21
50	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.21
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	3.21
	409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	3.21
	400836				3.20
	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	3.20
55	414343	AL036166	Hs.75914	NM_006815:Homo sapiens coated vesicle me	3.20
	447096	BE539199	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	3.20
	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.20
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.20
	407736	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.20
60	400845				3.20
	407082	Z47055			3.20
	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kinesi	3.20
	403217				3.20
	414249	AI797994	Hs.279929	(locuslink)NM_017510:Homo sapiens gp25L2	3.19
65	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.19
	417777	AI823763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis,	3.19
	457274	AW674193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	3.19
	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XIII	3.19
	430280	AA361258	Hs.237868	Hs.237868:Homo sapiens mRNA; cDNA DKFZp6	3.19
70	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	3.19
	422938	NM_001809	Hs.1594	NM_001809:Homo sapiens centromere protei	3.18
	435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.18
	449704	AK000733	Hs.23900	Hs.23900:Rac GTPase activating protein 1	3.18
	426925	NM_001196	Hs.172894	Hs.172894:BH3 interacting domain death a	3.18
75	414814	D14697	Hs.77393	(locuslink)NM_002004:Homo sapiens farnes	3.18
	405387				3.18
	444108	R55784	Hs.140942	Hs.140942:Homo sapiens cDNA FLJ38396 fis	3.18
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
80	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2-I	3.17
	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.17
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	3.17
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	3.17
	447032	AK000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.17
	410663	AA194952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.17

	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3)-glycopro	3.17
	451032	W03692	Hs.323079	Hs.323079:Homo sapiens mRNA; cDNA DKFZp5	3.17
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	3.17
5	417018	M16038	Hs.80887	Hs.80887:v-yes-1 Yamaguchi sarcoma viral	3.16
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.16
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	3.16
	432728	NM_006979	Hs.278721	NM_006979:Homo sapiens HLA class II regi	3.16
10	442643	U82756	Hs.374973	(locuslink)NM_004697:Homo sapiens PRP4 p	3.16
	418462	BE001596	Hs.85266	Hs.85266:integrin, beta 4	3.16
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	3.16
	429556	AW139399	Hs.314807	Hs.314807:hypothetical protein MGC2655	3.15
	418127	BE243982	Hs.83532	(locuslink)NM_002389:Homo sapiens membra	3.15
15	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	3.15
	435968	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens integr	3.15
	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.15
	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	3.15
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.14
20	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	3.14
	407961	AW672939	Hs.41694	Hs.41694:origin recognition complex, sub	3.14
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-II	3.14
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.14
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	3.14
25	450295	AI766732	Hs.210628	Hs.210628:ESTs	3.14
	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
	452695	AW780199	Hs.30327	NM_003668:Homo sapiens mitogen-activated	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.13
30	424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (renal a	3.13
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	3.13
	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	3.12
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	3.12
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	3.12
35	438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
	424727	AW590378	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.12
	435975	AL118990	Hs.373554	(locuslink)NM_130786:Homo sapiens alpha-	3.12
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	3.12
	412326	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
40	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	3.12
	428699	AW578252	Hs.190161	Hs.190161:LRB protein	3.12
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	3.12
	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.12
	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	3.12
45	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	3.12
	410240	AL157424	Hs.61289	Hs.61289:synaptojanin 2	3.12
	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	3.11
	406865	AI025931	Hs.181357	Hs.181357:laminin receptor 1 (67kD, ribo	3.11
	405203				3.11
50	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	3.11
	417211	T97617	Hs.269092	Hs.269092:ESTs	3.11
	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	3.11
	429824	AA296363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.11
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	3.11
55	408805	H69912	Hs.48269	NM_003384:Homo sapiens vaccinia related	3.10
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	3.10
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	3.10
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	3.10
	429597	NM_003816	Hs.2442	Hs.2442:a disintegrin and metalloprotein	3.10
60	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.10
	429238	NM_002849	Hs.198288	NM_002849:Homo sapiens protein tyrosine	3.10
	433409	AI278802	Hs.25661	Hs.25661:ESTs, Moderately similar to hyp	3.10
	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.10
	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.10
65	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	3.10
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic I	3.10
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	3.10
70	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.10
	433435	BE545277	Hs.340959	NM_005726:Homo sapiens Ts translation el	3.09
	408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	3.09
	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-II	3.09
	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	3.09
75	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.09
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	3.09
	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	3.09
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	3.09
	430066	AI929659	Hs.237825	Hs.237825:signal recognition particle 72	3.09
80	428044	AA093322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	3.09
	426989	AI815206	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (	3.08
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	3.08
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	3.08
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	3.08



	410668	BE379794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	3.08
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.08
	419757	AA773820	Hs.63970	Hs.63970:ESTs	3.08
5	427725	U66839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	3.08
	424408	AI754813	Hs.146428	Hs.146428:collagen, type V, alpha 1	3.08
	453914	NM_000507	Hs.574	NM_000507:Homo sapiens fructose-1,6-bisph	3.08
	420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	3.08
10	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	3.07
	411423	AW845987	Hs.68864	(locuslink)NM_139248:Homo sapiens membra	3.07
	449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	3.07
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to choli	3.07
	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antimicr	3.07
15	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 l	3.07
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	3.07
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	3.07
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	3.07
	436553	AW407157	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.06
20	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	3.06
	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	3.06
	418062	AW630656	Hs.83383	NM_006406:Homo sapiens peroxiredoxin 4 (	3.06
	407223	H96850		H96850:yw03b12.s1 Soares melanocyte 2NbH	3.06
	418641	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.06
25	450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXYP d	3.06
	408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	3.06
	435550	AI224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	3.06
	421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.05
	440246	W52010	Hs.191379	Hs.191379:ESTs	3.05
30	446770	AV660309	Hs.154986	Hs.154986:ESTs, Weakly similar to PLLP_H	3.05
	440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	3.05
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	3.05
	453830	AA534296	Hs.20953	Hs.20953:hypothetical protein BC010003	3.05
	412867	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	3.05
35	422032	AA476966	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	3.05
	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	3.05
	408524	D87942	Hs.46328	Hs.46328:fucosyltransferase 2 (secretor	3.05
	408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	3.05
	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	3.04
40	432281	AK001239	Hs.274263	Hs.274263:hypothetical protein FLJ10377	3.04
	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	3.04
	423570	AW836306	Hs.129819	NM_018344:Homo sapiens hypothetical prot	3.04
	443653	AA137043	Hs.9663	NM_013374:Homo sapiens programmed cell d	3.04
45	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	3.04
	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	3.04
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	3.04
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.04
50	453450	AW797627	Hs.347459	Hs.347459:Homo sapiens cDNA FLJ13900 fis	3.04
	412708	R26830	Hs.106137	Hs.106137:Homo sapiens mRNA for OK/SW-CL	3.04
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	3.04
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	3.03
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	3.03
	412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	3.03
	444309	U83236	Hs.10803	Hs.10803:calcium and integrin binding 1	3.03
55	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	3.03
	430354	AA954810	Hs.239784	Hs.239784:scribble	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	3.03
	421179	U72664	Hs.148495	NM_002810:Homo sapiens proteasome (proso	3.02
60	451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	3.02
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	3.02
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.02
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.02
	417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	3.02
65	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	3.02
	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis,	3.01
	414421	AI521130	Hs.355126	(locuslink)NM_144586:Homo sapiens hypoth	3.01
	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Not56 (D. melanog	3.01
	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	3.01
70	437651	BE560672	Hs.13543	(locuslink)NM_145214:Homo sapiens tripar	3.01
	436540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	3.00
	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protei	3.00
	415697	AI365603	Hs.279696	Hs.279696:DKFZP566I1024 protein	3.00
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	3.00
75	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	3.00
	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	3.00
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.00
	406868	AA505445	Hs.300697	Hs.300697:immunoglobulin heavy constant	3.00
	424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	3.00
80	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	3.00
	417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rh-related antige	3.00

TABLE 11B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	406685	0_0	M18728
10	432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
15	459306	223120_-4	AW578452
	452098	161393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 AI858183
	451129	1495511_1	BE072881 AI762181 BE072946

TABLE 11C

20 Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 25 Nt\_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
	406399	9256288	Minus	63448-63554
30	403220	7630969	Plus	64338-64517
	403218	7630969	Plus	58039-58149
	403221	7630969	Plus	66294-66438,66936-67124
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
	400529	9796988	Plus	138232-138423
35	405556	1552511	Plus	163497-163623,164715-164968,165369-16550
	403739	7630882	Plus	44563-44766,48209-48483,52255-52495
	403219	7630969	Plus	61858-61995
	404826	6572184	Plus	47726-48046
	400750	8119067	Plus	198991-199168,199316-199548
40	400846	9188605	Plus	39310-39474
	401179	9438647	Plus	113477-113893
	400847	9188605	Plus	44643-44835
	404854	7143420	Plus	14260-14537
	400448	9887687	Minus	177372-177674
45	404240	5002624	Minus	116132-116407,116653-116922
	402829	8918414	Plus	101532-101852,102006-102263
	406363	9256114	Plus	14403-14602,17000-17147,17241-17368
	402104	8119072	Plus	122409-122600
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
50	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	400836	8954179	Plus	677-1188
	400845	9188605	Plus	34428-34612
	403217	7630969	Plus	54089-54163,55427-55623
	405387	6587915	Minus	3769-3833,5708-5895
55	405203	7230116	Plus	125295-125463

60 Table 12A lists about 1006 genes up-regulated in cervical cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" cervical cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" cervical cancer level was set to the 93<sup>rd</sup> percentile value amongst cervical cancers. The "average" normal adult tissue level was set to the 93<sup>rd</sup> percentile value amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15<sup>th</sup> percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

65 TABLE 12A: 1006 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 70 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
75	402075	U19557	Hs.123035	squamous cell carcinoma antigen 2 (SCCA2)	81.1
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	43.6
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial coll	38.9
	435094	AI560129	Hs.329062	EST	30.3
	439606	W79123	Hs.58561	G protein-coupled receptor 87	28.8
80	452240	AI591147	Hs.61232	ESTs	27.0
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin bi	26.0
	417034	NM_006183	Hs.80962	neurotensin	25.5
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, cl	24.5
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	23.7

	435505	AF200492	Hs.211238	interleukin-1 homolog 1	21.2
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	20.5
	418345	AJ001696	Hs.241407	serine proteinase inhibitor 13 (PI13; serpin	20.1
5	452461	N78223	Hs.108106	transcription factor	19.8
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor, cl	19.2
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	17.5
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-type,	16.4
	435243	AW292886	Hs.261373	hypothetical protein dJ434O14.3	16.3
10	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.2
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-C	15.9
	421373	AA808229	Hs.167771	ESTs	15.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	15.4
	441459	AI919142	Hs.214233	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.6
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	13.8
15	412719	AW016610	Hs.129911	ESTs	13.4
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	13.3
	431753	X76029	Hs.2841	neuromedin U	13.2
	438817	AI023799	Hs.163242	ESTs	13.1
20	404996			Target Exon	13.1
	443211	AI128388	Hs.143655	ESTs	12.9
	414764	AW013887	Hs.72047	ESTs	12.9
	428618	AA885360	Hs.160199	Target CAT	12.7
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.7
25	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribosomal	12.6
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.6
	432666	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein produ	12.6
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaphyseal	12.6
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin D 24	12.3
30	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.2
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	11.6
	415989	AI267700	Hs.317584	ESTs	11.5
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	11.4
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	11.3
35	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	11.0
	449260	AA741180	Hs.29879	ESTs	11.0
	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN HOMEOB	10.7
	406467			Target Exon	10.5
40	439926	AW014875	Hs.137007	ESTs	10.2
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, pr	10.2
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	10.2
	414422	AA147224	Hs.337232	Homeo box A13	10.2
	442660	AW138174	Hs.130651	ESTs	10.1
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu or sig	10.0
45	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN ALU SU	9.9
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clo	9.8
	400195	NM_007057		NM_007057*:Homo sapiens ZW10 interactor (ZWIN	9.8
	422426	W79117	Hs.58559	ESTs	9.7
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical p	9.7
50	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN ALU SU	9.4
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR/MRP)	9.4
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothetical p	9.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	9.1
55	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT2RP40	9.1
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.0
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.0
	426427	M86699	Hs.169840	TTK protein kinase	9.0
60	429538	BE182592	Hs.11261	small proline-rich protein 2A	9.0
	446232	AI281848	Hs.194691	retinoic acid induced 3	8.9
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	8.9
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDNA clo	8.9
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	8.9
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	8.9
65	430486	BE062109	Hs.241551	chloride channel, calcium activated, family m	8.7
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	8.7
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	8.7
	407642	AW178963		gb:MR0-ST0032-200899-001-b11 ST0032 Homo sapi	8.7
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily, m	8.7
70	458027	L49054	Hs.85195	myeloid leukemia factor 1	8.4
	424086	AI351010	Hs.102267	lysyl oxidase	8.3
	420092	AA814043	Hs.88045	ESTs	8.3
	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	8.3
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human, odont	8.2
75	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	8.2
	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adren	8.2
	440834	AA907027	Hs.128606	ESTs	8.2
	452724	R84810	Hs.30464	cyclin E2	8.1
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (from c	8.1
80	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine h	8.0
	429228	AI553633	Hs.337139	ESTs	7.9
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome region 14	7.9
	425710	AF030880	Hs.159275	solute carrier family, member 4	7.8
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	7.8

	435159	AA668879	Hs.116649	ESTs	7.7
	439232	N48590	Hs.46693	ESTs	7.7
	437616	AI797163	Hs.207954	ESTs	7.6
	406554			Target Exon	7.4
5	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	7.4
	424098	AF077374	Hs.139322	small proline-rich protein 3	7.3
	418134	AA397769	Hs.86617	ESTs	7.2
	446364	AB006624	Hs.14912	KIAA0286 protein	7.2
10	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (yeast	7.1
	414148	BE084049		gb:PM0-BT0651-270400-003-f02 BT0651 Homo sapi	7.0
	429548	AW138872	Hs.135288	ESTs	7.0
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	7.0
	450192	AA263143	Hs.24596	RAD51-interacting protein	7.0
15	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila ho	6.9
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone COL0454	6.9
	427821	AA470158	Hs.98202	ESTs	6.9
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794 prote	6.9
	425761	AW664214	Hs.196729	ESTs	6.9
20	450028	AI912012	Hs.200737	ESTs	6.8
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated protein N	6.8
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	6.8
	413573	AI733859	Hs.149089	ESTs	6.8
	422330	D30783	Hs.115263	epiregulin	6.8
25	454988	AW850140		gb:IL3-CT0219-261099-023-D11 CT0219 Homo sapi	6.8
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010317E2	6.8
	403471			Target Exon	6.7
	409041	AB033025	Hs.50081	KIAA1199 protein	6.7
	407839	AA045144	Hs.161566	ESTs	6.6
30	415652	T79213	Hs.272073	ESTs	6.6
	420900	AL045633	Hs.44269	ESTs	6.6
	444271	AW452569	Hs.149804	ESTs	6.6
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	6.5
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.5
35	431622	AW979271	Hs.293184	ESTs	6.5
	457405	AA504860		gb:ab03a10.s1 Stratagene fetal retina 937202	6.4
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	6.4
	414812	X72755	Hs.77367	monokine induced by gamma interferon	6.4
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase	6.3
40	446435	AW206737	Hs.253582	ESTs	6.3
	421948	L42583	Hs.334309	keratin 6A	6.3
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	6.3
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-protein	6.2
	406747	AI925153	Hs.217493	annexin A2	6.2
45	453884	AA355925	Hs.36232	KIAA0186 gene product	6.2
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapiens c	6.2
	421773	W69233	Hs.112457	ESTs	6.2
	457435	AW972024	Hs.142653	ret finger protein	6.1
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HEMBB10	6.1
50	427043	AA397679	Hs.3991	ESTs	6.1
	409723	AW885757	Hs.257862	ESTs	6.1
	459462	AA481396	Hs.105167	ESTs	6.1
	423244	AL038379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	6.0
	427217	AA399272	Hs.144341	ESTs	6.0
55	441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein [H.s	6.0
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferritin a	6.0
	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	5.9
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein [H.s	5.9
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	5.9
60	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced prote	5.9
	414299	AA142989	Hs.71730	ESTs	5.8
	439292	AA090421	Hs.5555	hypothetical protein MGC5347	5.8
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin (140	5.8
	413625	AW451103	Hs.71371	ESTs	5.8
65	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	5.8
	415064	AA159804	Hs.149305	hypothetical protein MGC2603	5.7
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor ty	5.7
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	5.7
	415900	Z43758	Hs.26037	ESTs	5.7
70	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.7
	449611	AI970394	Hs.197075	ESTs	5.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo sapi	5.7
	438639	AI278360	Hs.31409	ESTs	5.7
	414972	BE263782	Hs.77695	KIAA0008 gene product	5.7
75	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1	5.6
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone COL0042	5.6
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	5.6
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	5.5
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase 3)	5.5
80	451307	AW293207	Hs.211516	ESTs	5.5
	441531	AW291239	Hs.271111	ESTs	5.5
	418663	AK001100	Hs.41690	desmocollin 3	5.5
	410659	AI080175	Hs.68826	ESTs	5.5
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo sapi	5.5

	431255	AA497043	Hs.115685	ESTs	5.5
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	5.5
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	5.4
5	418502	R99288	Hs.35152	ESTs	5.4
	440320	AA879294		gb:nw86e09.s1 NCL_CGAP_Pr12 Homo sapiens cDNA	5.4
	439579	AF086400		gb:Homo sapiens full length insert cDNA clone	5.4
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7 (gale	5.4
	408536	AW381532	Hs.135188	ESTs	5.4
10	408758	NM_003686	Hs.47504	exonuclease 1	5.4
	451411	AA017492	Hs.135655	EST	5.4
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.3
	407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	5.3
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin 6)	5.2
	420026	AI831190	Hs.166676	ESTs	5.2
15	427356	AW023482	Hs.97849	ESTs	5.2
	420440	NM_002407	Hs.97644	mammaglobin 2	5.2
	430082	AW514083	Hs.190135	ESTs	5.2
	445259	AI798994	Hs.152923	ESTs	5.2
	457345	AI699933	Hs.192175	ESTs	5.2
20	453161	AA628608	Hs.61656	ESTs	5.2
	445019	AI205540	Hs.281295	ESTs	5.2
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	5.2
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSO	5.2
25	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	5.2
	443179	AI928402	Hs.6933	hypothetical protein FLJ12684	5.2
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, choline, al	5.2
	441020	W79283	Hs.35962	ESTs	5.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	5.1
30	419520	AB009303	Hs.90800	matrix metalloproteinase 16 (membrane-inserte	5.1
	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	5.1
	405547			NM_018833*:Homo sapiens transporter 2, ATP-bi	5.1
	435206	AI432364	Hs.160594	ESTs	5.1
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	5.1
35	439223	AW238299	Hs.250618	UL16 binding protein 2	5.1
	413251	AI932903	Hs.211535	ESTs	5.1
	426320	W47595	Hs.169300	transforming growth factor, beta 2	5.1
	458829	AI557388		gb:PT2.1_6_G03.r tumor2 Homo sapiens cDNA 3',	5.0
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	5.0
40	432473	AI202703	Hs.152414	ESTs	5.0
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino acid	5.0
	423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	5.0
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, protein-gl	5.0
	432867	AW016936	Hs.233364	ESTs	5.0
45	449448	D60730	Hs.57471	ESTs	5.0
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (from c	4.9
	406547			C7000246:gil72477 pir DVHY1C multidrug resis	4.9
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromosomes 1	4.9
	446704	AI337228	Hs.197083	ESTs	4.9
50	443476	AA631492	Hs.23921	hypothetical protein DKFZp547A023	4.9
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypothetic	4.9
	421155	H87879	Hs.102267	lysyl oxidase	4.9
	443335	T89697	Hs.16645	ESTs	4.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell growt	4.8
55	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	4.8
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage elast	4.8
	441720	AI346487	Hs.28739	ESTs	4.8
	442980	AA857025	Hs.8878	kinesin-like 1	4.8
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12	4.8
60	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosome seg	4.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosyltran	4.8
	418939	AW630803	Hs.89497	lamin B1	4.7
	417235	AA810278	Hs.24250	ESTs	4.7
	411958	AA099020		gb:zn45h01.s1 Stratagene HeLa cell s3 937216	4.7
65	433858	N69243	Hs.192974	hypothetical protein FLJ12735	4.7
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	4.7
	418379	AA218940	Hs.137516	fidgetin-like 1	4.7
	401747			Homo sapiens keratin 17 (KRT17)	4.7
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clo	4.7
70	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	4.7
	457465	AW301344	Hs.122908	DNA replication factor	4.6
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.6
	412333	AW937485		gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapi	4.6
	401137			Target Exon	4.6
75	401575			Target Exon	4.6
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL0667	4.6
	421978	AJ243662	Hs.110196	NICE-1 protein	4.6
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	4.6
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PLACE10	4.6
80	450510	AA010056	Hs.242998	ESTs	4.6
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.6
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, type II	4.6
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino acid	4.5
	449416	AI651016	Hs.246311	ESTs	4.5

	416168	H23687		gb:yn72d12.r1 Soares adult brain N2b5HB55Y Ho	4.5
	447033	AI357412	Hs.157601	ESTs	4.5
	446353	AI290919	Hs.153661	ESTs	4.5
5	443715	AI583187	Hs.9700	cyclin E1	4.5
	454707	AW814989		gb:MR1-ST0206-170400-024-g05 ST0206 Homo sapi	4.5
	435435	T89473	Hs.192328	ESTs	4.5
	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	4.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	4.4
10	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.4
	430919	AA489041	Hs.295448	ESTs	4.4
	435313	AI769400	Hs.189729	ESTs	4.4
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	4.4
	433322	H50621	Hs.134156	ESTs, Weakly similar to I38022 hypothetical p	4.4
15	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (p150)	4.4
	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.4
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein ho	4.4
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	4.4
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor, cl	4.4
20	418216	AA662240	Hs.283099	AF15q14 protein	4.4
	446252	AI283125	Hs.150009	ESTs	4.4
	447519	U46258	Hs.339665	ESTs	4.4
	425916	NM_006786	Hs.162200	urotensin 2	4.3
	408420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalinin (10	4.3
25	416320	H47867	Hs.34024	ESTs	4.3
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth facto	4.3
	441582	BE550200	Hs.127197	ESTs	4.3
	414132	AI801235	Hs.48480	ESTs	4.3
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homology to	4.3
30	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (RHAMM)	4.3
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.3
	428613	AB037749	Hs.186928	KIAA1328 protein	4.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter tra	4.3
	447078	AW885727	Hs.301570	ESTs	4.3
35	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	4.3
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.3
	405708			Target Exon	4.3
	433405	AW157566	Hs.156892	ESTs	4.3
	456443	AW967500	Hs.133543	ESTs	4.3
40	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	4.2
	448621	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	4.2
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequence	4.2
	406887	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.2
	455365	AW948343		gb:RC0-MT0015-130400-031-c01 MT0015 Homo sapi	4.2
45	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypothetical p	4.2
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypothetical p	4.2
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	4.2
	427666	AI791495	Hs.180142	calmodulin-like skin protein	4.2
	444602	AI174456	Hs.271925	ESTs, Moderately similar to I38022 hypothetic	4.2
50	417791	AW965339	Hs.111471	ESTs	4.2
	444266	AI424984	Hs.125465	ESTs	4.2
	439394	AA149250	Hs.56105	ESTs	4.2
	457336	AW969657	Hs.291029	ESTs	4.2
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypothetical p	4.2
55	404440			NM_021048:Homo sapiens melanoma antigen, fami	4.2
	449228	AJ403107	Hs.148590	protein related with psoriasis	4.2
	437144	AL049466	Hs.7859	ESTs	4.2
	448599	AW860912		gb:QV0-CT0387-170200-121-c05 CT0387 Homo sapi	4.2
	431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like protein	4.2
60	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.2
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	4.2
	458116	AW977549	Hs.47367	KIAA1785 protein	4.1
	444105	AW189097	Hs.166597	ESTs	4.1
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	4.1
65	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor, cl	4.1
	408096	BE250162	Hs.83765	dihydrofolate reductase	4.1
	457620	AA602711	Hs.336753	EST	4.1
	402048			Target Exon	4.1
	427025	AA397589	Hs.97523	ESTs	4.1
70	423515	AA327017	Hs.162204	ESTs	4.1
	423891	AK002042	Hs.134795	Homo sapiens cDNA FLJ11180 fis, clone PLACE10	4.1
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo sapi	4.1
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	4.1
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	4.1
75	423738	AB002134	Hs.132195	airway trypsin-like protease	4.1
	448243	AW369771	Hs.52620	integrin, beta 8	4.1
	411559	BE144081		gb:MR0-HT0165-030200-007-d06 HT0165 Homo sapi	4.1
	423553	AA405635	Hs.96854	ESTs, Weakly similar to DYLC_HUMAN CYTOPLASMI	4.1
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	4.1
80	424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypothetical p	4.1
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PLACE10	4.1
	424745	AA214618	Hs.152759	activator of S phase kinase	4.0
	433384	AI021992	Hs.124244	ESTs	4.0
	448995	AI613276	Hs.5662	guanine nucleotide binding protein (G protein	4.0

	448504	AI858128	Hs.171136	ESTs	4.0
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (from c	4.0
	432441	AW292425	Hs.163484	ESTs	4.0
5	424794	M85646	Hs.210696	ESTs	4.0
	432184	AW971125		gb:EST383212 MAGE resequences, MAGL Homo sapi	4.0
	408321	AW405882	Hs.44205	cortistatin	4.0
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like repeat d	4.0
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.0
10	447724	AW298375	Hs.24477	ESTs	4.0
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y79AA10	4.0
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.0
	420252	AW270404	Hs.193161	ESTs	4.0
	412811	H06382	Hs.21400	ESTs	4.0
15	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	4.0
	438390	AI422017		gb:tt45f12.x1 NCL_CGAP_Brn23 Homo sapiens cDN	4.0
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	4.0
	429900	AA460421	Hs.30875	ESTs	4.0
	421270	H56037	Hs.108146	ESTs	3.9
20	430733	AW975920	Hs.283361	ESTs	3.9
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo sapi	3.9
	424131	AA335714	Hs.199665	ESTs	3.9
	457059	BE561665	Hs.177677	exosome component Rrp40	3.9
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	3.9
25	404959			NM_025001*:Homo sapiens hypothetical protein	3.9
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.9
	428536	AI143139	Hs.2288	visinin-like 1	3.9
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H.sapi	3.9
	432757	AF113013	Hs.278919	PRO0806 protein	3.9
30	418686	Z36830	Hs.87268	annexin A8	3.9
	437845	AA769578	Hs.90488	ESTs	3.9
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein produ	3.9
	419312	AA831850	Hs.58149	hypothetical protein MGC14136	3.9
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	3.9
35	410553	AW016824	Hs.255527	hypothetical protein MGC14128	3.9
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.9
	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HEMBB10	3.9
	442163	AI791749	Hs.128896	ESTs	3.9
	438656	H85310	Hs.209456	ESTs, Weakly similar to NG22 [H.sapiens]	3.9
40	406560			ENSP00000016943*:cDNA	3.8
	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33)	3.8
	404132			Target Exon	3.8
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	3.8
	439238	N47305	Hs.46668	ESTs	3.8
45	433289	AF005258		gb:Homo sapiens laminin alpha 3b chain mRNA,	3.8
	436149	AI754308	Hs.159452	ESTs	3.8
	446292	AF081497	Hs.279682	Rh type C glycoprotein	3.8
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-bind	3.8
	405545			(MDR/TAP) (TAP2)	3.8
50	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	3.8
	409687	T51125	Hs.8493	ESTs	3.8
	407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo sapie	3.8
	415532	R14780	Hs.12826	ESTs	3.8
	402047	AK001921	Hs.169575	hypothetical protein MGC2550	3.8
55	415317	Z43388		gb:HSC1AF121 normalized infant brain cDNA Hom	3.8
	438777	AA825487	Hs.142179	ESTs	3.8
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolysis bu	3.7
	405943			Target Exon	3.7
60	430686	NM_001942	Hs.2633	desmoglein 1	3.7
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP024	3.7
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	3.7
	418582	BE244318	Hs.213194	hypothetical protein MGC10895	3.7
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	3.7
65	433849	BE465884	Hs.280728	ESTs	3.7
	449592	AI655494	Hs.195718	ESTs	3.7
	453028	AB006532	Hs.31442	RecQ protein-like 4	3.7
	435612	AA693537	Hs.321411	ESTs	3.7
	417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clone 22d	3.7
70	418735	N48769	Hs.44609	ESTs	3.7
	444707	AI188613	Hs.41690	desmocollin 3	3.7
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.7
	450613	AI702055		gb:tg20g10.x1 NCL_CGAP_U11 Homo sapiens cDNA	3.7
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	3.7
75	432837	AA310693	Hs.87329	HSPC072 protein	3.7
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN ALU SU	3.7
	423441	R68649	Hs.278359	absent in melanoma 1 like	3.7
	449978	AI806335	Hs.200829	ESTs, Weakly similar to T30171 ninein - mouse	3.7
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo sapi	3.7
80	409582	R27430	Hs.271565	ESTs	3.6
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANTIGEN	3.6
	458446	AW394104	Hs.43744	ESTs, Moderately similar to I54374 gene NF2 p	3.6
	433040	H70423	Hs.300511	ESTs	3.6
	452193	AA987351	Hs.184993	ESTs	3.6

	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed-rect	3.6
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.6
	459575	BE080825		gb:QV1-BT0631-180200-078-c08 BT0631 Homo sapi	3.6
5	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.6
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	3.6
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.6
	427131	AA448460	Hs.112017	GE36 gene	3.6
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	3.6
10	420373	AW968228		gb:EST380198 MAGE resequences, MAGJ Homo sapi	3.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromosomes 2	3.6
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.6
	424639	AI917494	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HEMBA10	3.6
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.6
15	434321	AA629368		gb:zu78a1.1.s1 Soares_testis_NHT Homo sapiens	3.6
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	3.6
	427335	AA448542	Hs.251677	G antigen 7B	3.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	3.6
20	426749	AI623718	Hs.105618	ESTs	3.6
	443899	AW842283	Hs.79933	cyclin I	3.6
	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H.sapi	3.6
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	mammaglobin 1	3.5
25	408867	AA437199	Hs.656	cell division cycle 25C	3.5
	428508	BE252383	Hs.184668	SBB131 protein	3.5
	431120	AA492588		gb:ng99c08.s1 NCI_CGAP_Thy1 Homo sapiens cDNA	3.5
	401780			NM_005557*:Homo sapiens keratin 16 (focal non	3.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sapiens	3.5
30	456671	AB011142	Hs.114293	KIAA0570 gene product	3.5
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP10 (HT	3.5
	435244	N77221	Hs.187824	ESTs	3.5
	436246	AW450963	Hs.119991	ESTs	3.5
	431917	D16181	Hs.2868	peripheral myelin protein 2	3.5
35	443113	AI040686	Hs.132908	ESTs	3.5
	443341	AW631480	Hs.8688	ESTs	3.5
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.5
	418347	AA216419		gb:nc16e03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA	3.5
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo sapi	3.5
40	408633	AW963372	Hs.46677	PRO2000 protein	3.5
	427878	C05766	Hs.181022	CGI-07 protein	3.5
	419945	AW290975	Hs.118923	ESTs	3.5
	448372	AW445166	Hs.170802	ESTs	3.5
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen 1NFLS	3.5
45	411274	NM_002776	Hs.69423	kallikrein 10	3.5
	400666			NM_002425:Homo sapiens matrix metalloproteina	3.5
	426920	AA393351	Hs.132121	ESTs	3.5
	402639			Target Exon	3.4
50	454891	AW837349		gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapi	3.4
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet-de	3.4
	456296	AA829976	Hs.239114	mannosidase, alpha, class 1A, member 2	3.4
	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.4
	429274	AI379772	Hs.99206	ESTs	3.4
	430704	AW813091	Hs.335799	ESTs	3.4
55	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo sapi	3.4
	451778	AI826131	Hs.71243	ESTs, Weakly similar to zinc finger protein [	3.4
	430397	AI924533	Hs.105607	bicarbonate transporter related protein 1	3.4
	432113	AA935065	Hs.152385	ESTs	3.4
	449722	BE280074	Hs.23960	cyclin B1	3.4
60	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapi	3.4
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.4
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.4
	417009	AA191719	Hs.314714	ESTs	3.4
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moiety X	3.4
65	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen induci	3.4
	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PLACE20	3.4
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	3.4
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens cDNA	3.4
	403274			Target Exon	3.4
70	435360	AF105366	Hs.4876	solute carrier family 12 (potassium/chloride	3.4
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2 prote	3.4
	443462	AI064690	Hs.171176	ESTs	3.3
	444910	AI201849		gb:qs76g04.x1 NCI_CGAP_Pr28 Homo sapiens cDNA	3.3
75	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (from c	3.3
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	3.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE066	3.3
	419751	AW195581	Hs.93121	KIAA0761 protein	3.3
80	404782			C7001692*:gil6724096[gb]AAF26844.1 (AF195021	3.3
	415613	R20233		gb:yg18h11.r1 Soares infant brain 1NIB Homo s	3.3
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypothetical p	3.3
	406599			Target Exon	3.3
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.3



5	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo sapi	3.3
	421107	AA283822	Hs.55606	ESTs, Weakly similar to S47072 finger protein	3.3
	436985	AA740946	Hs.150895	ESTs	3.3
	443903	AI220547	Hs.135223	ESTs	3.3
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (from c	3.3
10	447153	AA805202	Hs.315562	ESTs	3.3
	450769	AA057418	Hs.33654	ESTs	3.3
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-C	3.3
	402481			NM_001821*:Homo sapiens choroideremia-like (R	3.3
	459394	BE409894	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, complete	3.3
15	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-1 [H.	3.3
	417708	N74392	Hs.50495	ESTs	3.3
	414869	AA157291	Hs.21479	ubiquitin 1	3.3
	441690	R81733	Hs.33106	ESTs	3.3
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.3
20	412246	AI160873	Hs.69233	zinc finger protein	3.3
	412903	BE007967	Hs.155795	ESTs	3.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placental)	3.3
	451177	AI969716	Hs.13034	ESTs	3.3
	409990	AA079337		gb:zm95b09.r1 Stratiagene colon HT29 (937221)	3.3
25	418462	BE001596	Hs.85266	integrin, beta 4	3.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92k	3.3
	405196			C2000662*:gi 7512792 pir T12482 hypothetical	3.3
	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA libra	3.3
	432917	NM_014125	Hs.279812	PRO0327 protein	3.3
30	448251	BE280486	Hs.84045	hypothetical protein FLJ20288	3.3
	415025	AW207091	Hs.72307	ESTs	3.3
	420218	AW958037	Hs.286	ribosomal protein L4	3.2
	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fis, clone HEMBB10	3.2
	447762	AI939461	Hs.161370	ESTs	3.2
35	414147	BE091634		gb:IL2-BT0731-240400-069-C03 BT0731 Homo sapi	3.2
	445038	AI635444	Hs.143917	dJ467N11.1 protein	3.2
	448666	NM_014953	Hs.323346	KIAA1008 protein	3.2
	402800			Target Exon	3.2
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated	3.2
40	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cere	3.2
	455203	AW865450		gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapi	3.2
	459666	W27362		gb:30g7 Human retina cDNA randomly primed sub	3.2
	401458			Target Exon	3.2
	432361	AI378562	Hs.159585	ESTs	3.2
45	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLICING F	3.2
	405336			Target Exon	3.2
	446563	BE326588	Hs.141454	ESTs	3.2
	449276	AW241510	Hs.252713	ESTs	3.2
	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo sapi	3.2
50	420591	X53655	Hs.99171	neurotrophin 3	3.2
	401486			C4000647*:gi 4758508 ref NP_004253.1  airway	3.2
	432979	AA573263	Hs.120860	ESTs	3.2
	413833	Z15005	Hs.75573	centromere protein E (312kD)	3.2
	438325	AA804258	Hs.123229	ESTs	3.2
55	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha-1C-a	3.2
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cysteine-r	3.2
	421777	BE562088	Hs.108196	HSPC037 protein	3.2
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone ADKA02	3.2
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone LNG004	3.2
60	402337			Target Exon	3.2
	420930	AW888650		gb:CM4-NT0007-130500-551-f06 NT0007 Homo sapi	3.2
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HEMBA10	3.2
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.1
	437641	AA811452	Hs.291911	ESTs	3.1
65	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.1
	434208	T92641	Hs.127648	hypothetical protein PRO2176	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.1
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	3.1
	458923	Y12812	Hs.24422	regulatory factor X-associated protein	3.1
70	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A receptor, ep	3.1
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDNA clo	3.1
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevisiae,	3.1
	445885	AI734009	Hs.127699	KIAA1603 protein	3.1
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP010	3.1
75	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine protein k	3.1
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo sapi	3.1
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription factor	3.1
	455987	BE178323		gb:RC3-HT0600-240400-023-g05 HT0600 Homo sapi	3.1
	421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA, part	3.1
80	423887	AL080207	Hs.134585	DKFZP434G232 protein	3.1
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.1
	447815	AI432199	Hs.247084	ESTs	3.1
	441974	AI683782	Hs.128245	ESTs	3.1
	446474	AI301227	Hs.150186	hypothetical protein DKFZp566K1946	3.1
	452166	AI948607	Hs.264680	ESTs	3.1
	451659	BE379761	Hs.14248	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1

	447701	BE619526	Hs.255527	hypothetical protein MGC14128	3.1
	443648	AI085377	Hs.143610	ESTs	3.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.1
5	449441	AI656040	Hs.196532	ESTs	3.1
	458145	AI239457	Hs.130794	ESTs	3.1
	444588	AI221321	Hs.167559	ESTs	3.1
	450832	AW970602	Hs.105421	ESTs	3.1
	449425	AW103433	Hs.195684	ESTs	3.1
10	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT2RP30	3.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	3.1
	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB55Y Ho	3.1
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S. cere	3.1
	404107			Target Exon	3.1
15	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.1
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (from c	3.1
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM040	3.1
	442824	BE178065	Hs.144081	ESTs	3.1
	435061	AI651474	Hs.163944	ESTs	3.1
20	420589	AA419360	Hs.192708	ESTs	3.0
	434569	AI311295	Hs.8294	KIAA0196 gene product	3.0
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B, membe	3.0
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional act	3.0
	402892			Target Exon	3.0
25	406087			Target Exon	3.0
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	3.0
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbHPU Ho	3.0
	435990	AI015862	Hs.131793	ESTs	3.0
	442577	AA292998	Hs.163900	ESTs	3.0
30	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitter tra	3.0
	458154	AW816379	Hs.335018	ESTs	3.0
	416809	N67253	Hs.271691	ESTs	3.0
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	3.0
	437938	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapiens cDN	3.0
35	413281	AA861271	Hs.222024	transcription factor BMAL2	3.0
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810027O1	3.0
	445505	AI971156	Hs.148891	ESTs	3.0
	425005	AI565851		gb:tn07g03.x1 NCI_CGAP_Brn25 Homo sapiens cDN	3.0
40	435673	AF202961	Hs.284200	Homo sapiens uncharacterized gastric protein	3.0
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA	3.0
	453509	AL040021	Hs.252674	ESTs, Weakly similar to alternatively spliced	3.0
	455750	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapi	3.0
	407777	AA161071	Hs.71465	squalene epoxidase	3.0
	424441	X14850	Hs.147097	H2A histone family, member X	3.0
45	417734	Z42667	Hs.6724	ESTs	3.0
	449676	AW380579	Hs.209657	ESTs	3.0
	445425	AI223511	Hs.300722	ESTs	3.0
	427061	AB032971	Hs.173392	KIAA1145 protein	3.0
	433584	AW295399		gb:Ul-H-BI2-ahv-h-03-0-Ul.s1 NCI_CGAP_Sub4 Ho	3.0
50	444477	AI150548	Hs.23155	ESTs	3.0
	446255	AI283257	Hs.257090	ESTs	3.0
	400612			C10001034:gil7513113 pir T13078 KIAA0992 pro	3.0
	450841	AI741466	Hs.270515	ESTs	3.0
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	3.0
55	433871	W02410	Hs.205555	ESTs	3.0
	401994			Target Exon	3.0
	449272	AW137656	Hs.197645	ESTs	3.0
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 kD)	3.0
	400250			Eos Control	3.0
60	408015	AW136771	Hs.244349	epidermal differentiation complex protein lik	3.0
	436414	BE264633	Hs.143638	WD repeat domain 4	3.0
	432220	AI571306	Hs.232224	ESTs	3.0
	420831	AA280824	Hs.190035	ESTs	3.0
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_Ul2 Homo sapiens cDNA	3.0
65	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG repeat r	3.0
	428262	AI651324	Hs.7298	biphenyl hydrolase-like (serine hydrolase; br	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone COL070	3.0
	417308	H60720	Hs.81892	KIAA0101 gene product	3.0
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	3.0
70	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2 (dihy	3.0
	423556	R72694	Hs.7720	dynein, cytoplasmic, heavy polypeptide 1	3.0
	426890	AA393167	Hs.41294	ESTs	2.9
	436333	AA709270	Hs.136672	EST	2.9
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.9
75	402556			C1001383*:gil538695 pir A61183 hypothetical	2.9
	411098	AW817238		gb:QV0-ST0247-090200-105-b07 ST0247 Homo sapi	2.9
	435399	AA679463		gb:ac50c03.s1 Stratagene hNT neuron (937233)	2.9
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.9
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone HEP016	2.9
80	410658	AW105231	Hs.192035	ESTs	2.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	2.9
	412279	BE245511		gb:TCBAP1D3235 Pediatric pre-B cell acute lym	2.9
	405277			ENSP00000211621*:Keratin, type II cytoskeleta	2.9
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapiens c	2.9

5	455319	AW895387		gb:QV4-NN0038-300300-157-c10 NN0038 Homo sapi	2.9
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	2.9
	413306	AW303544	Hs.118654	ESTs	2.9
	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.9
	434423	NM_006769	Hs.3844	LIM domain only 4	2.9
10	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	2.9
	412367	AW945964		gb:QV0-ET0001-050500-228-e09 ET0001 Homo sapi	2.9
	436148	BE005252	Hs.321583	Homo sapiens cDNA FLJ20779 fis, clone COL0507	2.9
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.9
	404981			ENSP00000252242::Keratin, type II cytoskeleta	2.9
15	448796	AA147829	Hs.301431	endothelial zinc finger protein induced by tu	2.9
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA, part	2.9
	401760			Target Exon	2.9
	443859	NM_013409	Hs.9914	folliculin	2.9
	404253			NM_021058::Homo sapiens H2B histone family, m	2.9
20	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	2.9
	435867	AA654229	Hs.114052	ESTs	2.9
	429035	BE549781	Hs.270475	ESTs	2.9
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega-hydr	2.9
	446417	AI299050		gb:qn14d12.x1 NCLCGAP_Lu5 Homo sapiens cDNA	2.9
25	437637	AJ003029	Hs.65792	syntrophin, gamma 2	2.9
	452452	BE393822	Hs.29645	Homo sapiens mRNA; cDNA DKFZp761C029 (from cl	2.9
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	2.9
	450698	W31489	Hs.95044	ESTs, Weakly similar to I38022 hypothetical p	2.9
	439430	AF124250	Hs.6564	cervical cancer anti-estrogen resistance 3	2.9
30	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	2.9
	438268	AA782163	Hs.293502	ESTs	2.9
	401781			Target Exon	2.9
	439625	AF086453	Hs.58611	ESTs	2.9
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothetical p	2.9
35	410743	AA089474	Hs.272153	ESTs	2.9
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog o	2.9
	449746	AI688594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOCHROME	2.9
	443479	AF027219	Hs.9443	zinc finger protein 202	2.9
	442601	AI684969	Hs.46772	ESTs	2.9
40	405932			C15000305:gi 3806122 gb AAC69198.1  (AF097887	2.9
	405454			C12000541:gi 5729884 ref NP_006539.1  IGF-II	2.9
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	2.9
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, parti	2.9
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransf	2.9
45	414581	AA256213	Hs.72010	ESTs	2.9
	411268	AK000512	Hs.69388	hypothetical protein FLJ20505	2.9
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_1NFLS	2.9
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	2.9
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	2.9
50	400631	AF173937	Hs.109494	secreted protein of unknown function	2.9
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein produ	2.9
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothetical p	2.9
	435711	AF226667	Hs.58553	CTP synthase II	2.9
	419088	AI538323	Hs.52620	integrin, beta 8	2.8
55	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clone IF	2.8
	429299	AI620463	Hs.293984	hypothetical protein MGC13102	2.8
	451702	AW665452	Hs.246503	ESTs	2.8
	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	2.8
	405281			NM_002864:Homo sapiens pregnancy-zone protein	2.8
60	438161	BE089028	Hs.20158	ESTs, Weakly similar to S34159 transcription	2.8
	409103	AF251237	Hs.112208	XAGE-1 protein	2.8
	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.8
	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mis5, S	2.8
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.8
65	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-like	2.8
	452730	AA027952	Hs.165216	ESTs	2.8
	413083	BE064528		gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapi	2.8
	437030	AA742577	Hs.303781	EST	2.8
	438113	AI467908	Hs.8882	ESTs	2.8
70	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone LNG096	2.8
	440994	AI160011	Hs.193341	ESTs	2.8
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HEMBA10	2.8
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	2.8
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin, tissu	2.8
75	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.8
	433788	AI810534	Hs.161275	ESTs	2.8
	403806			Target Exon	2.8
	437182	AL080098		gb:Homo sapiens mRNA; cDNA DKFZp564C1072 (fro	2.8
	453955	AW579207	Hs.304666	ESTs, Weakly similar to I78885 serine/threoni	2.8
80	420795	AA323037	Hs.128645	sorting nexin 16	2.8
	452696	AI826645	Hs.211534	ESTs	2.8
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.8
	438052	AA776564	Hs.41891	zinc finger 1111	2.8
	441755	AW450826	Hs.127786	ESTs	2.8
	427961	AW293165	Hs.143134	ESTs	2.8
	449785	AI225235	Hs.288300	hypothetical protein FLJ23231	2.8
	450451	AW591528	Hs.202072	ESTs	2.8

5	406831	N73448	Hs.50272	ESTs, Weakly similar to RS1A_HUMAN 40S RIBOSO	2.8
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A receptor, pi	2.8
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.8
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.8
	448979	AI611378	Hs.192610	ESTs	2.8
10	409143	AW025980	Hs.138965	ESTs, Weakly similar to I38022 hypothetical p	2.8
	410664	NM_006033	Hs.65370	lipase, endothelial	2.8
	444550	BE250716	Hs.87614	ESTs	2.8
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.8
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.8
15	445941	AI267371	Hs.172636	ESTs	2.8
	459719	AW749511	Hs.301554	ESTs, Weakly similar to AF133298 1 cytochrome	2.8
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT2RP20	2.8
	456456	AA477609	Hs.89563	nuclear cap binding protein subunit 1, 80kD	2.8
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothetical p	2.8
20	403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	2.8
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	2.8
	439846	T63959	Hs.228320	hypothetical protein FLJ23537	2.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	2.8
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	2.8
25	455091	BE079752		gb:RC6-BT0627-140200-011-A04 BT0627 Homo sapi	2.8
	410049	AW579475		gb:RC0-DT0076-110100-031-d10 DT0076 Homo sapi	2.8
	452571	W31518	Hs.34665	ESTs	2.8
	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	2.8
	426343	NM_014642	Hs.169387	KIAA0036 gene product	2.8
30	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-associated	2.8
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromosomes 4	2.7
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.7
	429128	AA446869	Hs.119316	ESTs	2.7
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MAMMA10	2.7
35	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.7
	403763			NM_001059*:Homo sapiens tachykinin receptor 3	2.7
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypothetic	2.7
	406753	AA505665	Hs.217493	annexin A2	2.7
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sapiens	2.7
40	419875	AA853410	Hs.93557	proenkephalin	2.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical p	2.7
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.7
	456181	L36463	Hs.1030	ras inhibitor	2.7
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen 1NFLS	2.7
45	417995	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICROTUBUL	2.7
	435347	AW014873	Hs.116963	ESTs	2.7
	457339	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC FINGE	2.7
	417398	N78541	Hs.177366	ESTs	2.7
	408380	AF123050	Hs.44532	diubiquitin	2.7
50	437724	AW444828	Hs.184323	ESTs	2.7
	408680	AK000093	Hs.46821	hypothetical protein FLJ20086	2.7
	454202	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo sapi	2.7
	414362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli RecA ho	2.7
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.7
55	406092			Target Exon	2.7
	447748	AI422023	Hs.161338	ESTs	2.7
	443236	AI079496	Hs.134169	ESTs	2.7
	433743	AF075312	Hs.236760	Homo sapiens clone HQ0262	2.7
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related protein	2.7
60	405675			Target Exon	2.7
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila inaD-like)	2.7
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	2.7
	448592	N69546	Hs.44563	hypothetical protein	2.7
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MAMMA10	2.7
65	407287	AI678812		gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA	2.7
	448275	BE514434	Hs.20830	kinesin-like 2	2.7
	412977	AA125910	Hs.191461	ESTs	2.7
	431721	AB032996	Hs.268044	KIAA1170 protein	2.7
	417357	AF260257	Hs.131917	retinitis pigmentosa GTPase regulator interac	2.7
70	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the p	2.7
	416294	D86980	Hs.79170	KIAA0227 protein	2.7
	458201	AI989961	Hs.233477	ESTs, Moderately similar to A Chain A, Cyclop	2.7
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolog 2	2.7
	401230			NM_014191*:Homo sapiens sodium channel, volta	2.7
75	422058	AA862231	Hs.334443	ESTs	2.7
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.7
	430152	AB001325	Hs.234642	aquaporin 3	2.7
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.7
	443500	AV646388	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (from cl	2.7
80	418030	BE207573	Hs.83321	neuromedin B	2.7
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	2.7
	418869	AW516565		gb:xq01d05.x1 Soares_NHCeC_cervical_tumor Hom	2.7
	431688	AA513906		gb:ng67c08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	2.7
	427579	AA366143	Hs.179669	hypothetical protein FLJ20637	2.7
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.7
	414737	AI160386	Hs.125087	ESTs	2.7
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.7

	446659	AI335361	Hs.226376	ESTs	2.7
	419833	AA251131	Hs.220697	ESTs	2.7
	411819	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo sapi	2.6
5	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypothetical p	2.6
	446102	AW168067	Hs.252956	ESTs	2.6
	441408	AI733249	Hs.126897	ESTs	2.6
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse transc	2.6
	416283	NM_005429	Hs.79141	vascular endothelial growth factor C	2.6
10	421470	R27496	Hs.1378	annexin A3	2.6
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	2.6
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.6
	431832	AW276866	Hs.192715	ESTs	2.6
	426698	AA394104	Hs.97489	ESTs	2.6
	433288	AI368873	Hs.271257	ESTs, Weakly similar to I38022 hypothetical p	2.6
15	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.6
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypothetical p	2.6
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo sapi	2.6
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein [H.s	2.6
	401260			C1001031*:gij7305041[ref]NP_038876.1} erythro	2.6
20	435136	R27299	Hs.10172	ESTs	2.6
	412108	AA100293	Hs.185043	ESTs	2.6
	434442	AA737415	Hs.152826	ESTs	2.6
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	2.6
25	419667	AU077005	Hs.92208	a disintegrin and metalloproteinase domain 15	2.6
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	2.6
	409594	AA076118		gb:zm18e06.s1 Stratagene pancreas (937208) Ho	2.6
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (937208) Ho	2.6
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.6
30	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth factor	2.6
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.6
	434444	AI765276	Hs.101257	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	2.6
	411465	AW847663		gb:IL3-CT0213-280100-056-F02 CT0213 Homo sapi	2.6
35	408625	AW243323	Hs.266785	ESTs	2.6
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.6
	439245	NM_013381	Hs.6510	thyrotropin-releasing hormone degrading ectoe	2.6
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit of	2.6
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin)	2.6
40	401050			NM_014155*:Homo sapiens HSPC063 protein (HSPC	2.6
	405897			Target Exon	2.6
	451153	BE092900		gb:CM2-BT0742-100400-147-h04 BT0742 Homo sapi	2.6
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC FINGE	2.6
	440159	AI637599	Hs.126127	ESTs	2.6
45	404184			NM_030903*:Homo sapiens olfactory receptor, f	2.6
	428552	AW274560	Hs.129520	ESTs	2.6
	401367			Target Exon	2.6
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
50	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated fac	2.6
	449432	AW451361	Hs.196529	ESTs	2.6
	425062	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger protein)	2.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PLACE10	2.6
	450705	U90304	Hs.25351	iroquois homeobox protein 5	2.6
55	421506	BE302766	Hs.105097	thymidine kinase 1, soluble	2.6
	408391	AW859276		gb:MR1-CT0352-240200-105-d02 CT0352 Homo sapi	2.6
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mouse)	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to ARL-	2.6
60	453331	AI240665	Hs.8895	ESTs	2.6
	447175	AI365208	Hs.293606	ESTs	2.6
	451878	AI821027	Hs.8429	ESTs	2.6
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	2.6
	418282	AA215535	Hs.98133	ESTs	2.6
65	434557	AW855466	Hs.271866	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.6
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.6
	420894	AA744597	Hs.88854	ESTs	2.6
	435663	AI023707	Hs.134273	ESTs	2.6
	448037	AW195634	Hs.170401	ESTs	2.6
70	418067	AI127958	Hs.83393	cystatin E/M	2.6
	439524	BE542950	Hs.155548	ESTs	2.6
	402298			Target Exon	2.6
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.6
	407471	D55644		gb:Human spleen PABL (pseudautosomal boundar	2.6
75	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, complete	2.6
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from c	2.6
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothetical p	2.6
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (from c	2.6
	425415	M13903	Hs.157091	involucrin	2.6
80	444826	AI674482	Hs.148441	ESTs	2.6
	413331	BE083950		gb:PM0-BT0651-260200-001-b11 BT0651 Homo sapi	2.6
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.6
	405041			C3001706*:gij1345652[sp]P15989[CA36_CHICK COL	2.6
	413864	BE175582		gb:RC5-HT0580-100500-022-C01 HT0580 Homo sapi	2.6

	438746	AI885815	Hs.184727	ESTs	2.5
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo sapi	2.5
	433365	AF026944	Hs.293797	ESTs	2.5
5	412723	AA648459	Hs.335951	hypothetical protein AF301222	2.5
	422656	AI870435	Hs.1569	LIM homeobox protein 2	2.5
	411171	AW820260		gb:QV2-ST0296-150200-040-c10 ST0296 Homo sapi	2.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapi	2.5
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telencepha	2.5
10	414883	AA926960	Hs.334883	CDC28 protein kinase 1	2.5
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.5
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (from cl	2.5
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associated fac	2.5
	455549	AW994222		gb:RC3-BN0036-250200-012-e02 BN0036 Homo sapi	2.5
15	409676	AA077118	Hs.197298	NS1-binding protein	2.5
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	2.5
	429413	NM_014058	Hs.201877	DESC1 protein	2.5
	424420	BE614743	Hs.146688	prostaglandin E synthase	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypep	2.5
20	452834	AI638627	Hs.105685	KIAA1688 protein	2.5
	424354	NM_014314	Hs.145612	RNA helicase	2.5
	455095	AW855598		gb:CM1-CT0278-031199-032-e08 CT0278 Homo sapi	2.5
	431241	AA496799	Hs.36958	ESTs	2.5
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (connexin	2.5
25	427239	BE270447	Hs.174070	ubiquitin carrier protein	2.5
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.5
	458175	AW296024	Hs.150434	ESTs	2.5
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein type	2.5
	453379	AA035261	Hs.61753	ESTs	2.5
30	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothetical p	2.5
	412313	AW936832		gb:PM2-DT0023-050400-003-h03 DT0023 Homo sapi	2.5
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro	2.5
	443757	H05479	Hs.62314	ESTs	2.5
	449300	AI656959	Hs.222165	ESTs	2.5
35	434913	AW872860	Hs.11056	RALBP1 protein	2.5
	448946	AI652855	Hs.23363	hypothetical protein FLJ10983	2.5
	437327	AL353942	Hs.306504	Homo sapiens mRNA; cDNA DKFZp761L23121 (from	2.5
	450262	AW409872	Hs.184846	Homo sapiens, Similar to zinc finger protein	2.5
	453204	R10799	Hs.191990	ESTs	2.5
40	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	2.5
	449344	AI640355	Hs.312691	ESTs	2.5
	439436	BE140845	Hs.57868	ESTs	2.5
	449867	AI672379	Hs.122970	hypothetical protein FLJ21579	2.5
	452220	BE158006	Hs.212296	ESTs	2.5
45	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.5
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapien	2.5
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	2.5
	415030	D31118	Hs.191735	hypothetical protein MGC10520	2.5
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	2.5
50	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	2.5
	400301	X03635	Hs.1657	estrogen receptor 1	2.5
	429386	AK001795	Hs.201179	hypothetical protein FLJ10933	2.5
	423949	AI014546	Hs.130912	ESTs	2.5
	411768	NM_013371	Hs.71979	interleukin 19	2.5
55	436961	AW375974	Hs.156704	ESTs	2.5
	431124	AF284221	Hs.59506	doublesex and mab-3 related transcription fac	2.5
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	2.5
	418717	AI334430	Hs.86984	ESTs	2.5
	443270	NM_004272	Hs.337737	Homer, neuronal immediate early gene, 1B	2.5
60	448454	NM_005879	Hs.21254	TRAF interacting protein	2.5
	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogene hom	2.5
	442966	AI394036	Hs.132237	ESTs, Weakly similar to DUS8_HUMAN DUAL SPECI	2.5
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN ALU SU	2.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription factor	2.5
65	440381	AA917808	Hs.190495	ESTs	2.5
	403983			Target Exon	2.5
	451340	AW936273		gb:QV0-DT0020-090200-107-g07 DT0020 Homo sapi	2.5
	447888	BE620911	Hs.126889	ESTs	2.5
	441794	AW197794	Hs.253338	ESTs	2.5
70	424153	AA451737	Hs.141496	MAGE-like 2	2.5
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.5
	435647	AI653240	Hs.49823	ESTs	2.5
	428780	AI478578	Hs.50636	ESTs	2.5
	439108	AW163034	Hs.6467	synaptogyrin 3	2.5
75	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fascin h	2.5
	428054	AI948688	Hs.266619	ESTs	2.5
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	2.5
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S. cere	2.5
	443362	AI053464	Hs.166505	ESTs	2.5
80	433183	AF231338	Hs.222024	transcription factor BMAL2	2.5
	438214	H06076	Hs.26320	TRABID protein	2.5
	446745	AW118189	Hs.156400	ESTs	2.5
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.5
	426333	AW269088	Hs.118183	hypothetical protein FLJ22833	2.5

TABLE 12B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
407642	1007175_1	AW178963 AW845721 BE141041 AW806977 AW845690 AW845691 AW845724 AW176564 AW845705 AW845603 AW845729 AW845722 AW178966 AW845693 AW845585 AW845707 BE141053 BE141046 AW845570 AW845575 BE141043 BE141039 BE141070 AW062443 AW806980 AW845643 AW806969 AW845686 BE141054 BE141040 BE141044 BE141042 AW845571 AW845604 BE141047 BE141071 AW062442 AW845633 AW178968
408391	1055687_1	AW859276 AW859274 AW190959 T91463
408690	107490_1	AW864542 AA056567 AW882724
409594	114249_1	AA076118 AA975618 AA076220
409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
409990	116644_1	AA079337 AA079338 AW272100
410008	116812_1	AA079552 BE142525 BE142527
410049	1172307_1	AW579475 AW939654 AW939655
410784	1221005_1	AW803201 BE079700 BE062940
411098	1232093_1	AW817238 AW993985 AW993998
411171	1234393_1	AW820260 AW820332 R94406
411465	1246768_1	AW847663 AW847861 AW861080
411559	1249417_1	BE144081 BE144190 AW851155
411819	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
411958	126717_1	AA099020 AW751275 AW751276 AW751289
412279	1287332_1	BE245511 BE246133 AW935247
412313	1288355_1	AW936832 AW936609 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW936760 AW936819 AW937485 AW937589 AW937658 AW937654 AW937492
412333	1289037_1	AW945964 AW946020 AW946034 AW946027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016 AW946039
412367	1291505_1	AW946045 AW946028 AW946036
412879	1334272_1	BE092219 BE092361 BE006789
413083	1348639_1	BE064528 BE064589 BE064561
413331	1361726_1	BE083950 BE084017 BE084016
413864	1395788_1	BE175582 BE175514 BE175505 BE175591 BE175530
414147	142127_1	BE091634
414148	142133_1	BE084049 AW292907 AA135984
415317	1533847_1	Z43388 F05453 R19673 R20275 H06917
415613	1540602_1	R20233 F12901 T74740
415747	155189_1	AA381209 AA381245 AA167683
416120	1571266_1	H46739 H51513 H19779
416168	1574545_1	H23687 H46460 H40239
416548	1600181_1	H62953 N76608 N72413
417742	1696282_1	R64719 Z44680 R12451
418347	174149_1	AA216419 F03238 AA229517
418869	179863_1	AW516565 AA229762 AA230035
419807	188252_1	R77402 AA262462 AA250988 R06794
420373	193194_1	AW968228 AA259146 W01465
420637	195241_1	AW976153 AA278945 AA747691
420930	197736_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
422689	219896_1	AW856665 AA315006 AW954733
423733	231476_1	AA330281 AA330232 AW962521
423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA649496
423841	232507_1	AW753967 AA370795 AA331630 AW962550
425005	245908_1	AI565851 AA349656 R24798
429163	300543_1	AA884766 AW974271 AA592975 AA447312
431120	328264_1	AA492588 AA492498 AA492571
431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
431688	336609_1	AA513906 AA847734 AI357044
432184	342677_1	AW971125 AA527731 N52655 AI821508 AA532420
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432869	355475_1	AW974094 AA569074 AA602574
433289	36202_1	AF005258
433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
433644	371919_1	AW342028 AA641080 AA603282
434321	383473_1	AA629368 AW849574 AW849573
435399	405576_1	AA679463 AW813779 AW813709
437182	43421_1	AL080098 AL037472 AA432051
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005 AI422017 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AI423279 AI423645 AI424090 AI359637 AL044732 D17003
438390	45662_1	AW979074 AA834841 AA828650
438966	467436_1	AA828995 AA834879 AI926361
438993	467651_1	

439579 47404\_1 AF086400 W79232 W73990  
 440320 491930\_1 AA879294 N67538 A1474541  
 444910 624951\_1 A1201849 BE069007 AW946544  
 446417 676384\_1 A1299050 BE256910  
 447197 711623\_1 R36075 A1366546 R36167  
 448599 770766\_1 AW860912 A1540866  
 449034 794817\_1 A1624049 AW117770 A1858360  
 450024 82296\_1 AA005129 AA679084 AA694399  
 450613 840016\_1 A1702055 R89204 R86260  
 451105 859083\_1 A1761324 AW880941 AW880937  
 451153 86054\_1 BE092900 AA015877 AA018521  
 451340 86640\_1 AW936273 AW340350 AA017208  
 454202 1050507\_1 AW178363 AW846011 AW845964 AW845988 AW845977 AW846002  
 454241 1067807\_1 BE144666 BE184942 AW238414 BE184946  
 454707 1230250\_1 AW814989 AW814852 AW814808  
 454891 1239217\_1 AW837349 AW837355 AW882717  
 454988 1248607\_1 AW850140 AW850195 AW850192  
 455091 1252939\_1 BE079752 BE079868 BE148989 AW855532 BE148818 BE148815 BE148796  
 455092 1252971\_1 BE152428 AW855572 AW855607  
 455095 1252987\_1 AW855598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855601 AW855605  
 455203 1259973\_1 AW865450 AW865119 AW865452 AW865461 AW865325 AW865114 AW865116 AW865321 AW865590 AW865390  
 455310 1278158\_1 AW893961 AW893998 AW894034 AW894019  
 455319 1279172\_1 AW895387 AW895547 AW895564 AW895323 AW895405 AW895539 AW895538  
 455365 1284681\_1 AW948343 AW948341 AW902855 AW984737  
 455549 1324696\_1 AW994222 AW994377  
 455666 1349545\_1 BE065813 BE065788 BE065889 BE065832  
 455750 1355998\_1 BE075114 BE075283 BE075118  
 455838 1374605\_1 BE145808 BE145807 BE181883  
 455987 1397735\_1 BE178323 BE177978  
 457405 333127\_1 AA504860 AA504911  
 458829 773443\_1 A1557388 BE158936  
 459267 966605\_1 AJ003631 AJ003650 AJ003651

TABLE 12C

Pkey: Unique number corresponding to an Eos probe set  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400612	9929646	Minus	151513-151662
400666	8118496	Plus	17982-18115,20297-20456
401050	8117628	Minus	78449-79425
401137	2547238	Minus	598-1009
401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
401260	8076883	Minus	86008-86355
401367	9796198	Minus	145356-145807
401458	9187886	Plus	76485-77597
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
401575	7229804	Minus	76253-76364
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402048	8072512	Plus	43936-44078
402298	6598824	Plus	36758-37953
402337	6957691	Plus	4116-4286,16811-16973,17107-17256,19715-20040,22029-22205
402481	9797406	Plus	87891-88991
402556	9863723	Plus	13579-14026
402639	9958129	Minus	20167-22383
402800	6010175	Plus	43921-44049,46181-46273
402892	8086844	Minus	194384-194645
403274	8072441	Minus	104069-104179,105683-105859
403471	9930659	Minus	85867-85983
403763	7229888	Minus	43575-43887
403806	8140491	Plus	146390-146678
403983	8576059	Minus	82441-82701
404107	8099028	Minus	201699-202363
404132	6981900	Plus	11307-12434
404184	4581418	Minus	12652-13548
404253	9367202	Minus	55675-56055
404440	7528051	Plus	80430-81581
404782	9910094	Minus	15455-15589
404959	7407964	Plus	45243-45368
404981	4432779	Minus	20626-20770,22513-22721
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405041	7547195	Plus	121230-121714
405196	7230083	Minus	135716-135851



405277	3980473	Plus	23471-23572
405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
405336	6094635	Plus	33267-33563
405454	7656675	Plus	133807-134053
405545	1054740	Plus	118677-118807,119091-119296,121626-121823
405547	1054740	Plus	124361-124520,124914-125050
405657	4827303	Minus	104132-104293
405675	4557087	Plus	70304-70630
405708	4156182	Plus	55030-55604
405897	6758795	Plus	59828-60535
405932	7767812	Minus	123525-123713
405943	6758796	Plus	20605-20812
406087	9123919	Minus	7234-7626
406092	9123919	Plus	251370-251797,252168-252882
406467	9795551	Plus	182212-182958
406554	7711566	Plus	106956-107121
406560	7711569	Minus	35162-35292
406599	8248616	Plus	10933-11086

TABLE 13A: 465 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES, LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 13A lists about 465 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 12A, except that the ratio was greater than or equal to 1.7, and the 96<sup>th</sup> percentile value amongst cervical cancers was greater than or equal 100 units, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 PPDomains: Predicted Protein Domains  
 Unigene Title: Unigene gene title  
 R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigenelD	PPDomains	Unigene Title	R1
425650	NM_001944	Hs.1925	TM,cadherin,Cadherin_C_term	desmoglein 3 (pemphigus vulgaris antigen)	43.6
418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interstitial)	38.9
439606	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87	28.8
452240	AI591147	Hs.61232	TM	ESTs	27.0
424046	AF027866	Hs.138202	SS,TM,serpin	serine (or cysteine) proteinase inhibitor	24.5
400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (stromelysin	20.5
418345	AJ001696	Hs.241407	SS,TM,serpin	serine proteinase inhibitor 13(P113; se	20.1
423017	AW178761	Hs.227948	SS,serpin	serine (or cysteine) proteinase inhibitor	19.2
428227	AA321649	Hs.2248	SS,TM,IL8	small inducible cytokine subfamily B (Cys	15.9
447164	AF026941	Hs.17518	TM,IBR	Homo sapiens cig5 mRNA, partial sequence	13.8
414764	AW013887	Hs.72047	TM	ESTs	12.9
416661	AA634543	Hs.79440	TM	IGF-II mRNA-binding protein 3	12.7
427585	D31152	Hs.179729	SS,C1q,Collagen	collagen, type X, alpha 1 (Schmid metaphy	12.6
406467			TM,elfhand	Target Exon	10.5
428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromelysin 1	10.2
418882	NM_004996	Hs.89433	TM,ABC_membrane,ABC_tran	ATP-binding cassette, sub-family C (CFTR/	9.4
419247	S65791	Hs.89764	TM,KH-domain	fragile X mental retardation 1	9.1
446232	AI281848	Hs.194691	TM,7tm_3Ribosomal_L13	retinoic acid induced 3	8.9
424905	NM_002497	Hs.153704	TM,pkinase	NIMA (never in mitosis gene a)-related ki	8.9
422420	U03398	Hs.1524	TM,tubulin,TNF	tumor necrosis factor (ligand) superfamil	8.7
427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA1794 p	6.9
444342	NM_014398	Hs.10887	Lamp	similar to lysosome-associated membrane g	6.8
422330	D30783	Hs.115263	SS,TM,EGF	epiregulin	6.8
447342	AI199268	Hs.19322	SS,lipocalin	Homo sapiens, Similar to RIKEN cDNA 20103	6.8
407839	AA045144	Hs.161566	TM,cadherin,Cadherin_C_term	ESTs	6.6
410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
414812	X72755	Hs.77367	SS,TM,IL8	monokine induced by gamma interferon	6.4
421773	W69233	Hs.112457	SS	ESTs	6.2
413385	M34455	Hs.840	TM,IDO	indoleamine-pyrrole 2,3 dioxygenase	5.9
413753	U17760	Hs.75517	SS,laminin_EGF,laminin_Nterm,adh_short	laminin, beta 3 (nicein (125kD), kalinin	5.8
432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collagenase	5.5
418663	AK001100	Hs.41690	TM,cadherin	desmocollin 3	5.5
407366	AF026942		TM,IBR	gb:Homo sapiens cig33 mRNA, partial seque	5.5
433091	Y12642	Hs.3185	SS,TM,UPAR_LY6	lymphocyte antigen 6 complex, locus D	5.4
408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Cation_ATPase_C, N	ESTs	5.4
420440	NM_002407	Hs.97644	SRCLUteroglobin	mammaglobin 2	5.2
437044	AL035864	Hs.69517	TM	cDNA for differentially expressed CO16 ge	5.1
405547			SS,TM,ABC_membrane,ABC_tran,ig	NM_018833*:Homo sapiens transporter 2, AT	5.1
439223	AW238299	Hs.250618	SS	UL16 binding protein 2	5.1
426320	W47595	Hs.169300	SS,TM,TGF-beta,TGFb_propeptide	transforming growth factor, beta 2	5.1
423634	AW959908	Hs.1690	TM	heparin-binding growth factor binding pro	5.0
426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 3 (E polypeptide, protei	5.0
409744	AW675258	Hs.56265	TM,metalthio,Kelch	Homo sapiens mRNA; cDNA DKFZp586P2321 (fr	4.9

	444461	R53734	Hs.25978	TM	ESTs, Weakly similar to 2109260A B cell g	4.8
	410361	BE391804	Hs.62661	SS,TM,GBP	guanylate binding protein 1, interferon-i	4.8
	423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrophage e	4.8
5	450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep,Repolysin	a disintegrin and metalloproteinase domai	4.8
	401575	NA		TM	Target Exon	4.6
	428484	AF104032	Hs.184601	TM	solute carrier family 7 (cationic amino a	4.5
	425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, iodothyronine, type II	4.4
	431808	M30703	Hs.270833	SS,TM,EGF	amphiregulin (schwannoma-derived growth f	4.3
10	434699	AA643687	Hs.149425	TM,Nucleoside_tra2	Homo sapiens cDNA FLJ11980 fis, clone HEM	4.3
	406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprotein 9	4.2
	404440			TM,MAGE	NM_021048:Homo sapiens melanoma antigen,	4.2
	449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
	444105	AW189097	Hs.166597	TM,cdherin	ESTs	4.1
15	409632	W74001	Hs.55279	SS,serpin	serine (or cysteine) proteinase inhibitor	4.1
	423515	AA327017	Hs.162204	SS,TM,UPAR_LY6	ESTs	4.1
	423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
	423553	AA405635	Hs.96854	TM	ESTs, Weakly similar to DYLL_HUMAN CYTOPL	4.1
	445537	AJ245671	Hs.12844	TM,ras	EGF-like-domain, multiple 6	4.0
20	446989	AK001898	Hs.16740	TM	hypothetical protein FLJ11036	4.0
	428536	AI143139	Hs.2288	TM,efhand,Syndecan	visinin-like 1	3.9
	413801	M62246	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	3.9
	429441	AJ224172	Hs.204096	Uteroglobulin	lipophilin B (uteroglobulin family member),	3.9
	409601	AF237621	Hs.80828	TM,filamentfilament,C2	keratin 1 (epidermolytic hyperkeratosis)	3.8
25	439238	N47305	Hs.46668	TM	ESTs	3.8
	446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
	405545			SS,TM,proteasome,ig,ABC_memb,tranABC_tran,	(MDR/TAP) (TAP2)	3.8
	422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	SS,TM,fn3,vwa,Collagen,Kunitz_BPTI	collagen, type VII, alpha 1 (epidermolyti	3.7
30	430686	NM_001942	Hs.2633	SS,TM,cdherin,Cadherin_C_term	desmoglein 1	3.7
	444707	AI188613	Hs.41690	TM,cdherin	desmocollin 3	3.7
	409582	R27430	Hs.271565	TM	ESTs	3.6
	408771	AW732573	Hs.47584	TM,K_tetra,ion_trans	potassium voltage-gated channel, delayed-	3.6
	400441	M15530	Hs.99879	TM,G-alpha	B-cell growth factor 1 (12kD)	3.6
35	413278	BE563085	Hs.833	TM,ubiquitinlaminin_G,laminin_EGF,kazal	interferon-stimulated protein, 15 kDa	3.6
	426514	BE616633	Hs.170195	SS,TGFb_propeptide,TGF-beta	bone morphogenetic protein 7 (osteogenic	3.6
	424927	AW973666	Hs.153850	SS	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	SS,TM,Uteroglobulin	mammaglobin 1	3.5
	407756	AA116021	Hs.38260	SS,UCH-1,UCH-2	ubiquitin specific protease 18	3.5
40	407137	T97307		TM,GDA1_CD39	gb:ye53h05.s1 Soares fetal liver spleen 1	3.5
	411274	NM_002776	Hs.69423	trypsin	kallikrein 10	3.5
	400666			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metalloprot	3.5
	412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Cam_acyltransf	endothelial cell growth factor 1 (platele	3.4
45	450650	T65617	Hs.101257	TM	hypothetical protein MGC3295	3.4
	451778	AI826131	Hs.71243	ig	ESTs, Weakly similar to zinc finger prote	3.4
	430397	AI924533	Hs.105607	SS,TM	bicarbonate transporter related protein 1	3.4
	449722	BE280074	Hs.23960	TM,cyclin	cyclin B1	3.4
	422487	AJ010901	Hs.198267	TM,vwd	mucin 4, tracheobronchial	3.4
	449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
50	418994	AA296520	Hs.89546	SS,TM,lectin_c,sushi,EGF	selectin E (endothelial adhesion molecule	3.3
	421379	Y15221	Hs.103982	SS,TM,IL8	small inducible cytokine subfamily B (Cys	3.3
	414774	X02419	Hs.77274	SS,kringle,trypsin	plasminogen activator, urokinase	3.3
	431958	X63629	Hs.2877	SS,TM,Cadherin_C_term,cdherin	cadherin 3, type 1, P-cadherin (placental	3.3
	418462	BE001596	Hs.85266	SS,TM,integrin_B,fn3	integrin, beta 4	3.3
55	424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatinase B,	3.3
	401486	NA		SS,TM,trypsin	C4000647*gi4758508 ref NP_004253.1  air	3.2
	408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, clone AD	3.2
	427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	3.2
	452934	AA581322	Hs.4213	SS,TM,ig	hypothetical protein MGC16207	3.1
60	448988	Y09763	Hs.22785	SS,TM	gamma-aminobutyric acid (GABA) A receptor	3.1
	439750	AL359053	Hs.57664	TM,integrin_B,Ricin_B_lectinrm	Homo sapiens mRNA full length insert cDNA	3.1
	414696	AF002020	Hs.76918	SS,TM,Patched	Niemann-Pick disease, type C1	3.1
	435604	AA625279	Hs.26892	TM	uncharacterized bone marrow protein BM040	3.1
	453883	AI638516	Hs.22630	TM,Ets,SAM_PNT	cofactor required for Sp1 transcriptional	3.0
65	448733	NM_005629	Hs.187958	SS,TM,SNF,ABC_tran,isodh,pkinase,DSPC,Ribosomal_	solute carrier family 6 (neurotransmitter	3.0
	444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
	437938	AI950087		TM,histone,ig,MHC_I	gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapiens	3.0
	424441	X14850	Hs.147097	TM,histone	H2A histone family, member X	3.0
	427061	AB032971	Hs.173392	TM	KIAA1145 protein	3.0
70	409703	NM_006187	Hs.56009	SS	2'-5'-oligoadenylate synthetase 3 (100 kD	3.0
	447313	U92981	Hs.18081	TGF-beta	Homo sapiens clone DT1P1B6 mRNA, CAG repe	3.0
	431070	AW408164	Hs.249184	ABC_tran	transcription factor 19 (SC1)	2.9
	446269	AW263155	Hs.14559	TM	hypothetical protein FLJ10540	2.9
	421190	U95031	Hs.102482	TM,vwd	mucin 5, subtype B, tracheobronchial	2.9
75	452732	BE300078	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.9
	443859	NM_013409	Hs.9914	SS,kazal	folistatin	2.9
	446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid omega-	2.9
	449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOCH	2.9
	418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
80	414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kinase,SCO1-SenC	ESTs	2.9
	413629	AU077025	Hs.265827	SS,IRNA_antish2,SH3,pkinase	interferon, alpha-inducible protein (clon	2.8
	445873	AA250970	Hs.251946	SS,rm,PABPpkinase,14-3-3,rm	poly(A)-binding protein, cytoplasmic 1-li	2.8
	438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
	410310	J02931	Hs.62192	SS,TM,Tissue_fac	coagulation factor III (thromboplastin, t	2.8

	411558	AA102670	Hs.70725	SS,TM	gamma-aminobutyric acid (GABA) A receptor	2.8
	413273	U75679	Hs.75257	TM,ig,pkinase	stem-loop (histone) binding protein	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product	2.8
5	433345	AI681545	Hs.152982	SS	hypothetical protein FLJ13117	2.7
	452234	AW084176	Hs.223296	TM	ESTs, Weakly similar to I38022 hypothetic	2.7
	456181	L36463	Hs.1030	TM,RA,VPS9	ras inhibitor	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor,sushi	diubiquitin	2.7
	422278	AF072873	Hs.114218	TM,Frizzled,Fz	frizzled (Drosophila) homolog 6	2.7
10	446839	BE091926	Hs.16244	TM	mitotic spindle coiled-coil related prote	2.7
	416250	AA581386	Hs.73452	TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Claudin	hypothetical protein MGC10791	2.7
	407287	AI678812		TM,rascadherin	gb:tu59d08.x1 NCL_CGAP_Gas4 Homo sapiens	2.7
	412977	AA125910	Hs.191461	TGF-beta	ESTs	2.7
	400298	AA032279	Hs.61635	TM	six transmembrane epithelial antigen of t	2.7
15	425483	AF231022	Hs.158159	EGF,cadherin,laminin_G	FAT tumor suppressor (Drosophila) homolog	2.7
	430152	AB001325	Hs.234642	SS,TM,MIP	aquaporin 3	2.7
	444006	BE395085	Hs.10086	SS,TM	type I transmembrane protein Fn14	2.7
	418869	AW516565		TM,RasGAP,IQ,WW	gb:xq01d05.x1 Soares_NHCeC_cervical_tumor	2.7
	416658	U03272	Hs.79432	SS,TM,EGF,TB	fibrillin 2 (congenital contractual arac	2.6
20	410290	AA402307	Hs.322844	SS,TM,Sema,TIG,Plexin_repeat	hypothetical protein DKFZp564A176	2.6
	419667	AU077005	Hs.92208	SS,TM,disintegrin,Repolyisin,Pep_M12B_propep	a disintegrin and metalloproteinase domai	2.6
	406671	AA129547	Hs.285754	TM,pkinase,Plexin_repeat,Sema,TIG,LIM	met proto-oncogene (hepatocyte growth fac	2.6
	434444	AI765276	Hs.101257	TM	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	TM,ABC_tran,ABC_membrane,Rhomboid	ATP-binding cassette, sub-family C (CFTR/	2.6
25	431890	X17033	Hs.271986	vwa,FG-GAP,integrin_A	integrin, alpha 2 (CD49B, alpha 2 subunit	2.6
	452281	T93500	Hs.28792	TGF-beta,TGFB_propeptide	Homo sapiens cDNA FLJ11041 fls, clone PLA	2.6
	421506	BE302796	Hs.105097	TM,TK	thymidine kinase 1, soluble	2.6
	453331	AI240665	Hs.8895	TM,disintegrin,Pep_M12B_propep,Repolyisin	ESTs	2.6
	447197	R36075		TM,SDF	gb:yh88b01.s1 Soares_placenta Nb2HP Homo	2.5
30	459688	U72671	Hs.151250	SS,TM,ig	intercellular adhesion molecule 5, telenc	2.5
	437412	BE069288	Hs.34744	TM,ABC_tran,ABC_membrane,Rhomboid	Homo sapiens mRNA; cDNA DKFZp547C136 (fro	2.5
	429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
	424420	BE614743	Hs.146688	TM,MAPEG	prostaglandin E synthase	2.5
	427239	BE270447	Hs.174070	TM,UQ_con	ubiquitin carrier protein	2.5
35	407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170	2.5
	431130	NM_006103	Hs.2719	SS,TM,wap	epididymis-specific, whey-acidic protein	2.5
	453379	AA035261	Hs.61753	PAN,kringle,trypsin	ESTs	2.5
	421733	AL119671	Hs.1420	SS,TM,ig,pkinase	fibroblast growth factor receptor 3 (acho	2.5
	452220	BE158006	Hs.212296	TM,integrin_A,FG-GAP	ESTs	2.5
40	417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	2.5
	440381	AA917808	Hs.190495	TM	ESTs	2.5
	441794	AW197794	Hs.253338	TM	ESTs	2.5
	439108	AW163034	Hs.6467	SS,TM	synaptogyrin 3	2.5
	401103	NA		TM,vwd	C12001233:gil7305361[ref NP_038652.1] oto	2.4
45	430630	AW269920	Hs.2621	TM,cystatin	cystatin A (stefin A)	2.4
	430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
	415621	AI648602	Hs.55468	TM,histone,Sec1sugar_tr	ESTs	2.4
	402745			SS,TM,EGF,ldl_recepLb,thyroglobulin_1	NM_002508:Homo sapiens nidogen (enactin)	2.4
	407758	D50915	Hs.38365	SS,TM	KIAA0125 gene product	2.4
50	457570	AA579426		TM	gb:nf37c09.s1 NCL_CGAP_Pr2 Homo sapiens c	2.4
	429574	BE268321	Hs.208912	SS,TM	hypothetical protein MGC861	2.4
	431211	M86849	Hs.323733	SS,TM,connexin	gap junction protein, beta 2, 26kD (conne	2.4
	452865	AI924046	Hs.119567	SS,TM,PMP22_Claudin	ESTs, Weakly similar to A47582 B-cell gro	2.4
	420511	AF052692	Hs.98485	SS,TM,connexin	gap junction protein, beta 3, 31kD (conne	2.4
55	437897	AA770561	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969	2.4
	437846	AA773866	Hs.244569	TM	esophagus cancer-related gene-2	2.4
	418432	M14156	Hs.85112	Insulin	insulin-like growth factor 1 (somatomedin	2.3
	438108	AI471795	Hs.287776	TM	vanilloid receptor-related osmotically ac	2.3
	453406	AI192987	Hs.61784	pkinase,Furin-like,Recep_L_domain	hypothetical protein FLJ14451	2.3
60	435542	AA687376	Hs.269533	pkinase,RhoGEF,ig,PH,SH3	ESTs	2.3
	434517	AA635690	Hs.337251	TM	hypothetical protein MGC2487	2.3
	431630	NM_002204	Hs.265829	SS,TM,FG-GAP,integrin_A	integrin, alpha 3 (antigen CD49C, alpha 3	2.3
	422310	AA316622	Hs.98370	SS,TM,fn3,ig,pkinase,Ribosomal_L36e,p450	cytochrome P450, subfamily IIS, polypepti	2.3
	441954	AI744935	Hs.8047	TM,Band_7,AAA,cdc48_N	Fanconi anemia, complementation group G	2.3
65	416091	AF295370	Hs.283082	SS,TM,Defensin_beta	defensin, beta 3	2.3
	429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membrane-ins	2.3
	409402	AF208234	Hs.695	TM,cystatin	cystatin B (stefin B)	2.3
	432284	AA532807	Hs.105822	TM,pkinase	ESTs	2.3
	408243	Y00787	Hs.624	SS,TM,IL8	interleukin 8	2.3
70	423229	AC003965	Hs.125532	SS,trypsin	protease, serine, 26	2.3
	408713	NM_001248	Hs.47042	GDA1_CD39	ectonucleoside triphosphate diphosphohydr	2.3
	440502	AI824113	Hs.78281	RGS,GoLoco,RBD	regulator of G-protein signalling 12	2.3
	429929	AB014583	Hs.226275	TM	KIAA0683 gene product	2.3
	439963	AW247529	Hs.6793	TM,p450Ets	platelet-activating factor acetylhydrolas	2.3
75	428953	AA306610	Hs.194676	SS,TM,TNFR_c6,arf,Statthmin,DEAD	tumor necrosis factor receptor superfamil	2.2
	439398	AA284267	Hs.221504	SS	ESTs	2.2
	440371	BE268550	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.2
	452203	X57522	Hs.158164	SS,TM,ABC_tran,ABC_membrane	transporter 1, ATP-binding cassette, sub-	2.2
80	407811	AW190902	Hs.40098	SS	cysteine knot superfamily 1, BMP antagoni	2.2
	432078	BE314877	Hs.24553	TM	hypothetical protein FLJ12541 similar to	2.2
	429113	D28235	Hs.196384	SS,TM,EGF	prostaglandin-endoperoxide synthase 2 (pr	2.2
	452755	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypothetic	2.2
	428434	AW363590	Hs.65551	SS	Homo sapiens, Similar to DNA segment, Chr	2.2
	429922	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0	2.2

5	417903	NM_002342	Hs.1116	SS,TM,ASC,TNFR_c6	lymphotoxin beta receptor (TNFR superfami	2.2
	422012	AW403423	Hs.110746	SS,homeobox,pou	HCR (a-helix coiled-coil rod homologue)	2.2
	433090	AI720050	Hs.145362	SS,TM	immortalization-upregulated protein	2.2
	417576	AA339449	Hs.82285	TM,AIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltransfera	2.2
	409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor; SREC	2.2
	417433	BE270266	Hs.82128	SS,TM,LRRCT,LRRNT,LRR	5T4 oncofetal trophoblast glycoprotein	2.2
	416763	AI908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators of di	2.2
	425999	AW513051	Hs.332981	TM,FAD_binding_2,P53PA,Ribosomal_S2,FAD_bindi	ESTs, Weakly similar to I38022 hypothetic	2.2
10	452799	AI948829	Hs.213786	TM	ESTs	2.2
	414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficient (S.	2.2
	448153	Y10805	Hs.20521	SS,TM,Na_Ca_Ex	HMT1 (hnRNP methyltransferase, S. cerevis	2.2
	428969	AF120274	Hs.194689	SS	artemin	2.2
	443171	BE281128	Hs.9030	SS,TM,7tm_1,rm	TONDU	2.2
15	408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
	409533	AW969543	Hs.21291	TM	mitogen-activated protein kinase kinase k	2.2
	408201	AK000568	Hs.43654	TM	hypothetical protein FLJ20561	2.1
	408996	AI979168	Hs.82226	TM	glycoprotein (transmembrane) nmb	2.1
	417900	BE250127	Hs.82906	TM,WD40,pro_isomerase	CDC20 (cell division cycle 20, S. cerevis	2.1
20	437191	NM_006846	Hs.331555	SS,TM,kazal	serine protease inhibitor, Kazal type, 5	2.1
	412834	R77123	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	2.1
	431117	AF003522	Hs.250500	SS,TM,DSL,EGF	delta (Drosophila)-like 1	2.1
	447674	BE270640	Hs.19192	TM,kinaseras,arf	cyclin-dependent kinase 2	2.1
	409651	H96643	Hs.283565	bZIPcofilin_ADF,EGF	FOS-like antigen-1	2.1
25	440495	AA887212	Hs.14161	TM,NSFNa_Ca_Ex	hypothetical protein DKFZp434I1930	2.1
	429415	NM_002593	Hs.202097	SS,CUB,NTR,MAM,TIL,TiLa,vwd,EPO_TPO	procollagen C-endopeptidase enhancer	2.1
	421013	M62397	Hs.1345	TM	mutated in colorectal cancers	2.1
	447827	U73727	Hs.19718	SS,TM,Y_phosphatase,fn3,ig,MAM	protein tyrosine phosphatase, receptor ty	2.1
	449224	AW995911	Hs.299883	fn3	hypothetical protein FLJ23399	2.1
30	452679	Z42387	Hs.83883	TM	transmembrane, prostate androgen induced	2.1
	409956	AW103364	Hs.727	SS,TGF-beta,TGFB_propeptide	inhibin, beta A (activin A, activin AB al	2.1
	438580	AA811262	Hs.299202	TM,kinasesugar_tr	ESTs	2.1
	406400			SS,TM,trypsin	NM_007196:Homo sapiens kallikrein 8 (neur	2.1
	424965	AW956282	Hs.144609	TM	Homo sapiens, Similar to RIKEN cDNA 57305	2.1
35	412270	AC005262	Hs.73797	TM,G-alpha	guanine nucleotide binding protein (G pro	2.1
	428471	X57348	Hs.184510	TM,14-3-3	stratifin	2.1
	427375	AL035460	Hs.177536	SS,Zn_carbOpept,hormone5Reprolysin	metallocarboxypeptidase CPX-1	2.1
	416498	U33632	Hs.79351	TM	potassium channel, subfamily K, member 1	2.1
	423453	AW450737	Hs.128791	SS,Granin,CDP-OH_P_transf	CGI-09 protein	2.1
40	417944	AU077196	Hs.82985	SS,COLFI,Collagen,vwc	collagen, type V, alpha 2	2.1
	424197	AF096834	Hs.142989	SS,TM,CSD	germ cell specific Y-box binding protein	2.1
	446163	AA026880	Hs.25252	TM,fn3	prolactin receptor	2.1
	417331	AW411297	Hs.81972	TM,SH2,PID	SHC (Src homology 2 domain-containing) tr	2.1
	430413	AW842182	Hs.241392	IL8,PX	small inducible cytokine A5 (RANTES)	2.1
45	421685	AF189723	Hs.106778	TM,E1-E2_ATPase,HydrolaseE1-E2_ATPase	ATPase, Ca transporting, type 2C, member	2.1
	407305	AA715284		TM,kinase,Sema,Plaxin_repeat,TIG,LIM	gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens c	2.1
	407792	AI077715	Hs.39384	SS	putative secreted ligand homologous to fj	2.0
	418695	AA447014	Hs.193261	SS	hypothetical protein MGC2991	2.0
	439738	BE246502	Hs.9598	TM,RasGAP,IQ,VW	sema domain, immunoglobulin domain (Ig),	2.0
50	433398	AW843150	Hs.112412	TM,PMP22_Claudin	ESTs	2.0
	456327	H68741	Hs.38774	TM,Glyco_transf_8	ESTs	2.0
	446872	X97058	Hs.16362	TM	pyrimidinergic receptor P2Y, G-protein co	2.0
	419726	U50330	Hs.1274	SS,TM,Astacin,CUB,EGF	bone morphogenetic protein 1	2.0
	410116	AW630671	Hs.58636	SS,TM	squamous cell carcinoma antigen recognize	2.0
55	426500	NM_014638	Hs.170156	TM	KIAA0450 gene product	2.0
	452194	AI694413	Hs.332649	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily I	2.0
	418140	BE613836	Hs.83551	TM,E1-E2_ATPase	microfibrillar-associated protein 2	2.0
	425855	AF135025	Hs.159679	SS,trypsin	kallikrein 12	2.0
	434346	AA630445	Hs.116773	TM,Ferric_reduct	ESTs	2.0
	426274	D38122	Hs.2007	TM,TNF	tumor necrosis factor (ligand) superfamil	2.0
60	440008	AW051683	Hs.277686	TM,RhoGEF,FYVE,PH	ESTs	2.0
	424634	NM_003613	Hs.151407	ig,tsp_1	cartilage intermediate layer protein, nuc	2.0
	446641	AL049229	Hs.15787	TM,kinase,rm	Homo sapiens mRNA; cDNA DKFZp564O1016 (fr	2.0
	418851	AI417828	Hs.192435	TM	ESTs	2.0
65	440351	AF030933	Hs.7179	TM,Rad1,Cadherin_C_term	RAD1 (S. pombe) homolog	2.0
	439496	BE616501	Hs.32343	SS	Homo sapiens, Similar to RIKEN cDNA 11100	2.0
	454197	BE140966		TM,Ammonium_transpkinasin,Ammonium_transp	gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
	433573	AF234887	Hs.57652	TM,7tm_2,GPSIRNA-synt_2b,Seryl_tRNA_N	cadherin, EGF LAG seven-pass G-type recep	2.0
	429211	AF052693	Hs.198249	TM,connexin	gap junction protein, beta 5 (connexin 31	2.0
70	420737	L08096	Hs.99899	SS,TM,TNF	tumor necrosis factor (ligand) superfamil	2.0
	455333	AW897851		TM,Glyco_hydro_2	gb:RC1-NN0063-100500-022-c08 NN0063 Homo	2.0
	414784	NM_000344	Hs.288986	SS,TM,BIR	survival of motor neuron 1, telomeric	2.0
	435836	AW292532	Hs.250175	TM,GNS1_SUR4	homolog of yeast long chain polyunsaturat	2.0
	411789	AF245505	Hs.72157	TM,ig,LRRCT	DKFZP564I1922 protein	2.0
	441455	AJ271671	Hs.7854	TM,ras,DENN	zinc/iron regulated transporter-like	2.0
75	426068	AF029778	Hs.166154	SS,TM,DSL,EGF,NUDIX	jagged 2	2.0
	439733	AL365412	Hs.107203	TM,Sm	hypothetical protein from EUROIMAGE 17593	2.0
	435014	BE560898	Hs.10026	TM,Ribosomal_L17	mitochondrial ribosomal protein L17	1.9
	457819	AA057484	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	1.9
80	422737	M26939	Hs.119571	SS,Collagen,COLFI	collagen, type III, alpha 1 (Ehlers-Danlo	1.9
	431104	AW970859	Hs.313503	Sema,ig	ESTs	1.9
	432210	AI567421	Hs.273330	TM,laminin_G,laminin_EGF,kazalubiquitin	Homo sapiens, clone IMAGE:3544662, mRNA,	1.9
	436511	AA721252	Hs.291502	TM,disintegrin,Reprolysin,Pep_M12B_propep,kinase,	ESTs	1.9
	419216	AU076718	Hs.164021	SS,IL8	small inducible cytokine subfamily B (Cys	1.9

	432169	Y00971	Hs.2910	TM,Pribosyltran	phosphoribosyl pyrophosphate synthetase 2	1.9
	441128	AA570256	Hs.54628	TM,ras	ESTs, Weakly similar to T23273 hypothetic	1.9
	447160	AA330310	Hs.24181	TM	ESTs	1.9
5	419138	U48508	Hs.89631	TM,RYDR_ITPR,RyR,SPRY	ryanodine receptor 1 (skeletal)	1.9
	457817	AA247751	Hs.79572	TM,hemopexin,Peptidase_M10	calhepsin D (lysosomal aspartyl protease)	1.9
	431009	BE149762	Hs.48956	SS,TM,connexin	gap junction protein, beta 6 (connexin 30)	1.9
	428957	NM_003881	Hs.194679	SS,TM,vwc,IGFBP,tsp_1	WNT1 inducible signaling pathway protein	1.9
	418546	AA224827		TM,vwa,FG-GAP,integrin_A	gb:nc32g04.s1 NCL_CGAP_Pr2 Homo sapiens c	1.9
10	400749			SS,TM,ldl_recept_a,fn3,ldl_recept_b	NM_003105*:Homo sapiens sortilin-related	1.9
	408369	R38438	Hs.182575	F-protein	solute carrier family 15 (H???) transporte	1.9
	422765	AW409701	Hs.1578	TM,BIR	baculoviral IAP repeat-containing 5 (surv	1.9
	417409	BE272506	Hs.82109	TM,Syndecan	syndecan 1	1.9
	407720	AB037776	Hs.38002	TM,calponin,CH	KIAA1355 protein	1.9
15	418830	BE513731	Hs.88959	TM,CDP-OH_P_transf,MCM	hypothetical protein MGC4816	1.9
	434769	AA648884	Hs.134278	TM,CDP-OH_P_transf,MCM	Homo sapiens cDNA FLJ12676 fis, clone NT2	1.9
	421593	NM_017436	Hs.105956	SS,TM	globotriaosylceramide/CD77 synthase; Gb3/	1.9
	426064	BE387014	Hs.166146	TM,WH1	Homer, neuronal immediate early gene, 3	1.9
	404604	NA		TM	Target Exon	1.9
20	422753	AI928995	Hs.1575	SS,TM,Sm	small nuclear ribonucleoprotein D3 polype	1.9
	422739	H20106	Hs.119591	SS,ClaI_adaptor_s	adaptor-related protein complex 2, sigma	1.9
	433068	NM_006456	Hs.288215	SS,Pribosyltran	sialyltransferase	1.9
	419594	AA013051	Hs.91417	TM	topoisomerase (DNA) II binding protein	1.9
	428188	M98447	Hs.22	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 1 (K polypeptide epiderm	1.9
25	428343	AL043021	Hs.12705	TM,Rhomboid,HMG_boxTPR	ESTs	1.9
	429592	AB029041	Hs.209646	Troponin	KIAA1118 protein	1.9
	431620	AA126109	Hs.264981	C2,PH,RasGAP,NTP_transf_2	2'-5'-oligoadenylate synthetase 2 (69-71	1.9
	424670	W61215	Hs.116651	ig	epithelial V-like antigen 1	1.9
	428373	AI751656	Hs.183986	SS,TM,ig	poliovirus receptor-related 2 (herpesviru	1.9
30	453449	W16752	Hs.32981	SS,ig,Sema	sema domain, immunoglobulin domain (Ig),	1.9
	432304	AA932186	Hs.69297	TM,7tm_1	ESTs	1.9
	432673	AB028859	Hs.278605	TM,DnaJ,DnaJ_CDnaJ	DnaJ (Hsp40) homolog, subfamily B, member	1.9
	416207	NM_014745	Hs.336433	SS,TM,zf-DHHC	Homo sapiens, clone MGC:2908, mRNA, compl	1.9
	408988	AL119844	Hs.49476	TM,Plexin_repeat,Sema,tsp_1	Homo sapiens clone TUA8 Cri-du-chat regio	1.9
35	417426	NM_002291	Hs.82124	SS,laminin_EGF,laminin_Nterm	laminin, beta 1	1.9
	443883	AA114212	Hs.9930	SS,TM,serpin,Marek_A	serine (or cysteine) proteinase inhibitor	1.9
	433328	AW298159	Hs.23644	SS,TM	ESTs, Weakly similar to S65824 reverse tr	1.9
	419981	AA897581	Hs.128773	TM,Skl_Sno	ESTs	1.8
	420931	AF044197	Hs.100431	SS,TM,IL8	small inducible cytokine B subfamily (Cys	1.8
40	415023	AA932146	Hs.133494	TM,Ribosomal_S17Ribosomal_L13	Homo sapiens clone TCCCA00164 mRNA seque	1.8
	413644	BE154910	Hs.278793	TM,Glyco_hydro_2	ESTs, Weakly similar to Z195_HUMAN ZINC F	1.8
	449987	AW079749	Hs.184719	TM,ABC_tran,ABC_membraneion_trans	ESTs, Weakly similar to ALU1_HUMAN ALU SU	1.8
	421340	F07783	Hs.1369	SS,sushi	decay accelerating factor for complement	1.8
	417866	AW067903	Hs.82772	SS,TM,Collagen,COLFI,TSPN	collagen, type XI, alpha 1	1.8
45	430259	BE550182	Hs.127826	TM,transmembrane4RasGEF,RA	RalGEF-like protein 3, mouse homolog	1.8
	432998	AA835948	Hs.153307	TM,SDF	ESTs	1.8
	431671	NM_016937	Hs.267289	TM,NA	polymerase (DNA directed), alpha	1.8
	411773	NM_006799	Hs.72026	trypsin	protease, serine, 21 (testisin)	1.8
	425247	NM_005940	Hs.155324	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 11 (stromelysin	1.8
50	422976	AU076657	Hs.1600	TM,cpn60_TCP1,Sema	chaperonin containing TCP1, subunit 5 (ep	1.8
	425159	NM_004341	Hs.154868	SS,TM,GATase,OTCace,CPSase_L_chain,Dihydrooro	carbamoyl-phosphate synthetase 2, asparta	1.8
	447776	AI525625	Hs.130181	Ricin_B_lectin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.8
	426908	AW815163	Hs.172851	SS,TM,fusion_gly,Myosin_tailadh_short	arginase, type II	1.8
	408116	AA251393	Hs.289052	TM,Na_Ca_ExCam_acyltransf	Homo sapiens, Similar to RIKEN cDNA 54304	1.8
55	417847	AI521558	Hs.7331	Uteroglobulin	hypothetical protein FLJ22316	1.8
	415791	H09366	Hs.78853	SS,TM,UNG	uracil-DNA glycosylase	1.8
	407903	AI287341	Hs.154029	TM,ubiquitin,laminin_G,laminin_EGF,kazal	bHLH factor Hes4	1.8
	422511	AU076442	Hs.117938	TM,p450	collagen, type XVII, alpha 1	1.8
	414117	W88559	Hs.1787	TM,ion_trans,K_tetra	proteolipid protein 1 (Pelizaeus-Merzbach	1.8
60	426841	AI052358	Hs.193726	TM,asp	ESTs	1.8
	415272	AA164215	Hs.203186	TM,TPR,pkinase,Ig,B56	ESTs	1.8
	426440	BE382756	Hs.169902	TM,sugar_tr,Fork_head	solute carrier family 2 (facilitated gluc	1.8
	419488	AA316241	Hs.90691	FGF	nucleophosmin/nucleoplasm 3	1.8
	418452	BE379749	Hs.85201	SS,TM,lectin_c	C-type (calcium dependent, carbohydrate-r	1.8
65	431363	M86528	Hs.266902	SS,NGF	neurotrophin 5 (neurotrophin 4/5)	1.8
	440975	AW499914	Hs.7579	SS,TM	hypothetical protein FLJ10402	1.8
	438962	BE046594		TGF-beta,bZIP	gb:hn41c11.x1 NCL_CGAP_RDF2 Homo sapiens	1.8
	414602	AW630088	Hs.76550	SS	Homo sapiens mRNA; cDNA DKFZp564B1264 (fr	1.8
70	418054	NM_002318	Hs.83354	TM,mito_carr,Lysyl_oxidase	lysyl oxidase-like 2	1.8
	440501	AA887391	Hs.202229	TM,Galactosyl_T	ESTs	1.8
	449309	AW589823	Hs.224189	TM	ESTs	1.8
	421461	AW291023	Hs.97255	TM,Lysyl_oxidase,SCP2,Band_7	ESTs, Weakly similar to A46010 X-linked r	1.8
	412584	X54870	Hs.74085	TM,lectin_c	DNA segment on chromosome 12 (unique) 248	1.8
	441565	AW953575	Hs.303125	TM	p53-induced protein PIGPC1	1.8
75	431837	T79326	Hs.326553	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily I	1.8
	436251	BE515065	Hs.296585	SS,Y_phosphataseTIG	nucleolar protein (KKE/D repeat)	1.8
	448633	AA311426	Hs.21635	TM,EGF,laminin_G,fibrinogen_C,F5_F8_type_C,tubulin	tubulin, gamma 1	1.8
	424291	AL120051	Hs.144700	TM,Ephrin,Hist_deacetyl	ephrin-B1	1.8
	415388	AF018081	Hs.78409	SS,TM,TSPN,Collagen	collagen, type XVIII, alpha 1	1.8
80	435550	AI224456	Hs.4934	TM,LRR,LRRCT	H.sapiens polyA site DNA	1.8
	448568	AA149121	Hs.71947	TM,LRRCT	ESTs	1.8
	439246	AI498072	Hs.77783	SS,TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Cla	membrane-associated tyrosine- and threoni	1.8
	410001	AB041036	Hs.57771	SS,TM,trypsin	kallikrein 11	1.8
	417312	AW888411	Hs.81915	SS,Stathmin	leukemia-associated phosphoprotein p18 (s	1.8

	444152	AI125694	Hs.149305	TM	hypothetical protein MGC2603	1.8
	453454	AW052006	Hs.8551	TM	PRP4/STK/WD splicing factor	1.8
	449320	AB030835	Hs.23476	SS,adenylatekinase	Cip1-interacting zinc finger protein	1.8
5	428329	AA426091	Hs.98453	TM,Gal-bind_lectin	ESTs, Moderately similar to R27328 2 [H.s	1.8
	452875	BE275760	Hs.30928	TM,Apolipoproteinig	DNA segment on chromosome 19 (unique) 117	1.8
	444031	BE271513	Hs.25303	TM,Peptidase_M10,hemopexin	hypothetical protein FLJ13154	1.8
	443534	AI076123		TM	gb:oy92e04.x1 Soares_fetal_liver_spleen_1	1.8
	413313	NM_002047	Hs.75280	TM,WHEP-TRS,7tm_2	glycyl-IRNA synthelase	1.8
10	452874	AK001061	Hs.30925	SS	hypothetical protein FLJ10199	1.8
	453140	AA032238	Hs.170531	TM	ESTs	1.8
	418641	BE243136	Hs.86947	SS,TM,disintegrin,Pep_M12B_propep,Repolyisin	a disintegrin and metalloproteinase domai	1.8
	432925	AA878324	Hs.192734	SS	ESTs	1.8
	453857	AL080235	Hs.35861	TM	DKFZP586E1621 protein	1.8
15	457663	AW371946	Hs.337459	TM	ESTs	1.8
	452873	AK001247	Hs.30922	TM	hypothetical protein FLJ10385	1.8
	436396	AI683487	Hs.152213	SS,wnt	wingless-type MMTV integration site famil	1.8
	452835	AK001269	Hs.30738	TM	hypothetical protein FLJ10407	1.7
	459647	R34107	Hs.198287	ig	pregnancy specific beta-1-glycoprotein 11	1.7
20	418245	AA088767	Hs.83883	TM,PEPCK	transmembrane, prostate androgen induced	1.7
	448484	BE613340	Hs.334725	TM	Homo sapiens, Similar to RIKEN cDNA 94300	1.7
	431369	BE184455	Hs.251754	SS,wap	secretory leukocyte protease inhibitor (a	1.7
	434877	AW974792	Hs.292171	TM	ESTs	1.7
	428923	BE047698	Hs.188785	TM	ESTs	1.7
25	402915	NA		TM,HCO3_cotransp	ENSP00000202587*:Bicarbonate transporter-	1.7
	420185	AL044056	Hs.158047	TM	ESTs	1.7
	445739	AW136354	Hs.145303	TM	ESTs	1.7
	409435	AI810721	Hs.95424	TM,p450	ESTs	1.7
	408688	AI634522	Hs.152925	TM	KIAA1268 protein	1.7
30	420085	AI741909	Hs.44680	TM	hypothetical protein FLJ20979	1.7
	433933	AI754389	Hs.133494	TM,Ribosomal_S17Ribosomal_L13	Homo sapiens clone TCCCA00164 mRNA seque	1.7
	430965	AA489732	Hs.154918	hormone_rec,Prog_receptor,zf-C4	ESTs	1.7
	414703	BE243877	Hs.76941	SS,TM,Na_K-ATPaseE2F_TDP	ATPase, Na? transporting, beta 3 polypept	1.7
	423464	NM_016240	Hs.128856	TM,Collagen	CSR1 protein	1.7
35	416737	AF154335	Hs.79691	SS,TM,LIM,PDZsugar_tr,PDZ,LIM	LIM domain protein	1.7
	409012	AL117435	Hs.49725	TM,RhoGEFzf-DHHC,adh_short	DKFZP434I216 protein	1.7
	423804	AW403448	Hs.1706	TM,IRF	interferon-stimulated transcription facto	1.7
	410418	D31382	Hs.63325	SS,TM,trypsin,Idl_recept_a	transmembrane protease, serine 4	1.7
	440028	AW473675	Hs.125843	TM	ESTs, Weakly similar to T17227 hypothetic	1.7
40	457646	AA725650	Hs.112948	TM,SPRY	ESTs	1.7
	445439	BE243084	Hs.12719	SS,TGF-beta	regulator of nonsense transcripts 1	1.7
	420426	AA262045	Hs.36567	TM,Galactosyl_T_2ATP-synt_C	Homo sapiens cDNA FLJ14227 fis, clone NT2	1.7
	431341	AA307211	Hs.251531	TM,proteasome	proteasome (prosome, macropain) subunit,	1.7
	412338	AA151527	Hs.69485	TM,Sema,Plexin_repeatTIG,Plexin_repeat	hypothetical protein FLJ12436	1.7
45	414799	AI752416	Hs.77326	SS,thyroglobulin_1,IGFBP	insulin-like growth factor binding protei	1.7
	452700	AI859390	Hs.288940	TM,DIX,RGS,thiod	five-span transmembrane protein M83	1.7
	430877	NM_005269	Hs.2693	GST_C,IRNA-synt_1,WHEP-TRS,TGF-beta	glioma-associated oncogene homolog (zinc	1.7
	428624	AI125222	Hs.98712	TM,thiod,Y_phosphatase,MAM,ig,fn3MSP_domain	hypothetical protein DKFZp434H0311	1.7
	444065	AW449415	Hs.10260	TM,ion_trans	Homo sapiens cDNA FLJ11341 fis, clone PLA	1.7
50	416319	AI815601	Hs.79197	SS,TM,ig	CD83 antigen (activated B lymphocytes, im	1.7
	429367	AB007867	Hs.278311	Sema,Plexin_repeat,TIG	plexin B1	1.7
	430425	AA531428	Hs.241412	TM	apolipoprotein L, 2	1.7
	441668	AI611973	Hs.127525	TM,Ammonium_transp	ESTs	1.7
	418469	U34879	Hs.85279	SS,TM,adh_short	hydroxysteroid (17-beta) dehydrogenase 1	1.7
55	450835	BE262773	Hs.25584	TM,ArfGap	hypothetical protein FLJ10767	1.7
	418859	AA229558		TM	gb:nc15d10.s1 NCL_CGAP_Pr1 Homo sapiens c	1.7
	425304	AA463844	Hs.31339	TM,ig,ITAM	fibroblast growth factor 11	1.7
	423635	X85019	Hs.130181	TM,Ricin_B_lectin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.7
	414820	AA371931	Hs.77422	TM,ion_trans,LIM,Synaptophysin	proteolipid protein 2 (colonic epithelium	1.7
60	440654	AW014242	Hs.159998	TM,connexin	ESTs	1.7
	412276	BE262621	Hs.73798	SS,MIF	macrophage migration inhibitory factor (g	1.7
	422087	X58968	Hs.111301	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 2 (gelatinase A,	1.7
	407151	H25836	Hs.301527	SS,TNF	ESTs, Moderately similar to unknown [H.sa	1.7
	410726	AI623859	Hs.15936	TM,PX	ESTs	1.7
65	452012	AA307703	Hs.279766	TM,kinesin	kinesin family member 4A	1.7
	433627	AF078866	Hs.284296	TM,SURF4,SURF1,DEADlipocalin	Homo sapiens cDNA: FLJ22993 fis, clone KA	1.7
	409220	BE243323	Hs.51233	TM,death,TNFR_c6	tumor necrosis factor receptor superfamil	1.7
	427082	AB037858	Hs.173484	TM,mito_carr	hypothetical protein FLJ10337	1.7
	426410	BE298446	Hs.305890	TM,Bcl-2,BH4	BCL2-like 1	1.7
70	433598	AI762836	Hs.271433	TM,Cytidylyltransf,SIR27tm_2	ESTs, Moderately similar to ALU2_HUMAN AL	1.7
	436495	BE258948	Hs.290874	TM,Armadillo_seg	ESTs, Weakly similar to ALU8_HUMAN ALU SU	1.7
	422032	AA476966	Hs.110857	TM,TFIIS,RNA_POL_M_15KDserpin,hormone_rec,zf-C4	polymerase (RNA) III (DNA directed) polyp	1.7
	429736	AF125304	Hs.212680	SS,TNFR_c6	tumor necrosis factor receptor superfamil	1.7
	427600	AW630918	Hs.179774	TM,Transglutamin_C,Transglutamin_N,Transglut_core	proteasome (prosome, macropain) activator	1.7
75	431981	AA664069	Hs.115779	laminin_B,laminin_EGF	ESTs	1.7
	407736	N41744	Hs.19978	TM,Sulfatase	CGI-30 protein	1.7
	420187	AK001714	Hs.95744	TM	hypothetical protein similar to ankyrin r	1.7
	424620	AA101043	Hs.151254	SS,TM,trypsin	kallikrein 7 (chymotryptic, stratum come	1.7
	430488	D19589	Hs.13453	TM	hypothetical protein FLJ14753	1.7
80	423393	R37772	Hs.21420	TM,thiodpk kinase	p21-activated protein kinase 6	1.7
	444051	N48373	Hs.10247	SS,ig		

TABLE 13B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
408344	105240_1	AA053843 BE162213
418546	176677_1	AA224827 T59708 T59843 BE156903
418859	179717_1	AA229558 AA345492 AA229582
418869	179863_1	AW516565 AA229762 AA230035
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875
		AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
		AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062
		AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642
		AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499
		AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996
		AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531
		H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
438962	467390_1	BE046594 BE046667 AA828585 AI207343
443534	572957_1	AI076123 AI244834 AI695239
447197	711623_1	R36075 AI366546 R36167
454197	1050392_1	BE140966 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969
		BE141673 BE141650 BE141674 BE141550 BE141688 AW178241 BE140994 BE141666 BE140998 BE141008 BE140988 BE141011 BE140975
		BE141667 BE141675 BE141657 BE141681 BE141656 BE141672 BE141680 AW178237 BE141012 BE140990 BE141658 BE141648 BE141013
		BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646
		BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671
		AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141556
455333	1281044_1	AW897851 AW897852
457570	357443_1	AA579426 AA579436 AA573735

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400666	8118496	Plus	17982-18115,20297-20456
400749	7331445	Minus	9162-9293
401103	8568122	Minus	98330-98449
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
401575	7229804	Minus	76253-76364
402745	9212200	Minus	76516-76690
402915	7406502	Minus	140-276
404440	7528051	Plus	80430-81581
404604	9212537	Minus	72019-72509
405545	1054740	Plus	118677-118807,119091-119296,121626-121823
405547	1054740	Plus	124361-124520,124914-125050
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406467	9795551	Plus	182212-182958

TABLE 14A: 209 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES THAT ARE LIKELY TO ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES

Table 14A lists about 209 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 12A, except that the ratio was greater than or equal to 2.0, and the 96<sup>th</sup> percentile value amongst cervical cancers was greater than or equal 40 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulatable by small molecules (e.g. pkinase, peptidase, phosphatase, ATPase, or ion\_transporter domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
 ExAccon: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 PPDomains: Predicted Protein Domains  
 Unigene Title: Unigene gene title  
 R1: Ratio of tumor to normal adult tissues

Pkey	ExAccon	UnigenelD	PPDomains	Unigene Title	R1
418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interst	38.9
439606	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87	28.8
400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (stroma	20.5
415817	U88967	Hs.78867	SS,TM,Y_phosphatase,carb_anhyd	protein tyrosine phosphatase, recep	16.4
416209	AA236776	Hs.79078	TM,HORMA	MAD2 (mitotic arrest deficient, yea	15.4
404996	NM_001333	Hs.87417	Peptidase_C1	CTSL2 Cathepsin L2	13.1

	428618	AA885360	Hs.160199	kinase	Target CAT	12.7
	429486	AF155827	Hs.203963	helicase_C,SNF2_Nhelicase_C	hypothetical protein FLJ10339	12.6
	419183	U60669	Hs.89663	p450	cytochrome P450, subfamily XXIV (vi	12.3
5	428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromel	10.2
	420759	T11832	Hs.127797	helicase_C	Homo sapiens cDNA FLJ11381 fis, clo	10.2
	458194	AW383618	Hs.265459	p450	ESTs, Moderately similar to ALU2_HU	9.4
	446232	AI281848	Hs.194691	TM,7tm_3Ribosomal_L13	retinoic acid induced 3	8.9
	424905	NM_002497	Hs.153704	TM,kinase	NIMA (never in mitosis gene a)-rela	8.9
10	452291	AF015592	Hs.28853	TM,kinase	CDC7 (cell division cycle 7, S. cer	8.7
	424086	AI351010	Hs.102267	Lysyl_oxidase	lysyl oxidase	8.3
	425710	AF030880	Hs.159275	TM,Sulfate_transp,STAS	solute carrier family, member 4	7.8
	433133	AB027249	Hs.104741	TM,Collagen,kinase	PDZ-binding kinase; T-cell original	7.4
	447254	NM_004153	Hs.17908	SS,AAA,BAH	origin recognition complex, subunit	7.1
15	431941	AK000106	Hs.272227	kinase,Furin-like,Recep_L_dom	Homo sapiens cDNA FLJ20099 fis, clo	6.9
	427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
	436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA	6.9
	403471	NA		SS,TM,trypsin	Target Exon	6.7
	410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
20	457405	AA504860		TM,7tm_2	gb:ab03a10.s1 Stratagene fetal reti	6.4
	421948	L42583	Hs.334309	filament,HCO3_cotranspfilament	keratin 6A	6.3
	439292	AA090421	Hs.5555	TM,AAA,Ferric_reduct	hypothetical protein MGC5347	5.8
	413625	AW451103	Hs.71371	TM,E1-E2_ATPase,Hydrolase	ESTs	5.8
	425695	NM_005401	Hs.159238	TM,Band_41,Y_phosphatase	protein tyrosine phosphatase, non-r	5.7
25	438394	BE379623	Hs.27693	SS,pro_isomerase	peptidylprolyl isomerase (cyclophil	5.6
	432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collag	5.5
	408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Cation_ATPa	ESTs	5.4
	432226	AW182766	Hs.273558	Cytidylyltransf	phosphate cytidylyltransferase 1, c	5.2
	419520	AB009303	Hs.90800	TM,hemopexin,Peptidase_M10	matrix metalloproteinase 16 (membra	5.1
30	426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutam	transglutaminase 3 (E polypeptide,	5.0
	421155	H87879	Hs.102267	SS,Lysyl_oxidase,Aldose_epim,E	lysyl oxidase	4.9
	423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrop	4.8
	450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep	a disintegrin and metalloproteinase	4.8
	418379	AA218940	Hs.137516	AAA	fidgetin-like 1	4.7
35	457465	AW301344	Hs.122908	Pribosyltran,Sulfatase	DNA replication factor	4.6
	412333	AW937485		TM,7tm_1	gb:QV3-DT0044-221299-045-b09 DT0044	4.6
	450510	AA010056	Hs.242998	DNA_topoisomII,DNA_topoisomVIGF	ESTs	4.6
	436291	BE568452	Hs.5101	abhydrolase	protein regulator of cytokinesis 1	4.6
	446353	AI290919	Hs.153661	HECTkinase	ESTs	4.5
40	435435	T89473	Hs.192328	lipase,PLAT	ESTs	4.5
	425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, iodothyronine, type II	4.4
	433322	H50621	Hs.134156	TM,ion_transNB-ARC,CARD_mito_c	ESTs, Weakly similar to I38022 hypo	4.4
	406908	BE296227	Hs.250822	TM,kinase	serine/threonine kinase 15	4.4
	444781	NM_014400	Hs.11950	PH,lactamase_B	GPI-anchored metastasis-associated	4.4
45	428479	Y00272	Hs.184572	kinase	cell division cycle 2, G1 to S and	4.2
	406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprot	4.2
	423035	AW449679	Hs.156739	TM,Glyco_transf_8	H.sapiens XG mRNA (clone PEP11)	4.2
	449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
	423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
50	457030	AI301740	Hs.173381	TM,Dihydroorotase	dihydropyrimidinase-like 2	4.1
	448995	AI613276	Hs.5662	adenylatekinase	guanine nucleotide binding protein	4.0
	415857	AA866115	Hs.127797	helicase_C	Homo sapiens cDNA FLJ11381 fis, clo	4.0
	438390	AI422017		TM,DSL,7tm_17tm_1	gb:tf45f12.x1 NCI_CGAP_Brn23 Homo s	4.0
	429900	AA460421	Hs.30875	kinase	ESTs	4.0
55	446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
	422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
	408771	AW732573	Hs.47584	TM,K_tetra,ion_trans	potassium voltage-gated channel, de	3.6
	424296	AI631874	Hs.155140	kinase	casein kinase 2, alpha 1 polypeptid	3.6
	436246	AW450963	Hs.119991	connexinhormone_rec,zf-C4	ESTs	3.5
60	411274	NM_002776	Hs.69423	trypsin	kallikrein 10	3.5
	400666			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metal	3.5
	426920	AA393351	Hs.132121	PDEase	ESTs	3.5
	412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Carn_acy	endothelial cell growth factor 1 (p	3.4
	430704	AW813091	Hs.335799	Epimerase	ESTs	3.4
65	455092	BE152428		Sulfatase	gb:CM0-HT0323-151299-126-b04 HT0323	3.4
	453775	NM_002916	Hs.35120	AAA,PI3_P14_kinase,PI3Ka,PI3K_	replication factor C (activator 1)	3.4
	438993	AA828995		integrin_B	gb:od77b08.s1 NCI_CGAP_Ov2 Homo sap	3.4
	426572	AB037883	Hs.170623	hormone_rec,zf-C4	hypothetical protein FLJ11183	3.4
	449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
70	427660	AI741320	Hs.114121	hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23228 fis, cl	3.3
	402481			TM,GDI,7tm_1	NM_001821*:Homo sapiens choroiderem	3.3
	414774	X02419	Hs.77274	SS,kringle,trypsin	plasminogen activator, urokinase	3.3
	412246	AI160873	Hs.69233	SulfotransferACOX	zinc finger protein	3.3
	418462	BE001596	Hs.85266	SS,TM,integrin_B,fn3	integrin, beta 4	3.3
75	424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatin	3.3
	401486	NA		SS,TM,trypsin	C4000647*:gil4758508[ref]NP_004253.	3.2
	408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, cl	3.2
	427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, cl	3.2
	402337			SS,p450	Target Exon	3.2
80	420930	AW888650		ribonuclease_T2	gb:CM4-NT0007-130500-551-f06 NT0007	3.2
	443426	AF098158	Hs.9329	kinase	chromosome 20 open reading frame 1	3.1
	439750	AL359053	Hs.57664	TM,integrin_B,Ricin_B_tectinrr	Homo sapiens mRNA full length inser	3.1
	420039	NM_004605	Hs.94581	CARD,SulfotransferDAGKc	sulfotransferase family, cytosolic,	3.0
	448733	NM_005629	Hs.187958	SS,TM,SNF,ABC_tran,isodh,pkina	solute carrier family 6 (neurotrans	3.0



	444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
	450841	AI741466	Hs.270515	pro_isomerase	ESTs	3.0
	428262	AI651324	Hs.7298	death,pkinase	biphenyl hydrolase-like (serine hyd	3.0
5	435399	AA679463		pkinase	gb:ac50c03.s1 Stratagene hNT neuron	2.9
	446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid	2.9
	449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN	2.9
	418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
	414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kin	ESTs	2.9
10	431629	AU077025	Hs.265827	SS,iRNA_antiSH2,SH3,pkinase	interferon, alpha-inducible protein	2.8
	445873	AA250970	Hs.251946	SS,rm,PABPpkinase,14-3-3,rm	poly(A)-binding protein, cytoplasmic	2.8
	438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
	422689	AW856665		helicase_C,SNF2_Nhelicase_C	gb:RC3-CT0297-290100-013-d03 CT0297	2.8
	439453	BE264974	Hs.6566	SS,AAA	thyroid hormone receptor interactor	2.8
15	413582	AW295647	Hs.71331	carb_anhydrase	hypothetical protein MGC5350	2.8
	410664	NM_006033	Hs.65370	TM,lipase,PLAT	lipase, endothelial	2.8
	456456	AA477609	Hs.89563	FBPase	nuclear cap binding protein subunit	2.8
	413273	U75679	Hs.75257	TM,lg,pkinase	stem-loop (histone) binding protein	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product	2.8
20	403763			TM,7tm_1	NM_001059*:Homo sapiens tachykinin	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor	diubiquitin	2.7
	401230			SS,TM,ion_trans,IQ	NM_014191*:Homo sapiens sodium chan	2.7
	418030	BE207573	Hs.83321	SS,TM,Peptidase_S26,Bombesin	neuromedin B	2.7
	445640	AW969626	Hs.31704	TM,alpha-amylase	ESTs, Weakly similar to KIAA0227 [H	2.7
25	432865	AI753709	Hs.152484	TM,ion_transNB-ARC,CARD,WD40,m	ESTs, Weakly similar to I38022 hypo	2.6
	419667	AU077005	Hs.92208	SS,TM,disintegrin,Reprolysin,P	a disintegrin and metalloproteinase	2.6
	406671	AA129547	Hs.285754	TM,pkinase,Flexin_repeat,Sema,	met proto-oncogene (hepatocyte grow	2.6
	412530	AA766268	Hs.266273	abhydrolase	hypothetical protein FLJ13346	2.6
	431890	X17033	Hs.271986	vwa,FG-GAP,integrin_A	integrin, alpha 2 (CD49B, alpha 2 s	2.6
30	404184	NA		SS,TM,7tm_1	NM_030903*:Homo sapiens olfactory r	2.6
	428450	NM_014791	Hs.184339	pkinase,KA1	KIAA0175 gene product	2.6
	425698	NM_016112	Hs.159241	TM,pkinase,ion_trans	polycystic kidney disease 2-like 1	2.6
	453331	AI204665	Hs.8895	TM,disintegrin,Pep_M12B_propep	ESTs	2.6
	444826	AI674482	Hs.148441	pkinase,SAM	ESTs	2.6
35	414987	AA524394	Hs.294022	connexinhormone_rec,zf-C4,conn	hypothetical protein FLJ14950	2.6
	438746	AI885815	Hs.184727	Ribosomal_S2,transferrin	ESTs	2.5
	429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
	407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170	2.5
	453379	AA035261	Hs.61753	PAN,kringle,trypsin	ESTs	2.5
40	421733	AL119671	Hs.1420	SS,TM,lg,pkinase	fibroblast growth factor receptor 3	2.5
	452220	BE158006	Hs.212296	TM,integrin_A,FG-GAP	ESTs	2.5
	417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	2.5
	400301	X03635	Hs.1657	TM,Oest_recep,zf-C4,hormone_re	estrogen receptor 1	2.5
	408938	AA059013	Hs.22607	Y_phosphatase	ESTs	2.4
45	411643	AI924519	Hs.192570	DEAD,helicase_C	hypothetical protein FLJ22028	2.4
	446638	AL133063	Hs.15783	TM,pkinase	Homo sapiens mRNA; cDNA DKFZp434P11	2.4
	430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
	417655	AA780791	Hs.14014	Peptidase_M41,AAApkinase	hypothetical protein FLJ14813	2.4
	448005	AW207437	Hs.170378	pkinase	ESTs	2.4
50	423973	AF038461	Hs.136574	TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase, 12R t	2.4
	437897	AA770561	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969	2.4
	425397	J04088	Hs.156346	DNA_topoisomII,DNA_topoisomVIGF	topoisomerase (DNA) II alpha (170kD	2.4
	432777	AA564991	Hs.269477	alpha-amylase	ESTs	2.4
	421247	BE391727	Hs.102910	TM,iRNA-synt_1,SPRYF5_F8_type_	general transcription factor IIH, p	2.4
55	425465	L18964	Hs.1904	TM,pkinase,DAG_PE-bind,OPR,pki	protein kinase C, iota	2.4
	419281	H96452	Hs.42189	TM,E1-E2_ATPase,HMA,Hydrolase	ESTs	2.4
	434205	AF119861	Hs.283032	SH3,effhand,C2,PH,RhoGEF,AAA,PG	hypothetical protein PRO2015	2.4
	453406	AI192987	Hs.61784	pkinase,Furin-like,Recep_L_dom	hypothetical protein FLJ14451	2.3
	435542	AA687376	Hs.269533	pkinase,RhoGEF,lg,PH,SH3	ESTs	2.3
60	443151	AI827193	Hs.132714	DNA_mis_repair,HATPase_cAcy/iph	ESTs	2.3
	431630	NM_002204	Hs.265829	SS,TM,FG-GAP,integrin_A	integrin, alpha 3 (antigen CD49C, a	2.3
	422310	AA316622	Hs.98370	SS,TM,fn3,jg,pkinase,Ribosomal	cytochrome P450, subfamily IIS, pol	2.3
	441954	AI744935	Hs.8047	TM,Band_7,AAA,cdc48_N	Fanconi anemia, complementation gro	2.3
	414907	X90725	Hs.77597	SS,TM,pkinase,POLO_box	polo (Drosophila)-like kinase	2.3
65	439810	AL109710	Hs.85568	aconitase,Aconitase_C	EST	2.3
	429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membra	2.3
	432284	AA532807	Hs.105822	TM,pkinase	ESTs	2.3
	452947	AW130413		alpha-amylase	gb:xf50f04.x1 NCI_CGAP_Gas4 Homo sa	2.3
70	423229	AC003965	Hs.125532	SS,trypsin	protease, serine, 26	2.3
	453941	U39817	Hs.36820	DEAD,HRDC,helicase_C	Bloom syndrome	2.3
	439963	AW247529	Hs.6793	TM,p450Ets	platelet-activating factor acetylhy	2.3
	424439	AA579635	Hs.1770	DNA_ligase	ligase I, DNA, ATP-dependent	2.2
	452755	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypo	2.2
	429922	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0	2.2
75	434149	Z43829	Hs.19574	TM,EPH_lbd,fn3,pkinase,SAM	hypothetical protein MGC5469	2.2
	417576	AA339449	Hs.82285	TM,AlRS,formyl_transf,GARS	phosphoribosylglycinamide formyltra	2.2
	409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor, SREC	2.2
	416763	AI908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators	2.2
	414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficien	2.2
80	443171	BE281128	Hs.9030	SS,TM,7tm_1,rm	TONDU	2.2
	430637	BE160081	Hs.256290	S_100Peptidase_M16	S100 calcium-binding protein A11 (c	2.2
	452367	U71207	Hs.29279	SS,Hydrolase	eyes absent (Drosophila) homolog 2	2.2
	408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
	417900	BE250127	Hs.82906	TM,WD40,pro_isomerase	CDC20 (cell division cycle 20, S. c	2.1

5	424490	AJ278016	Hs.55565	TM, pkinase, ank	ankyrin repeat domain 3	2.1
	412834	R77123	Hs.79881	TM, 7Im_1	Homo sapiens cDNA: FLJ23006 fis, cl	2.1
	410855	X97795	Hs.66718	SNF2_N, helicase_C	RAD54 (S.cerevisiae)-like	2.1
	418804	AA809632		HATPase_c, HSP90, PHD, zf-C2H2	gb:nz17n04.s1 NCL_CGAP_GCB1 Homo sa	2.1
	447674	BE270640	Hs.19192	TM, pkinaseras, arf	cyclin-dependent kinase 2	2.1
	450663	H43540	Hs.25292	SS, TM, RNase_HII	ribonuclease HI, large subunit	2.1
	408805	H69912	Hs.48269	TM, pkinase	vaccinia related kinase 1	2.1
	429415	NM_002593	Hs.202097	SS, CUB, NTR, MAM, TIL, TILa, vwd, EP	procollagen C-endopeptidase enhance	2.1
10	447827	U73727	Hs.19718	SS, TM, Y_phosphatase, fn3, Ig, MAM	protein tyrosine phosphatase, recep	2.1
	428273	AI867228	Hs.303211	Glycos_transf_2	ESTs	2.1
	404274			SS, TM, pkinase, fn3	NM_002944*:Homo sapiens v-ros avian	2.1
	403133			pkinaase, K_tetra, Band_41, RhoGEF	Target Exon	2.1
	440249	AI246590	Hs.337275	VHL, TatD_DNase	ESTs	2.1
15	438580	AA811262	Hs.299202	TM, pkinasesugar_tr	ESTs	2.1
	406400			SS, TM, trypsin	NM_007196:Homo sapiens kalikrein 8	2.1
	427375	AL035460	Hs.177536	SS, Zn_carbOpept, hormone5Reprol	metallocarboxypeptidase CPX-1	2.1
	423453	AW450737	Hs.128791	SS, Granin, CDP-OH_P_transf	CGI-09 protein	2.1
	433716	AA608808	Hs.225118	Acylphosphatase	ESTs	2.1
20	420757	X78592	Hs.99915	TM, hormone_rec, Androgen_recep,	androgen receptor (dihydrotestoster	2.1
	425018	BE245277	Hs.154196	DNase_I, K_tetra	E4F transcription factor 1	2.1
	421685	AF189723	Hs.106778	TM, E1-E2_ATPase, HydrolaseE1-E2	ATPase, Ca transporting, type 2C, m	2.1
	457288	AA521458	Hs.192738	pro_isomerase	ESTs	2.1
	407305	AA715284		TM, pkinase, Sema, Plexin_repeat,	gb:nv35f03.r1 NCL_CGAP_Br5 Homo sap	2.1
25	456327	H68741	Hs.38774	TM, Glyco_transf_8	ESTs	2.0
	422429	AA310527		pkinaase, RGS, PHpkinase, PH, RGS	gb:EST181333 Jurkat T-cells V Homo	2.0
	402974	NM_001501	Hs.129715	GnRHhormone5, hormone4	gonadotropin-releasing hormone 2	2.0
	458016	AW188099	Hs.131813	pkinaase	ESTs	2.0
	452194	AI694413	Hs.332649	TM, 7Im_3, ANF_receptor, sushi	olfactory receptor, family 2, subfa	2.0
30	428028	U52112	Hs.182018	TM, pkinase, MBD	interleukin-1 receptor-associated k	2.0
	427747	AW411425	Hs.180655	pkinaase, lipoxigenase, PLATilipox	serine/threonine kinase 12	2.0
	452841	T17431	Hs.65412	TM, DEAD, helicase_C	DEAD/H (Asp-Glu-Ala-Asp/His) box po	2.0
	449539	W80363	Hs.58446	pkinaase, Furin-like, Recep_L_dom	ESTs	2.0
	418140	BE613836	Hs.83551	TM, E1-E2_ATPase	microfibrillar-associated protein 2	2.0
35	430076	AA465115	Hs.318773	AAA, BAH	KIAA1836 protein	2.0
	425749	AW328587	Hs.159448	Ribosomal_L7Ae, LRR, LRRCT, pkina	surfeit 2	2.0
	425855	AF135025	Hs.159679	SS, trypsin	kalikrein 12	2.0
	400135	L40027	Hs.118890	pkinaase	glycogen synthase kinase 3 alpha	2.0

## 40 TABLE 14B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

45	Pkey	CAT number	Accessions
			*
50	412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492
	418804	179138_1	AA809632 AI917245 AI701732 AA228406
	420930	197736_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
	422429	216469_1	AA310527 AW962295 Z44865 H05641
	422689	219896_1	AW856665 AA315006 AW954733
	435399	405576_1	AA679463 AW813779 AW813709
55	438390	45662_1	AI422017 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AI423279 AI423645 AI424090 AI359637 AL044732 D17003
	438993	467651_1	AA828995 AA834879 AI926361
	452947	939810_1	AW130413 AI932362
	455092	1252971_1	BE152428 AW855572 AW855607
	457405	333127_1	AA504860 AA504911

## 60 TABLE 14C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

70	Pkey	Ref	Strand	Nt_position
	400666	8118496	Plus	17982-18115, 20297-20456
	401230	9929527	Minus	33835-34006, 34539-34592, 36461-36745, 48925-49098, 52604-52758
	401486	7341763	Plus	32585-32756, 36281-36540, 40791-40933, 44018-44179
75	402337	6957691	Plus	4116-4286, 16811-16973, 17107-17256, 19715-20040, 22029-22205
	402481	9797406	Plus	87891-88991
	403133	7331427	Plus	38314-38634
	403471	9930659	Minus	85867-85983
	403763	7229888	Minus	43575-43887
80	404184	4581418	Minus	12652-13548
	404274	9885189	Plus	104127-104318
	406400	9256298	Plus	1553-1712, 1878-2140, 4252-4385, 5922-6077

TABLE 15A: 752 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

Table 15A lists about 752 genes up-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 12A, except that the ratio was greater than or equal to 7.0, the denominator was the median value for three non-malignant cervical specimens, and the 96<sup>th</sup> percentile value amongst cervical cancers was greater than or equal 80 units.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of cervical cancer to normal cervix

Pkey	ExAccn	UnigenelD	Unigene Title	R1
414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	58.3
411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HEMBA1004341	36.2
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-Cys), mem	35.6
421508	NM_004833	Hs.105115	absent in melanoma 2	33.6
443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit, beta type, 1	32.0
454390	AB020713	Hs.56966	KIAA0906 protein	30.5
416065	BE267931	Hs.78996	proliferating cell nuclear antigen	30.4
433226	AW503733	Hs.9414	KIAA1488 protein	30.0
413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein,	29.4
411669	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	28.9
414132	AI801235	Hs.48480	ESTs	28.3
422809	AK001379	Hs.121028	hypothetical protein FLJ10549	28.1
448569	BE382657	Hs.21486	signal transducer and activator of transcription 1, 9	27.4
432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	27.2
418963	BE304571	Hs.89529	aldo-keto reductase family 1, member A1 (aldehyde red	26.9
439963	AW247529	Hs.6793	platelet-activating factor acetylhydrolase, isoform I	26.5
449722	BE280074	Hs.23960	cyclin B1	26.2
414812	X72755	Hs.77367	monokine induced by gamma interferon	25.3
408405	AK001332	Hs.44672	hypothetical protein FLJ10470	25.1
432917	NM_014125	Hs.279812	PRO0327 protein	24.6
412530	AA766268	Hs.266273	hypothetical protein FLJ13346	23.6
457465	AW301344	Hs.122908	DNA replication factor	23.1
408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone COL06049	22.9
429083	Y09397	Hs.227817	BCL2-related protein A1	22.9
401405			Target Exon	22.8
426272	AW450671	Hs.189284	ESTs	22.7
424878	H57111	Hs.221132	ESTs	22.6
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakbinesin 6)	22.5
444371	BE540274	Hs.239	forkhead box M1	22.2
418030	BE207573	Hs.83321	neuromedin B	22.0
452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolog)-	21.6
400196			Eos Control	21.3
416795	AI497778	Hs.20509	HBV pX associated protein-8	21.2
424865	AF011333	Hs.153563	lymphocyte antigen 75	21.0
438011	BE466173	Hs.145696	splicing factor (CC1.3)	20.7
428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, progelatin	20.3
436923	AW293704	Hs.122658	ESTs	20.2
415791	H09366	Hs.78853	uracil-DNA glycosylase	20.0
448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moiety X)-type m	19.6
435647	AI653240	Hs.49823	ESTs	19.6
431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene trap PA	19.5
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	19.5
428433	AA521410	Hs.41371	ESTs	19.4
418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK2-associated	19.3
417308	H60720	Hs.81892	KIAA0101 gene product	19.2
429574	BE268321	Hs.208912	hypothetical protein MGC861	19.2
407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	19.0
408901	AK001330	Hs.48855	hypothetical protein FLJ10468	19.0
438899	AF085833	Hs.135624	ESTs	19.0
456362	AW973003	Hs.179909	hypothetical protein FLJ22995	18.9
438598	AI805943	Hs.326067	hypothetical protein MGC5178	18.8
408908	BE296227	Hs.250822	serine/threonine kinase 15	18.8
427488	M91401	Hs.178658	RAD23 (S. cerevisiae) homolog B	18.6
400195			NM_007057*:Homo sapiens ZW10 interactor (ZWINT), tran	18.5
414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin)	18.4
410324	AW292539	Hs.30177	ESTs	18.3
453028	AB006532	Hs.31442	RecQ protein-like 4	18.1
410608	AI538438	Hs.159087	ESTs	18.1
432503	AA551196	Hs.188952	ESTs	17.9
430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	17.7
430709	R34366		gb:yh85d01.s1 Soares placenta Nb2HP Homo sapiens cDNA	17.6
449962	AA004879	Hs.187820	ESTs	17.3
425408	AB002375	Hs.156814	KIAA0377 gene product	17.1
440774	AI420611	Hs.127832	ESTs	16.8
408201	AK000568	Hs.43654	hypothetical protein FLJ20561	16.7
436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothetical protein [	16.7
426897	AW976570	Hs.97387	ESTs	16.5
447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical protein F	16.5

	433159	AB035898	Hs.150587	kinesin-like protein 2	16.3
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	16.3
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional activation,	16.3
5	453941	U39817	Hs.36820	Bloom syndrome	16.1
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	16.0
	407999	AI126271	Hs.49433	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTE	16.0
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12961 fis, clone NT2RP2006454	15.7
	407720	AB037776	Hs.38002	KIAA1355 protein	15.6
10	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1 protein - mou	15.6
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage elastase)	15.5
	419777	D60134	Hs.270975	ESTs	15.3
	453886	R66282	Hs.20247	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	15.2
	443715	AI583187	Hs.9700	cyclin E1	15.2
	407786	AA687538	Hs.38972	tetraspan 1	15.2
15	431910	AK000142	Hs.101774	hypothetical protein FLJ23045	15.2
	417634	W27202	Hs.82327	glutathione synthetase	15.1
	432692	AW974944	Hs.200577	ESTs	15.1
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cys-Cys), membe	15.1
20	427999	AI435128	Hs.181369	ubiquitin fusion degradation 1-like	15.0
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	15.0
	431629	AI077025	Hs.265827	interferon, alpha-inducible protein (clone IFI-6-16)	14.9
	435354	AA678267	Hs.117115	ESTs	14.8
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	14.8
25	416109	AI20311	Hs.126550	suppressor of K transport defect 1	14.8
	417933	X02308	Hs.82962	thymidylate synthetase	14.7
	438970	AA837782	Hs.321058	ESTs	14.7
	409680	W31092	Hs.55847	mitochondrial ribosomal protein 64	14.7
	432401	NM_013330	Hs.274479	NME7	14.6
30	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.5
	420734	AW972872	Hs.293736	ESTs	14.5
	434256	AI378817	Hs.191847	ESTs	14.5
	418269	AA806113	Hs.189025	ESTs	14.3
	427372	AW960673	Hs.177530	ATP synthase, H transporting, mitochondrial F1 comple	14.3
35	427081	AI474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN !!!! ALU CLASS	14.2
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	14.2
	429966	BE081342	Hs.283037	HSPC039 protein	14.2
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-inducible, 67	14.1
	443957	AA521049	Hs.34487	hypothetical protein FLJ23412	14.0
40	418803	U50079	Hs.88556	histone deacetylase 1	14.0
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	14.0
	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	13.9
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin binding pr	13.9
	433255	AI274270	Hs.96840	KIAA1527 protein	13.9
45	431838	AI097229	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	13.8
	449801	AA477355	Hs.288300	hypothetical protein FLJ23231	13.8
	447078	AW885727	Hs.301570	ESTs	13.8
	441240	AA923749	Hs.132442	ESTs	13.8
	439398	AA284267	Hs.221504	ESTs	13.6
50	404630			Target Exon	13.6
	408321	AW405882	Hs.44205	cortistatin	13.6
	426427	M86699	Hs.169840	TTK protein kinase	13.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	13.5
	403055			C2002219*.g 12737280 ref XP_006682.2  keratin 18 [Ho	13.5
55	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	13.5
	425261	BE385099	Hs.334727	hypothetical protein MGC3017	13.3
	439926	AW014875	Hs.137007	ESTs	13.3
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated kinesin	13.2
	451141	AW772713	Hs.247186	ESTs	13.2
60	447390	X95384	Hs.18426	translational inhibitor protein p14.5	13.2
	419828	T81422	Hs.14922	ESTs	13.2
	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109260A B cell growth factor	13.2
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	13.1
	407595	BE350012	Hs.248365	ESTs	13.1
65	432721	AL121478	Hs.180532	glucose phosphate isomerase	13.1
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associ	13.0
	413314	BE081585		gb:QV2-BT0635-210400-156-b07 BT0635 Homo sapiens cDNA	13.0
	430929	AA489166	Hs.156933	ESTs	12.9
	449571	AW016812	Hs.200266	ESTs	12.9
70	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the prostate	12.8
	417105	X60992	Hs.81226	CD6 antigen	12.6
	434263	N34895	Hs.44648	ESTs	12.6
	412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferritin associate	12.6
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	12.5
75	437056	AI147061		gb:ok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	12.5
	438768	AI307416	Hs.184675	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY	12.5
	444478	W07318	Hs.240	M-phase phosphoprotein 1	12.5
	450738	AA010907	Hs.184456	hypothetical protein	12.4
	418205	L21715	Hs.83760	troponin I, skeletal, fast	12.4
80	442994	AI026718	Hs.16954	ESTs	12.4
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone HEP20977	12.4
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	12.4
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylgl	12.3
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (survivin)	12.3

	410245	C17908	Hs.194125	ESTs	12.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	12.3
	418941	AA452970	Hs.155218	E1B-55kDa-associated protein 5	12.3
5	432325	AW973209	Hs.261782	ESTs	12.3
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	12.3
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dystonia)	12.2
	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone LNG00818	12.2
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501	12.2
10	427295	AW291212	Hs.293943	hypothetical protein MGC11266	12.2
	415443	T07353	Hs.7948	ESTs	12.1
	429770	AI766047	Hs.99736	ESTs	12.1
	428955	AA579297	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	12.1
	435244	N77221	Hs.187824	ESTs	12.1
	432810	AA863400	Hs.23054	ESTs	12.1
15	434423	NM_006769	Hs.3844	LIM domain only 4	12.0
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit, beta type, 9	12.0
	459273	AW608906	Hs.334767	hypothetical protein MGC5629	12.0
	419945	AW290975	Hs.118923	ESTs	11.9
20	442159	AW163390	Hs.278554	heterochromatin-like protein 1	11.9
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MAMMA1002566	11.9
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	11.8
	401557			Target Exon	11.8
	434408	AI031771	Hs.132586	ESTs	11.8
25	406747	AI925153	Hs.217493	annexin A2	11.8
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein (EGP) (KSA)	11.8
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor 1	11.8
	445655	AA873830	Hs.167746	B cell linker protein	11.7
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	11.7
30	427527	AI809057	Hs.302063	immunoglobulin heavy constant mu	11.7
	432287	AK001057	Hs.274268	Homo sapiens cDNA FLJ10195 fis, clone HEMBA1004771	11.6
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C W	11.6
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 kD)	11.6
	447082	T85314	Hs.42644	thioredoxin-like	11.5
35	409931	BE293233	Hs.129771	ESTs	11.4
	426172	AA371307	Hs.125056	ESTs	11.4
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(hnRNP methyltr	11.4
	456880	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcriptional enha	11.4
	433849	BE465884	Hs.280728	ESTs	11.4
40	430519	AF129534	Hs.49210	F-box only protein 4	11.4
	434442	AA737415	Hs.152826	ESTs	11.3
	457205	AI905780	Hs.198272	Target CAT	11.3
	422713	AA902780	Hs.119325	Huntingtin-interacting protein A	11.3
	443491	AW499665	Hs.9456	SWI/SNF related, matrix associated, actin dependent r	11.3
45	424339	BE257148	Hs.145416	endoglycan	11.3
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	11.3
	450208	AI686945	Hs.272062	ESTs	11.2
	446849	AU076617	Hs.16251	cleavage and polyadenylation specific factor 3, 73kD	11.2
	424965	AW956282	Hs.144609	Homo sapiens, Similar to RIKEN cDNA 5730578N08 gene,	11.2
50	442737	AB002319	Hs.8663	KIAA0321 protein	11.2
	409113	AA074897		gb:zm85a05.r1 Stratagene ovarian cancer (937219) Homo	11.2
	415782	AA169345	Hs.123177	ESTs	11.1
	417958	AA767382	Hs.193417	ESTs	11.1
	402539	AW502761	Hs.30909	KIAA0430 gene product	11.0
55	413677	AW503116	Hs.301819	zinc finger protein 146	11.0
	414706	AW340125	Hs.76989	KIAA0097 gene product	11.0
	421632	AA825426	Hs.238832	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	11.0
	438995	AI277986	Hs.164875	ESTs	11.0
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	10.9
60	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 3'	10.9
	451655	H85689	Hs.225560	ESTs	10.9
	429237	AA448417	Hs.104990	ESTs	10.9
	427719	AI393122	Hs.134726	ESTs	10.9
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	10.8
65	410093	AW589558	Hs.296120	ESTs, Weakly similar to KIAA0970 protein [H.sapiens]	10.8
	400080			Eos Control	10.8
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643	10.8
	401539			NM_002675:Homo sapiens promyelocytic leukemia (PML),	10.8
	446099	T93096	Hs.17126	hypothetical protein MGC15912	10.7
70	451066	AI758660	Hs.206132	ESTs	10.7
	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypothetical protein [	10.7
	451730	AF095687	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	10.7
	428054	AI948688	Hs.266619	ESTs	10.6
	441636	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (from clone DKFZ	10.6
75	438654	AI005270	Hs.123543	ESTs	10.6
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kinase	10.6
	449035	AI815728	Hs.19980	DNA polymerase epsilon p12 subunit	10.6
	436137	AI056769	Hs.133512	ESTs	10.6
	417863	AB000450	Hs.82771	vaccinia related kinase 2	10.6
80	439975	AW328081	Hs.6817	inosine triphosphatase (nucleoside triphosphate pyrop	10.6
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen inducible gene	10.6
	454355	AW812535		gb:CM4-ST0182-051099-021-c09 ST0182 Homo sapiens cDNA	10.6
	435542	AA687376	Hs.269533	ESTs	10.6
	431386	AA504359	Hs.110067	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	10.5

	416564	AW795793	Hs.179827	Homo sapiens cDNA FLJ12257 fis, clone MAMMA1001501, h	10.5
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT2RM4002390	10.5
	408329	AF155510	Hs.44227	heparanase	10.5
5	410146	AW592655		gb:hf45f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA c	10.5
	427600	AW630918	Hs.179774	proteasome (prosome, macropain) activator subunit 2 (	10.4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	10.4
	407241	M34516		gb:Human omega light chain protein 14.1 (lg lambda ch	10.4
	435061	AI651474	Hs.163944	ESTs	10.4
10	409653	AW451693	Hs.220826	ESTs	10.4
	428294	AA425488		gb:zw46d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapie	10.4
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sensitivity prote	10.4
	408809	AW274673	Hs.279706	ESTs, Weakly similar to A47582 B-cell growth factor p	10.4
	410174	AA306007	Hs.59461	DKFZP434C245 protein	10.4
15	424792	U92538	Hs.153138	origin recognition complex, subunit 5 (yeast homolog)	10.3
	422406	AF025441	Hs.116206	Opa-interacting protein 5	10.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92kD gelati	10.3
	413809	L25851	Hs.851	integrin, alpha E (antigen CD103, human mucosal lymph	10.3
	413507	BE145360	Hs.190064	ESTs, Weakly similar to I38022 hypothetical protein [	10.3
20	448119	H38587	Hs.82295	dedicator of cyto-kinesis 1	10.2
	457288	AA521458	Hs.192738	ESTs	10.2
	402025			NM_021624:Homo sapiens histamine H4 receptor (HRH4),	10.2
	440572	AW183778	Hs.249584	ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN	10.2
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside transporters), m	10.2
25	443780	NM_012068	Hs.9754	activating transcription factor 5	10.1
	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapiens cDNA 5' en	10.1
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	10.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	10.1
30	430848	AW021726		gb:df27e02.y1 Morton Fetal Cochlea Homo sapiens cDNA	10.1
	422470	AB017919	Hs.117232	peptidyl arginine deiminase, type V	10.1
	449501	AI652924	Hs.231942	ESTs	10.1
	420731	AL042052	Hs.104432	ESTs	10.1
	404345	AA730407	Hs.159156	protocadherin 11	10.1
	400438	AF185611		Target	10.1
35	438170	AI916685	Hs.194601	ESTs	10.1
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	10.1
	458715	AK000973	Hs.16725	hypothetical protein FLJ10111	10.1
	427766	AA412258	Hs.188817	ESTs	10.1
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	10.0
40	403038			Target Exon	10.0
	434674	AA831879	Hs.136985	ESTs	10.0
	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKHEAD BOX PROTE	10.0
	439428	AA835825	Hs.190490	ESTs	10.0
	403310			Target Exon	9.9
45	408392	U28831	Hs.44566	KIAA1641 protein	9.9
	421849	AW410872	Hs.108894	hypothetical protein FLJ20411	9.9
	433384	AI021992	Hs.124244	ESTs	9.9
	443343	BE409809	Hs.301005	purine-rich element binding protein B	9.9
	437267	AW511443	Hs.258110	ESTs	9.9
50	455978	AI310151	Hs.173524	ESTs	9.9
	435851	AA700946	Hs.191933	ESTs	9.9
	452243	AL355715	Hs.28555	programmed cell death 9	9.9
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	9.9
	414001	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY	9.9
55	436669	AA535975	Hs.174308	Homo sapiens, clone IMAGE:3453347, mRNA, partial cds	9.8
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate), member 2	9.8
	417087	AA193193	Hs.188325	Homo sapiens cDNA FLJ11484 fis, clone HEMBA1001835	9.8
	455855	BE147440		gb:RC1-HT0229-080100-015-f09 HT0229 Homo sapiens cDNA	9.8
	410390	AA876905	Hs.125286	ESTs	9.8
60	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid transpo	9.8
	442660	AW138174	Hs.130651	ESTs	9.8
	436186	BE390717	Hs.5074	similar to S. pombe dim1	9.8
	426773	NM_015556	Hs.172180	KIAA0440 protein	9.8
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	9.7
65	418347	AA216419		gb:nc16e03.s1 NCLCGAP_Pr1 Homo sapiens cDNA clone si	9.7
	448752	AA593867	Hs.300842	KIAA1608 protein	9.7
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone THYRO1001322	9.7
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	9.7
	430752	AA485330	Hs.303278	ESTs	9.7
70	436523	BE612990	Hs.5212	single-strand selective monofunctional uracil DNA gly	9.7
	415740	N80486	Hs.39911	Homo sapiens mRNA for FLJ00089 protein, partial cds	9.7
	411930	F06485	Hs.7740	oxysterol binding protein-like 1	9.7
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H	9.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical protein [	9.6
75	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA1011 protein	9.6
	434957	AF283775	Hs.35380	x 001 protein	9.6
	407292	AA876638		gb:nz45e06.s1 NCLCGAP_Pr12 Homo sapiens cDNA clone s	9.6
	459109	AW292447	Hs.140821	ESTs	9.6
	457892	AA744389		gb:ny51e10.s1 NCLCGAP_Pr18 Homo sapiens cDNA clone s	9.6
80	432074	AA525248	Hs.149723	ESTs	9.6
	440463	AI733087	Hs.129994	ESTs	9.6
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	9.6
	445326	AI220072	Hs.165993	ESTs	9.6
	434953	BE049102	Hs.121573	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALI [H.sap	9.6

	420361	N92054	Hs.194718	zinc finger protein 265	9.6
	415853	H06016	Hs.100855	ESTs	9.6
	429599	AA806106	Hs.123664	ESTs	9.6
5	417037	BE083936	Hs.80976	antigen identified by monoclonal antibody Ki-67	9.6
	449317	AW293413	Hs.132906	19A24 protein	9.6
	436588	AA759233	Hs.126506	ESTs	9.6
	409261	BE315042	Hs.19210	hypothetical protein MGC11308	9.5
	401069			C11000374*:gi 10764778 gb AAG22817.1 AF302150_1 (AF30	9.5
10	414065	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PLACE1008851	9.5
	409902	AI337658	Hs.156351	ESTs	9.5
	432258	AW973078	Hs.293039	ESTs	9.5
	438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serine/threonine-s	9.5
	405536			NM_005805:Homo sapiens 26S proteasome-associated pad1	9.5
15	418216	AA662240	Hs.283099	AF15q14 protein	9.5
	434573	AW372340	Hs.159717	ESTs	9.5
	439354	AF086174		gb:Homo sapiens full length insert cDNA clone ZB94A08	9.5
	455410	AW936678		gb:PM2-DT0023-080300-004-a04 DT0023 Homo sapiens cDNA	9.5
	400736			Target Exon	9.5
20	419474	AW968619	Hs.155849	ESTs	9.4
	406464			C17000168:gi 7294725 gb AAF50062.1  (AE003544) CG7547	9.4
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	9.4
	427258	AA400091	Hs.39421	ESTs	9.4
	404680			Target Exon	9.4
25	433840	AA129782	Hs.3576	Homo sapiens mRNA full length insert cDNA clone EURO1	9.4
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	9.4
	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapiens]	9.4
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	9.4
	451846	T65840	Hs.11762	ESTs	9.4
30	419988	W39388	Hs.55336	Homo sapiens, clone MGC:17421, mRNA, complete cds	9.4
	402967			Target Exon	9.3
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.3
	441075	AA915991	Hs.179214	ets variant gene 3	9.3
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (UBE3B) mRNA, p	9.3
	404649			Target Exon	9.3
35	420897	AW139261	Hs.232280	ESTs	9.3
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	9.3
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	9.3
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypothetical protein [	9.3
40	420101	AW500529	Hs.95180	KIAA0767 protein	9.3
	428166	AA423849	Hs.79530	M5-14 protein	9.3
	420022	AA256253	Hs.120817	ESTs	9.3
	444020	R92962	Hs.35052	ESTs	9.3
	454765	AW819629		gb:RC5-ST0293-140200-014-H05 ST0293 Homo sapiens cDNA	9.3
45	415021	R54409	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA, partial cds	9.3
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	9.3
	415009	C75253	Hs.220950	ESTs	9.3
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.3
	433348	AA877996	Hs.125376	ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase	9.2
50	417881	AI879117		gb:au54g09.y1 Schneider fetal brain 00004 Homo sapien	9.2
	446354	AW449650	Hs.202249	ESTs	9.2
	427018	AA397538	Hs.136280	Homo sapiens cDNA: FLJ22288 fis, clone HRC04157	9.2
	434410	AA632644		gb:np87b07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone s	9.2
	448072	AI459306	Hs.24908	ESTs	9.2
55	457322	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257	9.2
	424317	AI865032	Hs.26017	ESTs	9.2
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	9.2
	404112	BE302729	Hs.173162	neighbor of COX4	9.2
60	433334	AI927208	Hs.231958	matrix metalloproteinase 28	9.1
	434960	AW374941	Hs.72545	ESTs	9.1
	431658	BE409917	Hs.266935	tRNA selenocysteine associated protein	9.1
	439158	R60323	Hs.193888	ESTs	9.1
	443081	H86858	Hs.132909	ESTs	9.1
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	9.1
65	452706	AW449390	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN SURFEIT LOCUS	9.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	9.1
	430780	N95102	Hs.334858	hypothetical protein MGC12250	9.1
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defective, S. cere	9.1
	418379	AA218940	Hs.137516	fidgetin-like 1	9.1
70	431405	AI470895	Hs.252574	ribosomal protein L10a	9.0
	405454			C12000541:gi 5729884 ref NP_006539.1  IGF-II mRNA-bin	9.0
	438362	AA805678	Hs.12326	ESTs	9.0
	401940			Target Exon	9.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.0
75	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	9.0
	459086	AA021163	Hs.22287	ESTs	9.0
	418653	AI734064	Hs.136212	ESTs	9.0
	444152	AI125694	Hs.149305	hypothetical protein MGC2603	9.0
	437534	AA814471	Hs.291800	ESTs	9.0
	435074	AI760944	Hs.116937	ESTs	9.0
80	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA, complete cds	9.0
	442829	AW263123	Hs.127554	ESTs	9.0
	431675	AA699965	Hs.202375	ESTs	9.0
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	8.9

	420183	W92885	Hs.143408	ESTs	8.9
	421133	AA814971	Hs.257634	ESTs	8.9
	407605	W03512	Hs.6479	hypothetical protein MGC13272	8.9
5	441370	AI242433	Hs.270085	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	8.9
	437966	AW891130	Hs.38173	ESTs	8.9
	426360	AW290981	Hs.211296	ESTs, Weakly similar to 2109260A B cell growth factor	8.8
	448111	AA053486	Hs.20315	interferon-induced protein with tetratricopeptide rep	8.8
	408021	AW137133	Hs.245867	ESTs	8.8
10	429228	AI553633	Hs.337139	ESTs	8.8
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1) mRNA, partial	8.8
	431184	AW970116	Hs.310616	ESTs	8.8
	425219	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	8.8
	439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDNA clone EUROI	8.8
15	432573	AA553612	Hs.324696	KIAA1594 protein	8.8
	450881	W60462	Hs.270521	ESTs, Highly similar to ALU2_HUMAN ALU SUBFAMILY SB S	8.8
	437835	AI146771	Hs.158008	ESTs	8.8
	453204	R10799	Hs.191990	ESTs	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
20	408805	H69912	Hs.48269	vaccinia related kinase 1	8.7
	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuolar proton pu	8.7
	422583	AA410506	Hs.27973	KIAA0874 protein	8.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	8.7
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapiens]	8.7
25	454132	AW131759	Hs.248286	ESTs	8.7
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-inducing)	8.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-like	8.7
	441525	AW241867	Hs.127728	ESTs	8.7
	459539	AI279186		gb:qm24a04.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone 3'	8.7
30	443148	AI034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX S	8.7
	424255	AI192657	Hs.143897	dysferlin, limb girdle muscular dystrophy 2B (autosom	8.7
	459435	AA320038		gb:EST22383 Adipose tissue, white II Homo sapiens cDN	8.7
	443117	AI248826	Hs.42029	ESTs	8.6
35	457434	AW628192	Hs.18851	hypothetical protein FLJ10875	8.6
	442505	AW003775	Hs.198248	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, p	8.6
	430901	AA488833	Hs.126711	ESTs, Weakly similar to I38588 reverse transcriptase	8.6
	439223	AW238299	Hs.250618	UL16 binding protein 2	8.6
	417739	Z43995		gb:HSC1QB121 normalized infant brain cDNA Homo sapien	8.6
40	415961	H10983	Hs.155919	ESTs	8.6
	424042	Y10601	Hs.137674	ankyrin-like with transmembrane domains 1	8.6
	451035	AU076785	Hs.430	plastin 1 (I isoform)	8.6
	447155	AA100605	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPOSIS LOCUS PRO	8.6
	412668	AA456195	Hs.10056	hypothetical protein FLJ14621	8.6
	458042	AW058464	Hs.6430	protein with polyglutamine repeat; calcium (ca2) home	8.6
45	456530	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone DKF	8.6
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	8.6
	445006	W91903	Hs.124814	ESTs	8.6
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast homolo	8.5
	455161	BE145900		gb:MRO-HT0208-221299-204-b12 HT0208 Homo sapiens cDNA	8.5
50	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cerevisiae)	8.5
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	8.5
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interacting protein	8.5
	415018	U49395	Hs.77807	purinergic receptor P2X, ligand-gated ion channel, 5	8.5
	404534			C11001758* gij 12621132 ref NP_075243.1  MEGF1 [Rattus	8.5
55	438451	AI081972	Hs.220261	ESTs	8.5
	435176	AA744875	Hs.189413	ESTs	8.5
	443245	AI040955	Hs.151973	hypothetical protein FLJ23511	8.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	8.5
	457478	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), catalytic subuni	8.5
60	403839			Target Exon	8.5
	434932	BE613162	Hs.284135	hypothetical protein MGC3036	8.5
	420991	AW504814	Hs.121004	Homo sapiens mRNA for FLJ00111 protein, partial cds	8.4
	457854	BE547674	Hs.204169	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	8.4
	455994	BE179190		gb:RC0-HT0613-210300-032-f07 HT0613 Homo sapiens cDNA	8.4
65	402796			Target Exon	8.4
	423426	AW389579	Hs.128434	Homo sapiens ELISC-1 mRNA, partial cds	8.4
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (from clone DKF	8.4
	404110			NM_020245*:Homo sapiens tubby super-family protein (T	8.4
	424441	X14850	Hs.147097	H2A histone family, member X	8.4
70	433155	AL037035	Hs.100426	Homo sapiens cervical cancer metastasis-suppressor 1 (B	8.4
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	8.4
	406867	AA157857	Hs.182265	keratin 19	8.4
	418278	AI088489	Hs.83937	hypothetical protein	8.4
75	458696	AW375333	Hs.199890	ESTs	8.4
	456248	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	8.4
	403152	AA576664	Hs.37078	v-crk avian sarcoma virus CT10 oncogene homolog-like	8.4
	407649	BE066724	Hs.37427	erythrocyte membrane protein band 4.1 (elliptocytosis	8.4
	448387	AI874402	Hs.170810	ESTs	8.4
	433671	AW138797	Hs.132906	19A24 protein	8.4
80	425891	AI041717	Hs.132141	ESTs	8.4
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 protein [H.sapie	8.4
	439079	AF085937	Hs.38348	ESTs	8.4
	458115	BE091587		gb:IL2-BT0731-240400-069-H04 BT0731 Homo sapiens cDNA	8.4
	428144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associated	8.4



	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	8.3
	443056	AI457996	Hs.132578	ESTs	8.3
	410391	H17881	Hs.15043	Homo sapiens clone FLB5227 PRO1367 mRNA, complete cds	8.3
5	407989	AW135208	Hs.256092	ESTs	8.3
	410536	N39533		gb:yv27d04.s1 Soares fetal liver spleen 1NFLS Homo sa	8.3
	452273	AI870685	Hs.231022	ESTs	8.3
	454297	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	8.3
	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, calcium-indepe	8.3
10	401654			NM_007242:Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) b	8.3
	432891	AF161483	Hs.279761	HSPC134 protein	8.3
	419923	AW081455	Hs.120219	ESTs	8.2
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone KAT11914	8.2
	435452	AA831004	Hs.124874	ESTs	8.2
	418683	U90908	Hs.87241	hypothetical protein from clones 23549 and 23762	8.2
15	440065	W03476	Hs.266331	hypothetical protein MGC4595	8.2
	439752	T78968	Hs.14411	ESTs	8.2
	447983	AW612726	Hs.282113	ESTs, Weakly similar to I38022 hypothetical protein [	8.2
	441966	AA568689	Hs.16131	hypothetical protein FLJ12876	8.2
20	408182	AA047854		gb:zf49g04.r1 Soares retina N2b4HR Homo sapiens cDNA	8.2
	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	8.2
	436005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 fis, clone OVARC1002143	8.2
	414962	AF273304	Hs.235376	XPMC2 protein	8.2
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), soluble	8.2
25	408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	8.2
	413940	AI633205	Hs.159914	ESTs, Weakly similar to I78885 serine/threonine-speci	8.2
	437277	AA748016	Hs.123370	ESTs	8.2
	431445	AA505135	Hs.44037	ESTs	8.1
	418927	BE349635	Hs.190284	ESTs	8.1
30	452446	AA086123	Hs.297856	ESTs	8.1
	445380	AI222019	Hs.144838	ESTs	8.1
	421174	AW969058	Hs.291974	ESTs, Moderately similar to A46010 X-linked retinopat	8.1
	444374	AA009841	Hs.11039	hypothetical protein MGC2722	8.1
	417247	N58024		gb:yv63c01.s1 Soares fetal liver spleen 1NFLS Homo sa	8.1
35	438335	AI498421	Hs.243168	ESTs	8.1
	445235	AI564022	Hs.138207	ESTs	8.1
	422585	NM_016186	Hs.118620	protein Z-dependent protease inhibitor precursor	8.1
	442522	AI087038	Hs.146592	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	8.1
	430684	AI808979	Hs.293193	ESTs	8.1
40	446442	BE221533	Hs.257858	ESTs	8.1
	441410	AA932689	Hs.233304	ESTs, Weakly similar to I38022 hypothetical protein [	8.0
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein product [H.sa	8.0
	449539	W80363	Hs.58446	ESTs	8.0
	406663	U24683	Hs.302063	immunoglobulin heavy constant mu	8.0
45	423767	H18283	Hs.132753	F-box only protein 2	8.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protein 1	8.0
	430977	AA490069	Hs.306676	Homo sapiens cDNA FLJ14302 fis, clone PLACE2000003	8.0
	455677	BE066061	Hs.8867	cysteine-rich, angiogenic inducer, 61	8.0
	436706	AA725808	Hs.194609	ESTs	8.0
50	459407	N92114		gb:za22h11.r1 Soares fetal liver spleen 1NFLS Homo sa	8.0
	444132	AK000452	Hs.10340	hypothetical protein FLJ20445	8.0
	437149	AI686651	Hs.202234	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2	8.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	8.0
	411298	AW835858		gb:PM0-LT0017-031299-001-h07 LT0017 Homo sapiens cDNA	8.0
55	432571	AF151054	Hs.278429	hepatocellular carcinoma-associated antigen 59	8.0
	416295	AI064824	Hs.193385	ESTs	8.0
	427485	AF039652	Hs.178655	ribonuclease H1	8.0
	409857	AW501908		gb:UI-HF-BR0p-ajp-c-12-0-UI.r1 NIH_MGC_52 Homo sapien	7.9
	433854	AA610649	Hs.333239	ESTs	7.9
60	458080	BE142728		gb:MR0-HT0157-021299-004-d08 HT0157 Homo sapiens cDNA	7.9
	423573	AA328504		gb:EST31993 Embryo, 12 week I Homo sapiens cDNA 5' en	7.9
	404495			C8001441*gi 8923061 ref NP_060114.1  hypothetical pr	7.9
	443135	AI376331	Hs.156103	ESTs	7.9
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	7.9
65	413283	R78669	Hs.23756	hypothetical protein similar to swine acylneuraminat	7.9
	443987	AW163123	Hs.10071	seven transmembrane protein TM7SF3	7.9
	434197	AA627223		gb:nq63b04.s1 NCL_CGAP_Ov6 Homo sapiens cDNA clone si	7.9
	436882	AW016722	Hs.194976	SH2 domain-containing phosphatase anchor protein 1	7.9
	434502	AW974915	Hs.116550	ESTs	7.9
70	435507	AI143579	Hs.26510	vacuolar protein sorting 33B (yeast homolog)	7.9
	444896	AI201480	Hs.144856	ESTs	7.9
	419320	H96666	Hs.6137	ESTs	7.9
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	7.9
	425569	AA359597	Hs.301701	Homo sapiens cDNA FLJ12073 fis, clone HEMBB1002387	7.9
75	445209	AW294230	Hs.80988	collagen, type VI, alpha 3	7.9
	449193	AI637997	Hs.195653	ESTs	7.9
	447397	BE247676	Hs.18442	E-1 enzyme	7.9
	455037	BE144549		gb:MR0-HT0167-081199-001-a02 HT0167 Homo sapiens cDNA	7.9
	453367	AW732847	Hs.70573	PKC1-1-related HIT protein	7.8
80	439317	AF086127	Hs.50600	ESTs, Weakly similar to T47156 hypothetical protein D	7.8
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	7.8
	406562			NM_004520*:Homo sapiens kinesin heavy chain member 2	7.8
	435192	AK000739	Hs.4835	eukaryotic translation initiation factor 3, subunit 8	7.8
	413500	BE144914		gb:CM3-HT0183-181099-023-b05 HT0183 Homo sapiens cDNA	7.8

	436216	AA380887	Hs.5085	dolichyl-phosphate mannosyltransferase polypeptide 1,	7.8
	418623	AW194757	Hs.266804	ESTs	7.8
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapiens cDNA	7.8
5	430146	AW815330		gb:QV0-ST0215-060100-083-a09 ST0215 Homo sapiens cDNA	7.8
	441841	AA971819	Hs.176083	ESTs	7.8
	457677	AA628890	Hs.158701	ESTs	7.8
	421090	BE301870	Hs.101813	solute carrier family 9 (sodium/hydrogen exchanger),	7.8
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzy	7.8
10	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo sapiens cDNA	7.8
	406410			C5000010*:gij10440464[dbj]BAB15765.1[ AK024475) FLJ0	7.8
	453579	AI204463	Hs.61857	ESTs	7.8
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogene homolog-lik	7.7
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone COL05135	7.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa protein.	7.7
15	440777	AA994020	Hs.128553	ESTs	7.7
	446424	AW134529	Hs.244647	ESTs	7.7
	448004	AW451477	Hs.257456	ESTs	7.7
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP S	7.7
20	427080	AW068287	Hs.173466	ras-related C3 botulinum toxin substrate 2 (rho famil	7.7
	451693	BE220445	Hs.279635	ESTs	7.7
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	7.7
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	7.7
	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (polypyrimidin	7.7
25	425423	NM_005897	Hs.157180	intracisternal A particle-promoted polypeptide	7.7
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	7.7
	432585	AA705591	Hs.190209	ESTs	7.7
	402682			Target Exon	7.7
	400247			Eos Control	7.7
30	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	7.7
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (from clone DKF	7.7
	405514			ENSP00000241075:TRRAP PROTEIN.	7.7
	412406	AW948172		gb:RC0-MT0013-280300-021-b06 MT0013 Homo sapiens cDNA	7.7
	440226	AA873387	Hs.207330	ESTs	7.7
35	435625	H50654	Hs.113999	ESTs	7.7
	418529	AW005695	Hs.250897	TRK-fused gene	7.6
	407758	D50915	Hs.38365	KIAA0125 gene product	7.6
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	7.6
	449938	AW970612	Hs.172635	Homo sapiens cDNA: FLJ21367 fis, clone COL03051	7.6
40	422893	X98411	Hs.121555	myosin IF	7.6
	451593	AF151879	Hs.26706	CGI-121 protein	7.6
	424148	BE242274	Hs.1741	integrin, beta 7	7.6
	447519	U46258	Hs.339665	ESTs	7.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog 1	7.6
45	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	7.6
	426523	S68616	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger),	7.6
	456926	AB018284	Hs.158688	KIAA0741 gene product	7.6
	416294	D86980	Hs.79170	KIAA0227 protein	7.6
	409206	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo sapiens cDNA	7.6
50	417086	AA194446	Hs.73451	ESTs, Weakly similar to S55024 nebulin, skeletal musc	7.6
	418181	U37012	Hs.83727	cleavage and polyadenylation specific factor 1, 160kD	7.5
	436910	AA926944		gb:om68g01.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone 3'	7.5
	401008			Target Exon	7.5
	413245	BE244334	Hs.75249	ADP-ribosylation factor-like 6 interacting protein	7.5
55	446820	AW295037	Hs.254986	ESTs	7.5
	439279	AI039473	Hs.130636	ESTs	7.5
	426116	AA868729	Hs.144694	ESTs	7.5
	410098	BE326839	Hs.17433	hypothetical protein FLJ20967	7.5
	422326	AI114875	Hs.78592	eukaryotic translation initiation factor 2B, subunit	7.5
60	435513	AW404075	Hs.42785	DC11 protein	7.5
	421629	N80121	Hs.4983	ESTs	7.4
	434663	AA641972	Hs.130058	ESTs	7.4
	452461	N78223	Hs.108106	transcription factor	7.4
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	7.4
65	405417			CX001144*:gij7242973[dbj]BAA92547.1[ (AB037730) KIAA1	7.4
	414076	AA467736		gb:nc74e05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone, m	7.4
	435014	BE560898	Hs.10026	mitochondrial ribosomal protein L17	7.4
	449610	AI242042	Hs.14044	ESTs	7.4
	403397			Target Exon	7.4
70	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant; spastin)	7.4
	404914			NM_004046*:Homo sapiens ATP synthase, H+ transporting	7.4
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-activating fact	7.4
	432820	AI554057	Hs.152477	ESTs	7.4
75	418978	T85295	Hs.268606	ESTs	7.4
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonine kinase 21)	7.4
	454639	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo sapiens cDNA	7.4
	434522	AF189259	Hs.283081	gamma-aminobutyric acid (GABA) receptor, theta	7.4
	458236	AW297043	Hs.255604	ESTs, Weakly similar to A47234 homeobox protein H6 [H	7.4
80	441043	AA913422	Hs.192104	ESTs	7.4
	422838	AA524065	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone HSI08202	7.3
	455096	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapiens cDNA	7.3
	442307	AW027690	Hs.90037	ESTs	7.3
	425453	AW374284	Hs.297215	Homo sapiens chromosome 19, cosmid R26894	7.3

	455327	AW896238	Hs.334805	Homo sapiens cDNA FLJ14604 fis, clone NT2RP1000363, m	7.3
	420982	AW576160	Hs.100729	KIAA0692 protein	7.3
	424563	AA446932	Hs.151428	ret finger protein 2	7.3
5	417125	AW181998	Hs.81248	CUG triplet repeat, RNA-binding protein 1	7.3
	453902	BE502341	Hs.3402	ESTs	7.3
	446842	AI343510	Hs.176992	ESTs	7.3
	454128	AL031259	Hs.41639	programmed cell death 2	7.3
	427011	BE302729	Hs.173162	neighbor of COX4	7.3
10	450872	AI742594		gb:wg55h05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	7.3
	451512	AI800236	Hs.207080	ESTs	7.3
	405708	AI282759		gb:ql84a01.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone I	7.3
	432576	AW157424	Hs.165954	ESTs, Weakly similar to I38022 hypothetical protein I	7.3
	459304	AW005809	Hs.281076	ESTs, Weakly similar to CHD4_HUMAN CHROMODOMAIN HELIC	7.3
15	401375			NM_020999*:Homo sapiens neurogenin 3 (NEUROG3), mRNA.	7.3
	413258	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapiens cDNA	7.3
	406016			Target Exon	7.3
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	7.3
	422742	AA316117	Hs.337128	ESTs	7.3
20	440031	BE045970	Hs.244746	ESTs	7.3
	429389	AA454779	Hs.201441	Homo sapiens cDNA FLJ11079 fis, clone PLACE1005111	7.3
	449656	AA002008	Hs.188633	ESTs	7.3
	444310	AI140432	Hs.175936	ESTs	7.3
	459274	AA382590	Hs.170980	KIAA0948 protein	7.3
25	425404	BE048060	Hs.133494	Homo sapiens clone TCCCA00164 mRNA sequence	7.3
	431150	T63857		gb:yc16e01.s1 Stratagene lung (937210) Homo sapiens c	7.2
	443217	NM_001545	Hs.9078	immature colon carcinoma transcript 1	7.2
	413405	AW022253	Hs.215976	ESTs	7.2
	447653	BE327277	Hs.161145	ESTs	7.2
30	414704	NM_014757	Hs.76986	mastermind (Drosophila), homolog of	7.2
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, clade B (o	7.2
	409188	AW363284	Hs.32553	ESTs	7.2
	453493	AL039478	Hs.304447	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	456111	AK000150	Hs.78185	MAX-like bHLHZIP protein	7.2
35	400297	AI127076	Hs.334473	hypothetical protein DKFPz56401278	7.2
	446364	AB006624	Hs.14912	KIAA0286 protein	7.2
	432215	AL076609	Hs.2934	ribonucleotide reductase M1 polypeptide	7.2
	436943	AA773838	Hs.5353	caspase 10, apoptosis-related cysteine protease	7.2
	446336	AW815036	Hs.151251	ESTs	7.2
40	418469	U34879	Hs.85279	hydroxysteroid (17-beta) dehydrogenase 1	7.2
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	7.2
	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP3002304	7.2
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polypeptide 1	7.2
	416450	AA180467		gb:zp14g08.s1 Stratagene fetal retina 937202 Homo sap	7.2
45	449714	AB033015	Hs.23941	KIAA1189 protein	7.2
	455447	AW947507		gb:RCO-MT0002-140300-011-a12 MT0002 Homo sapiens cDNA	7.2
	437154	AI023133	Hs.10739	ESTs	7.2
	423059	AW378445	Hs.123080	Homo sapiens unknown protein mRNA, partial cds	7.2
	419092	J05581	Hs.89603	mucin 1, transmembrane	7.2
50	426736	AA431615	Hs.130722	ESTs	7.2
	417748	Z43011	Hs.21169	ESTs	7.2
	434748	AI862604	Hs.211884	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	438929	AW195515	Hs.253177	ESTs	7.2
	452061	AI074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	7.1
55	446416	AV658299	Hs.163959	ESTs	7.1
	415023	AA932146	Hs.133494	Homo sapiens clone TCCCA00164 mRNA sequence	7.1
	434766	AA742222	Hs.120634	ESTs	7.1
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell growth factor	7.1
	420252	AW270404	Hs.193161	ESTs	7.1
60	435403	AA779987	Hs.269658	ESTs	7.1
	430151	AW968203		gb:EST380398 MAGE resequences, MAGJ Homo sapiens cDNA	7.1
	427908	AA417272	Hs.24122	ESTs	7.1
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitter transporter	7.1
	400098			Eos Control	7.1
65	412647	AW975090		gb:EST387196 MAGE resequences, MAGN Homo sapiens cDNA	7.1
	437234	AI472213	Hs.247711	hypothetical protein FLJ20557	7.1
	453366	AW958751	Hs.28921	zinc finger protein	7.1
	425803	AI825204	Hs.211408	ESTs	7.1
70	447383	N24231		gb:yx22a11.r1 Soares melanocyte 2NbHM Homo sapiens cD	7.1
	423864	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (gamma)	7.1
	450799	AW407504		gb:UI-HF-BMO-adj-g-12-0-UI.r1 NIH_MGC_38 Homo sapiens	7.1
	409592	BE280951	Hs.55058	EH-domain containing 4	7.1
	453945	NM_005171	Hs.36908	activating transcription factor 1	7.1
	425196	AL037915	Hs.155097	carbonic anhydrase II	7.0
75	439778	AL109729	Hs.99364	putative transmembrane protein	7.0
	417662	R07478	Hs.268845	ESTs	7.0
	438087	AI863770	Hs.190422	ESTs	7.0
	452724	R84810	Hs.30464	cyclin E2	7.0
	448633	AA311426	Hs.21635	tubulin, gamma 1	7.0
80	433154	AA578526	Hs.160994	ESTs	7.0
	440094	AI651558	Hs.270372	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.0
	409253	H91200	Hs.52002	CD5 antigen-like (scavenger receptor cysteine rich fa	7.0
	431270	BE046609		gb:hn41e11.x1 NCL_CGAP_RDF2 Homo sapiens cDNA clone 3	7.0
	407629	AA649242	Hs.62632	ESTs	7.0

5	408296	AL117452	Hs.44155	DKFZP586G1517 protein	7.0
	445439	BE243084	Hs.12719	regulator of nonsense transcripts 1	7.0
	427106	AA398193	Hs.97584	ESTs	7.0
	408623	AW811978	Hs.254037	ESTs	7.0
	426561	AA381437		gb:EST94514 Activated T-cells I Homo sapiens cDNA 5'	7.0
10	408492	AA555217	Hs.183684	eukaryotic translation initiation factor 4 gamma, 2	7.0
	428894	AA437066	Hs.271736	ESTs	7.0
	419102	AA234098	Hs.42424	ESTs, Weakly similar to 2004399A chromosomal protein	7.0
	429067	AA446019	Hs.104967	ESTs	7.0
	422684	BE561617	Hs.119192	H2A histone family, member Z	7.0
15	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase 5	7.0
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H.	7.0
	443599	AI079559	Hs.134125	ESTs	7.0
	400715			ENSP00000237081*KIAA1217 PROTEIN (FRAGMENT).	7.0
	446514	AW449233	Hs.150847	ESTs	7.0
20	413992	W26276	Hs.136075	RNA, U2 small nuclear	7.0
	402442			Target Exon	7.0
	419497	NM_006410	Hs.90753	Tat-interacting protein (30kD)	7.0
	439575	W79259		gb:zd75c06.r1 Soares_fetal_heart_NbHH19W Homo sapiens	7.0
	407027	U63312		gb:Human cosmid LL12NC01-242E1, ETV6 gene, exons 1B a	7.0

Table 15B

25	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
30	Pkey	CAT Number	Accessions	
	408182	104479_1	AA047854 AA057506 AA053841	
	409113	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204	
35			AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070	
			AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209	
			AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053	
40			AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA065051 AA079143 AA071110	
			AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200	
			AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929	
45	409206	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659	
	409857	1156298_1	AW501908 AW502959 AW502540	
	410146	1178974_1	AW592655 R05927 R06916	
50	410536	1207322_1	N39533 AW753094 AW753093	
	411298	1237955_1	AW835858 AW835836 AW835823 AW835834 AW835831 AW835832 AW835843 AW835816 AW835833 AW835815 AW835849 AW835835	
			AW835848 AW835851 AW835852 AW835862 AW835855 AW835825 AW835847 AW835838	
55	412406	1293055_1	AW948172 AW948178 AW948169 AW948176 AW948191 AW948186 AW948184 AW948187 AW948188 AW948189 AW948181	
			AW948177 AW948171 AW948183 AW948173	
	412647	1317604_1	AW975090 N44182	
60	413258	1355998_1	BE075114 BE075283 BE075118	
	413314	1360034_1	BE081585 BE081717 BE081863 BE081794 BE081659	
	413500	1373933_1	BE144914 BE394989	
65	414076	141490_1	AA467736 AA135210 AW968166 AA467804	
	416450	159551_1	AA180467 AA449184 AA464831 AA505048	
	417247	1660859_1	N58024 T58194 T11693 N64222 T05848	
70	417739	1696198_1	Z43995 R12357 R34740	
	417881	170544_1	AI879117 AW161351 Z45755 BE003661 AA206949 AA476541	
	418347	174149_1	AA216419 F03238 AA229517	
75	422429	216469_1	AA310527 AW962295 Z44865 H06641	
	423573	229714_1	AA328504 AA327783 AW962370	
	426561	269158_1	AA361437 AA628833 AW407275	
80	428294	289365_1	AA425488 AA496895 F23221	
	430146	313562_1	AW815330 AW968170 AI732687 AI732725 AA468343 AA467817 AW063961	
	430151	313668_1	AW968203 AI732757 AA470353 AA468025 AA468479 AI734151	
85	430709	322338_1	R34356 AW969880 AA484613	
	430848	324621_1	AW021726 AA487752 AA488085	
	431150	328626_1	T63857 AW971220 AA493469 T63699	
90	431270	330676_1	BE046609 BE046118 AA501504	
	432363	345469_1	AA534489 AW970240 AW970323	
	434197	381655_1	AA627223 AA643443 AA650519 AA643463 AA643453 AA643439 AA643438 AW802964 AW821595 AW821594 AA643431 AA643432	
95			AW827513	
	434407	385744_1	AW815333 AW815409 AA632563	
	434410	385798_1	AA632644 AA635376 AA664188	
100	436910	429182_1	AA926944 AA767974 AA737237	
	437056	432262_1	AI147061 AA743380 AA765223 AW976398 AI803927	
	439354	47146_1	AF086174 W31796 W04694	
105	439575	47400_1	W79259 AF086396 W73927	
	444314	600667_1	AI140497 AW749625 AW749626 AW749644	
	447197	711623_1	R36075 AI366546 R36167	
110	447383	71990_1	N24231 BE617964 N36313	
	450799	847242_1	AW407504 W31274 AI738877	
	450872	849959_1	AI742594 AI761397 R31198 AI819332 R31257	
115	454355	1130264_1	AW812535 AW812536 AW390307	
	454639	1227728_1	AW811633 AW811652 AW811898	
	454765	1233905_1	AW819629 AW854320	



BE075431 AW815917 AW998359 AW799883 AW603782 AA557480 AW841444 BE075915 AA548034 AW843393 AW391559 BE083265 AW939721  
 AW800857 AW079109 AW364901 AI435993 AA985526 AW799848 BE182463 AA776111 AW799915 BE008399 BE075377 AW577809 BE010272  
 BE182443 BE010296 AW577806 BE008415 BE184036 BE076597 AI817413 AW795053 AW896761 AW841433 BE182458 AW603796 AW842676  
 BE085455 AW884879 BE075414 AW838836 AW878273 AW998088 AW799778 AW899125 BE082247 AA774870 BE001401 BE001485 AW817297  
 AW796670 AW394063 BE001396 AW394070 AW603797 BE182447 AW582483 AW843283 AW749520 AW867449 AW899274 AW578232  
 AW603765 AW843919 AW578235 BE184139 AW997742 BE183923 BE084210 AW802033 AW748724 AW939018 AW997459 AW842742 AA213697  
 BE182308 BE011078 AW607702 AW882623 BE080016 AW580994 BE076531 AA443462 AW607407 AW883382 AW939399 AW605627 AW844615  
 AW939724 AW815931 AW883765 AA287421 BE075626 AW946171 AW841445 AW797994 AW815957 AA683300 AW369004 BE075368 BE081560  
 AW605626 AW939398 AA507280 AA506317 AW841230 AW992519 AA465332 AA425246 BE090234 BE090236 AA483259 AA451961 AA535566  
 AA506406 AA888571 AA503568 AA507130 AA532944 AA501672 BE168634 AA492022 AA507662 AW842286 AA494226 AA776038 AA442419  
 AW579900 BE171816 AA863065 AA491916 AA447490 AA461423 AA434543 AA243279 AW997466 AW603740 BE000295 AA658571

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA  
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400715	8118885	Minus	80151-80297
400736	8118985	Plus	143447-143851
401008	8117391	Minus	81421-81551,82364-82512,82862-82938
401069	3927852	Minus	45682-45831
401375	7417809	Minus	6121-6766
401405	7768126	Minus	69276-69452,69548-69958
401539	8072433	Minus	62028-62608
401557	8099866	Minus	112785-112924
401654	9097132	Minus	64695-64797
401940	3738108	Plus	153460-153592
402025	7547159	Plus	173835-173998
402442	9796503	Plus	141714-141842,142010-142122
402682	8138477	Minus	147522-147795
402796	3646083	Minus	6126-6265,6416-6689
402967	5360987	Minus	33518-34546
403038	7717439	Minus	290021-290284
403055	8748904	Minus	109532-110225
403310	8139936	Minus	183883-184026
403397	9438368	Minus	84481-84655
403839	4176355	Plus	21201-22223
404110	9212839	Minus	18344-18510
404495	8151634	Minus	59449-60477
404534	8247909	Minus	147853-148086
404630	9796665	Plus	74495-74715
404649	9796926	Minus	100027-100399
404680	9797204	Minus	159810-159979,160213-160321,161023-161304,162862-163140,164490-164644,166404-166530,166936-167083,167392-167522
404914	7341760	Plus	92603-92827
405417	4753290	Minus	50704-51499
405454	7656675	Plus	133807-134053
405510	7630909	Minus	101028-101174
405514	9454624	Plus	35953-36151
405536	9795661	Plus	164091-164162,164397-164516,166720-166790,167785-167935
406016	8272661	Plus	41341-41940
406410	9256394	Minus	115806-116104
406464	9789674	Plus	72161-72562
406562	7711584	Plus	37316-37426

TABLE 16A: 200 GENES DOWN-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

Table 16A shows 200 genes down-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 15A, except that the numerator and denominator were switched, the median value amongst normal cervixes was greater than or equal 40 units, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal cervix).

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of cervical cancer to normal cervix

Pkey	ExAccn	UnigenelD	Unigene Title	R1
453596	AA441838	Hs.62905	hypothetical protein FLJ14834	18.1
443912	R37257	Hs.184780	ESTs	16.8
420923	AF097021	Hs.273321	differentially expressed in hematopoietic lineages	13.6
414422	AA147224	Hs.337232	Homeo box A13	13.1
420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT2RP2002672	12.9
412639	AW961284	Hs.296235	ESTs	12.4

	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	12.4
	407938	AA905097	Hs.85050	phospholamban	11.3
	410544	AI446543	Hs.95511	ESTs	11.3
5	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	11.1
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 protein [H.sapiens]	11.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	10.9
	453060	AW294092	Hs.21594	hypothetical protein MGC15754	10.6
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia induci	10.5
10	452106	AI141031	Hs.21342	ESTs	9.5
	428780	AI478578	Hs.50636	ESTs	9.5
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	9.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PLACE1002968	9.0
	430468	NM_004673	Hs.241519	angiopoietin-like 1	9.0
15	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	8.7
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activin receptor inte	8.6
	401486	NA		C4000647*:gij4758508[ref NP_004253.1 ] airway trypsin-li	8.4
	417511	AL049176	Hs.82223	chordin-like	8.3
	429900	AA460421	Hs.30875	ESTs	8.2
20	411908	L27943	Hs.72924	cytidine deaminase	8.0
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiesterase	8.0
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFp586P1124 (from clone DKFZp	8.0
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	8.0
	421666	AL035250	Hs.1408	endothelin 3	7.9
25	450164	AI239923	Hs.30098	ESTs	7.9
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A; scatter factor	7.7
	425608	AA360486	Hs.92448	ESTs	7.6
	442748	AI016713	Hs.135787	ESTs	7.3
	415672	N53097	Hs.193579	ESTs	7.2
30	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	7.2
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	7.0
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nucleotide pyroph	6.7
	414214	D49958	Hs.75819	glycoprotein M6a	6.5
	436637	AI783629	Hs.26766	ESTs	6.5
35	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	6.5
	432101	AI918950	Hs.123642	EphA3	6.3
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA, complete cds	6.3
	424153	AA451737	Hs.141496	MAGE-like 2	6.3
	420228	R25023	Hs.12369	ESTs	6.2
40	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myotilin)	6.1
	444931	AV652066	Hs.75113	general transcription factor IIIA	6.1
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HEMBA1002970	6.1
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	6.1
	410425	BE278367	Hs.63510	KIAA0141 gene product	6.0
45	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	6.0
	424973	X92521	Hs.154057	matrix metalloproteinase 19	6.0
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like 1	5.9
	429414	AI783656	Hs.202095	empty spiracles (Drosophila) homolog 2	5.9
	440594	AW445167	Hs.126036	ESTs	5.9
50	452768	AW069459	Hs.61539	ESTs	5.9
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 protein [H.sapiens	5.9
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	5.9
	425010	T16837	Hs.4241	ESTs	5.9
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.8
55	437980	R50393	Hs.278436	KIAA1474 protein	5.8
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	5.7
	404097	NA		C5000242*:gij9369379[gb]AAF87128.1 AC006434_24 (AC00643	5.7
	422546	AB007969	Hs.301478	KIAA0500 protein	5.7
	445872	AI681573	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HEMBB1001458	5.7
60	429999	AI761902	Hs.99597	ESTs	5.6
	453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB1002492	5.6
	442082	R41823	Hs.7413	ESTs	5.5
	452073	AA625150	Hs.82098	ESTs	5.4
	430032	AW936136	Hs.99610	ESTs	5.4
65	408767	AA057279	Hs.211928	ESTs	5.4
	433234	AB040928	Hs.65366	KIAA1495 protein	5.3
	431708	AI698136	Hs.108873	ESTs	5.3
	421200	AA284811	Hs.264433	ESTs	5.2
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HEMBA1001008	5.2
70	409643	AW450866	Hs.257359	ESTs	5.1
	416676	AW392022	Hs.79507	KIAA0582 protein	5.1
	420357	U94333	Hs.97199	complement component C1q receptor	5.0
	417355	D13168	Hs.82002	endothelin receptor type B	5.0
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL06674	5.0
75	430965	AA489732	Hs.154918	ESTs	4.9
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	4.9
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	4.8
	404485	NA		Target Exon	4.8
	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fis, clone HEMBB1001024	4.8
80	417692	R09338	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OVARC1000640	4.8
	432304	AA932186	Hs.69297	ESTs	4.7
	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.7
	448851	AI582207	Hs.177166	ESTs	4.7
	405523			C8001409*:gij7441226[pir]S31212 collagen alpha 1(XIV)	4.7

	450656	AA010539	Hs.18912	ESTs	4.6
	422942	AF054839	Hs.122540	tetraspan 2	4.6
	401479	T49304	Hs.110950	Rag C protein	4.6
5	444192	AW469413	Hs.151145	ESTs	4.6
	439648	AW780192	Hs.267596	ESTs	4.5
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, member 4	4.5
	444702	AI220122	Hs.326560	hypothetical protein MGC2780	4.5
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX	4.5
10	452249	BE394412	Hs.202095	empty spiracles (Drosophila) homolog 2	4.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	4.5
	411037	BE145915	Hs.99472	ESTs	4.4
	442803	AI675298	Hs.199917	ESTs	4.4
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulatory, type II, be	4.4
15	400628	NA		C10001871*:gij1705533[sp P32018]CA1E_CHICK COLLAGEN ALP	4.3
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage serine esterase	4.3
	437110	AL049240	Hs.144995	ESTs	4.2
	410646	W79408	Hs.50745	ESTs	4.2
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens cDNA clone, mRNA	4.2
20	401270			Target Exon	4.2
	419447	BE092696	Hs.75928	ESTs	4.2
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	4.2
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	4.2
	434469	AA634806		gb:ab28c02.r1 Stratagene lung (937210) Homo sapiens cDN	4.1
25	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR	4.1
	418947	W52990	Hs.22860	ESTs	4.1
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.0
	454736	BE184348		gb:CM0-HT0676-010500-355-e11 HT0676 Homo sapiens cDNA,	4.0
	407945	X69208	Hs.606	ATPase, Cu transporting, alpha polypeptide (Menkes synd	4.0
30	447499	AW262580	Hs.147674	protocadherin beta 16	4.0
	430686	NM_001942	Hs.2633	desmoglein 1	4.0
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (cardiovascula	3.9
	419047	AW952771	Hs.90043	ESTs	3.9
	414272	AI651603	Hs.46988	ESTs	3.9
35	443808	AW377736	Hs.12420	ESTs	3.9
	426883	H21520	Hs.35088	ESTs	3.9
	410659	AI080175	Hs.68826	ESTs	3.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.9
	432181	AA527650	Hs.156037	ESTs	3.9
40	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.8
	453296	AA034413	Hs.62560	ESTs	3.8
	400878	NA		Target Exon	3.8
	401103	NA		C12001233:gij7305361[ref NP_038652.1  otogelin [Mus mus	3.8
45	436670	AI690021	Hs.201536	ESTs	3.7
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface receptor	3.7
	408793	BE258371	Hs.254660	ESTs	3.7
	419093	AI804054	Hs.112885	spinal cord-derived growth factor-B	3.7
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	3.7
	450776	NM_007250	Hs.320861	Kruppel-like factor 8	3.7
50	437140	AA312799	Hs.283689	activator of CREM in testis	3.6
	418421	R58620	Hs.85050	phospholamban	3.6
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOTHETICAL PROTEIN	3.6
	417194	N53793		gb:yz07a01.r1 Soares_multiple_sclerosis_2NbHMSF Homo sa	3.6
	443567	AI077540	Hs.134090	ESTs	3.6
55	451879	AI821030		gb:yb52f11.y5 Stratagene ovary (937217) Homo sapiens cD	3.6
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.5
	451896	AF196304	Hs.27197	SUMO-1-specific protease	3.5
	413237	AI468574	Hs.171965	ESTs	3.5
	424636	AA453734	Hs.10198	ESTs	3.5
60	432660	AI288430	Hs.64004	ESTs	3.5
	414681	AL079440	Hs.74002	nuclear receptor coactivator 1	3.5
	400802	NA		Target Exon	3.5
	430015	AW768399	Hs.112157	ESTs	3.5
	451978	AW813747	Hs.27371	Homo sapiens mRNA; cDNA DKFZp566J123 (from clone DKFZp5	3.5
65	449088	AI654048	Hs.196556	ESTs	3.5
	425113	AI936992	Hs.154658	pleckstrin and Sec7 domain protein	3.5
	458459	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone COL09609	3.5
	420249	BE262895	Hs.276916	nuclear receptor subfamily 1, group D, member 1	3.5
	401159	NA		Target Exon	3.5
70	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQ	3.5
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5 [H.sapiens]	3.4
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC FINGER PROTEIN	3.4
	423587	AA328074	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia induci	3.4
	443178	AI631241	Hs.47312	ESTs	3.4
75	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTONE H2B H [H.sap	3.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Drosophila) homol	3.4
	437950	U79244	Hs.112642	ESTs	3.3
	419368	AI753518	Hs.209464	KIAA1604 protein	3.3
	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	3.3
80	451398	AI793124	Hs.144479	ESTs	3.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	3.3
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, expressed in pro	3.3
	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	3.3
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	3.3



444216	D25303	Hs.222	integrin, alpha 9	3.3
418771	AA807881	Hs.25329	ESTs	3.3
433036	AA574091	Hs.105964	ESTs	3.2
404584			Target Exon	3.2
404195			NM_015718*:Homo sapiens NADPH oxidase 3 (NOX3), mRNA. V	3.2
428819	AL135623	Hs.193914	KIAA0575 gene product	3.2
425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
420833	R47948	Hs.188732	ESTs	3.1
413156	AA127133		gb:zl87e03.r1 Stratagene colon (937204) Homo sapiens cD	3.1
413607	T64741		gb:yc48f11.r1 Stratagene liver (937224) Homo sapiens cD	3.1
443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.1
428790	AF023456	Hs.193558	protein phosphatase, EF hand calcium-binding domain 2	3.1
434520	AA205273	Hs.177011	hypothetical protein	3.1
432247	AA531287	Hs.105805	ESTs	3.1
429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	3.1
439734	AC005013	Hs.149	cAMP response element-binding protein CRE-BPa	3.1
433546	AI075877	Hs.125461	hypothetical protein FLJ11539	3.0
430317	AB020645	Hs.239189	glutaminase	3.0
425130	AA448208	Hs.99163	ESTs	3.0
444195	AB002351	Hs.10587	KIAA0353 protein	3.0
409007	AL122107	Hs.49599	Homo sapiens mRNA; cDNA DKFZp434G0827 (from clone DKFZp	3.0
453773	AL133761		gb:DKFZp761C1413_r1 761 (synonym: hamy2) Homo sapiens c	3.0
442974	AI025670	Hs.109308	ESTs, Weakly similar to leucine-rich glioma-inactivated	3.0
446936	H10207	Hs.47314	ESTs	3.0
454086	AW885909	Hs.6975	PRO1073 protein	3.0
420271	AI954365	Hs.42892	ESTs	3.0
435545	AA687415	Hs.28107	ESTs	3.0
445175	AV652851	Hs.20255	ESTs	3.0

TABLE 16B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
413156	135116_1	AA127133 AA384396 AW958912 T72119
413607	1379911_1	T64741 BE158393 BE152805
417194	1657323_1	N53793 N53716 N53739
434469	387447_1	AA634806 C18732 AA729161 AA729860
451879	888642_1	AI821030 T47126 AI821318
453773	980699_1	AL133761 AL133767
454736	1232235_1	BE184348 AW817453 BE011068
456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101

TABLE 16C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400628	3818355	Plus	41851-41984
400802	8567867	Minus	174571-174856
400878	9864757	Plus	31493-32842
401103	8568122	Minus	98330-98449
401159	6067118	Minus	3180-3953
401270	9797168	Minus	141659-141813
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
404097	7770701	Plus	55512-55781
404195	3805917	Minus	39186-39332
404485	8096921	Plus	75166-75264,124036-124232
404584	9857511	Plus	138651-139153
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

TABLE 17A: 605 genes upregulated in testicular cancer relative to normal body tissues

Table 17A lists about 605 genes upregulated in cervical cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar accession number, GenBank accession number  
UniGeneID: UniGene number  
Pred.Proto.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M,

UniGene Title: likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).  
 R1 UniGene gene title  
 95th percentile of cervical cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigenID; Unigene Title; Pred.Prot.Domains; R1

408522; AI541214; Hs.46320; Small proline-rich protein SPRK [human; ; none,Cornifin; 33.942  
 422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psorias; ehand,S\_100;TM=M;SS=N; 33.05  
 424098; AF077374; Hs.139322; small proline-rich protein 3; Cornifin;TM=M;SS=N; 32.856  
 422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap;TM=M;SS=Y; 29.604  
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR\_LY6,toxin,Activin\_recpt;TM=M;SS=Y; 27.95054945  
 421948; L42583; Hs.334309; keratin 6A; filament,RhoGAP,DUF286,bZIP,Tropomyosin,tubulin,DUF164,TBCA,Collagen;TM=M;SS=N; 26.778  
 446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium\_transp,FecCD;TM=Y;SS=M; 26.1133829  
 407242; M18728; ; gb:Human nonspecific crossreacting antig; ig;TM=M;SS=M; 23.382  
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2,hemopexin,Peptidase\_M10;; 22.522  
 412719; AW016610; Hs.816; ESTs; none,none; 21.198  
 406690; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; ig;TM=M;SS=M; 20.028  
 402075; ; ENSP00000251056\*:Plasma membrane calcium; none;; 19.038  
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin,Cadherin\_C\_term;TM=Y;SS=M; 17.92061281  
 412471; M63193; Hs.73946; endothelial cell growth factor 1 (platelet; Glycos\_transf\_3,Glycos\_trans\_3N;TM=M;SS=M; 17.8978979  
 417308; H60720; Hs.81892; KIAA0101 gene product; none;TM=M;SS=N; 17.08333333  
 429259; AA420450; Hs.380088; Plakophilin; none,none; 17.08235294  
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;; 16.91568628  
 439926; AW014875; Hs.137007; ESTs; none,none; 16.69  
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1\_PLM\_MAT8;TM=Y;SS=M; 16.365  
 413753; U17760; Hs.75517; laminin, beta 3 (nicein (125kD), kalinin; laminin\_EGF,laminin\_Nterm;; 15.75294118  
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin;; 15.48600509  
 401781; ; Target Exon; filament;TM=M;SS=N; 15.43668831  
 420440; NM\_002407; Hs.97644; mammaglobin 2; Uteroglobin;; 15.394  
 441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none;TM=M;SS=M; 15.12264151  
 452240; AI591147; Hs.61232; ESTs; none,none; 14.63  
 428957; NM\_003681; Hs.194679; WNT1 inducible signaling pathway protein; tsp\_1,vwc,IGFBP;TM=M;SS=M; 14.49772727  
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;SS=N; 14.4389313  
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis, clone PL; none,none; 14.00909091  
 400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin,Peptidase\_M10,Astacin;; 13.824  
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 13.7754386  
 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;; 13.74595843  
 400284; ; NM\_000125\*:Homo sapiens estrogen recepto; hormone\_rec,zf-C4,Oest\_recep;TM=M;SS=M; 13.31578947  
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 13.05294118  
 411274; NM\_002776; Hs.69423; kallikrein 10; trypsin;TM=M;SS=N; 13.038  
 406687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase\_M10;; 13.00311527  
 427666; AI791495; Hs.180142; calmodulin-like skin protein (CLSP); ehand;TM=M;SS=N; 12.79  
 400301; X03635; Hs.1657; estrogen receptor 1; F-box,hormone\_rec,zf-C4,Oest\_recep,adh\_zinc,ketoacyl-synt,pp-binding,Acyl\_transf,Thioesterase,ketoacyl-synt\_C,AAA,E7,RFX\_DNA\_binding;TM=M;SS=N; 12.472  
 410001; AB041036; Hs.57771; kallikrein 11; trypsin;TM=M;SS=M; 12.47  
 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none,pkinase,fn3,ig; 12.28597122  
 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M;SS=N; 12.13379205  
 437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none;TM=M;SS=M; 12.04945055  
 418462; BE001596; Hs.85266; integrin, beta 4; fn3,integrin\_B,Ca1x-beta,EGF;TM=M;SS=M; 11.95538462  
 443859; NM\_013409; Hs.9914; follistatin; kazal;; 11.95467422  
 426350; NM\_003245; Hs.2022; transglutaminase 3 (E polypeptide, prote; Transglutamin\_N,Transglutamin\_C,Transglut\_core;TM=M;SS=N; 11.61  
 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;SS=N; 11.564  
 444781; NM\_014400; Hs.11950; GPI-anchored metastasis-associated prote; UPAR\_LY6,lactamase\_B; 11.55285714  
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ; aa\_permeases,pyridoxal\_deC,bromodomain,PHD,MBD,AT\_hook,DDT,PI3\_Pi4\_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 11.47956989  
 418663; AK001100; Hs.41690; desmocollin 3; cadherin,Cadherin\_C\_term,none; 11.456  
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none;; 11.45352113  
 423217; NM\_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolys; Kunitz\_BPTI,fn3,vwa,Collagen,beta-lactamase;TM=M;SS=M; 11.32234432  
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7trn\_3;TM=Y;SS=M; 11.28686327  
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none,none; 11.076  
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo\_seg;TM=M;SS=N; 11.0381579  
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 11  
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin,Peptidase\_M10;TM=M;SS=M; 11  
 425071; NM\_013989; Hs.154424; deiodinase, iodothyronine, type II; T4\_deiodinase;TM=M;SS=Y; 10.93859649  
 437938; AI950097; Hs.369628; gb:wq05c02.x1 NCI\_CGAP\_Kid12 Homo sapien; none,none; 10.78064516  
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 10.74825175  
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1\_HUMAN DEATH; none,none; 10.542  
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC,none; 10.49538462  
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none;TM=M;SS=Y; 10.48210736  
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A recepto; Neur\_chan\_LBD,Neur\_chan\_memb;TM=Y;SS=M; 10.26714286  
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC\_tran,M,SMC\_N,SMC\_C,DUF164,none; 10.142  
 421508; NM\_004833; Hs.105115; absent in melanoma 2; PAAD\_DAPIN,HIN;TM=M;SS=N; 10.1  
 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin,Repolyisin,Pep\_M12B\_propep,EGF;TM=Y;SS=M; 10.072  
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA\_gyraseB,DNA\_topoisolV,HATPase\_;; 9.996363636  
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor; serpin;; 9.896825397  
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M;SS=N; 9.888888889  
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 9.876056338  
 424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD\_NFYB\_HMF;; 9.851635514  
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone\_rec,zf-C4,none; 9.840720222  
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM\_PNT,none; 9.823170732  
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); ehand,spectrin,GAS2,SH3,Plectin,RA,Xylose\_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,Idh\_C,CH,AIP3;TM=M;SS=N; 9.812

- 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S.; MCM,aldo\_ket\_red;TM=M;SS=N; 9.787878788  
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;SS=N; 9.637037037  
 425650; NM\_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin;TM=M;SS=M; 9.596  
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevi; WD40;TM=M;SS=N; 9.558  
 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase\_2;TM=Y;SS=M; 9.55  
 421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 9.529085873  
 408591; AF015224; Hs.46452; mammaglobin 1; Uterogloblin;TM=M;SS=M; 9.506  
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 9.477961433  
 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; ldl\_recept\_a,PKD,MHC\_I;TM=M;SS=Y; 9.415151515  
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8;; 9.408  
 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 atrophin-; ras;TM=M;SS=N; 9.36  
 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo\_seg;TM=M;SS=N; 9.315693431  
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 9.31  
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 9.29  
 454034; NM\_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh;; 9.264  
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN\_MK;TM=M;SS=Y; 9.241561181  
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank;; 9.207272727  
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 9.195167286  
 439223; AW238299; Hs.256018; UL16 binding protein 2; ldl\_recept\_a,PKD,MHC\_I;TM=M;SS=Y; 9.108  
 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA;TM=Y;SS=N; 9.028  
 421777; BE562088; Hs.108196; HSPC037 protein; none;TM=M;SS=N; 9.004  
 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A recepto; Neur\_chan\_LBD,Neur\_chan\_memb;TM=Y;SS=M; 9.001096491  
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;SS=N; 9.942  
 455601; A1368680; Hs.816; SRY (sex determining region Y)-box 2; HMG\_box;; 8.87  
 429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin;TM=Y;SS=M; 8.77131783  
 456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4,Cbl\_N,Cbl\_N3;TM=M;SS=N; 8.738  
 430397; A1924533; Hs.105607; bicarbonate transporter related protein ; HCO3\_cotransp;TM=Y;SS=N; 8.736  
 417034; NM\_006183; Hs.80962; neurotensin; none;; 8.592  
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 8.536  
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm\_3,none; 8.49  
 439285; A1133916; Hs.47860; hypothetical protein FLJ20093; ig, pkinase,LRR,LRRNT,LRRCT,none; 8.460655738  
 409420; Z15008; Hs.54451; laminin, gamma 2 (nicein (100kD), kalini; laminin\_B,laminin\_EGF;; 8.414  
 438746; A1885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanylate\_kin,PDZ,SH3; 8.376205788  
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm\_1;TM=Y;SS=M; 8.37  
 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 8.364  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSFp,Y\_phosphatase,Ribosomal\_S3\_N;TM=M;SS=N; 8.266  
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 8.248314607  
 431620; AA126109; Hs.264981; 2'-5'-oligoadenylate synthetase 2 (69-71; NTP\_transf\_2;TM=M;SS=N; 8.156  
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M;SS=N; 8.142857143  
 448733; NM\_005629; Hs.187958; solute carrier family 6 (neurotransmitte; SNF;TM=Y;SS=N; 8.137559809  
 427557; NM\_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR\_LY6,ET,PLA2\_inh;; 8.043478261  
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; DNA\_ligase;; 8.038194444  
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y\_phosphatase,DSFp;TM=M;SS=N; 8.024752475  
 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none;TM=Y;SS=M; 8  
 424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibitor; serpin;TM=M;SS=N; 7.982  
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.973684211  
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR\_c6,Acyl-CoA\_hydro; 7.892  
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 7.824  
 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC\_tran,ABC\_membrane,SRP54,Thymidylate\_kin;TM=Y;SS=M; 7.823874755  
 431630; NM\_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP,Rhabd\_glycop,integrin\_A;TM=Y;SS=M; 7.758985201  
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3;TM=M;SS=Y; 7.75887574  
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC\_tran,CoaE;TM=M;SS=N; 7.757751938  
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd\_glycop;TM=Y;SS=M; 7.624  
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone\_rec,zf-C4,none; 7.605660377  
 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M;SS=N; 7.578  
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 7.476  
 429299; A1620463; Hs.347408; hypothetical protein MGC13102; none;TM=Y;SS=N; 7.442528736  
 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm\_3,none; 7.442495127  
 446163; AA026880; Hs.25252; prolactin receptor; none;NA;NA; 7.436781609  
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant\_thionins;; 7.435897436  
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,pkinase,Recep\_L\_domain,YLP,none; 7.398360656  
 432636; AA340864; Hs.278562; claudin 7; PMP22\_Claudin;TM=Y;SS=M; 7.394039735  
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subuni; vwa,integrin\_A,FG-GAP;TM=Y;SS=M; 7.383419689  
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none,none; 7.382  
 436972; AA284679; Hs.25640; claudin 3; PMP22\_Claudin;TM=Y;SS=M; 7.327160494  
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 7.316  
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT\_bind,STAT\_prot;TM=M;SS=N; 7.315412186  
 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;SS=N; 7.2984375  
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 7.28  
 451253; H48299; Hs.26126; claudin 10; PMP22\_Claudin,Peptidase\_M1,K\_tetra;TM=Y;SS=M; 7.256802721  
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase;; 7.234455959  
 421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC\_tran,ABC\_membrane,GTP\_EFTU;TM=M;SS=M; 7.162534435  
 451035; AU076785; Hs.430; plastin 1 (I isoform); ehfand,CH,Adaptin\_N;; 7.145454546  
 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm\_1;TM=Y;SS=M; 7.126  
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm\_1;TM=Y;SS=M; 7.122413793  
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX ; Troponin,Exo\_endo\_phos,IQ;TM=M;SS=N; 7.106719368  
 430890; X54232; Hs.2699; glypican 1; Glypican;TM=M;SS=M; 7.088937093  
 407792; A1077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 7.052  
 426514; BE616633; Hs.170195; bone morphogenetic protein 7 (osteogenic; TGF-beta,TGFB\_propeptide;; 7.042  
 431241; AA496799; Hs.36958; ESTs; SH2,RasGEF,none; 7.03  
 437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm\_1;TM=Y;SS=M; 7.03  
 420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-530115; none,none; 7.026  
 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none;TM=M;SS=N; 7.008

- 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3,PX;TM=M;SS=N; 6.991626794  
 416250; AA581386; Hs.73452; Kremen 2; kringle,CUB,WSC;; 6.972  
 430770; AA765694; Hs.123296; ESTs; none,none; 6.95  
 418869; AW516565; ; gb:qx01d05.x1 Soares\_NHCCc\_cervical\_tumo; none,RasGAP,WW,IQ; 6.948  
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily; 60s\_ribosomal,Ribosomal\_L10,TNFR\_c6,DEAD;; 6.914  
 418283; S79895; Hs.83942; cathepsin K (pseudosyostosis); Peptidase\_C1;; 6.876190476  
 419667; AU077005; Hs.92208; a disintegrin and metalloproteinase domain; disintegrin,Repolyisin,Pep\_M12B\_propep;TM=M;SS=M; 6.862970711  
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing Ig; ig,LRR,LRNT,LRCT;TM=M;SS=M; 6.849056604  
 456181; L36463; Hs.1030; ras inhibitor; RA,SH2,VPS9;TM=M;SS=N; 6.762  
 436856; A169355; Hs.127310; ESTs; pkinase,rrm;TM=M;SS=N; 6.721428571  
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 6.720348837  
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH\_C,IMPDH\_N,CBS,integrin\_B,Ricin\_B\_lectin; 6.717307692  
 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2;TM=Y;SS=M; 6.715240642  
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo\_seg,UQ\_con,none; 6.688194444  
 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema,PSI,integrin\_B;TM=Y;SS=N; 6.670553936  
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;; 6.662921348  
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM,PDZ,pkinase;; 6.653713299  
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD\_DAPIN,HIN;; 6.652671756  
 426500; NM\_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M;SS=N; 6.639655172  
 438113; A1467908; Hs.8882; ESTs; 7tm\_1,none; 6.6  
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH,none; 6.6  
 408482; NM\_000676; Hs.45743; adenosine A2b receptor; 7tm\_1;TM=Y;SS=M; 6.548148148  
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin\_B;TM=Y;SS=M; 6.532763533  
 414809; A1434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=N; 6.526951673  
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar\_tr;TM=Y;SS=M; 6.512704174  
 420039; NM\_004605; Hs.376147; sulfotransferase family, cytosolic, 2B;; Sulfotransfer; 6.496  
 423031; A1278995; Hs.374579; ESTs; none,none; 6.447658402  
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion\_trans,K\_tetra,asp; 6.426666667  
 433933; A1754389; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none,NA,NA; 6.4  
 435094; A1560129; Hs.289008; EST; none,none; 6.312  
 432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3,PDZ,Guanylate\_kin,none; 6.276556777  
 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST\_C,EF1G\_domain,GST\_N,S1,Fz,Frizzled,calreticulin,7tm\_2,rrm,PAP\_assoc;TM=Y;SS=M; 6.272727273  
 435232; NM\_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank;TM=M;SS=N; 6.269720102  
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 6.219081272  
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin;TM=M;SS=N; 6.19  
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD,helicase\_C,CARD;TM=M;SS=N; 6.188888889  
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; ig,Isodh,Ribosomal\_L6,F-box;TM=Y;SS=M; 6.188046647  
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-Ii; AAA,NB-ARC,PAAD\_DAPIN,NA,NA; 6.15503876  
 450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta,TGFb\_propeptide;; 6.152  
 432314; AA533447; Hs.285173; ESTs; Xlink,none; 6.123040752  
 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase,PLAT;TM=M;SS=N; 6.12  
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; ig,pkinase;TM=Y;SS=M; 6.095758355  
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial; mito\_carr;TM=M;SS=N; 6.089164786  
 452683; A1089575; Hs.374574; progesterone membrane binding protein; homeobox,none; 6.06284153  
 445537; AJ245671; Hs.12844; EGF-like domain, multiple 6; EGF,MAM;; 6.05513308  
 444309; U83236; Hs.10803; calcium and integrin binding protein (DN; ehband;; 6.04015544  
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase\_C,rrm,Ndr,Cys\_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPC,isp\_1,Ribosomal\_S21,rvp;TM=M;SS=N; 6.009562842  
 438108; A1471795; Hs.287776; vanilloid receptor-related osmotically a; ank,ion\_trans;TM=Y;SS=N; 6.004  
 413869; NM\_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 5.984536083  
 405484; ; ; C3002124; gi|12737280|ref|XP\_006682.2| k; none;; 5.978964401  
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal\_L37ae,pkinase,POLO\_box,tRNA-synt\_1b,dynammin,dynammin\_2,GED,bZIP,M;; 5.978431373  
 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8;; 5.976  
 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y\_phosphatase;TM=M;SS=N; 5.969387755  
 411756; BE294350; Hs.71891; discoidin domain receptor family, member; pkinase,F5\_F8\_type\_C;TM=Y;SS=M; 5.95184136  
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 5.951550388  
 453459; BE047032; Hs.257789; ESTs; none,none; 5.95  
 456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=N; 5.938  
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-in; hemopexin,Peptidase\_M10;TM=M;SS=M; 5.917857143  
 414703; BE243877; Hs.380063; ATPase, Na? transporting, beta 3 polypep; Na\_K-ATPase;TM=Y;SS=M; 5.910455487  
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moi; NUDIX;TM=M;SS=M; 5.901886793  
 452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none,none; 5.868362832  
 418345; AJ001696; Hs.241407; serine (or cysteine) proteinase inhibitor; serpin;TM=Y;SS=M; 5.842  
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 11; Euk\_porin;TM=M;SS=M; 5.816363636  
 439625; AF086453; Hs.58611; ESTs; Fork\_head,glycolytic\_enzym,Na\_sulph\_symp; 5.811594203  
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 5.81  
 422765; AW049701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR;TM=M;SS=N; 5.806  
 415198; AW009480; Hs.943; natural killer cell transcript 4; none;TM=M;SS=N; 5.804137931  
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase,Furin-like,Recep\_L\_domain,none; 5.8  
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone\_rec,zf-C4,Metallothio\_5;TM=M;SS=N; 5.794  
 439335; AA742697; Hs.62492; NM\_052863;Homo sapiens secretoglobulin, fa; none;; 5.778588808  
 439246; A1498072; Hs.351474; membrane-associated tyrosine- and threon; ank,pkinase,UPF0073;; 5.763492064  
 452461; N78223; Hs.108106; transcription factor; zf-C3HC4,ubiquitin,PHD,YDG\_SRA;TM=M;SS=N; 5.728  
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 5.714634146  
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2,STAT,STAT\_bind,STAT\_prot,none; 5.701666667  
 419056; M89957; Hs.89575; CD79B antigen (immunoglobulin-associated; ig,ITAM;TM=Y;SS=M; 5.692  
 432269; NM\_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase,Sema,PSI,TIG,A4\_EXTRA;TM=M;SS=M; 5.686  
 452696; A1826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate\_kin,PDZ,SH3; 5.683673469  
 411030; BE387193; Hs.67896; 7-60 protein; none;TM=M;SS=N; 5.676767677  
 447131; NM\_004585; Hs.17466; retinoic acid receptor responder (tazaro; none;TM=Y;SS=N; 5.672977625  
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm\_1;TM=Y;SS=M; 5.666  
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; ptkB;TM=M;SS=N; 5.655616943

427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M; SS=N; 5.6485623  
 415010; NM\_004203; Hs.77783; membrane-associated tyrosine- and threonine; ank, pkinase, UPF0073; 5.648  
 452690; AI536070; Hs.15085; ESTs; pou, homeobox, lig\_chan, ANF\_receptor; 5.646  
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2, SH3, pkinase; TM=M; SS=N; 5.642405063  
 418703; NM\_014448; Hs.87435; Rho guanine exchange factor (GEF) 16; SH3, PH, RhoGEF, Birna\_VP3; TM=M; SS=N; 5.636  
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122; TM=M; SS=N; 5.635087719  
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M; SS=N; 5.620930233  
 432065; AA01039; Hs.2903; protein phosphatase 4 (formerly X), cata; Metallophos; TM=M; SS=N; 5.608352145  
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related; SH2, SH3, pkinase; TM=M; SS=N; 5.596052632  
 430696; AA531276; Hs.59509; ESTs; pkinase, PP2C, none; 5.575112108  
 435017; AA336522; Hs.12854; angiotensin II, type I receptor-associated; none; TM=Y; SS=M; 5.556910569  
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH, Lipase\_GDSL; TM=M; SS=N; 5.556195965  
 415012; NM\_004383; Hs.77793; c-src tyrosine kinase; SH2, SH3, pkinase; TM=M; SS=N; 5.555421687  
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; 5.549751244  
 413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidyl); SH2, SH3, C2, PH, PI-PLC-Y, PI-PLC-X, PDGF; 5.541366907  
 406621; X57809; Hs.181125; immunoglobulin lambda locus; ig, HSP70, Ppx-GppA; TM=M; SS=N; 5.54076087  
 417700; M36542; Hs.1101; POU domain, class 2, transcription factor; homeobox, pou; TM=M; SS=N; 5.536  
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M; SS=N; 5.52661597  
 436576; AI458213; Hs.77542; ESTs; 7tm\_1, DnaJ; 5.52638191  
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase, DAG\_PE-bind, pkinase\_C, OPR; TM=M; SS=N; 5.519672131  
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (f; MIF, sugar\_tr, none; 5.516453382  
 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR, LRRNT, LRRCT; TM=Y; SS=M; 5.514964789  
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; fn3, ig\_Y, phosphatase, MAM; TM=Y; SS=M; 5.494202899  
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC\_tran, ABC\_membrane; TM=Y; SS=M; 5.471947195  
 410608; AI538438; Hs.159087; ESTs; ubiquitin, integrin\_B, UBA, none; 5.465384615  
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin; TM=M; SS=N; 5.460076046  
 408716; AI567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein; ; UvrD-helicase, RNB, Runt; TM=M; SS=N; 5.450413223  
 426410; BE298446; Hs.305890; BCL2-like 1; Bcl-2, BH4, none; 5.444805195  
 457819; AA057484; Hs.35400; FLJ20522 Hypothetical protein FLJ20522; none, none; 5.444281525  
 422597; BE245909; Hs.118634; ATP-binding cassette, sub-family B (MDR); ABC\_tran, ABC\_membrane, PRK; TM=Y; SS=N; 5.437931035  
 429191; AF065215; Hs.198161; phospholipase A2, group IVB (cytosolic); C2, PLA2\_B, jmjC; TM=M; SS=N; 5.4375  
 449961; AW265634; Hs.133100; ESTs; pkinase, Furin-like, Recep\_L\_domain, none; 5.435211268  
 409012; AL117435; Hs.489725; DKFZP434I216 protein; PH, RhoGEF; TM=M; SS=M; 5.433333333  
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible Ik; pkinase, RIO1; TM=M; SS=N; 5.429657795  
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C, none; 5.423322684  
 423189; M59371; Hs.171596; EphA2; fn3, pkinase, SAM, EPH\_lbd; TM=Y; SS=M; 5.421621622  
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae); pkinase; TM=M; SS=N; 5.412  
 432527; AW975028; Hs.102754; ESTs; none, none; 5.40625  
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz, Frizzled, 7tm\_2; TM=Y; SS=M; 5.405504587  
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M; SS=N; 5.396  
 434467; BE552368; Hs.231853; Homo sapiens cDNA FLJ13445 f1, clone PL; 7tm\_1, none; 5.391472868  
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ; 5.389250814  
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC004358 3 U1 sm; none, none; 5.382  
 437016; AU076916; Hs.5398; guanine monophosphate synthetase; PHD, SET, zf-  
 CXXC, EGF, ank, notch, WW, FCH, GATase, GMP\_synt\_C, Occludin, YEATS, metalthio, EB, heme\_1, RCC1, ZZ, FeThRed\_A, ENTH, Band\_41, HECT; TM=M; SS=N; 5.373937677  
 424848; AI263231; Hs.327090; EST; SH3, PDZ, Guanylate\_kin, none; 5.36  
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate); MORN, sugar\_tr; TM=Y; SS=M; 5.35971223  
 405932; ; C15000305.gi3806122[gblAAC69198.1] (AF0); ras; TM=M; SS=N; 5.349226804  
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated); ig, ITAM, Zn\_clus; TM=Y; SS=M; 5.346153846  
 453143; AA382234; Hs.356289; protein tyrosine phosphatase, receptor t; serpin; 5.333667335  
 423973; AF038461; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase, PLAT; TM=M; SS=N; 5.33  
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none, none; 5.328  
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 5.316  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 5.309638554  
 410165; BE560228; Hs.71869; apoptosis-associated speck-like protein; PAAD, DAPI, CARD; TM=M; SS=N; 5.293560606  
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-t; fn3, Y\_phosphatase, carb\_anhydase; TM=Y; SS=M; 5.28  
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none, spectrin, SH3, PH, CH; 5.278947368  
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y; SS=N; 5.274746193  
 416207; NM\_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, comp; none; TM=Y; SS=M; 5.272222222  
 415117; AF120499; Hs.78016; polynucleotide kinase 3-phosphatase; Viral\_helicase1; TM=M; SS=N; 5.27  
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3, RhoGAP, FCH; TM=M; SS=N; 5.251865672  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc, Rhodanese, none; 5.248  
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 5.232  
 422017; NM\_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2; 5.212418301  
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; 5.209259259  
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphatase); Ribosomal\_L20, Na\_Pi\_cotrans; TM=Y; SS=N; 5.202  
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo\_endo\_phos, SH2; TM=M; SS=N; 5.19979716  
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC\_tran, GTP\_EFTU, ABC\_membrane, none; 5.199074074  
 416602; NM\_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF, ywc, TSPN; 5.198224852  
 429556; AW139399; Hs.314807; ESTs; none; TM=M; SS=N; 5.192439863  
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin\_head, IQ, zf-MYND; TM=M; SS=M; 5.190251572  
 400517; ; lengsin; none; TM=M; SS=N; 5.18  
 413436; AF238083; Hs.68061; sphingosine kinase 1; DAGKc; TM=M; SS=N; 5.172881356  
 423527; AI206965; Hs.105861; hypothetical protein FLJ13824; none; TM=M; SS=N; 5.165060241  
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion\_trans, SPRY, RYDR, ITPR, RyR, MIR; TM=Y; SS=N; 5.156976744  
 437809; AL137723; Hs.5855; Homo sapiens mRNA; cDNA DKFZp434D0818 (f; none, none; 5.154676259  
 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos; TM=M; SS=N; 5.152360515  
 409340; BE174629; Hs.321130; hypothetical protein MGC2771;  
 aa\_permeases, pyridoxal\_deC, bromodomain, PHD, MBD, AT\_hook, DDT, PI3\_PI4\_kinase, FAT, FATC, BoA, RUN; TM=M; SS=N; 5.144859813  
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K\_tetra, DUF51, none; 5.142  
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3, PH, WW, RhoGAP; 5.141534392  
 434808; AF155108; Hs.256150; NY-REN-41 antigen; none; TM=M; SS=N; 5.14  
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M; SS=N; 5.13968254

- 431685; AW296135; Hs.267659; vav 3 oncogene; CH,DAG\_PE-bind,PH,RhoGEF,SH2,SH3,DC1;TM=M;SS=N; 5.129476584  
 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase\_C,HR1;TM=M;SS=N; 5.121527778  
 433573; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G-type rece; 7tm\_2,EGF,cadherin,laminin\_EGF,laminin\_G,Trypan\_glycop,GPS,HRM;TM=Y;SS=M; 5.107438017  
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC\_tran,arf;TM=M;SS=M; 5.10251046  
 419493; AF001212; Hs.90744; proteasome (prosome, macropain) 26S subu; CDK5\_activator,PCI,none; 5.095194085  
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor; ; inositol\_P,ig;TM=M;SS=N; 5.092  
 435243; AW292886; Hs.348932; hypothetical protein dJ43O14.3; IRF,none; 5.092  
 434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp586F2224 (f; DSPc,none; 5.091922006  
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 5.088932806  
 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA;; 5.082840237  
 420030; BE503994; Hs.146233; KIAA0418 gene product; SH3,none; 5.080645161  
 440665; AW449415; Hs.10260; Homo sapiens cDNA FLJ11341 fis, clone PL; SH3;; 5.063953488  
 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo\_seg,IBB; 5.056  
 411165; NM\_000169; Hs.69089; galactosidase, alpha; Melibiase;; 5.054133858  
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE\_p10,ICE\_p20;TM=M;SS=M; 5.054  
 423883; AF250238; Hs.134514; ATP-binding cassette, sub-family A (ABC1; ABC\_tran,photoRC,SRP54,Ca\_channel\_B,Pterin\_4a;TM=Y;SS=M; 5.051724138  
 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3\_P14\_kinase,PI3Ka;TM=M;SS=N; 5.051282051  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y\_phosphatase;TM=M;SS=N; 5.047311828  
 410026; AI912061; Hs.55016; hypothetical protein FLJ21935; none,none; 5.04674221  
 426395; BE151985; Hs.355669; hypothetical protein FLJ23316; pkinase,none; 5.040298508  
 418054; NM\_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl\_oxidase;TM=M;SS=M; 5.030390393  
 444895; AI674383; Hs.22891; solute carrier family 7 (cationic amino; ASC,death,TNFR\_c6; 5.037151703  
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF;TM=Y;SS=M; 5.034  
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1\_rep;TM=M;SS=N; 5.03030303  
 410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Topoisom\_bac,Toprim;; 5.027985075  
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase; pkinase,CNH;TM=M;SS=N; 5.014652015  
 415166; NM\_003652; Hs.78068; carboxypeptidase Z; Zn\_carbOpept,Dioxygenase,Fz;; 5.012269939  
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion\_trans;TM=Y;SS=M; 5.001811594  
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl\_oxidase;; 4.997983871  
 430024; AI808780; Hs.227730; integrin, alpha 6; integrin\_A,FG-GAP;TM=Y;SS=M; 4.994871795  
 409220; BE243323; Hs.51233; tumor necrosis factor receptor superfam; TNFR\_c6,death,Lipoprotein\_5,TIL;TM=Y;SS=M; 4.987135506  
 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 4.985185185  
 423011; NM\_000683; Hs.123022; adrenergic, alpha-2C-, receptor; 7tm\_1;TM=Y;SS=M; 4.984  
 419577; L36531; Hs.91296; integrin, alpha 8; integrin\_A,FG-GAP;TM=Y;SS=N; 4.968  
 402328; ; Target Exon; pkinase;TM=M;SS=N; 4.96728972  
 421242; AW161386; Hs.13561; hypothetical protein MGC4692; none;NA;NA; 4.966334165  
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 4.964491363  
 414203; BE262170; Hs.78629; ATPase, Na? transporting, beta 1 polypep; none,none; 4.961956522  
 409582; R27430; Hs.271565; ESTs; none,Neur\_chan\_LBD,Neur\_chan\_memb; 4.946  
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;SS=N; 4.943181818  
 453449; W17652; Hs.32981; sema domain, immunoglobulin domain (Ig); ; Ig,Sema,PSI;; 4.930508475  
 425233; Z17861; Hs.155218; E1B-55kDa-associated protein 5; SPRY,SAP,pkinase,fn3,ig; 4.925347222  
 425247; NM\_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase\_M10;; 4.92  
 422282; AF019225; Hs.114309; apolipoprotein L; MoTA\_ExbB;TM=Y;SS=M; 4.912181303  
 442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 4.910224439  
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.909972299  
 449523; NM\_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm\_1;TM=Y;SS=M; 4.904  
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M;SS=N; 4.897338403  
 411770; NM\_014278; Hs.71992; heat shock protein (hsp110 family); HSP70;TM=M;SS=N; 4.894  
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm\_1;TM=Y;SS=M; 4.886  
 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese,none; 4.884  
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 4.876379691  
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevi; NusG;; 4.876117497  
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfam; SRP14,TNFR\_c6;; 4.873684211  
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase\_M49,EGF,ig,Neuregulin;TM=M;SS=N; 4.872641509  
 421541; NM\_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase\_C;TM=M;SS=N; 4.869318182  
 429619; AL120751; Hs.211568; eukaryotic translation initiation factor; none,none; 4.868073879  
 458873; AW150717; Hs.345728; STAT induced STAT inhibitor 3; none,none; 4.861538462  
 437669; AI358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA; none,pkinase,pkinase\_C; 4.854651163  
 405545; ; Target Exon; ABC\_tran,SRP54,ABC\_membrane;TM=Y;SS=M; 4.85  
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 4.848387097  
 424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus; fn3,ig,IRK;TM=Y;SS=M; 4.846153846  
 425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar\_tr;TM=Y;SS=M; 4.843694494  
 421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, polyp; pkinase,pkinase\_C;TM=M;SS=N; 4.842532468  
 418736; T18979; Hs.87908; Snf2-related CBP activator protein; helicase\_C,AT\_hook,SNF2\_N;TM=M;SS=N; 4.842  
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2,none; 4.841071429  
 417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2,PID,zf-C2H2,SCAN,AMP-binding,KRAB;TM=M;SS=N; 4.839464883  
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar\_tr; 4.837837838  
 434521; NM\_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo\_seg,IBB;TM=M;SS=N; 4.833333333  
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 4.821666667  
 453082; H18835; Hs.31608; hypothetical protein FLJ20041; ion\_trans;TM=Y;SS=M; 4.820936639  
 417949; AL049795; Hs.83004; interleukin 14; none,Armadillo\_seg,IBB,WD40; 4.81443299  
 439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR\_c6,granulin,CUB,Keratin\_B2,TIL;TM=M;SS=M; 4.81  
 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 4.805063291  
 432194; AL040801; Hs.273219; breast cancer anti-estrogen resistance 1; SH3;; 4.803191489  
 431472; AK001023; Hs.256549; nucleotide binding protein 2 (E.coli Min; fer4\_NiH,ParA,APS\_kinase,ArsA\_ATPase;TM=M;SS=N; 4.800990099  
 450690; AA296696; Hs.333418; FYXD domain-containing ion transport reg; ATP1G1\_PLM\_MAT8;TM=Y;SS=M; 4.795480881  
 448950; AF286887; Hs.9275; CGI-152 protein; E1-E2\_ATPase,Hydrolase;TM=Y;SS=N; 4.776923077  
 427681; AB018263; Hs.284232; tumor necrosis factor receptor superfam; death,TNFR\_c6,PH,Xlink,RhoGEF,Metallothio\_5;TM=M;SS=M; 4.772196262  
 432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH,RhoGAP,SH3;TM=M;SS=N; 4.760115607  
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE\_p10,ICE\_p20;; 4.751162791  
 419981; AA897581; Hs.128773; ESTs; pkinase,DAG\_PE-bind,pkinase\_C,OPR,none; 4.748  
 431657; AI345227; Hs.105448; ESTs, Weakly similar to B34087 hypotheti; pkinase,PA28\_alpha,PA28\_beta,Cu\_amine\_oxid,Cu\_amine\_oxidN2,Cu\_amine\_oxidN3; 4.746

412958; BE391579; Hs.75087; Fas-activated serine/threonine kinase; none;; 4.736781609  
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor;; Ig, pkinase; TM=Y; SS=N; 4.733  
 419250; AW770185; Hs.356066; U5 snRNP-specific protein, 116 kD; 7tm\_1, BAH, zf-CXXC, DNA\_methylase; 4.725454546  
 417903; NM\_002342; Hs.1116; lymphotoxin beta receptor (TNFR superfam; TNFR\_c6; TM=M; SS=M; 4.718858132  
 5 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK\_CoaE;; 4.718836565  
 426059; BE292842; Hs.166120; interferon regulatory factor 7; IRF;; 4.718543046  
 414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase; TM=M; SS=N; 4.708  
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC; TM=Y; SS=M; 4.707920792  
 10 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase, DCX; TM=M; SS=N; 4.707671958  
 407143; C14076; Hs.332329; EST; none; TM=Y; SS=M; 4.682675815  
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 4.681818182  
 408806; AW847814; Hs.75608; Homo sapiens cDNA: FLJ21532 fis, clone C; SH3, PDZ, Guanylate\_kin, none; 4.680440771  
 448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate\_rec, MIP; TM=M; SS=M; 4.679841897  
 15 418936; AI655499; Hs.161712; ESTs; pkinase, Activin\_rec, PDZ, ZU5, death; 4.679180887  
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; ig, kringle, pkinase, Fz; TM=Y; SS=M; 4.675342466  
 414665; AA160873; Hs.356307; serum amyloid A1; zf-C2H2, BTB, K\_tetra, none; 4.674474796  
 449843; R85337; Hs.24030; solute carrier family 31 (copper transp; none; TM=Y; SS=M; 4.673701299  
 428245; AF151048; Hs.183180; anaphase promoting complex subunit 11 (y; none;; 4.656756757  
 20 417088; M54915; Hs.81170; p1m-1 oncogene; pkinase; TM=M; SS=N; 4.656190476  
 420340; NM\_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TIT3 com; ITAM; TM=M; SS=M; 4.65  
 425966; NM\_001761; Hs.1973; cyclin F; cyclin, F-box, cyclin\_C; TM=M; SS=N; 4.644  
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; ig, abhydrolase; 4.640384615  
 430603; AA148164; Hs.247280; HBV associated factor; zf-C3HC4, zf-RanBP, pkinase; 4.630653266  
 25 419273; BE271180; Hs.293490; ESTs, Weakly similar to I38022 hypotheti; none, none; 4.628  
 453880; AI803166; Hs.135121; ESTs, Weakly similar to I38022 hypotheti; HSP70, none; 4.619047619  
 459399; BE407712; Hs.153998; creatine kinase, mitochondrial 1 (ubiqui; none, none; 4.618577075  
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese, DSPC;; 4.616  
 433577; AW007080; Hs.284192; ESTs; none, none; 4.614  
 444838; AV651680; Hs.208558; ESTs; integrin\_A, FG-GAP, none; 4.612149533  
 30 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/pep; PTR2; TM=Y; SS=N; 4.602  
 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ, Guanylate\_kin;; 4.596875  
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22, Claudin, none; 4.587931035  
 433083; AL042759; Hs.191762; ESTs; SH3, PX; TM=M; SS=N; 4.586  
 35 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, ; ig; TM=Y; SS=M; 4.58557047  
 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS;; 4.579087049  
 422009; AI742845; Hs.110713; DEK oncogene (DNA binding); SAP;; 4.576347305  
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none, lectin\_c; 4.57312253  
 414561; AI064813; Hs.195155; Homo sapiens amino acid transport system; Aa\_trans; TM=Y; SS=N; 4.573015873  
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC\_tran, ABC\_membrane, GTP\_EFTU; TM=M; SS=M; 4.570526316  
 40 459053; AI807052; Hs.97792; ESTs; none, 7tm\_2, GPS; 4.569230769  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, ig, FAD\_Synth, Idh, Idh\_C, pkinase;; 4.566195373  
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p\_like; TM=M; SS=N; 4.56056338  
 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.558  
 408051; AI623351; Hs.172148; ESTs; PH, RhoGAP, none; 4.552307692  
 45 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; ehtand, Idl\_recept\_a;; 4.547761194  
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7tm\_1, LRR; TM=Y; SS=N; 4.547169811  
 426201; AW182614; Hs.128499; ESTs; SH3, none; 4.541666667  
 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; SS=N; 4.536  
 445229; BE276013; Hs.343828; Homo sapiens mRNA for FLJ00086 protein, ; G-alpha; TM=M; SS=N; 4.530588235  
 50 413109; AW389845; Hs.110855; ESTs; PHO4, none; 4.529761905  
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolo; EGF, cadherin, laminin\_G; TM=Y; SS=M; 4.529710145  
 402330; ; Target Exon; pkinase, none; 4.528070175  
 439238; N47305; Hs.302161; EDG-8 (endothelial differentiation, sph; 7tm\_1; TM=Y; SS=M; 4.524  
 55 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE\_p10, ICE\_p20;; 4.523715415  
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenas; CBS, IMPDH\_C, IMPDH\_N, NPD; TM=M; SS=N; 4.522900763  
 431429; AF072813; Hs.252831; reticulon 3; Reticulon, Fz, ig, kringle, pkinase; TM=Y; SS=N; 4.512  
 424078; AB006625; Hs.139033; paternally expressed 3; zf-C2H2, KRAB, none; 4.512  
 420602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS; TM=M; SS=N; 4.51  
 60 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm\_1; TM=Y; SS=M; 4.506  
 408157; AA047685; Hs.62946; ESTs; none, pkinase; 4.504  
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M; SS=Y; 4.50215208  
 431326; AW970580; Hs.198689; KIAA0728 protein; none, none; 4.501  
 428072; BE258602; Hs.182366; heat shock protein 75; HATPase\_c, HSP90; TM=M; SS=N; 4.48828125  
 65 415149; X12451; Hs.78056; cathepsin L; Peptidase\_C1;; 4.484375  
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypept; p450; TM=Y; SS=M; 4.48  
 445143; U29171; Hs.378918; casein kinase 1, delta; zf-C3HC4, Filamin, zf-B\_box, NHL, pkinase, zf-MIZ; TM=M; SS=N; 4.478092784  
 421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen; none; TM=Y; SS=M; 4.477337111  
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none; TM=M; SS=N; 4.476  
 70 438774; AA431620; Hs.379034; hypothetical protein MGC2745; none, none; 4.474874372  
 410726; AI623859; Hs.15936; ESTs; pkinase, pro\_isomerase, none; 4.47  
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory su; CDK5\_activator, none; 4.468  
 426485; NM\_006207; Hs.170040; platelet-derived growth factor receptor;; ig;; 4.464944649  
 433646; AA603319; Hs.155195; ESTs; pou, homeobox, lig\_chan, ANF\_receptor; 4.458  
 75 410293; AK000047; Hs.61960; hypothetical protein; K\_tetra; TM=M; SS=N; 4.453020134  
 453464; AI884911; Hs.32989; receptor (calcitonin) activity modifying; none; TM=Y; SS=N; 4.448198198  
 410593; AW770280; Hs.36258; ESTs, Moderately similar to JC5238 galac; SH3, PDZ, Guanylate\_kin, none; 4.446927374  
 441455; AJ271671; Hs.7854; zinc/iron regulated transporter-like; Zip; TM=Y; SS=M; 4.445010183  
 453064; R40334; Hs.89463; potassium large conductance calcium-acti; none, none; 4.436480187  
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase, ICE\_p10, ICE\_p20; TM=M; SS=M; 4.433411215  
 80 411825; AK000334; Hs.352415; solute carrier family 39 (zinc transport; SNF, Zip; TM=Y; SS=N; 4.432765152  
 428376; AF119665; Hs.184011; pyrophosphatase (inorganic); Pyrophosphatase; TM=M; SS=N; 4.428571429  
 429592; AB029041; Hs.209646; KIAA1118 protein; Troponin, Exo\_endo\_phos, IQ; TM=M; SS=N; 4.428  
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); ank, DAGKa, DAGKc, DAG\_PE-bind; TM=M; SS=N; 4.426229508



- 427138; N77624; Hs.173717; phosphatidic acid phosphatase type 2B; PAP2,none; 4.4234375  
 414496; W73853; Hs.355424; ESTs; pkinase,F5\_F8\_type\_C,adh\_short,none; 4.42114094  
 429432; A1678059; Hs.202676; synaptonemal complex protein 2; none;TM=M;SS=N; 4.42  
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker\_histone;TM=M;SS=N; 4.419207317  
 5 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L2; none;TM=M;SS=N; 4.418181818  
 435411; AW444619; Hs.138211; ESTs; none,pkinase; 4.414  
 414581; AA256213; Hs.72010; ESTs; none,Carn\_acyltransf,Choline\_kinase,SCO1-SenC,Glycos\_transf\_3,Glycos\_trans\_3N; 4.41  
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domain; death,DED;; 4.408523909  
 10 442259; A1690269; Hs.201345; ESTs; Acetyltransf,RhoGAP,FCH,SH3,Kelch,fn3; 4.406  
 415860; D56051; Hs.78888; diazepam binding inhibitor (GABA receptor; ACBP;TM=M;SS=N; 4.404678363  
 434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPC;TM=M;SS=N; 4.404  
 404440; ; NM\_021048;Homo sapiens melanoma antigen; MAGE;TM=M;SS=N; 4.4  
 435542; AA687376; Hs.351226; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 4.394  
 15 413367; NM\_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar\_tr;TM=Y;SS=N; 4.39028777  
 435732; AF229178; Hs.123136; leucine rich repeat and death domain con; none,none; 4.38490566  
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm\_1,none; 4.382129278  
 425749; AW328587; Hs.159448; surfeit 2; none;; 4.382  
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y\_phosphatase;TM=Y;SS=N; 4.381422925  
 20 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 4.380681818  
 431837; T79326; Hs.331967; olfactory receptor, family 2, subfamily ; none,7tm\_3,sushi,ANF\_receptor; 4.376  
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm,pkinase;; 4.370247934  
 434876; AF160477; Hs.61460; Ig superfamily receptor LNIR; ig,Rhbd\_glycop;TM=Y;SS=M; 4.37  
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion\_trans;TM=Y;SS=M; 4.367777778  
 25 403912; ; C5000394;gij12737280[ref]XP\_006682.2] k; none;TM=M;SS=N; 4.367684478  
 426268; AF083420; Hs.168913; serine/threonine kinase 24 (Ste20, yeast; pkinase;; 4.366348449  
 434263; N34895; Hs.79187; ESTs; ig,none; 4.358527132  
 404760; ; Target Exon; cadherin;TM=M;SS=M; 4.356  
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M;SS=N; 4.35472973  
 30 420757; X78592; Hs.99915; androgen receptor (dihydrotestosterone r; hormone\_rec,zf-C4,Androgen\_recep;TM=M;SS=N; 4.354  
 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chlo; none;TM=Y;SS=N; 4.353244838  
 431674; AA088901; Hs.301642; G-protein coupled receptor; none,GCV\_H; 4.35  
 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M;SS=N; 4.347893916  
 447719; BE387402; Hs.19333; hypothetical protein FLJ10349; adenylatekinase,ATP-bind;TM=M;SS=N; 4.346007605  
 35 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerev; Acetyltransf;TM=M;SS=N; 4.344  
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone K; none,none; 4.334722222  
 411768; NM\_013371; Hs.71979; interleukin 19; IL10;; 4.322  
 445350; AF052112; Hs.12540; lysophospholipase 1; abhydrolase\_2;TM=M;SS=N; 4.320359281  
 425964; AW889928; Hs.9071; progesterone membrane binding protein; homeobox,none; 4.318867925  
 40 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; rrm;TM=M;SS=N; 4.316573557  
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;; 4.316  
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; none,Cys\_knot; 4.314728682  
 438899; AF085833; Hs.135624; ESTs; none,PI3\_P14\_Kinase,PI3Ka,PI3K\_C2,PI3K\_rbd,PI3K\_p85B; 4.314084507  
 418883; BE387036; Hs.12111; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 4.312121212  
 45 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; IMP4;TM=M;SS=N; 4.304407714  
 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo\_seg,HEAT;TM=M;SS=N; 4.304  
 430017; AA263172; Hs.35; protein tyrosine phosphatase, non-recept; Y\_phosphatase;TM=M;SS=M; 4.302  
 447224; BE617125; Hs.142076; gb:601441664F1 NIH\_MGC\_65 Homo sapiens c; none,NA;NA; 4.302  
 425424; NM\_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;SS=N; 4.301639344  
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 4.30141844  
 50 446143; BE245342; Hs.306079; sec61 homolog; NUDIX,secY,E1\_dehydrog,transket\_pyr;TM=Y;SS=M; 4.300872093  
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2\_HUMAN ALU S; none,rm; 4.292620865  
 432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2;TM=M;SS=N; 4.290258449  
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 4.288405797  
 55 421921; H83363; Hs.355993; translocase of inner mitochondrial membr; zf-Tim10,DDP,efhand,CH,spectrin,serpin;TM=M;SS=N; 4.284  
 448564; AL044962; Hs.21453; inositol 1,4,5-trisphosphate 3-kinase C; IPK;; 4.28057554  
 453941; U39817; Hs.36820; Bloom syndrome; DEAD,helicase\_C,HRDC;TM=M;SS=N; 4.28  
 437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor ; Tropomyosin,pkinase,LRR,LRRCT,Hydantoinase\_B,Hydantoinase\_A;TM=M;SS=N; 4.277477478  
 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin\_EGF,laminin\_Nterm,integrin\_B; 4.276162791  
 60 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none,none; 4.273927393  
 438012; AA393254; Hs.43619; ESTs; Armadillo\_seg,none; 4.273134328  
 409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG;TM=M;SS=N; 4.273109244  
 418529; AW005695; Hs.250897; TRK-fused gene; Band\_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;SS=N; 4.272123894  
 65 415214; A1445236; Hs.125124; EphB2; fn3,pkinase,SAM,EPH\_Ibd;TM=Y;SS=M; 4.268  
 438233; W52448; Hs.56147; ESTs; Neur\_chan\_LBD,Neur\_chan\_memb,MAGE; 4.26284585  
 429019; AA443280; Hs.279907; myosin IIIA; myosin\_head,pkinase,PRK,IQ;TM=M;SS=N; 4.262  
 424959; NM\_005781; Hs.153937; activated p21cdc42Hs kinase; ldn,ldh\_C,SH3,pkinase,UBA;TM=M;SS=N; 4.258695652  
 453655; AW960427; Hs.342874; transforming growth factor, beta recepto; zona\_pellucida,none; 4.257208766  
 70 417414; AA434589; Hs.367676; dUTP pyrophosphatase; dUTPase,KRAB; 4.251785714  
 453905; NM\_002314; Hs.36566; LIM domain kinase 1; pkinase,LIM,PDZ,zf-PARP;TM=M;SS=N; 4.249116608  
 424232; AB015982; Hs.143460; protein kinase C, nu; pkinase,DAG\_PE-bind,PH;TM=M;SS=N; 4.247692308  
 404883; ; ENSP00000216009;Sodium-glucose cotranspo; SSF;TM=Y;SS=M; 4.242424242  
 412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH\_Ibd;TM=Y;SS=M; 4.239285714  
 75 411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none,none; 4.237313433  
 436957; AA902488; Hs.122952; ESTs; none,DAGKc,DAGKa,RA,DAG\_PE-bind; 4.236  
 452568; AA805634; Hs.300870; Homo sapiens mRNA; cDNA DKFZp547M072 (fr; PI3\_P14\_Kinase;TM=M;SS=M; 4.23537415  
 433535; AF111106; Hs.3382; protein phosphatase 4, regulatory subunit; HEAT;TM=M;SS=N; 4.234793187  
 432728; NM\_006979; Hs.278721; HLA class II region expressed gene KE4; Zip,lig\_chan;TM=Y;SS=M; 4.234545455  
 80 416350; AF188625; Hs.189507; phospholipase A2, group IID; phoslip;TM=M;SS=Y; 4.234  
 409533; AW969543; Hs.144609; mitogen-activated protein kinase kinase ; Peptidase\_C48,none; 4.230666667  
 427127; AW802254; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 4.228009259  
 403362; ; NM\_001615;Homo sapiens actin, gamma 2 ; actin;; 4.22688478  
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin\_G,CorA;; 4.226388889



428897; AJ245719; Hs.194385; hypothetical protein FLJ20234; SH2; TM=M; SS=N; 4.224731183  
 425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinase; SH2, SH3, pkinase, PH, BTK; TM=M; SS=N; 4.223684211  
 418566; C21220; Hs.321717; hypothetical protein FLJ10875; zf-C2H2, BTB, K\_tetra, 7tm\_1; 4.222807018  
 454098; W27953; Hs.217493; Plakophilin; none, none; 4.22  
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); pkinase, FHA, DnaJ; TM=M; SS=N; 4.21875  
 419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4; TM=Y; SS=M; 4.217130215  
 436756; Z18364; Hs.198298; v-src avian sarcoma (Schmidt-Ruppin A-2); none, none; 4.216  
 450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2; TM=M; SS=N; 4.215163934  
 416224; NM\_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand; 4.212041885  
 432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; none, DS, UPF0139, Glyco\_hydro\_38; 4.207407407  
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain, rrm; TM=M; SS=N; 4.206  
 432284; AA532807; Hs.287740; ESTs; pkinase, none; 4.205454546  
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase, RIO1; TM=M; SS=N; 4.204142012  
 450056; BE047394; Hs.502; ESTs; Weakly similar to S71512 hypothe; ABC\_tran, ABC\_membrane, Ig, MHC\_II\_beta, SRP54, proteasome, ABC\_membrane, ABC\_tran; 4.202572347  
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subu; PC\_rep; TM=M; SS=N; 4.202061856  
 425394; AA356730; Hs.323949; kangai 1 (suppression of tumorigenicity; transmembrane4, none; 4.195014663  
 449335; AW150717; Hs.345728; STAT induced STAT inhibitor 3; SH2; TM=M; SS=N; 4.192248062  
 415023; AA932146; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none, NA; NA; 4.192  
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none; TM=M; SS=Y; 4.191878981  
 445330; R52656; Hs.21691; ESTs; 7tm\_1, none; 4.189922481  
 430016; NM\_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX, EXS; TM=Y; SS=N; 4.188333333  
 434633; AI189587; Hs.120915; ESTs; SH3, PH, RhoGAP, none; 4.187106918  
 452908; AB001451; Hs.30965; neuronal Shc adaptor homolog; SH2, PID, Zn\_carbOpept; TM=M; SS=N; 4.186885246  
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm\_2, CytC\_asm, GPS; TM=Y; SS=M; 3.930957684  
 432201; AI538613; Hs.298241; Transmembrane protease, serine 3; Idl\_receptL\_a, trypsin; TM=Y; SS=M; 3.893103448  
 428969; AF120274; Hs.194689; artemin; TGF-beta; 3.884030418  
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ig; TM=Y; SS=M; 3.831669044  
 432305; M62402; Hs.274313; insulin-like growth factor binding prole; thyroglobulin\_1, IGFBP, A2M\_N; TM=M; SS=N; 3.742996346  
 405547; ; NM\_018833; Homo sapiens transporter 2, A; ABC\_tran, SRP54, ABC\_membrane; TM=Y; SS=M; 3.676  
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none; TM=M; SS=Y; 3.634  
 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 3.562  
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q, Collagen; 3.49  
 405546; ; NM\_018833; Homo sapiens transporter 2, A; ABC\_tran, SRP54, ABC\_membrane; TM=Y; SS=M; 3.422661871  
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length insert cDN; none, none; 3.402  
 404210; ; NM\_005936; Homo sapiens myeloid/lymphoid; FHA, PDZ, RA, DIL; TM=M; SS=N; 3.368807339  
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase, pkinase\_C; 3.213402062  
 418678; NM\_001327; Hs.87225; cancer/testis antigen (NY-ESO-1); none; TM=M; SS=N; 3.084  
 451106; BE382701; Hs.25960; N-MYC oncogene; HLH, Myc\_N\_term; TM=M; SS=N; 1.55

## TABLE 17B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
418869	12789_14	AA229762 AA230035

## TABLE 17C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035, 122804-122921, 124019-12416
401781	7249190	Minus	83215-83435, 83531-83656, 83740-83901, 8423
405484	5922025	Plus	199214-199579, 199672-199920, 200262-20049
405932	7767812	Minus	123525-123713
400517	9796686	Minus	49996-50346
402328	4464283	Minus	13758-13922, 14558-14752
405545	1054740	Plus	118677-118807, 119091-119296, 121626-12182
402330	4464283	Minus	15325-15380, 15484-15588, 15842-15915
404440	7528051	Plus	80430-81581
403912	7710730	Minus	72000-72290, 72431-72700, 72929-73199
404760	7767724	Plus	223266-223352, 224472-224585
404883	5101762	Minus	94626-94730, 96998-97069
403362	8571772	Plus	64099-64260
405547	1054740	Plus	124361-124520, 124914-125050
405546	1054740	Plus	124010-124183
404210	5006246	Plus	169926-170121

Table 18A: 194 Up-Regulated Genes in Uterine Cancer Versus Normal Adult Tissues

Table 18A lists about 194 genes up-regulated in uterine cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" uterine cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" uterine cancer level was set to the 2<sup>nd</sup> highest amongst uterine cancers. The "average" normal adult tissue level was set to the 90<sup>th</sup> percentile value amongst non-malignant tissues. In order to remove gene-specific background

levels of non-specific hybridization, the 15<sup>th</sup> percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor vs. normal tissue			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA	55.7
	435094	AI560129	Hs.277523	EST	45.2
	438817	AI023799	Hs.163242	ESTs	42.6
15	421478	AI683243	Hs.97258	ESTs	35.2
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	27.3
	450451	AW591528	Hs.202072	ESTs	26.0
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252	24.8
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49) (HG38)	24.2
20	438993	AA828995	Hs.52620	integrin; beta 8	16.7
	436775	AA731111	Hs.291891	ESTs	14.3
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDNA clo	13.5
	441377	BE218239	Hs.202656	ESTs	13.5
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	12.3
25	400292	AA250737	Hs.72472	BMPR-Ib; bone morphogenetic protein receptor Ib	10.7
	403899			predicted exon	10.1
	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA	10.0
	447350	AI375572	Hs.1939	HER4 (c-erb-B4)	9.8
	453964	AI961486	Hs.12744	ESTs	9.7
30	443830	AI142095	Hs.143273	ESTs	9.1
	459325	AW088369	Hs.282184	ESTs	9.0
	415245	N59650	Hs.27252	ESTs	8.9
	446608	N75217	Hs.257846	ESTs	8.9
	426635	BE395109	Hs.129327	ESTs	8.8
35	433426	H69125	Hs.133525	ESTs	8.7
	437960	AI669586	Hs.222194	ESTs	8.5
	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b [H	8.3
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [H.s	7.3
	447835	AW591623	Hs.164129	ESTs	7.2
40	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone THYRO10	7.1
	412925	AI089319	Hs.179243	ESTs	7.0
	408562	AI436323	Hs.31141	Roundabout homolog 2 transmembrane receptor (robo2)	7.0
	429272	W25140	Hs.110667	ESTs	6.9
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAM	6.3
45	437938	AI950087		ESTs; Weakly similar to Gag-Pol polyprotein	6.2
	420610	AI683183	Hs.99348	distal-less homeo box 5	6.2
	448672	AI955511	Hs.225106	ESTs	6.1
	452461	N78223	Hs.108106	transcription factor	6.1
	413335	AI613318	Hs.48442	ESTs	6.1
50	449611	AI970394	Hs.197075	ESTs	6.0
	449260	AA741180	Hs.29879	ESTs	6.0
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	6.0
	443715	AI583187	Hs.9700	cyclin E1	6.0
	432113	AA935065	Hs.152385	ESTs	5.9
55	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.7
	410658	AW105231	Hs.192035	ESTs	5.7
	426465	AI758948		gb:ty16f07.x1 NCI_CGAP_Ut3 Homo sapiens cDNA	5.7
	446704	AI337228	Hs.197083	ESTs	5.5
	419503	AA243642	Hs.137422	ESTs	5.5
60	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	5.4
	436076	AI193277	Hs.120954	ESTs	5.4
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.3
	445258	AI635931	Hs.147613	ESTs	5.3
	440901	AA909358	Hs.128612	ESTs	5.3
65	434636	AA083764	Hs.241334	ESTs	5.3
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone LNG020	5.2
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.2
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapiens cDN	5.2
	436787	AA908554	Hs.192756	ESTs	5.2
70	400301	X03635	Hs.1657	Estrogen receptor 1	5.1
	428771	AB028992	Hs.193143	KIAA1069 protein	5.1
	444929	AI685841	Hs.161354	ESTs	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
	405609			predicted exon	5.0
75	410102	AW248508	Hs.279727	ESTs;	5.0
	433283	BE041135	Hs.175622	ESTs	4.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	4.8
	410247	AF181721	Hs.61345	RU2S	4.7
	422589	AA312735	Hs.179725	ESTs	4.7
80	452771	T05477		gb:EST03366 Fetal brain, Stratagene (cat93620	4.7
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens cDNA	4.7
	420440	NM_002407	Hs.97644	mammaglobin 2	4.6
	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	4.6

	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypept	4.6
	424115	AA335497	Hs.293965	ESTs	4.6
	414245	BE148072	Hs.75850	WAS protein family, member 1	4.6
5	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	4.5
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	4.5
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone LNG076	4.4
	458861	AI630223		PHD finger DNA binding protein isoform 1 (int	4.4
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	4.3
10	420149	AA255920	Hs.88095	ESTs	4.3
	433479	AW511459	Hs.249972	ESTs	4.3
	449416	AI651016	Hs.246311	ESTs	4.3
	457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone HEP106	4.3
	450109	AI539295	Hs.17967	ESTs	4.3
15	436954	AA740151	Hs.130425	ESTs	4.3
	415511	AI732617	Hs.182362	ESTs	4.3
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT2RM40	4.3
	406411			predicted exon	4.2
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	4.2
20	416456	H57052	Hs.176626	hypothetical protein EDAG-1	4.2
	454692	AW813350		gb:MR3-ST0192-100100-024-g07	4.1
	452249	BE394412	Hs.61252	ESTs	4.1
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	4.1
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN ALU SUB	4.1
25	434988	AI418055	Hs.161160	ESTs	4.1
	423515	AA327017	Hs.162204	ESTs	4.0
	435407	AI149774	Hs.117178	ESTs	4.0
	440886	AW511032	Hs.190516	ESTs	4.0
	444783	AK001468	Hs.62180	ESTs	4.0
30	452039	AI922988	Hs.172510	ESTs	4.0
	407300	AA102616	Hs.120769	Homo sapiens cDNA FLJ20463 fis, clone KAT0614	4.0
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	4.0
	449433	AI672096	Hs.9012	ESTs	3.9
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone NT2RP20	3.9
35	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFp5861518	3.9
	453096	AW294631	Hs.11325	ESTs	3.9
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP010	3.9
	445034	AW293376	Hs.160323	ESTs	3.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	3.8
40	422219	AW978073		gb:EST390182 MAGE resequences	3.8
	440304	BE159984	Hs.125395	ESTs	3.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFp434P228	3.8
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK	3.8
	400250			predicted exon	3.8
45	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN	3.8
	420092	AA814043	Hs.88045	ESTs	3.8
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	3.8
	437212	AI765021	Hs.210775	ESTs	3.8
	409867	AW502161		gb:UI-HF-BR0p-ajr-g-12-0-UI.r1 NIH_MGC_52	3.7
50	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	3.7
	427119	AW880562	Hs.114574	ESTs	3.7
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234	3.7
	434539	AW748078	Hs.214410	ESTs	3.7
	424717	H03754	Hs.152213	wingless-type MMTV integration site family	3.7
55	412078	X69699	Hs.73149	paired box gene 8 (PAX-8)	3.7
	447342	AI199268	Hs.19322	ESTs; Weakly similar to !!! ALU SUBFAMILY J	3.7
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.7
	446619	AI076643	Hs.313	secreted phosphoprotein 1 (osteopontin)	3.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDNA clo	3.7
60	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapiens c	3.6
	441285	NM_002374	Hs.167	microtubule-associated protein 2	3.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	3.6
	417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC052	3.6
	441484	AA935481	Hs.58972	ESTs	3.6
65	415802	AA169515	Hs.6006	ESTs	3.6
	448112	AW245919	Hs.301018	ESTs	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	3.6
	402606			predicted exon	3.6
	407905	AW103655	Hs.252905	ESTs	3.6
70	424917	AI636208	Hs.96901	Homo sapiens cDNA: FLJ23049 fis, clone LNG025	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	3.6
	451842	AI820539	Hs.267087	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.6
	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	3.6
	431731	BE266322	Hs.211374	ESTs, Weakly similar to SP49_HUMAN SPLICEOSOM	3.6
75	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retinal sh	3.6
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	3.6
	406030			predicted exon	3.5
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA Libr	3.5
	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.5
80	437641	AA811452	Hs.291911	ESTs	3.5
	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN	3.4
	443450	N66045	Hs.133529	ESTs	3.4
	457438	NM_014053	Hs.270594	FLVCR protein	3.4
	451254	AI571016	Hs.172967	ESTs	3.4

5	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.4
	427778	AA412323	Hs.105323	ESTs	3.3
	435031	AI632091	Hs.116877	ESTs	3.3
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	3.3
	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-187J11 on c	3.3
	431548	AI834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP30	3.2
	432415	T16971	Hs.289014	ESTs	3.2
	423126	AA322245	Hs.290165	ESTs	3.2
10	433420	AI674093	Hs.293961	ESTs	3.2
	435174	AA687378	Hs.194624	ESTs	3.2
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linked moiety X	3.2
	452588	AA889120	Hs.110637	Homeo box A10	3.2
	427304	AA761526	Hs.163853	ESTs	3.2
15	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (from cl	3.1
	417728	AW138437	Hs.24790	KIAA1573 protein	3.1
	419356	AI656166	Hs.7331	ESTs	3.1
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [	3.1
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrolase 1	3.1
20	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone COL064	3.1
	405174			predicted exon	3.1
	403776			predicted exon	3.1
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily, m	3.1
	431255	AA497043	Hs.115685	ESTs	3.1
25	442353	BE379594	Hs.49136	ESTs	3.1
	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (formerl	3.1
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	3.1
	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens cDNA c	3.1
	406400			kallikrein 8 (neuropsin/ovasin)	3.0
30	439949	AW979197	Hs.292073	ESTs	3.0
	430704	AW813091		gb:RC3-ST0186-240400-111-d07 ST0186 Homo sapi	3.0
	401517			predicted exon	3.0
	417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncog	3.0
	435267	N23797	Hs.110114	ESTs	3.0
35	426384	AI472078		ESTs	3.0
	422797	AB033064	Hs.120908	KIAA1238 protein	3.0
	428832	AA578229		gb:nl22b12.s1 NCI_CGAP_HSC1 Homo sapiens cDNA	3.0
	449722	BE280074	Hs.23960	cyclin B1	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A	3.0
40	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	3.0

TABLE 18B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT number	Accession
50	409745	115237_1 AA077391 AI347618 AI361453 AI088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
	409867	1156530_1 AW502161 AW502587 AW502345
	422219	213547_1 AW978073 AW978072 AA807550 AA306567
	422689	219896_1 AW856665 AA315006 AW954733
	426384	266211_1 AI472078 AA377209 AA865807
55	426465	267664_1 AI758948 AA379527 AA379948 AA379262 AW963933
	428832	296144_1 AA578229 AA436432 AA481375 AA481363
	430704	322217_1 AW813091 AW206655 AA484440
	431322	331543_1 AW970622 AA503009 AA502998 AA502989 AA502805 T92188
60	437938	44573_2 AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598
		AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
		AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915
		AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975
		AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669
		AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628
65		N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056
		AI002839 R67840 AA300207 AW959581 T63226 F04005
	438993	467651_1 AA828995 AA834879 AI926361
	442438	542469_1 AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
	443613	575391_1 AI079356 W23287
70	449034	794817_1 AI624049 AW117770 AI858360
	451105	859083_1 AI761324 AW880941 AW880937
	452771	930983_1 T05477 T07855 AI917711
	454392	115882_1 BE260893 AA078319 R85057 AW803024 H85811 AA078293
	454692	1229118_1 AW813350 AW816082 AW813476 AW813383
75	455666	1349545_1 BE065813 BE065788 BE065889 BE065832
	458154	491768_1 AW816379 AA888282 AA879046 AA879195
	458861	798085_1 AI630223 AI630470

TABLE 18C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

5	Pkey	Ref	Strand	Nt_position
	401517	7677912	Plus	29278-29770
	402606	9909429	Minus	81747-82094
	403776	7770611	Minus	1414-1513,1624-1756
10	403899	7381715	Minus	9144-9350
	405174	7108030	Minus	102814-103063
	405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
	406030	8312328	Minus	96123-96547
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
15	406411	9256407	Plus	7400-7527

Table 19A: 225 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, UTERINE Cancer Versus Normal Adult Tissues

Table 19A lists about 225 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 PSDomain: Protein Structural Domain  
 R1: Ratio of tumor vs. normal tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	PSDomain	R1
35	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	TM	27.3
	438993	AA828995	Hs.52620	integrin; beta 8	SS,TM,integrin_B	16.7
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stroma	SS,hemopexin	12.3
	446608	N75217	Hs.257846	ESTs	TM	8.9
	433426	H69125	Hs.133525	ESTs	TM	8.7
40	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clo	TM,PAX	7.1
	408562	AI436323	Hs.31141	Roundabout homolog 2 transmembrane	SS,TM,ig,fn3	7.0
	420610	AI683183	Hs.99348	distal-less homeo box 5	TM,homeobox	6.2
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rab	TM,kinesin	6.0
	443715	AI583187	Hs.9700	cyclin E1	TM,cyclin	6.0
	432113	AA935065	Hs.152385	ESTs	TM	5.9
45	419503	AA243642	Hs.137422	ESTs	TM	5.5
	444342	NM_014398	Hs.10887	similar to lysosome-associated memb	TM,Lamp	5.4
	436076	AI193277	Hs.120954	ESTs	TM	5.4
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	TM,hemopexin	5.3
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.2
50	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo s	TM	5.2
	400301	X03635	Hs.1657	Estrogen receptor 1	TM,hormone_rec,zf-C4	5.1
	405609			predicted exon	TM,Myosin_tail,myosin_head	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazol	TM	5.0
	410102	AW248508	Hs.279727	ESTs;	SS,TM,	5.0
55	433283	BE041135	Hs.175622	ESTs	TM	4.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gen	TM	4.8
	410247	AF181721	Hs.61345	RU2S	TM	4.7
	422589	AA312735	Hs.179725	ESTs	TM	4.7
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sap	TM	4.7
60	420440	NM_002407	Hs.97644	mammaglobin 2	TM,Uteroglobin	4.6
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediat	TM,Ribosomal_S27e	4.6
	424115	AA335497	Hs.293965	ESTs	TM	4.6
	414245	BE148072	Hs.75850	WAS protein family, member 1	TM,WH2	4.6
	458861	AI630223		PHD finger DNA binding protein isof	TM,PHD	4.4
65	449416	AI651016	Hs.246311	ESTs	SS,TM,	4.3
	420149	AA255920	Hs.88095	ESTs	TM	4.3
	433479	AW511459	Hs.249972	ESTs	TM	4.3
	457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, cl	TM	4.3
	406411			predicted exon	TM,vwa,FG-GAP	4.2
70	416456	H57052	Hs.176626	hypothetical protein EDAG-1	TM	4.2
	454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192	TM	4.1
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	TM	4.1
	434988	AI418055	Hs.161160	ESTs	TM	4.1
	444783	AK001468	Hs.62180	ESTs	TM,PH	4.0
75	440886	AW511032	Hs.190516	ESTs	TM,FG-GAP	4.0
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HU	TM,Glyco_transf_29,TEA	4.0
	445034	AW293376	Hs.160323	ESTs	TM	3.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box	TM,HMG_box	3.8
	400250			predicted exon	TM,Hist_deacetyl	3.8
80	428227	AA321649	Hs.2248	interferon-gamma induced protein	TM,IL8	3.8
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 T	TM,Kunitz_BPTI,G-gamma	3.8
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234	TM,WW	3.7
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	TM	3.7

	413472	BE242870	Hs.75379	solute carrier family 1 (glial high	TM,SDF	3.7
	447342	AI199268	Hs.19322	ESTs; Weakly similar to !!! ALU SU	TM	3.7
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopon	TM,Osteopontin	3.7
5	453891	AB037751	Hs.36353	Homo sapiens mRNA full length inser	TM	3.7
	441285	NM_002374	Hs.167	microtubule-associated protein 2	TM,tubulin-binding	3.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuro	TM,Thymosin	3.6
	441484	AA935481	Hs.58972	ESTs	TM,fn3,ig,Y_phosphatase	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrily	SS,Peptidase_M10	3.6
10	407905	AW103655	Hs.252905	ESTs	SS,TM,Ephrin	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellula	SS,TM,	3.6
	402606			predicted exon	TM	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1	TM	3.6
	437641	AA811452	Hs.291911	ESTs	TM	3.5
15	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFA	TM,IQ,Rlla	3.4
	443450	N66045	Hs.133529	ESTs	TM	3.4
	457438	NM_014053	Hs.270594	FLVCR protein	TM	3.4
	435031	AI632091	Hs.116877	ESTs	TM,RhoGEF,PH	3.3
	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-1	TM	3.3
20	435174	AA687378	Hs.194624	ESTs	TM,SPRY	3.2
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linke	TM,mulT	3.2
	433420	AI674093	Hs.293961	ESTs	TM	3.2
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E23	TM	3.1
	417728	AW138437	Hs.24790	KIAA1573 protein	TM	3.1
25	403776			predicted exon	SS,TM,IL8	3.1
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) supe	TM,TNF	3.1
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, cl	TM,Ets	3.1
	405174			predicted exon	TM	3.1
30	431255	AA497043	Hs.115685	ESTs	TM	3.1
	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog	TM,homeobox	3.1
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	TM,trypsin,pro_isomerase	3.1
	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapi	TM	3.1
	406400			kallikrein 8 (neuropsin/ovasin)	TM,trypsin	3.0
	401517			predicted exon	TM,HMG14_17	3.0
35	417830	AW504786	Hs.132808	epithelial cell transforming sequen	TM	3.0
	435267	N23797	Hs.110114	ESTs	TM	3.0
	449722	BE280074	Hs.23960	cyclin B1	TM,cyclin	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2	TM,ank	3.0
40	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297	TM,SNF2_N	3.0
	441794	AW197794	Hs.253338	ESTs	TM,ank	2.9
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractura	TM,EGF,TB	2.9
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic pr	SS,wap	2.9
	418113	AI272141	Hs.83484	ESTs	TM,HMG_box	2.9
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome	TM,TEA	2.9
45	431989	AW972870	Hs.291069	ESTs	SS	2.9
	400284			Estrogen receptor 1	TM,hormone_rec,zf-C4	2.9
	438578	AA811244	Hs.164168	ESTs	TM,formyl_transf,AIRS,GARS	2.9
	423513	AF035960	Hs.129719	transglutaminase 5	TM,Transglutamin_N	2.8
	448966	AW372914	Hs.287462	Homo sapiens cDNA FLJ11875 fis, clo	TM	2.8
50	431870	AW449902	Hs.105500	ESTs	TM,MHC_I,ig	2.8
	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276	TM	2.8
	438777	AA825487	Hs.142179	ESTs, Weakly similar to ORF2 [M.mus	TM	2.8
	451807	W52854	Hs.27099	DKFZP564J0863 protein	TM	2.8
	433326	AI379486	Hs.159430	ESTs	TM	2.8
55	448221	BE622615		gb:601440775T1 NIH_MGC_72 Homo sapi	TM	2.8
	448141	AI471598	Hs.197531	ESTs	TM,bZIP	2.8
	456311	AA225632	Hs.190016	ESTs	TM,Sec7	2.8
	405454			predicted exon	TM	2.8
60	459287	AL079369		gb:DKFZp564G2378_r1 564 (synonym: h	TM	2.8
	438935	H40665	Hs.31564	ESTs	TM	2.7
	421312	AA824627	Hs.291670	ESTs	TM,G-patch	2.7
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	TM,ABC_membrane,ABC_tran	2.7
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clo	TM	2.7
	417956	AA210704	Hs.190465	ESTs	SS,sushi	2.7
65	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,EGF	2.7
	448089	AI467945	Hs.173696	ESTs	SS,TM,	2.6
	446643	AA194417	Hs.282060	ESTs	TM,Clat_adaptor_s	2.6
	456671	AB011142	Hs.114293	KIAA0570 gene product	TM	2.6
	457256	AA459443	Hs.231816	ESTs	SS	2.6
70	438986	AF085888	Hs.269307	ESTs	TM,Spin-Ssty	2.5
	435313	AI769400	Hs.189729	ESTs	TM,MBD	2.5
	417351	T90278	Hs.15049	ESTs	TM,CH	2.5
	412198	AA937111	Hs.69165	ESTs	TM	2.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 k	TM,ubiquitin	2.5
75	421502	AF111856	Hs.105039	solute carrier family 34 (sodium ph	TM,Na_Pi_cotrans	2.5
	418092	R45154	Hs.106604	ESTs	TM,pkinase	2.5
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (	TM,FG-GAP	2.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	TM,ENTH,LWEEQ	2.5
80	431974	AW972689	Hs.200934	ESTs	TM,bZIP	2.5
	438209	AL120659	Hs.6111	KIAA0307 gene product	TM,HLH,PAS	2.5
	447578	AA912347	Hs.136585	ESTs	TM	2.5
	414812	X72755	Hs.77367	monokine induced by gamma interfero	SS,IL8	2.5
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase	TM,Glyco_transf_29	2.4
	416402	NM_000715	Hs.1012	complement component 4-binding prot	TM,sushi	2.4

5	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HU	TM	2.4
	428242	H55709	Hs.2250	leukemia inhibitory factor (choline	SS,LIF_OSM	2.4
	417693	AW959741	Hs.40368	adaptor-related protein complex 1,	TM,Clat_adaptor_s	2.4
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Hom	TM,HECT	2.4
	436311	AA708958	Hs.168732	ESTs	TM	2.4
	426920	AA393351	Hs.132121	ESTs	TM	2.4
	426698	AA394104	Hs.97489	ESTs	TM	2.4
	443426	AF098158	Hs.9329	Homo sapiens mRNA for fls353, compl	TM	2.4
10	406815	AA833930	Hs.288036	IRNA isopentenylpyrophosphate trans	TM,IPPT	2.4
	434808	AF155108	Hs.256150	ESTs, Highly similar to NY-REN-41 a	TM	2.3
	432441	AW292425	Hs.163484	EST	TM,Fork_head	2.3
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQ	TM	2.3
	402298			predicted exon	TM,zf-C2H2,KRAB	2.3
15	435542	AA687376	Hs.269533	ESTs	TM	2.3
	442952	AI743261	Hs.131860	ESTs	TM	2.3
	418203	X54942	Hs.83758	CDC28 protein kinase 2	TM,CKS	2.3
	429228	AI553633	Hs.104985	ESTs	TM	2.3
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	TM,SH3	2.3
20	447570	AI868315	Hs.99669	ESTs	TM,PHD	2.3
	405032			predicted exon	TM,FMO-like	2.3
	416566	NM_003914	Hs.79378	cyclin A1	TM,cyclin	2.3
	420900	AL045633	Hs.44269	ESTs	TM,FAD_binding_5	2.3
	430563	AA481269	Hs.178381	ESTs	TM,ABC_membrane,p450	2.3
25	417372	T99755	Hs.290814	ESTs	TM	2.3
	449083	AI948808	Hs.191144	ESTs	TM	2.3
	410361	BE391804	Hs.62661	guanylate binding protein 1, interf	TM,GBP	2.3
	434131	AI858275	Hs.143659	ESTs	TM	2.3
	431846	BE019924	Hs.271580	Uroplakin 1B	TM,transmembrane4	2.3
30	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific	TM	2.3
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	TM	2.3
	445870	AW410053	Hs.13406	syntaxin 18	TM	2.3
	430639	AW025427	Hs.233552	ESTs	TM,pkinase	2.3
35	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfam	SS,TM,	2.3
	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	SS,TM,Cu-oxidase	2.2
	411558	AA102670	Hs.70725	*Human GABA-A receptor pi subunit m	TM,neur_chan	2.2
	408380	AF123050	Hs.44532	diubiquitin	TM,7tm_3,ANF_receptor	2.2
	403721			predicted exon	TM	2.2
	440711	AA904389	Hs.143511	ESTs	TM,rrm	2.2
40	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1	TM,efhand	2.2
	422956	BE545072	Hs.122579	ESTs	TM	2.2
	433482	AI953499	Hs.152617	ESTs	TM	2.2
	431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fis, cl	TM	2.2
	420777	AA280223	Hs.130865	ESTs	TM	2.2
45	446659	AI335361	Hs.226376	ESTs	TM	2.2
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	TM	2.2
	422282	AF019225	Hs.114309	apolipoprotein L	TM	2.2
	431701	AW935490	Hs.14658	ESTs	TM,Occludin	2.2
	426910	AA470023	Hs.190089	ESTs	TM,MMR_HSR1	2.2
50	405636		Hs.153595	predicted exon	SS,TM,EGF_idl_recept_a	2.2
	401933			predicted exon	TM,ion_trans	2.1
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed pro	TM	2.1
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 pr	TM	2.1
	410664	NM_006033	Hs.65370	lipase, endothelial	SS,TM,Ribosomal_L22,lipase	2.1
55	449378	AW664026	Hs.59892	ESTs	TM	2.1
	433345	AI681545	Hs.152982	EST cluster (not in UniGene)	TM	2.1
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase	SS,TM,Branch	2.1
	431832	AW276866	Hs.192715	ESTs	TM,Ets,SAM_PNT	2.1
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating prot	TM,kinesin_abhydrolase_2	2.1
60	423049	X59373	Hs.188023	ESTs	TM,homeobox	2.1
	427510	Z47542	Hs.179312	small nuclear RNA activating comple	TM	2.1
	418076	R61388	Hs.6724	ESTs	TM	2.1
	413670	AB000115	Hs.75470	hypothetical protein, expressed in	TM	2.1
	429183	AB014604	Hs.197955	KIAA0704 protein	TM	2.1
65	439031	AF075079		gb:Homo sapiens full length insert	TM	2.1
	431060	AF039307	Hs.249171	homeo box A11	TM,homeobox	2.1
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HU	TM	2.1
	419978	NM_001454	Hs.93974	forkhead box J1	TM,Fork_head	2.1
	404535	Z25884	Hs.121483	chloride channel 1, skeletal muscl	SS	2.1
70	445181	AW338972	Hs.147471	ESTs	TM	2.1
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	TM,Hydrolase	2.1
	443591	AI078281	Hs.179240	ESTs	TM	2.1
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN	TM,trypsin	2.1
	424310	AA338648	Hs.50334	ESTs	TM	2.0
75	450193	AI916071	Hs.224623	ESTs	TM,pkinase	2.0
	436009	H57130	Hs.120925	ESTs	SS,TM,Ephrin	2.0
	453313	BE005771	Hs.153746	Homo sapiens cDNA: FLJ22490 fis, cl	TM	2.0
	419833	AA251131	Hs.220697	ESTs	TM,WHEP-TRS	2.0
	437555	AA759263	Hs.14041	ESTs	TM,Nramp	2.0
80	411828	AW161449	Hs.72290	wingless-type MMTV integration site	TM,wnt	2.0
	440052	AI633744	Hs.195648	ESTs	TM,PAC	2.0
	410718	AI920783	Hs.191435	ESTs	TM,SQS_PSY	2.0
	404767			predicted exon	TM	2.0
	447462	AW337214	Hs.158973	ESTs	TM	2.0

442255	AI701857	Hs.202388	ESTs	TM	2.0
410292	AA843087	Hs.124194	ESTs	TM	2.0
442748	AI016713	Hs.135787	ESTs	TM	2.0
458760	AI498631	Hs.111334	ferritin, light polypeptide	TM,HCO3_cotransp	2.0
409799	D11928	Hs.76845	phosphoserine phosphatase-like	TM,Hydrolase	2.0
401324			predicted exon	TM,myosin_head	2.0
432140	AK000404	Hs.272688	hypothetical protein FLJ20397	SS	2.0
447541	AK000288	Hs.18800	hypothetical protein FLJ20281	TM,zf-CCHC	2.0
421379	Y15221	Hs.103982	small inducible cytokine subfamily	SS,TM,IL8	2.0

TABLE 19B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
409457	1132521_1	AW818081 AW392887 AW514700 AW392881
410008	116812_1	AA079552 BE142525 BE142527
422689	219896_1	AW856665 AA315006 AW954733
428679	294049_1	AA431765 AA432015
438993	467651_1	AA828995 AA834879 AI926361
439031	46798_1	AF075079 H48601 H48795
448221	75534_1	BE622615
454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
454692	1229118_1	AW813350 AW816082 AW813476 AW813383
458154	491768_1	AW816379 AA888282 AA879046 AA879195
458861	798085_1	AI630223 AI630470
459287	977129_1	AL079369 D81804

TABLE 19C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401324	9863791	Plus	234057-234174
401517	7677912	Plus	29278-29770
401933	3810668	Minus	48725-49057,51864-51955,52424-52589
402298	6598824	Plus	36758-37953
402606	9909429	Minus	81747-82094
403721	7528046	Minus	156647-157366
403776	7770611	Minus	1414-1513,1624-1756
404767	7882827	Minus	23244-23759
405032	7107731	Minus	131945-132224
405174	7108030	Minus	102814-103063
405454	7656675	Plus	133807-134053
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
405636	5123990	Plus	56384-56587
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406411	9256407	Plus	7400-7527

Table 20A: 56 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, Uterine Cancer Versus Normal Adult Tissues

Table 20A lists about 56 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulated by small molecules (e.g. pkinase, peptidase, isomerase, transporters). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 PSDomain: Protein Structural Domain  
 R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigenelD	Unigene Title	PSDomain	R1
428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	7tm_1	24.2
400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromely	hemopexin	12.3
447350	AI375572	Hs.172634	HER4 (c-erb-B4)	kinase	9.8
420610	AI683183	Hs.99348	distal-less homeo box 5	homeobox	6.2
405609			predicted exon	Myosin_tail,myosin_head	5.0
458861	NM_007358	Hs.31016	PHD finger DNA binding protein	PHD	4.4
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone	NA	4.3



5	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	NA	4.1
	444783	AK001468	Hs.62180	ESTs	PH	4.0
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	HMG_box	3.8
	413472	BE242870	Hs.75379	solute carrier family 1	SDF	3.7
	443613	AI079356	Hs.21807	gb:oz39b09.s1 Soares_NhHMPu_S1 Homo s	zf-C2H2	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	Peptidase_M10	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 re	NA	3.6
	435031	AI632091	Hs.116877	ESTs	RhoGEF,PH	3.3
10	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-187	NA	3.3
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrola	NA	3.1
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	trypsin,pro_isomerase	3.1
	406400	AA343629	Hs.104570	kallikrein 8 (neuropsin/ovasin)	trypsin	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A	ank	3.0
	441794	AW197794	Hs.253338	ESTs	ank	2.9
15	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome de	TEA	2.9
	423513	AF035960	Hs.129719	transglutaminase 5	Transglutamin_N	2.8
	448141	AI471598	Hs.197531	ESTs	bZIP	2.8
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	guanylate_cyc	2.7
20	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	ABC_membrane,ABC_tran	2.7
	448435	BE293439	Hs.182278	calmodulin 2	NA	2.6
	417351	T90278	Hs.15049	ESTs	CH	2.5
	430372	AI206173	Hs.211375	ESTs	SH3,efhand,C2,PH	2.5
	431974	AW972689	Hs.200934	ESTs	bZIP	2.5
25	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hy	ank	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I	Glyco_transf_29	2.4
	403095			predicted exon	homeobox,PAX	2.4
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transfe	IPPT	2.4
	435615	Y15065	Hs.4975	potassium voltage-gated channel	ion_channel	2.3
30	402298			predicted exon	zf-C2H2,KRAB	2.3
	418203	X54942	Hs.83758	CDC28 protein kinase 2	CKS	2.3
	430563	AA481269	Hs.178381	ESTs	ABC_membrane,p450	2.3
	447570	AI868315	Hs.99669	ESTs	PHD	2.3
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily	NA	2.3
35	415539	AI733881	Hs.72472	BMPR-Ib;	bone morphogenetic protein NA	2.2
	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	Cu-oxidase	2.2
	408380	AF123050	Hs.44532	diubiquitin	ANF_receptor,sushi,7tm_1	2.2
	440711	AA904389	Hs.143511	ESTs	rm	2.2
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-	efhand	2.2
40	418506	AA084248	Hs.85339	G protein-coupled receptor 39	NA	2.2
	410664	NM_006033	Hs.65370	lipase, endothelial	Ribosomal_L22,lipase,PLAT	2.1
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1	Branch	2.1
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein	kinesin,PHD,abhydrolase_2	2.1
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-dom	rm,NTF2	2.1
45	404535	Z25884	Hs.121483	chloride channel 1, skeletal muscle	NA	2.1
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2	trypsin	2.1
	446342	BE298665	Hs.14846	Cationic amino acid transporter (ecto	NA	2.0
	458760	AI498631	Hs.111334	ferritin, light polypeptide	HCO3_cotransp,zf-C3HC4	2.0
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	Hydrolase	2.0
50	401324			predicted exon	myosin_head	2.0

TABLE 20B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT number	Accession
443613	575391_1	AI079356 W23287
458861	798085_1	AI630223 AI630470

TABLE 20C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401324	9863791	Plus	234057-234174
402298	6598824	Plus	36758-37953
403095	8954339	Plus	150025-150240,151564-151690
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 21A: 270 Up-Regulated Genes, Uterine Cancer Versus Normal Uterus

Table 21A lists about 270 genes up-regulated in uterine cancer compared to normal uterus. These were selected as for Table 18A, except that the ratio was greater than or equal to 5.0, and the denominator was the median value for six non-malignant uterine specimens.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of tumor vs. normal tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_Ut1 Homo sapiens	55.7
	435094	AI560129	Hs.277523	EST	45.2
15	438461	AW075485	Hs.286049	phosphoserine aminotransferase	19.5
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel	15.6
	441633	AW958544	Hs.112242	ESTs	15.2
	429183	AB014604	Hs.197955	KIAA0704 protein	14.6
20	436775	AA731111	Hs.291891	ESTs	14.3
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	14.0
	446921	AB012113	Hs.16530	CC chemokine SCYA18 (MIP-4) (PARC)	13.0
	413753	U17760	Hs.301103	Laminin, beta 3 (nicein (125kD), kalinin	12.9
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	12.2
25	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	12.0
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	11.7
	425196	AL037915	Hs.155097	carbonic anhydrase II	11.4
	444863	AW384082	Hs.301323	ESTs	11.3
	449785	AI225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	11.1
30	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	10.9
	449801	AA477355	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	10.3
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	10.3
	414812	X72755	Hs.77367	monokine induced by gamma interferon	10.2
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	10.1
35	423645	AI215632	Hs.147487	ESTs	10.1
	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens	10.0
	415786	AW419196	Hs.257924	ESTs	10.0
	458017	AA813426	Hs.192034	ESTs, Weakly similar to KIAA0705 protein	10.0
	435525	AI831297	Hs.123310	ESTs	9.9
40	413335	AI613318	Hs.48442	ESTs	9.7
	420297	AI628272	Hs.88323	ESTs	9.6
	452799	AI948829	Hs.213786	ESTs	9.6
	434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	9.4
	408243	Y00787	Hs.624	interleukin 8	9.3
45	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	9.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	9.2
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	9.2
	443830	AI142095	Hs.143273	ESTs	9.1
	442547	AA306997	Hs.268362	ESTs, Weakly similar to hypothetical pro	9.0
50	421633	AF121860	Hs.106260	sorting nexin 10	9.0
	403381			0	8.9
	426635	BE395109	Hs.129327	ESTs	8.8
	440500	AA972165	Hs.150308	ESTs	8.7
	436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulati	8.7
55	431668	AW969610	Hs.151179	ESTs	8.7
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	8.7
	424966	AI077312	Hs.153985	solute carrier family 7 (cationic amino	8.6
	425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	8.6
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9	8.5
60	438986	AF085888	Hs.269307	ESTs	8.4
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	8.4
	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin	8.3
	415992	C05837	Hs.145807	Homo sapiens cDNA FLJ13593 fis, clone PL	8.2
	431211	M86849	Hs.5566	Homo sapiens connexin 26 (GJB2) mRNA, co	8.2
65	409865	AW502208		gb:UL-HF-BR0p-aju-e-09-0-UL.r1 NIH_MGC_5	8.0
	448158	AI627292	Hs.190877	ESTs	8.0
	401519			0	7.9
	441730	AI243276	Hs.149017	ESTs	7.9
	432441	AW292425	Hs.163484	EST	7.8
70	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	7.8
	438424	AI912498	Hs.25895	ESTs, Weakly similar to PI-3 kinase [H.s	7.8
	447342	AI199268	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAM1	7.7
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	7.7
	423081	AF262992	Hs.123159	sperm associated antigen 4	7.6
75	414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	7.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	7.6
	459142	AI903396		gb:RC-BT029-120199-219_1 BT029 Homo sapi	7.5
	411094	BE066142		gb:CM4-BT0320-221199-047-g10 BT0320 Homo	7.5
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	7.5
80	452607	AI160029	Hs.61438	ESTs	7.5
	443171	BE281128	Hs.9030	TONDU	7.4
	459081	W07808		gb:zb03a12.r1 Soares_fetal_lung_NbHL19W	7.4
	431195	AA503083	Hs.79742	ESTs	7.4
	444459	AI680624	Hs.148676	ESTs	7.4

5	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	7.3
	414918	AI219207	Hs.72222	Hypothetical protein FLJ13459	7.3
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	7.3
	448865	R35027		gb:yg60g02.r1 Soares infant brain 1NIB H	7.3
	409219	AA393383	Hs.133331	ESTs	7.3
10	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	7.2
	403485			0	7.2
	408350	AW183350	Hs.250127	ESTs	7.2
	445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fis, clone L	7.1
	400995			0	7.1
15	406086			0	7.1
	403378			0	7.0
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	7.0
	422038	R39098	Hs.192028	ESTs	7.0
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	6.9
20	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.9
	427494	AI628365	Hs.130412	ESTs, Weakly similar to sre-2 [C.elegans	6.9
	429272	W25140	Hs.110667	ESTs	6.9
	427258	AA400091	Hs.39421	ESTs	6.9
	449309	AW59823	Hs.224189	ESTs	6.9
25	400104			0	6.9
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	6.8
	404767			0	6.8
	406690	M29540	Hs.220529	CEA (carcinoembryonic antigen-related ce	6.8
	439750	AL359053	Hs.57664	ESTs	6.8
30	403127	AI904493	Hs.99890	polymerase (DNA directed), delta 1, cata	6.8
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.8
	425858	AA364923		gb:EST75602 Pineal gland II Homo sapiens	6.8
	421712	AK000140	Hs.107139	hypothetical protein	6.7
	456903	D49441	Hs.155981	mesothelin	6.7
35	414564	AA164803	Hs.71994	ESTs	6.7
	457942	AW665665	Hs.153034	ESTs	6.7
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	6.7
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	6.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	6.7
40	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	6.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.6
	410664	NM_006033	Hs.65370	lipase, endothelial	6.6
	428575	M19684	Hs.184929	serine (or cysteine) proteinase inhibito	6.6
	406400			kallikrein 8 (neuropsin/ovasin)	6.6
45	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	6.5
	441460	AI962478	Hs.226804	ESTs, Moderately similar to ALUC_HUMAN !	6.5
	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, beta pol	6.5
	424349	AF141289	Hs.145550	solute carrier family 7 (cationic amino	6.5
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.4
50	445258	AI635931	Hs.147613	ESTs	6.4
	456032	AW957446	Hs.301711	ESTs	6.4
	404727			0	6.4
	422810	AA317400		gb:EST19374 Retina II Homo sapiens cDNA	6.4
	440044	AW665167	Hs.259563	EST	6.4
55	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	6.4
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	6.4
	422170	AI791949	Hs.112432	anti-Mullerian hormone	6.4
	449611	AI970394	Hs.197075	ESTs	6.4
	402539	AW502761	Hs.30909	KIAA0430 gene product	6.3
60	456983	AI081687	Hs.170225	thymopoietin	6.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	6.3
	457887	AI240007	Hs.148812	ESTs	6.3
	431765	AF124249	Hs.268541	novel SH2-containing protein 1	6.3
	420344	BE463721	Hs.97101	Putative G protein-coupled receptor GPCR	6.2
65	443494	T99719	Hs.270404	Homo sapiens cDNA: FLJ22389 fis, clone H	6.2
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	6.2
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	6.2
	413982	BE503035	Hs.279193	ESTs	6.2
	458091	AF150286		gb:AF150286 Human mRNA from cd34+ stem c	6.2
70	402104			0	6.2
	428771	AB028992	Hs.193143	KIAA1069 protein	6.1
	435313	AI769400	Hs.189729	ESTs	6.1
	441666	AI188346	Hs.301776	ESTs	6.1
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	6.1
75	427308	D26067	Hs.174905	KIAA0033 protein	6.1
	423069	W15613	Hs.1613	adenosine A2a receptor	6.1
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.1
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	6.1
	449409	AI650935	Hs.301694	ESTs	6.1
80	400855			0	6.1
	454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192 Homo	6.0
	414869	AA157291	Hs.72163	ESTs	6.0
	439662	H97552	Hs.269060	ESTs	6.0
	445181	AW338972	Hs.147471	ESTs	6.0
	437129	AL049327		gb:Homo sapiens mRNA; cDNA DKFZp564E016	6.0
	440128	AA962623	Hs.189144	ESTs, Weakly similar to NPT2_HUMAN RENAL	6.0
	443715	AI583187	Hs.9700	cyclin E1	6.0

	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3	5.9
	405291			0	5.9
	432113	AA935065	Hs.152385	ESTs	5.9
5	441236	AA923489	Hs.130432	ESTs	5.9
	424418	BE503432	Hs.66170	HSKM-B protein	5.9
	453028	AB006532	Hs.31442	RecQ protein-like 4	5.8
	407137	T97307	Hs.199067	EST	5.8
	443462	AI064690	Hs.171176	ESTs	5.8
10	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens c	5.8
	456311	AA225632	Hs.190016	ESTs	5.8
	446501	AI302616	Hs.150819	ESTs	5.8
	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	5.8
	409615	AW444861		gb:UI-H-BI3-ajz-a-04-0-UI.s1 NCI_CGAP_Su	5.8
15	459360	BE384526		gb:601277913F1 NIH_MGC_20 Homo sapiens c	5.8
	403824			0	5.8
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	5.8
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabbins)	5.7
	410658	AW105231	Hs.192035	ESTs	5.7
20	426465	AI758948		gb:ty16f07.x1 NCI_CGAP_UI3 Homo sapiens	5.7
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retin	5.7
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	5.7
	405392			0	5.7
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	5.7
25	449796	AA004321	Hs.194397	ESTs	5.7
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	5.7
	428987	NM_004751	Hs.194710	glucosaminyl (N-acetyl) transferase 3	5.7
	404220			0	5.6
	420973	AA743415	Hs.291368	ESTs	5.6
30	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	5.6
	442549	AI751601	Hs.8375	TNF receptor-associated factor 4	5.6
	409867	AW502161		gb:UI-HF-BR0p-ajr-g-12-0-UI.r1 NIH_MGC_5	5.6
	451110	AI955040	Hs.301584	ESTs	5.6
	418216	AA662240	Hs.283099	AF15q14 protein	5.6
35	411897	AW875066		gb:RC6-PT0001-180100-021-F04 PT0001 Homo	5.6
	456161	BE264645	Hs.282093	Homo sapiens cDNA: FLJ21918 fis, clone H	5.6
	406536			0	5.6
	432540	AI821517	Hs.105866	ESTs	5.6
	446315	NM_016293	Hs.14770	bridging integrator 2	5.6
40	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.6
	451035	AU076785	Hs.430	plastin 1 (I isoform)	5.6
	406685	M18728		gb:Human nonspecific crossreacting antig	5.5
	454590	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HE	5.5
	402430			0	5.5
45	446704	AI337228	Hs.197083	ESTs	5.5
	435282	AA677428	Hs.189731	ESTs	5.5
	426062	N57014	Hs.44013	ESTs	5.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	5.5
	456002	AI628729	Hs.191450	ESTs, Weakly similar to type II membrane	5.5
50	409613	AW444816	Hs.171537	Homo sapiens cDNA: FLJ21596 fis, clone C	5.5
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	5.5
	434609	R76593		gb:y160c11.r1 Soares placenta Nb2HP Homo	5.5
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	5.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	5.4
55	400379	NM_018432	Hs.283076	Homo sapiens ovarian cancer related prot	5.4
	436076	AI193277	Hs.120954	ESTs	5.4
	432119	T80289		gb:y03h04.r1 Soares infant brain 1NIB H	5.4
	417175	R44558	Hs.94002	ESTs	5.4
	445774	AI254165	Hs.145504	ESTs	5.4
60	455604	BE011183		gb:PM3-BN0218-100500-003-d09 BN0218 Homo	5.4
	411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	5.4
	445262	AW205650	Hs.253503	ESTs	5.4
	412517	BE271584		gb:601141065F1 NIH_MGC_9 Homo sapiens cD	5.4
	434756	AA827650	Hs.259307	ESTs	5.3
65	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	5.3
	439949	AW979197	Hs.292073	ESTs	5.3
	414995	C18200		gb:C18200 Human placenta cDNA (TFujiiwara	5.3
	428071	AF212848	Hs.182339	transcription factor ESE-3B	5.3
	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	5.3
70	434283	AW235341	Hs.58715	mouse thiamin pyrophosphokinase homolog	5.3
	447798	AI425049	Hs.119629	ESTs, Moderately similar to ALU1_HUMAN A	5.3
	401723			0	5.3
	406270			0	5.3
	452194	AI694413	Hs.298262	ESTs, Weakly similar to dJ88J8.1 [H.sapi	5.3
75	415757	AA830854	Hs.187810	ESTs	5.3
	430051	AA464611	Hs.52515	transducin (beta)-like 2	5.2
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	5.2
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	5.2
	449009	BE044755	Hs.224812	ESTs	5.2
80	424001	W67883	Hs.137476	KIAA1051 protein	5.2
	409479	BE163800	Hs.136912	ESTs	5.2
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	5.2
	435928	H64345	Hs.183961	ESTs	5.2
	447397	BE247676	Hs.18442	E-1 enzyme	5.2

449183	AW445022	Hs.196985	Homo sapiens cDNA: FLJ21135 fis, clone C	5.2
410146	AW592655		gb:hf45f12.x1 Soares_NFL_T_GBC_S1 Homo s	5.2
458164	AI208666	Hs.192081	ESTs	5.2
410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	5.1
439509	AF086332	Hs.58314	ESTs	5.1
422569	BE552132	Hs.118442	cyclin C	5.1
430664	AW969834		gb:EST381912 MAGE resequenes, MAGK Homo	5.1
411231	AW833501		gb:QV4-TT0008-091199-025-e09 TT0008 Homo	5.1
412194	AW900282	Hs.115412	Homo sapiens cDNA FLJ13881 fis, clone TH	5.1
425188	AK002052	Hs.155071	hypothetical protein FLJ11190	5.1
417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	5.1
433279	AW971745		gb:EST383834 MAGE resequenes, MAGL Homo	5.1
454112	NM_000885	Hs.301806	ESTs	5.1
423261	Z43509		gb:HSC1EA031 normalized infant brain cDN	5.1
434084	AI061640	Hs.192788	hypothetical protein PRO1905	5.1
446115	AI733075	Hs.292682	ESTs, Weakly similar to S69913 hypertens	5.1
416719	H79731		gb:yu81f12.r1 Soares fetal liver spleen	5.1
421462	AF016495	Hs.104624	aquaporin 9	5.1
424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	5.1
403383			0	5.1
430832	AI073913	Hs.100686	ESTs, Weakly similar to secreted cement	5.1
436070	AK000073		gb:Homo sapiens cDNA FLJ20066 fis, clone	5.0
416969	AI815443	Hs.283404	organic cation transporter	5.0
444929	AI685841	Hs.161354	ESTs	5.0
453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
439031	AF075079		gb:Homo sapiens full length insert cDNA	5.0
414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	5.0
425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	5.0
449986	AW864502		gb:PM4-SN0016-120400-004-b12 SN0016 Homo	5.0
418717	AI334430	Hs.86984	ESTs	5.0
438769	AA830684	Hs.163426	ESTs	5.0
441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1	5.0
446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase	5.0

TABLE 21B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT number	Accession
409615	1143425_1	AW444861 BE074994 BE074966 BE074992
409865	1156518_1	AW502208 AW502366 AW502148
409867	1156530_1	AW502161 AW502587 AW502345
410146	1178974_1	AW592655 R05927 R06916
411094	1231982_1	BE066142 AW817074
411231	1236356_1	AW833501 AW833506 AW833722 AW833332 AW833509 AW833511 AW833767 AW833339
411426	1245515_1	BE141714 AW845993 AW845989
411897	1264907_1	AW875066 AW875079 AW875075 AW875062 AW875061 AW875074
412323	1288770_1	AW937143 AW937150 AW937141 AW937151 AW937132 AW937160 AW937191 AW937174 AW937195 AW937173 AW937159 AW937139 AW937171 AW937142 AW937145 AW937165 AW937163 AW937164 AW937137 AW937179 AW937156 AW937140 AW937135 AW937170
412517	130281_1	BE271584 AA112511
414484	1452830_1	BE314385
414539	1460320_1	BE379046 BE395459
414995	1511736_1	C18200 D78681 T82025
416719	1611345_1	H79731 H79732
422731	220507_1	AL138411 AL138412 AA315860
422810	221630_1	AA317400 AA434584
423261	226553_1	Z43509 H09001 AA375202 AW954383
425858	257265_1	AA364923 AW963483 BE182774 C21461
426465	267664_1	AI758948 AA379527 AA379948 AA379262 AW963933
430664	321423_1	AW969834 AA528493 AA483165 AW969842
432119	34170_1	T80289 AF052168
433279	361800_1	AW971745 AA581359 AA581358
433921	377350_1	AA618174 AI114549 R36464 R36465
434609	38950_1	R76593 AF147390 R76594
436070	41426_1	AK000073 AA380183 AA380181 AW963533
437129	43343_1	AL049327 AA847105
439031	46798_1	AF075079 H48601 H48795
442438	542469_1	AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
448865	78535_1	R35027 R12034 BE407120
449034	794817_1	AI624049 AW117770 AI858360
449986	821463_1	AW864502 AW864369 AI678780
454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
454692	1229118_1	AW813350 AW816082 AW813476 AW813383
455604	1337197_1	BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
458091	472385_1	AF150286 AA835857
459081	889426_1	W07808 AI822066
459142	918906_1	AI903396 AI903361 AI903360

TABLE 21C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400855	1931571	Minus	17801-18228
400995	8099094	Plus	141186-141601
401519	6649315	Plus	157315-157950
401723	7656694	Plus	147273-147503
402104	8119072	Plus	122409-122600
402430	9796372	Minus	62382-62552
403378	9438244	Minus	44264-44443
403381	9438267	Minus	26009-26178
403383	9438267	Minus	119837-121197
403485	9966528	Plus	2888-3001,3198-3532,3655-4117
403824	9798468	Plus	473-887
404220	6706820	Plus	46107-46439
404727	8081050	Plus	115534-115747
404767	7882827	Minus	23244-23759
405291	3845420	Plus	19999-20473,20672-21036,21147-21285,21378-21667
405392	6624069	Minus	116167-116289,118879-119030
406086	7107817	Plus	9418-9573
406270	7534217	Plus	13136-13591
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
406536	7711478	Plus	25655-25782

TABLE 22A: 430 SIGNIFICANTLY DOWN-REGULATED GENES, UTERINE CANCER VERSUS NORMAL UTERUS

Table 22A lists about 430 genes significantly down-regulated in uterine cancer compared to normal uterus. These were selected as for Table 21A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 14 (i.e. 14-fold down-regulated in tumor vs. normal uterus).

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
414063	H26904	Hs.75736	apolipoprotein D	93.0
447990	BE048821	Hs.20144	small inducible cytokine subfamily A, member 14	75.7
407815	AW373860	Hs.301716	ESTs	68.7
452547	AA335295	Hs.74120	adipose specific 2	61.1
415165	AW887604	Hs.78065	complement component 7	55.1
453655	AW960427	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE	54.0
429350	AI754634	Hs.131987	ESTs	52.6
407228	M25079	Hs.155376	hemoglobin, beta	52.0
425869	AA524547	Hs.160318	FXD domain-containing ion transport regulator	51.6
416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	51.4
408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (from c	49.7
417542	J04129	Hs.82269	progesterone-associated endometrial protein (p	49.3
412295	AW088826	Hs.22971	ESTs	48.0
421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	47.0
452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (from c	46.7
429707	W76631	Hs.211819	matrix metalloproteinase 23B	45.7
416950	AL049798	Hs.80552	dermatopontin	45.6
408221	AA912183	Hs.47447	ESTs	44.6
406791	AI220684	Hs.272572	hemoglobin, alpha 2	43.0
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chromosome	42.6
407938	AA905097	Hs.85050	phospholamban	41.1
410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)	41.0
412524	AA417813	Hs.11177	ESTs	39.4
452426	AI904823	Hs.31297	Homo sapiens cDNA: FLJ23001 fis, clone LNG002	38.6
414290	AI568801	Hs.71721	ESTs	38.2
439627	BE621702	Hs.29076	Homo sapiens cDNA: FLJ21841 fis, clone HEP018	38.0
400258		Hs.79064	deoxyhypusine synthase	37.0
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	36.1
410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	35.4
407663	NM_016429	Hs.37482	COP22 for nonclathrin coat protein zeta-COP	34.3
410286	AI739159	Hs.61898	DKFZP586N2124 protein	33.8
418986	AI123555	Hs.81796	ESTs	33.1
409060	AI815867	Hs.50130	necdin (mouse) homolog	33.1
436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)	32.8
420674	NM_000055	Hs.1327	butyrylcholinesterase	32.6
417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, member	32.4
450810	BE207588	Hs.25511	transforming growth factor beta 1 induced tra	31.7
438150	AA037534	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE	31.6

	430468	NM_004673	Hs.130699	ESTs	31.5
	453060	AW294092	Hs.21594	ESTs	31.3
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vascular	30.8
5	422126	AW973784	Hs.112028	Missshapen/NIK-related kinase	30.5
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (isoform	30.3
	421639	NM_012082	Hs.297921	Homo sapiens mRNA full length insert cDNA clo	30.3
	402520				29.9
	418043	AW377752	Hs.83341	H.sapiens mRNA for tyrosine kinase receptor	29.7
10	443906	AA348031	Hs.7913	ESTs	29.7
	450958	AL137669	Hs.25700	Homo sapiens mRNA; cDNA DKFZp434M0435 (from c	29.4
	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-type 12-	29.4
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob dise	29.4
	429507	NM_003102	Hs.2420	superoxide dismutase 3, extracellular	29.2
	400545				29.1
15	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	29.1
	429942	AI338993	Hs.134535	ESTs	28.9
	438303	AB028998	Hs.6147	KIAA1075 protein	28.7
	419971	AA400027	Hs.296234	ESTs, Highly similar to mitogen-activated pro	28.7
20	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	28.7
	452877	AI250789	Hs.32478	ESTs	28.6
	412442	AI983730	Hs.26530	serum deprivation response (phosphatidylserin	28.6
	424378	W28020	Hs.184367	GTPase activating protein-like	28.6
	421823	N40850	Hs.28625	ESTs	27.9
25	447786	BE620810	Hs.39619	hypothetical protein LOC57333	27.6
	400023			AFFX control: 18S ribosomal RNA	27.5
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	27.2
	414134	X60188	Hs.861	mitogen-activated protein kinase 3	27.1
	428451	AW970451	Hs.98570	ESTs	26.9
30	435520	AA297990	Hs.9315	HNOEL-iso protein	26.6
	437179	AA393508	Hs.171409	serologically defined colon cancer antigen 8	26.4
	441481	AA935303	Hs.270553	ESTs	26.0
	450227	BE388192	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone COL001	25.6
	403731				25.5
35	452814	AI092790	Hs.55016	hypothetical protein FLJ21935	25.5
	410036	R57171	Hs.57975	calsequestrin 2, cardiac muscle	25.5
	416854	H40164	Hs.80296	Purkinje cell protein 4	25.4
	418421	R58620	Hs.85050	phospholamban	25.4
	407000	U12139		gb:Human alpha1(XI) collagen (COL11A1) gene,	25.3
40	421803	NM_012205	Hs.108441	3-hydroxyanthranilate 3,4-dioxygenase	25.3
	445613	BE550889	Hs.158491	ESTs	25.1
	432302	AA345857	Hs.274307	KIAA1442 protein	24.8
	420796	L34355	Hs.99931	sarcoglycan, alpha (50kD dystrophin-associate	24.8
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone COL021	24.7
	417302	BE245812	Hs.8941	ESTs	24.6
45	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mimecan)	24.6
	440130	AI083899	Hs.157527	ESTs	24.5
	431967	AJ243653	Hs.283404	organic cation transporter	24.5
	424580	AA446539	Hs.35092	ESTs	24.4
50	406907	Z25427		gb:H.sapiens protein-serine/threonine kinase	24.2
	443745	AB039670	Hs.9728	ALEX1 protein	24.1
	429101	AW452174	Hs.173780	ESTs	23.5
	410691	AW239226	Hs.65450	reticulon 4	23.4
	408853	AW291484	Hs.254967	ESTs	23.3
55	407979	AA046306	Hs.62927	ESTs	23.1
	448619	AI867182	Hs.202255	ESTs	22.8
	424585	AA464840		gb:zx43h11.1 Soares_total_fetus_Nb2HF8_9w Ho	22.7
	407891	AA486620	Hs.41135	Endomucin 2	22.6
	407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma virus (FB	22.5
60	426990	AL044315	Hs.173094	Homo sapiens mRNA; cDNA DKFZp564H142 (from cl	22.5
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endothelial cell)	22.1
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-like	22.0
	423690	AA329648	Hs.23804	ESTs	22.0
	402865				21.9
65	417387	AW021102	Hs.21509	ESTs	21.9
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	21.9
	459722			Homo sapiens cDNA: FLJ23449 fis, clone HSI058	21.8
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	21.8
	402195				21.7
70	418213	AW978753	Hs.127327	ESTs	21.6
	440274	R24595	Hs.7122	scrapie responsive protein 1	21.6
	455818	AI733747		gb:zn86d04.y5 Stratagene lung carcinoma 93721	21.4
	420861	AI039044	Hs.88827	Homo sapiens mRNA for FLJ00033 protein, parti	21.4
	405228				21.3
75	441292	AF131218	Hs.7765	chromosome 16 open reading frame 5	21.3
	432553	AA553334	Hs.211095	ESTs	21.3
	417098	AB017365	Hs.173859	frizzled (Drosophila) homolog 7	21.2
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	21.2
	405313				21.1
80	410243	D83402	Hs.289006	ESTs, Weakly similar to alternatively spliced	21.1
	413186	AU077141	Hs.75231	solute carrier family 16 (monocarboxylic acid	21.1
	425954	AK000633	Hs.164476	hypothetical protein FLJ20626	21.0
	421770	AA374192	Hs.108124	ribosomal protein L41	21.0
	435265	AA779958	Hs.185932	ESTs	20.8

	430036	AL050284	Hs.227782	DKFZP586M1019 protein	20.7
	430233	AW367902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (from c	20.7
	436130	AA341497	Hs.31408	ESTs	20.7
5	434843	R43707	Hs.133159	ESTs, Weakly similar to PIHUSD salivary proli	20.7
	429303	AW137635	Hs.44238	ESTs	20.6
	442422	AI344415	Hs.156082	ESTs	20.5
	410399	BE068889	Hs.63236	synuclein, gamma (breast cancer-specific prot	20.5
	435869	AF255910	Hs.54650	ESTs, Weakly similar to (define not availabl	20.5
10	447384	AI377221	Hs.40528	ESTs	20.5
	440610	AI733098	Hs.130800	ESTs	20.5
	445806	AL137516	Hs.13323	hypothetical protein FLJ22059	20.4
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	20.4
	436467	AW450278	Hs.91681	ESTs	20.3
15	440191	AI990417	Hs.116107	Homo sapiens genomic DNA, chromosome 21q, sec	20.2
	417511	AL049176	Hs.82223	chordin-like	20.2
	406976	M60299		gb:Human alpha-1 collagen type II gene, exons	20.1
	443547	AW271273	Hs.23767	ESTs	20.1
	417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo sapi	20.1
20	419313	AA843387	Hs.87279	ESTs	20.1
	408322	AW181985	Hs.249986	ESTs	20.0
	448422	BE263813		gb:601194177F1 NIH_MGC_7 Homo sapiens cDNA cl	20.0
	403121				19.9
25	424198	AB029010	Hs.143026	KIAA1087 protein	19.9
	459060	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein D (AU	19.9
	457829	AI742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [H.sapiens	19.9
	445029	AF196481	Hs.12256	midline 2	19.9
	424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (from c	19.8
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal monoa	19.7
30	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYDROXY	19.6
	435891	AW249394	Hs.5002	copper chaperone for superoxide dismutase	19.6
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac muscle,	19.6
	400637				19.5
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (car	19.4
35	430310	U60115	Hs.239069	four and a half LIM domains 1	19.4
	402741				19.4
	401703				19.3
	409229	H60333	Hs.251928	nuclear pore complex interacting protein	19.3
40	453856	AA804789	Hs.19447	Homo sapiens mRNA for FLJ00106 protein, parti	19.3
	430342	NM_005938	Hs.239663	myeloid/lymphoid or mixed-lineage leukemia (t	19.3
	404033				19.2
	411939	AI365585	Hs.146246	ESTs	19.2
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	19.1
	452669	AA216363	Hs.262958	ESTs, Weakly similar to alternatively spliced	19.1
45	439698	AW779654	Hs.55876	ESTs	18.9
	416253	BE250659	Hs.15463	ESTs	18.9
	418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo sapien	18.9
	408877	AA479033	Hs.130315	ESTs	18.9
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24kD	18.9
50	417054	AF017060	Hs.174151	aldehyde oxidase 1	18.8
	404654				18.8
	420174	AI824144	Hs.23912	ESTs	18.8
	400625				18.7
	406150				18.7
55	457835	BE256338	Hs.192375	ESTs, Highly similar to dJ127B20.3 [H.sapiens	18.6
	420105	AW015571	Hs.32244	ESTs	18.6
	404619	BE514535	Hs.77171	minichromosome maintenance deficient (S. cere	18.5
	423282	AL137563	Hs.126378	putative ABC transporter	18.5
	424097	M13981	Hs.1734	inhibin, alpha	18.5
60	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from c	18.5
	427605	NM_000997	Hs.179779	ribosomal protein L37	18.4
	406535				18.4
	418947	W52990	Hs.22860	ESTs	18.4
	414323	NM_014759	Hs.239500	KIAA0273 gene product	18.3
65	457111	AA482027	Hs.142569	ESTs	18.3
	418373	AW750770	Hs.84344	CGI-135 protein	18.3
	424461	D83542	Hs.148090	cadherin 15, M-cadherin (myotubule)	18.2
	451565	NM_000897	Hs.456	leukotriene C4 synthase	18.2
	407751	BE276096	Hs.38205	from HeLa cyclin-dependent kinase 2 interacti	18.2
70	432031	AF039196	Hs.284126	hairless (mouse) homolog	18.1
	404608	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	18.1
	451962	AW078832	Hs.226806	ESTs	18.1
	424100	AI793080	Hs.123525	ESTs, Weakly similar to NGAL RAT NEUTROPHIL G	18.1
	451509	AI969529	Hs.171637	Homo sapiens cDNA: FLJ21937 fis, clone HEP044	18.1
75	453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker protein	18.0
	429924	W39693	Hs.226138	Homo sapiens mRNA; cDNA DKFZp566H2446 (from c	17.9
	423780	AA352013		gb:EST59935 Infant brain Homo sapiens cDNA 5'	17.9
	427030	AA397600	Hs.97531	ESTs	17.9
	439872	T81058		gb:yd26c08.r1 Soares fetal liver spleen 1N1LS	17.9
80	407836	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone CAE112	17.9
	451427	AI091441	Hs.26401	tumor necrosis factor (ligand) superfamily, m	17.9
	424462	AU076666	Hs.148101	serum constituent protein	17.9
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidylserin	17.8
	422319	AW403342	Hs.115232	splicing factor 3a, subunit 2, 66kD	17.8



	400489				17.8
	454421	BE409759	Hs.59563	Homo sapiens mRNA for FLJ00007 protein, parti	17.8
	449282	AL048056	Hs.23437	Homo sapiens cDNA FLJ13555 fis, clone PLACE10	17.7
5	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (from c	17.7
	429790	AK001352	Hs.221737	hypothetical protein FLJ10490	17.7
	422796	AW897265		gb:CM0-NN0057-150400-335-a04 NN0057 Homo sapi	17.7
	427980	AA418305		gb:zv96g05.s1 Soares_NhHMPu_S1 Homo sapiens c	17.6
	409543	AW410200		gb:fh05b12.x1 NIH_MGC_17 Homo sapiens cDNA cl	17.6
10	440206	AI762232	Hs.46794	ESTs	17.6
	455904	BE156173		gb:QV0-HT0367-201299-079-a02 HT0367 Homo sapi	17.5
	427707	NM_005578	Hs.180398	LIM domain-containing preferred translocation	17.5
	437140	AA312799	Hs.283689	activator of CREM in testis	17.5
	417637	AA204969	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB10	17.5
15	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor type,	17.4
	417808	AF177909	Hs.12828	tweety (Drosophila) homolog 1	17.4
	426232	Z70024	Hs.168157	nuclear transcription factor Y, gamma	17.4
	440747	AW297226	Hs.137840	ESTs, Moderately similar to SIX1_HUMAN HOMEOB	17.4
	415307	F05232	Hs.27495	prostate cancer associated protein 7	17.3
20	407049	X72632		(NONE)	17.3
	454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT2RM40	17.3
	411085	AF022991	Hs.68398	period (Drosophila) homolog 1	17.3
	443104	AA088470	Hs.83135	p53-responsive gene 6	17.2
	424106	AA412442	Hs.98132	ESTs	17.2
25	446716	AA436575	Hs.16602	ESTs	17.1
	448677	AI560769	Hs.227051	ESTs	17.0
	434919	AI821740	Hs.116531	ESTs	17.0
	401171	AA360954	Hs.27268	Homo sapiens mRNA; cDNA DKFZp564N196 (from cl	17.0
	456804	AI421645	Hs.139851	caveolin 2	17.0
30	453621	AW749983		gb:QV3-BT0537-280100-070-e04 BT0537 Homo sapi	16.9
	413419	BE093686	Hs.48938	Homo sapiens cDNA: FLJ21802 fis, clone HEP007	16.9
	426515	BE394222	Hs.231444	ESTs	16.9
	428937	T82221	Hs.56729	lymphocyte-specific protein 1	16.9
	424562	AI420859	Hs.150557	basic transcription element binding protein 1	16.9
35	444655	AF088886	Hs.11590	cathepsin F	16.9
	447424	AI681105	Hs.181641	ESTs	16.8
	425439	D38024	Hs.157425	double homeobox, 2	16.8
	446707	AI591214	Hs.156336	ESTs	16.8
	405324				16.8
40	434340	AI193043	Hs.128685	ESTs	16.8
	422942	AF054839	Hs.122540	tetraspan 2	16.8
	421820	AW662990	Hs.108675	heme-binding protein	16.8
	420037	BE299598	Hs.135569	ESTs, Weakly similar to NEUROD [H.sapiens]	16.7
	428818	AI131291	Hs.98866	ESTs	16.7
45	426485	NM_006207	Hs.170040	platelet-derived growth factor receptor-like	16.7
	404947				16.6
	412677	AW029608	Hs.17384	ESTs	16.6
	401551				16.6
50	408053	AW139474	Hs.246862	ESTs	16.6
	425016	AA376049	Hs.154162	ADP-ribosylation factor-like 2	16.6
	418179	X51630	Hs.1145	Wilms tumor 1	16.6
	418994	AA296520	Hs.89546	Selectin E (endothelial adhesion molecule 1)	16.5
	457514	AA775208	Hs.136423	ESTs	16.5
	426275	BE151551		gb:RC0-HT0297-201199-031-f12 HT0297 Homo sapi	16.5
55	457924	AL390142	Hs.288697	Homo sapiens cDNA FLJ13861 fis, clone THYRO10	16.5
	430712	AW044647	Hs.196284	ESTs	16.5
	455144	AW875942		gb:CM1-PT0013-131299-067-b10 PT0013 Homo sapi	16.4
	407524	X64985		gb:H.sapiens mRNA HTPCRX11 for olfactory rece	16.4
	426712	AW173177	Hs.197755	ESTs	16.4
60	429954	AI918130	Hs.21374	ESTs	16.4
	446208	BE258323	Hs.225795	ESTs, Highly similar to OTX1_HUMAN HOMEBOX P	16.4
	442792	AI352340	Hs.131194	ESTs	16.3
	420485	AF218586	Hs.288835	cell death-inducing DFFA-like effector b	16.3
	426767	AA384398	Hs.192491	ESTs	16.3
65	436950	L05779	Hs.113	epoxide hydrolase 2, cytoplasmic	16.3
	415186	AK000150	Hs.78185	MAX-like bHLHZIP protein	16.3
	442197	AW837912		gb:QV3-LT0048-260100-068-c02 LT0048 Homo sapi	16.3
	433457	AA830194	Hs.199417	Homo sapiens mRNA for FLJ00027 protein, parti	16.2
	402316				16.2
70	409736	AA078628		gb:7P07H07 Chromosome 7 Placental cDNA Librar	16.2
	407964	AW130334	Hs.281111	ESTs	16.2
	433677	AI791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN ALU SU	16.2
	425507	AI684745	Hs.165983	hypothetical C2H2 zinc finger protein FLJ2250	16.2
	413724	AA131466	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT2RM40	16.2
75	408922	R87388		gb:ym88g04.r1 Soares adult brain N2b4HB55Y Ho	16.1
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-induc	16.1
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	16.1
	442208	AW296984	Hs.255595	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	16.1
	402426				16.0
80	412399	N53816	Hs.14394	hypothetical protein FLJ20157	16.0
	413200	AA127395	Hs.222414	ESTs	16.0
	404597				15.9
	453143	AA382234	Hs.170121	protein tyrosine phosphatase, receptor type,	15.9
	455984	BE177442		gb:RC1-HT0595-200400-012-f01 HT0595 Homo sapi	15.9

	416193	T25400		gb:PTH069 HTCDL1 Homo sapiens cDNA 5'/3' sim	15.9
	407065	Y10141		gb:H.sapiens DAT1 gene, partial, VNTR.	15.9
	441785	AW138139	Hs.244598	ESTs	15.9
5	413784	BE165819		gb:CMO-HT0486-220300-301-d12 HT0486 Homo sapi	15.9
	429092	AI190864	Hs.178226	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.8
	408499	AW205323	Hs.253475	ESTs	15.8
	453754	AW972580	Hs.172753	ESTs	15.8
	450826	U43030	Hs.25537	cardiotrophin 1	15.8
10	428486	AW583497	Hs.184604	pancreatic polypeptide	15.7
	405895				15.7
	409108	AA339443	Hs.48793	ESTs	15.7
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	15.6
	422948	AW810824	Hs.21351	ESTs	15.6
15	447852	AW504781		gb:Ul-HF-BN0-aln-c-04-0-Ul.r1 NIH_MGC_50 Homo	15.6
	419084	AA496539	Hs.179902	transporter-like protein	15.6
	456771	AW016739	Hs.232201	ESTs	15.6
	438564	AA381553	Hs.198253	major histocompatibility complex, class II, D	15.6
	448705	H05072	Hs.124984	ESTs, Moderately similar to unnamed protein p	15.6
20	454460	X66945	Hs.748	fibroblast growth factor receptor 1 (fms-rela	15.5
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.5
	426759	AI590401	Hs.21213	ESTs	15.5
	453769	R35261	Hs.24947	ESTs	15.4
	434179	AI743448	Hs.116177	ESTs	15.4
25	404111				15.4
	402056				15.4
	458602	AI262208	Hs.276489	ESTs	15.3
	427530	AA405093	Hs.126519	ESTs	15.3
	414716	AF199598	Hs.97044	Kv channel-interacting protein 2	15.3
30	400632				15.3
	443918	AA305475	Hs.22660	Homo sapiens cDNA FLJ11658 fis, clone HEMBA10	15.3
	432037	AW450592	Hs.300459	ESTs	15.3
	412921	BE009345	Hs.128942	ESTs	15.3
	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H.sapi	15.3
35	441704	AI458766	Hs.201988	ESTs	15.3
	414272	AI651603	Hs.46988	ESTs	15.3
	448224	R48700	Hs.20733	EH-domain containing 2	15.2
	404611	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	15.2
	448381	D61580	Hs.21036	Homo sapiens mRNA; cDNA DKFZp434A1010 (from c	15.2
40	454719	BE006547		gb:RC2-BN0130-040400-011-b03 BN0130 Homo sapi	15.2
	446973	H95724	Hs.4283	ESTs	15.2
	457760	AA668123	Hs.134170	ESTs	15.2
	440144	AW082297	Hs.88523	ESTs	15.2
	407387	AB000895		gb:Homo sapiens mRNA for cadherin FIB1, parti	15.2
45	427850	AA416756	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN ALU SU	15.2
	404244				15.1
	402959				15.1
	435487	W07343	Hs.182538	phospholipid scramblase 4	15.1
50	414213	BE297765		gb:601176246F1 NIH_MGC_17 Homo sapiens cDNA c	15.0
	455916	BE156710		gb:QV0-HT0368-310300-181-d01 HT0368 Homo sapi	15.0
	448943	AI608810	Hs.193288	ESTs	15.0
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	15.0
	454082	AF283508	Hs.63168	cell death regulator aven	14.9
55	453308	AW959731	Hs.32538	ESTs	14.9
	458823	AW207574	Hs.179501	ESTs	14.9
	452532	AI905811	Hs.110757	DNA segment on chromosome 21 (unique) 2056 ex	14.9
	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB55Y Ho	14.9
	409473	AL137716	Hs.296567	Homo sapiens mRNA; cDNA DKFZp434D2030 (from c	14.8
	449779	AA004258	Hs.25218	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU C	14.8
60	457546	AA568484	Hs.153632	ESTs	14.8
	403368				14.8
	432163	AK000440	Hs.272799	hypothetical protein FLJ20433	14.8
	421531	AA713505	Hs.291769	ESTs	14.8
	428283	AI439096	Hs.25832	Homo sapiens mRNA; cDNA DKFZp564P116 (from cl	14.8
65	443528	AK001778	Hs.9547	hypothetical protein FLJ10916	14.8
	402399				14.8
	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	14.8
	450300	AL041440	Hs.58210	ESTs	14.8
	403552				14.7
70	406929	U04690		gb:Human olfactory receptor (OR17-210) gene,	14.7
	436365	AW444548	Hs.163118	ESTs	14.7
	402550				14.7
	441782	AW140126	Hs.132357	ESTs	14.7
	415672	N53097	Hs.193579	ESTs	14.7
75	430582	AI215509	Hs.143964	ESTs	14.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (sacsin	14.7
	432683	AW995441	Hs.10475	ESTs	14.7
	441871	AI306150	Hs.153450	ESTs, Weakly similar to 1909123A Na glucose c	14.6
	447481	AF052151	Hs.18686	Mouse Mammary Tumor Virus Receptor homolog	14.6
80	405114				14.6
	401082				14.6
	454316	AW366144		gb:QV0-HT0101-051099-032-b12 HT0101 Homo sapi	14.6
	421572	AA531607	Hs.125143	ESTs, Weakly similar to POL2 MOUSE RETROVIRUS	14.6
	424591	R55704	Hs.150968	hypocretin (orexin) receptor 1	14.6

	441503	AW172263	Hs.185202	ESTs	14.6
	416199	R83537		gb:yq12a08.r1 Soares fetal liver spleen 1NFLS	14.6
	420360	U83171	Hs.97203	small inducible cytokine subfamily A (Cys-Cys	14.6
5	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	14.5
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, member	14.5
	405100				14.5
	454012	M76424	Hs.37014	carbonic anhydrase VII	14.5
	402457				14.5
10	454613	AW810814		gb:MR2-ST0129-201099-004-e01 ST0129 Homo sapi	14.5
	429821	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (from cl	14.5
	431073	BE254470	Hs.249186	cone-rod homeobox	14.5
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing leucine	14.5
	401223				14.4
15	438627	AI087335	Hs.123473	ESTs	14.4
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.4
	437217	AW779241	Hs.155316	ESTs	14.4
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G protein	14.4
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-biphosp	14.4
20	413237	AI468574	Hs.171965	ESTs	14.4
	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, SP-40,	14.4
	426488	X03350	Hs.4	alcohol dehydrogenase 2 (class I), beta polyp	14.4
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	14.4
	405479				14.3
25	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	14.3
	426316	NM_002430	Hs.301852	Human DNA sequence from clone 437G10 on chrom	14.3
	412171	AW897452		gb:CMO-NN0058-150400-337-b08 NN0058 Homo sapi	14.3
	447241	BE382838	Hs.19322	ESTs	14.3
	402100				14.2
30	438286	AW139266	Hs.134807	Homo sapiens cDNA FLJ12057 fis, clone HEMBB10	14.2
	407947	AI500332	Hs.102367	ESTs, Weakly similar to hTcf-4 [H.sapiens]	14.2
	402275				14.2
	402358				14.2
	439624	AA838771	Hs.124407	ESTs	14.2
35	444455	AI149879	Hs.175024	Homo sapiens cDNA: FLJ23447 fis, clone HSI033	14.2
	455314	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	14.2
	427872	AA835058	Hs.21111	ESTs	14.2
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	14.2
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene homolo	14.2
40	442682	AI014545	Hs.231027	EST	14.1
	457033	AF029674	Hs.173422	KIAA1605 protein	14.1
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	14.1
	401007				14.1
	458274	AF149297	Hs.8087	NAG-5 protein	14.1
45	454106	D19687	Hs.245146	ESTs	14.1
	432928	AA570454	Hs.186467	ESTs, Moderately similar to ALU1_HUMAN ALU SU	14.1
	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin/ bet	14.1
	433887	AW204232	Hs.279522	ESTs	14.1
	434927	H46612	Hs.293815	ESTs, Weakly similar to PLM_HUMAN PHOSPHOLEMM	14.1
50	404282				14.1
	422581	NM_016339	Hs.118562	Link guanine nucleotide exchange factor II	14.0
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	14.0
	408107	AA806754	Hs.62835	ESTs	14.0
	401577				14.0
55	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 proline-rich p	14.0
	408104	AW972927	Hs.293968	ESTs	14.0
	404642				14.0
	400675				14.0
	406059				14.0
60	448386	AB037750	Hs.21061	KIAA1329 protein	14.0
	407287	AI678812	Hs.201658	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	14.0

TABLE 22B

65	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
	Pkey	CAT number	Accession
70	408922	109017_1	R87388 R84328 AA058916
	409543	1138723_1	AW410200 AW409705 AW411433 BE296786 BE270309
	409736	115189_1	AA078628 R09051 AA078197 AA077334 AW748808 AW748807
	412171	1280759_1	AW897452 Z20302 D55805 D52877 D60432
75	413784	1389150_1	BE165819 BE165853 W01386
	414213	1426375_1	BE297765 BE262061 BE302686 T83915
	416193	1577102_1	T25400 H26834 H44554 R73193
	416199	1577561_1	R83537 W80940 H27368
80	417998	171375_1	AW967420 AA210915 AA236991 AA210916
	418464	1759038_2	R87580
	418556	1767866_1	T02850
	422796	221500_1	AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361
			T06241 AA326794 AL138130 AW407975 AW999277
	423780	231952_1	AA352013 AA330878 AA339379 AW966303

424585 241151\_1 AA464840 AA343628  
 426275 263712\_1 BE151551 AA373783 BE182852 BE008826 BE008827 BE008781 BE008699  
 427980 285225\_1 AA418305 AI264351  
 439872 47823\_1 T81058 AL357200 T70270  
 442197 535550\_1 AW837912 AW837934 AA984475 AW997490  
 447852 73973\_1 AW504781 BE620394  
 448422 762770\_1 BE263813 BE253504 AI500202 BE251145  
 453621 974526\_1 AW749983 AL045823  
 454316 1109350\_1 AW366144 AW366154 AW366142 AW366151 AW366140 AW366155 BE141715 BE141718 BE141698  
 454613 1226904\_1 AW810814 AW810787 AW810854 AW810773 AW810735 AW810785 AW810660 AW810834 AW810874 AW810723  
 AW810881 AW810791 AW810644 AW810659 AW810676  
 BE006547 AW815578 AW815311 AW856304  
 454719 1230646\_1 AW875942 AW858234 AW875938 AW875941 AW858235 AW875958  
 455144 1254914\_1 AI733747 AA129802  
 455818 137219\_1 BE156173 BE156305 BE156196  
 455904 1382290\_1 BE156710 BE156726 BE156712  
 455916 1382748\_1 BE177442 BE177439 BE177445 BE177440 BE177448 BE177444 BE177433  
 455984 1397288\_1

TABLE 22C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400489	8954013	Plus	131475-131652
400545	9800107	Minus	124618-124881
400625	7228177	Minus	117266-117441
400632	3818355	Plus	72875-73447,75874-76425
400637	8894326	Plus	68901-69507
400675	8118750	Plus	11223-11816
401007	8117333	Minus	140821-141050
401082	3242744	Plus	22937-23494,27677-27966
401223	8099088	Plus	148940-150214
401551	8096896	Minus	189824-190728
401577	9280797	Minus	139377-139674,141195-141281,142217-142340
401703	4826475	Plus	135-1229
402056	8084234	Plus	207002-207288
402100	8117697	Plus	133649-133792
402195	7689778	Minus	147901-148884
402275	2935596	Minus	31065-31233,33680-33771,34345-34411,38890-39125,39779-39943
402316	7527774	Minus	10751-10919,18817-19052,22131-22328
402358	8886976	Minus	131788-132729
402399	1905915	Minus	24502-24666,24985-25102
402426	9796361	Minus	73590-73824
402457	9796782	Minus	16513-16577,16838-16926
402520	7596899	Minus	171761-171996
402550	7652009	Minus	80413-80673
402741	9212200	Minus	18603-18760,19719-19890
402865	9716300	Plus	3197-3429,3722-3914,5795-5987,6802-6961,8653-8815,9292-9660
402959	9368493	Plus	36729-37084
403121	9180223	Plus	4059-4258
403368	4388738	Plus	70286-70429,75165-75258
403552	6862638	Minus	117504-117662
403731	7543752	Minus	144000-144618
404033	8122195	Plus	7976-8156
404111	9408736	Plus	161506-161781
404244	5672609	Minus	98173-98517
404282	2276311	Plus	61503-62205
404597	9958262	Minus	114369-114599
404642	9796810	Plus	102999-103145
404654	9797010	Plus	6275-6527
404947	7382205	Plus	29740-30105,30176-30412
405100	8076846	Plus	144114-144234
405114	8096938	Minus	97013-97560
405228	7248990	Plus	92234-95905
405313	3638954	Plus	68924-69093
405324	3342751	Minus	5475-5677
405479	6453391	Plus	1668-1844
405895	7677903	Minus	66990-67484
406059	9103984	Minus	13856-14004
406150	9886026	Minus	59331-59701
406535	7711477	Plus	83135-83362

TABLE 23A: 626 genes upregulated in uterine cancer relative to normal body tissues

Table 23A lists about 626 genes upregulated in uterine cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis

was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

- 5 Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar accession number, GenBank accession number  
UniGeneID: UniGene number  
Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
- 10 UniGene Title: UniGene gene title  
R1 95th percentile of uterine cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator
- 15 Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prot.Domains; R1
- 20 428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase\_M10; 35.11  
420440; NM\_002407; Hs.97644; mammaglobin 2; Uteroglobulin; 22.80  
439335; AA742697; Hs.62492; NM\_052863; Homo sapiens secretoglobulin, fa; none; 21.66  
425723; NM\_014420; Hs.159311; dickkopf (Xenopus laevis) homolog 4; none; 21.11  
421481; AW391972; Hs.104696; KIAA1324 protein; none; TM=M; SS=M; 20.20  
437938; AI950087; Hs.369628; gb:wq05c02.x1 NCI\_CGAP\_Kid12 Homo sapien; none, none; 19.83  
406687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin, Peptidase\_M10; 17.68  
446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin; 17.60  
25 418281; U09550; Hs.1154; oviductal glycoprotein 1, 120kD (mucin 9; Glyco\_hydro\_18; TM=M; SS=M; 17.48  
431130; NM\_006103; Hs.2719; HE4; epididymis-specific, whey-acidic pr; wap; TM=M; SS=Y; 16.59  
400301; X03635; Hs.1657; estrogen receptor 1; F-box, hormone\_rec, zf-C4, Oest\_recep, adh\_zinc, ketoacyl-synt, pp-binding, Acyl\_transf, Thioesterase, ketoacyl-synt\_C, AAA, E7, RFX\_DNA\_binding; TM=M; SS=N; 16.11  
30 419356; AI656166; Hs.7331; hypothetical protein FLJ22316; Asparaginase\_2, none; 15.90  
433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 15.39  
417931; W95642; Hs.82961; trefoil factor 3 (intestinal); trefoil; 15.39  
400284; ; NM\_000125; Homo sapiens estrogen recepto; hormone\_rec, zf-C4, Oest\_recep; TM=M; SS=M; 15.23  
456662; NM\_002448; Hs.1494; msh (Drosophila) homeo box homolog 1 (fo; homeobox, none; 15.04  
35 438817; AI023799; Hs.163242; ESTs; none, none; 13.72  
453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none; TM=Y; SS=M; 13.67  
424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin, Peptidase\_M10; 13.51  
458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (S; HMG\_box; TM=M; SS=N; 13.44  
410001; AB041036; Hs.57771; kallikrein 11; trypsin; TM=M; SS=M; 13.41  
421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion\_trans, K\_tetra, asp; 13.27  
40 449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp; TM=M; SS=M; 12.76  
436972; AA284679; Hs.25640; claudin 3; PMP22\_Claudin; TM=Y; SS=M; 12.59  
450693; AW450461; Hs.203965; ESTs; Sema, lg, none; 12.52  
415457; AW081710; Hs.7369; Homo sapiens testes specific A2 homolog ; MORN, sugar\_tr; TM=Y; SS=M; 12.46  
413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; 12.23  
45 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none; TM=M; SS=Y; 12.09  
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN\_MK; TM=M; SS=Y; 12.08  
407786; AA687538; Hs.38972; tetraspan 1; transmembrane4; TM=Y; SS=M; 11.91  
444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 11.86  
446608; N75217; Hs.175622; ESTs; Armadillo\_seg, HEAT\_PBS; TM=M; SS=M; 11.72  
50 447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022 hypothetl; none, UQ\_con; 11.59  
420181; AI380089; Hs.158951; ESTs; none, ig, pkinase, LRR, LRRCT; 11.49  
451253; H48299; Hs.26126; claudin 10; PMP22\_Claudin, Peptidase\_M1, K\_tetra; TM=Y; SS=M; 11.45  
453968; AA847843; Hs.62711; High mobility group (nonhistone chromoso; HMG\_box, none; 11.42  
448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate\_rec, MIP; TM=M; SS=M; 11.37  
55 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz, NTR; 11.08  
452367; U71207; Hs.29279; eyes absent (Drosophila) homolog 2; Hydrolase; 11.01  
409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm\_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B\_box; TM=Y; SS=M; 10.95  
415138; C18356; Hs.295944; tissue factor pathway inhibitor 2; Kunitz\_BPTI, none; 10.91  
416658; U03272; Hs.79432; fibrillin 2 (congenital contractural ara; EGF, TB, granulin, PSI, EB, TIL; TM=M; SS=M; 10.81  
60 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A recepto; Neur\_chan\_LBD, Neur\_chan\_memb; TM=Y; SS=M; 10.72  
438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone\_rec, zf-C4, none; 10.66  
425071; NM\_013989; Hs.154424; deiodinase, iodothyronine, type II; T4\_deiodinase; TM=M; SS=Y; 10.66  
430832; AI073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior ; none, none; 10.52  
451497; H83294; Hs.284122; Wnt inhibitory factor-1; EGF, WIF; 10.50  
65 421478; AI683243; Hs.97258; ESTs, Moderately similar to S29539 ribos; none, none; 10.50  
409231; AA446644; Hs.692; GA733-2 antigen; epithelial glycoprotein; thyroglobulin\_1; TM=Y; SS=M; 10.35  
443785; AW449952; Hs.190125; basic-helix-loop-helix-PAS protein; HLH, PAS; TM=M; SS=N; 10.34  
409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC\_tran, M, SMC\_N, SMC\_C, DUF164, none; 10.34  
70 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 10.34  
415539; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; pkinase, Activin\_rec, PDZ, ZU5, death; 10.31  
411274; NM\_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 10.24  
423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin, Peptidase\_M10; TM=M; SS=M; 10.24  
441377; BE218239; Hs.202656; ESTs; none, none; 10.17  
400292; AA250737; Hs.72472; NAME OMITTED ... receptor kinase; pkinase, Activin\_rec, PDZ, ZU5, death; 10.17  
75 452594; AU076405; Hs.29981; solute carrier family 26 (sulfate transp; xan\_ur\_permease, Sulfate\_transp, STAS, HMG\_box; 10.12  
429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, ; C2, PLA2\_B; TM=M; SS=N; 9.87  
413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM\_PNT, none; 9.87  
408562; AI436323; Hs.31141; roundabout (axon guidance receptor, Dros; ig, fn3; TM=M; SS=N; 9.86  
428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); melabo; 7tm\_3; TM=Y; SS=M; 9.72  
80 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone\_rec, zf-C4, none; 9.68  
411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none, none; 9.53  
450451; AW591528; Hs.202072; ESTs; none, none; 9.53  
456062; AI866286; Hs.71962; ESTs, Weakly similar to B36298 proline-r; none, none; 9.50

- 418113; AI272141; Hs.83484; SRY (sex determining region Y)-box 4; HMG\_box,homeobox;TM=M;SS=N; 9.38  
 412791; AI131192; Hs.143199; ESTs, Weakly similar to S72481 probable ; pkinase,PBD:none; 9.36  
 432435; BE218886; Hs.282070; ESTs; none,none; 9.35  
 5 416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyme); trypsin;TM=M;SS=M; 9.32  
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.23  
 445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM; 9.19  
 410407; X66839; Hs.63287; carbonic anhydrase IX; carb\_anhydrase;TM=M;SS=M; 9.19  
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate\_transp,STAS,HMG\_box; 9.17  
 10 453459; BE047032; Hs.257789; ESTs; none,none; 9.14  
 431674; AA098901; Hs.301642; G-protein coupled receptor; none,GCV\_H; 9.05  
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 9.00  
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 8.93  
 436954; AA740151; Hs.130425; ESTs; none,none; 8.91  
 15 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf\_5;TM=Y;SS=M; 8.89  
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA\_gyraseB,DNA\_topoisolV,HATPase\_cc; 8.85  
 407792; AI077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 8.80  
 451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN cDNA 2810; none,none; 8.79  
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 8.72  
 20 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxygenase; IDO;TM=M;SS=N; 8.70  
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodi; Somatomedin\_B,Endonuclease,Phosphodiast;TM=Y;SS=M; 8.69  
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phospho; Ribosomal\_L20,Na\_Pi\_cotrans;TM=Y;SS=N; 8.67  
 437935; AW939591; Hs.5940; mucin 13, epithelial transmembrane; EGF,SEA;TM=Y;SS=M; 8.56  
 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; DPPIV\_N\_term,Peptidase\_S9,none; 8.55  
 25 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 8.53  
 428187; AI687303; Hs.285529; G protein-coupled receptor 49; 7tm\_1,none; 8.49  
 448672; AI955511; Hs.374290; ESTs; lig\_chan,ANF\_receptor,SBP\_bac\_3;TM=Y;SS=M; 8.44  
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm\_2,HRM;TM=Y;SS=M; 8.40  
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 8.40  
 452093; AA447453; Hs.27860; Homo sapiens mRNA; cDNA DKFZp586M0723 (f; 7tm\_1,none; 8.33  
 30 407894; AJ278313; Hs.41143; phosphoinositide-specific phospholipase ; C2,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 8.23  
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 8.21  
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC\_tran,ABC\_membrane;TM=Y;SS=M; 8.20  
 424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD\_NFYB\_HMF; 8.20  
 35 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;SS=N; 8.00  
 415752; BE314524; Hs.78776; putative transmembrane protein; none;TM=Y;SS=N; 7.99  
 422608; AW160644; Hs.118695; potassium voltage-gated channel, subfam; ion\_trans,K\_tetra;TM=Y;SS=N; 7.99  
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none; 7.95  
 409649; AA159216; Hs.55505; hypothetical protein FLJ20442; Y\_phosphatase,DSPc;TM=M;SS=N; 7.95  
 424078; AB006625; Hs.139033; paternally expressed 3; zf-C2H2,KRAB,none; 7.86  
 40 432179; X75208; Hs.2913; EphB3; EPH\_lbd,fn3,pkinase,SAM;TM=Y;SS=M; 7.85  
 424581; M62062; Hs.150917; catenin (cadherin-associated protein), a; Vinculin,DNA\_ligase\_ZBD;TM=M;SS=N; 7.84  
 420610; AI683183; Hs.99348; distal-less homeo box 5; homeobox;TM=M;SS=N; 7.81  
 436856; AI469355; Hs.127310; ESTs; pkinase,rrm;TM=M;SS=N; 7.81  
 45 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 7.80  
 407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagon; TGF-beta,DAN; 7.78  
 424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 BT095 Homo ; none;TM=M;SS=M; 7.65  
 418836; AI655499; Hs.161712; ESTs; pkinase,Activin\_rec,PDZ,ZU5,death; 7.64  
 435793; AB037734; Hs.4993; KIAA1313 protein; none;TM=M;SS=N; 7.61  
 426201; AW182614; Hs.128499; ESTs; SH3,none; 7.59  
 50 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; zf-C3HC4;TM=Y;SS=M; 7.55  
 410850; AW362867; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate\_transp,STAS,HMG\_box; 7.55  
 453464; AI884911; Hs.32989; receptor (calcitonin) activity modifying; none;TM=Y;SS=N; 7.54  
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm,pkinase; 7.52  
 55 437897; AA770561; Hs.146170; hypothetical protein FLJ22959; zf-DHHC,none; 7.38  
 443991; NM\_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK\_channel,ion\_trans;TM=Y;SS=M; 7.36  
 414617; AI339520; Hs.288817; ESTs, Moderately similar to N Chain N, M; hexokinase,hexokinase2;TM=Y;SS=N; 7.35  
 422017; NM\_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2; 7.33  
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none,none; 7.30  
 409041; AB033025; Hs.50081; Hypothetical protein, XP\_051860 (KIAA119; none;TM=M;SS=M; 7.28  
 60 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; 7.28  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y\_phosphatase,Ribosomal\_S3\_N;TM=M;SS=N; 7.28  
 418506; AA084248; Hs.372651; Unknown protein for MGC:29643 (formerly ; none,none; 7.27  
 448913; AA194422; Hs.22564; myosin VI; rrm,zf-RanBP,pkinase,GST\_C,Ets,SAM\_PNT,ABC2\_membrane,myosin\_head,IQ,Myosin\_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT\_hook,SAM;TM=M;SS=N; 7.26  
 65 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa\_permeases,pyridoxal\_deC,bromodomain,PHD,MBD,AT\_hook,DDT,PI3\_P14\_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 7.26  
 424317; AI865032; Hs.26017; ESTs; none,pkinase; 7.21  
 410361; BE391804; Hs.62661; guanylate binding protein 1, interferon-; GBP,GBP\_C;TM=Y;SS=M; 7.21  
 70 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;SS=N; 7.14  
 438707; L08239; Hs.5326; amino acid system N transporter 2; porcu; ACAT,MBOAT;TM=Y;SS=M; 7.05  
 423011; NM\_000683; Hs.123022; adrenergic, alpha-2C-, receptor; 7tm\_1;TM=Y;SS=M; 7.03  
 435021; AA922192; Hs.73962; ESTs; EPH\_lbd,pkinase,fn3,SAM,none; 7.02  
 446163; AA026880; Hs.25252; prolactin receptor; none;NA;NA; 7.01  
 75 447768; X86400; Hs.19520; FXFD domain-containing ion transport reg; ATP1G1\_PLM\_MAT8;TM=M;SS=N; 7.00  
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC\_tran,CoaE;TM=M;SS=N; 6.99  
 451035; AU076785; Hs.430; platin 1 (I isoform); ehand,CH,Adaptin\_N; 6.99  
 450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta,TGFb\_propeptide; 6.95  
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 6.93  
 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUIA S-100 pro; none,none; 6.93  
 80 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ\_con;TM=M;SS=N; 6.92  
 419693; AA133749; Hs.301350; FXFD domain-containing ion transport reg; ATP1G1\_PLM\_MAT8;TM=Y;SS=M; 6.92  
 437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm\_1;TM=Y;SS=M; 6.87  
 418054; NM\_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl\_oxidase;TM=M;SS=M; 6.87

- 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 6.86  
 410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; Ski\_Sno;TM=M;SS=M; 6.86  
 425247; NM\_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase\_M10;; 6.85  
 453064; R40334; Hs.89463; potassium large conductance calcium-acti; none,none; 6.83  
 452046; AB018345; Hs.27657; KIAA0802 protein; none;TM=M;SS=N; 6.79  
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 6.79  
 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glut; aldedh,aakinas;TM=M;SS=N; 6.77  
 431470; AA832417; Hs.139650; ESTs; none,ig,pkinase,LRR,LRRCT; 6.76  
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none,none; 6.75  
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory su; SH2,none; 6.74  
 417886; AA214584; ; ESTs; SPRY,7tm\_3,ANF\_receptor,none; 6.72  
 412926; A1879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS;; 6.70  
 437960; A1669586; Hs.369312; ESTs; none,none; 6.68  
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfam; 60s\_ribosomal,Ribosomal\_L10,TNFR\_c6,DEAD;; 6.66  
 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; Idl\_recept\_a,PKD,MHC\_I;TM=M;SS=Y; 6.65  
 413040; AA193338; Hs.12321; sodium calcium exchanger; Na\_Ca\_Ex;TM=Y;SS=M; 6.64  
 449656; AA002008; Hs.188633; ESTs; PIP5K,none; 6.64  
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-induc; pyr\_redox;TM=M;SS=N; 6.62  
 446063; A1720140; Hs.151079; ESTs; ISK\_Channel,none; 6.61  
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none,none; 6.60  
 421554; AW137676; Hs.97775; ESTs; none,none; 6.59  
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 6.55  
 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase;TM=M;SS=N; 6.54  
 448730; AB032983; Hs.21894; KIAA1157 protein; PP2C;TM=M;SS=N; 6.54  
 433577; AW007080; Hs.284192; ESTs; none,none; 6.53  
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin,ABC\_tran,ABC\_membrane,GTP\_EFTU;TM=M;SS=M; 6.53  
 442133; AW874138; Hs.129017; ESTs; type Ia transmembrane protein; LRR,LRRNT,LRRCT;TM=Y;SS=M; 6.52  
 430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 6.52  
 434263; N34895; Hs.79187; ESTs; ig,none; 6.49  
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y\_phosphatase,DSPc;TM=M;SS=N; 6.48  
 419942; U25138; Hs.93841; potassium large conductance calcium-acti; CakB;TM=Y;SS=M; 6.47  
 421064; A1245432; Hs.101382; tumor necrosis factor, alpha-induced pro; none;TM=M;SS=N; 6.47  
 432636; AA340864; Hs.278562; claudin 7; PMP22\_Claudin;TM=Y;SS=M; 6.45  
 431685; AW296135; Hs.267659; vav 3 oncogene; CH,DAG\_PE-bind,PH,RhoGEF,SH2,SH3,DC1;TM=M;SS=N; 6.44  
 428832; AA578229; Hs.324239; ESTs, Moderately similar to ZN91\_HUMAN Z; Osteopontin,none; 6.39  
 436775; AA731111; Hs.372225; ESTs; none,none; 6.39  
 424343; AW956360; Hs.4748; adenylate cyclase activating polypeptide; 7tm\_2,HRM,none; 6.37  
 421071; A1311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen; none;TM=Y;SS=M; 6.37  
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear trans; HLH,PAS,IL8;TM=M;SS=N; 6.37  
 438993; AA828995; ; gb:od77b08.s1 NCL\_CGAP\_Ov2 Homo sapiens; EGF,metalthio,integrin\_B,PSI,none; 6.27  
 406400; ; kallikrein 8 (neuropsin/ovasin) (KLK8); trypsin;TM=M;SS=M; 6.27  
 429556; AW139399; Hs.314807; ESTs; none;TM=M;SS=N; 6.26  
 409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-like; H5AR g; Steroid\_dh;TM=Y;SS=M; 6.25  
 435732; AF229178; Hs.123136; leucine rich repeat and death domain con; none,none; 6.24  
 439668; A1091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm\_2,toxin\_2;TM=Y;SS=M; 6.24  
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (; MIF,sugar\_tr,none; 6.23  
 436961; AW375974; Hs.156704; ESTs; none,none; 6.23  
 434808; AF155108; Hs.256150; NY-REN-41 antigen; none;TM=M;SS=N; 6.22  
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-li; AAA,NB-ARC,PAAD\_DAPIN;NA;NA; 6.20  
 416224; NM\_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; ethand;; 6.20  
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase\_M49,EGF,ig,Neuregulin;TM=M;SS=N; 6.19  
 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 6.19  
 452551; L27071; Hs.29877; TKX tyrosine kinase; Beach,WD40,SH2,SH3,pkinase;TM=M;SS=N; 6.14  
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;SS=N; 6.12  
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 6.11  
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM,PDZ,pkinase;; 6.11  
 449700; L02867; Hs.78358; paraneoplastic antigen; none;TM=M;SS=N; 6.10  
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE\_p10,ICE\_p20;TM=M;SS=M; 6.10  
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient, yeast, h; HORMA;TM=M;SS=N; 6.09  
 433159; AB035898; Hs.150587; kinesin-like protein 2; bZIP,kinesin;; 6.08  
 432432; AA541323; Hs.115831; ESTs; ig,Sema,PSI,none; 6.07  
 409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG;TM=M;SS=N; 6.04  
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M;SS=N; 6.03  
 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip;TM=M;SS=Y; 6.03  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.00  
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing le; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 6.00  
 428677; A1657119; Hs.351582; troponin I, cardiac; none;TM=M;SS=N; 6.00  
 450098; W27249; Hs.8109; hypothetical protein FLJ21080; SET,zf-MYND;TM=M;SS=N; 6.00  
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, com; C1q,Collagen;; 5.99  
 419972; AL041465; Hs.182982; golgin-67; none,none; 5.99  
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ;; 5.97  
 403362; ; NM\_001615; Homo sapiens actin, gamma 2, ; actin;; 5.95  
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo\_seg;TM=M;SS=N; 5.95  
 420253; A1656055; Hs.96200; neighbor of A-kinase anchoring protein 9; none;NA;NA; 5.93  
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M;SS=N; 5.93  
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 5.92  
 450747; A1064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm,zf-RanBP,GAS2; 5.92  
 415211; R64730.comp; Hs.155986; DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; DEAD,helicase\_C,rrm,Ndr,Cys\_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPc,isp\_1,Ribosomal\_S21,rvp;TM=M;SS=N; 5.91  
 429910; NM\_000867; Hs.2507; 5-hydroxytryptamine (serotonin) receptor; 7tm\_1;TM=Y;SS=N; 5.90  
 447131; NM\_004585; Hs.17466; retinoic acid receptor responder (tazaro; none;TM=Y;SS=N; 5.89  
 437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none;TM=Y;SS=M; 5.89  
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 5.89

- 453102; NM\_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm\_2;TM=Y;SS=M; 5.87
- 426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 5.85
- 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 5.85
- 5 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;SS=N; 5.84
- 450502; T08065; Hs.118262; ESTs; ion\_trans,ion\_trans; 5.84
- 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; none;TM=M;SS=N; 5.83
- 424917; AI636208; Hs.96901; hypothetical protein FLJ23049; none;TM=M;SS=N; 5.83
- 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT\_bind,STAT\_prot;TM=M;SS=N; 5.82
- 10 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS\_C;TM=M;SS=N; 5.82
- 445133; AW157646; Hs.198689; ESTs; ehfand,spectrin,GAS2,SH3,Plectin,RA,Xylose\_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,ldh\_C,CH,AIP3;TM=M;SS=N; 5.79
- 426215; AW963419; Hs.155223; stanniocalcin 2; Stanniocalcin; 5.78
- 414482; S57498; Hs.76252; endothelin receptor type A; 7tm\_1;TM=Y;SS=M; 5.75
- 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=N; 5.74
- 452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox,none; 5.72
- 15 432201; AI538613; Hs.298241; Transmembrane protease, serine 3; tdl\_recept\_a,trypsin;TM=Y;SS=M; 5.72
- 429345; R11141; Hs.199695; hypothetical protein; K\_tetra,SAM; 5.72
- 449458; AI805078; Hs.208261; ESTs; Frizzled,Fz,none; 5.72
- 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 5.71
- 418848; AI820961; Hs.193465; ESTs; PDZ,pkinase,none; 5.70
- 20 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm\_1;TM=Y;SS=M; 5.69
- 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase\_C,HR1;TM=M;SS=N; 5.69
- 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin;TM=M;SS=N; 5.69
- 445136; AI348014; Hs.143949; ESTs, Weakly similar to Achaete-Scute ho; ion\_trans,ion\_trans; 5.69
- 409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory su; SH2,SH3,RhoGAP,none; 5.67
- 25 430016; NM\_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y;SS=N; 5.66
- 429638; AI916662; Hs.211577; kinesin 1 (kinesin receptor); bZIP,Tropomyosin,spectrin,LBP,BPL\_CETP,B56,M;TM=Y;SS=M; 5.65
- 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2;TM=Y;SS=M; 5.64
- 453950; AA156998; Hs.348037; eukaryotic translation initiation factor; none;; 5.64
- 30 425889; M57414; Hs.161305; tachykinin receptor 2; 7tm\_1;TM=Y;SS=M; 5.64
- 432527; AW975028; Hs.102754; ESTs; none,none; 5.64
- 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm\_3,none; 5.63
- 419080; AW150835; Hs.18878; hypothetical protein FLJ21620; 2OG-Fel1\_Oxy;TM=M;SS=N; 5.63
- 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5\_F8\_type\_C;TM=M;SS=M; 5.61
- 440422; AW452696; Hs.130760; myosin phosphatase, target subunit 2; BTB,Kelch,ank,none; 5.58
- 35 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome;TM=M;SS=N; 5.58
- 432805; X94630; Hs.3107; CD97 antigen; 7tm\_2,EGF,GPS,FecCD;TM=Y;SS=M; 5.55
- 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; lg,isodh,Ribosomal\_L6,F-box;TM=Y;SS=M; 5.55
- 441607; NM\_005010; Hs.7912; neuronal cell adhesion molecule; WD40,fn3,lg;TM=M;SS=N; 5.54
- 40 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none,none; 5.54
- 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 5.53
- 404210; ; NM\_005936;Homo sapiens myeloid/lymphoid ; FHA,PDZ,RA,DIL;TM=M;SS=N; 5.53
- 408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 5.53
- 436726; AA324975; Hs.198689; ESTs, Weakly similar to T00079 hypotheti; ehfand,spectrin,GAS2,SH3,Plectin,RA,Xylose\_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,ldh\_C,CH,AIP3;TM=M;SS=N; 5.53
- 45 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none,none; 5.52
- 428667; AI375550; Hs.346868; nucleolar protein p40; homolog of yeast ; none,none; 5.51
- 433907; AW296107; Hs.152686; ESTs; Armadillo\_seg,none; 5.50
- 442821; BE391929; Hs.8752; transmembrane protein 4; none;; 5.50
- 50 422282; AF019225; Hs.114309; apolipoprotein L; Mota\_ExbB;TM=Y;SS=M; 5.49
- 439820; AL360204; Hs.283853; Homo sapiens mRNA full length insert cDN; none,none; 5.49
- 428771; AB028992; Hs.193143; KIAA1069 protein; C2,PI-PLC-X,PI-PLC-X;TM=M;SS=N; 5.48
- 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HE; GDI,7tm\_1,none; 5.48
- 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C1; none,none; 5.48
- 55 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 5.47
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR;TM=M;SS=N; 5.47
- 420297; AI628272; Hs.128757; ESTs, Weakly similar to ALU1\_HUMAN ALU S; pkinase,TUDOR,none; 5.47
- 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3; 5.46
- 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2,STAT,STAT\_bind,STAT\_prot,none; 5.45
- 60 441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia vi; pkinase,Recep\_L\_domain,Furin-like,YLP,none; 5.44
- 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 5.43
- 450402; BE218027; Hs.89969; ESTs; SH3,none; 5.42
- 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ; aa\_permeases,pyridoxal\_deC,bromodomain,PHD,MBD,AT\_hook,DDT,PI3\_P14\_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 5.42
- 65 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 5.42
- 412350; AI659306; Hs.73826; protein tyrosine phosphatase, non-recept; Y\_phosphatase,Band\_41,PDZ;TM=M;SS=N; 5.42
- 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH,none; 5.41
- 448379; AI097463; Hs.21035; KIAA1130 protein; none,Zip; 5.41
- 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; rrm;TM=M;SS=N; 5.41
- 70 411817; BE302900; Hs.72241; mitogen-activated protein kinase kinase ; pkinase;TM=M;SS=M; 5.40
- 445413; AA151342; Hs.12677; CGI-147 protein; UPF0099;TM=M;SS=M; 5.39
- 451863; AL120634; Hs.331803; ATPase, Ca transporting, plasma membrane; cpn60\_TCP1,E1-E2\_ATPase,Cation\_ATPase\_C,Cation\_ATPase\_N,Hydrolase;; 5.38
- 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K\_tetra,DUF51,none; 5.38
- 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrola; PAF-AH\_Ib,Lipase\_GDSL;TM=M;SS=N; 5.36
- 75 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate\_kin;; 5.34
- 441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen\_C,G-alpha,arf;TM=M;SS=M; 5.33
- 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/pep; PTR2;TM=Y;SS=N; 5.33
- 435391; AA704588; Hs.58934; ESTs; PIP5K,none; 5.33
- 411779; AA292811; Hs.72050; non-metastatic cells 5, protein expresse; NDK;; 5.33
- 80 422170; AI791949; Hs.112432; anti-Mullerian hormone; TGF-beta;; 5.32
- 447350; AI375572; Hs.172634; v-erb-a avian erythroblastic leukemia vi; pkinase,Recep\_L\_domain,Furin-like,YLP,none; 5.32
- 449964; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase;TM=M;SS=N; 5.31
- 426427; M86699; Hs.169840; TTK protein kinase; pkinase;; 5.30
- 430407; H23551; Hs.30974; ESTs; pkinase,PBD,none; 5.29



- 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3;TM=M;SS=N; 5.27  
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; ig,kringle,pkinase,Fz;TM=Y;SS=M; 5.27  
 424596; AB020639; Hs.151017; estrogen-related receptor gamma; hormone\_rec,zf-C4;TM=M;SS=N; 5.27  
 428013; AF151020; Hs.181444; hypothetical protein; none;TM=Y;SS=M; 5.26  
 447384; AI377221; Hs.40528; ESTs; SH3,Sorb,none; 5.26  
 441824; AB007871; Hs.7977; KIAA0411 gene product; SH3,RhoGAP;TM=M;SS=N; 5.26  
 438493; AI130740; Hs.6241; phosphoinositide-3-kinase, regulatory su; SH2,SH3,RhoGAP;TM=M;SS=N; 5.26  
 428579; NM\_005756; Hs.184942; G protein-coupled receptor 64; 7tm\_2,GPS;TM=Y;SS=M; 5.25  
 414359; M62194; Hs.75929; cadherin 11, type 2, OB-cadherin (osteob; cadherin,Cadherin\_C\_term;TM=Y;SS=M; 5.25  
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar\_tr;TM=Y;SS=M; 5.24  
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;SS=N; 5.24  
 423685; BE350494; Hs.49753; uveal autoantigen with coiled coil domai; ank,bZIP,M,DUF164,AIP3;; 5.23  
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-pho; MORN,sugar\_tr;TM=Y;SS=M; 5.23  
 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M;SS=N; 5.23  
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin\_ADF;; 5.23  
 412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH\_1bd;TM=Y;SS=M; 5.23  
 426770; AI948618; Hs.150178; ESTs; Sulfate\_transp,STAS;TM=Y;SS=N; 5.23  
 422583; AA410506; Hs.27973; KIAA0874 protein; ank, G-alpha;TM=M;SS=N; 5.22  
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 5.22  
 448093; AW977382; Hs.15898; 2,4-dienoyl CoA reductase 2, peroxisomal; adh\_short;; 5.21  
 443646; AI085198; Hs.164226; Thrombospondin 1; EGF,tsp\_1,vwc,TSPN,tsp\_3,none; 5.18  
 457916; BE085271; Hs.8834; ring finger protein 3; pkinase,none; 5.18  
 433933; AI754389; Hs.355397; Homo sapiens clone TCCIA00164 mRNA sequ; none;NA;NA; 5.18  
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none;; 5.17  
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC\_tran,arf;TM=M;SS=M; 5.17  
 450511; R07423; Hs.85092; thyroid hormone receptor interactor 11; Myosin\_tail,EGF; 5.16  
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 no; none;TM=M;SS=N; 5.15  
 454438; AA224053; Hs.172405; cell division cycle 27; SPRY,7tm\_3,ANF\_receptor; 5.14  
 413869; NM\_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 5.14  
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial; mito\_carr;TM=M;SS=N; 5.14  
 415474; NM\_014252; Hs.78457; solute carrier family 25 (mitochondrial; mito\_carr;TM=M;SS=N; 5.14  
 411704; AI499220; Hs.71573; hypothetical protein FLJ10074; pkinase;TM=M;SS=N; 5.13  
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm\_2;TM=Y;SS=M; 5.13  
 454128; AL031259; Hs.367900; programmed cell death 2; zf-MYND;TM=M;SS=N; 5.13  
 431322; AW970622; Hs.376626; gb:EST382704 MAGE resequences, MAGK Homo; none,none; 5.13  
 444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none;TM=Y;SS=M; 5.12  
 422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; tsp\_3,EGF;; 5.12  
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion\_trans;TM=Y;SS=M; 5.11  
 436494; AA720997; Hs.128295; ESTs; none,CAP\_GLY,HCO3\_cotransp,Glyco\_hydro\_63,PH; 5.11  
 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA synthetas; WHEP-TRS,tRNA-synt\_1b,none; 5.10  
 453387; AI90741; Hs.252809; ESTs; Na\_Ca\_Ex,none; 5.07  
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M;SS=N; 5.07  
 456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4,Cbl\_N,Cbl\_N2,Cbl\_N3;TM=M;SS=N; 5.07  
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanlylate\_kin,PDZ,SH3; 5.07  
 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase,DCX;TM=M;SS=N; 5.06  
 413745; AW247252; Hs.75514; nucleoside phosphorylase; Mtap\_PNP;; 5.06  
 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, y; none,Ribosomal\_S13,Galactosyl\_T,Zip,adh\_short,zf-C3HC4; 5.06  
 421369; NM\_005089; Hs.171909; U2 small nuclear ribonucleoprotein auxil; rrm,zf-CCCH,lectin\_c,integrin\_B;TM=M;SS=N; 5.06  
 412170; D16532; Hs.73729; very low density lipoprotein receptor; ldl\_recept\_a,ldl\_recept\_b,EGF;TM=M;SS=M; 5.06  
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;SS=N; 5.05  
 421109; L32832; Hs.101842; AT-binding transcription factor 1; HMG14\_17,homeobox,zf-C2H2;TM=M;SS=M; 5.05  
 453880; AI803166; Hs.135121; ESTs, Weakly similar to I38022 hypotheiti; HSP70,none; 5.05  
 431512; BE270734; Hs.2795; lactate dehydrogenase A; ldh,ldh\_C,SH3,pkinase,UBA;TM=M;SS=N; 5.05  
 435411; AW444619; Hs.138211; ESTs; none,pkinase; 5.04  
 419088; AI538323; Hs.367688; integrin, beta 8; integrin\_B,none; 5.04  
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX; Troponin,Exo\_endo\_phos,IQ;TM=M;SS=N; 5.04  
 428376; AF119665; Hs.184011; pyrophosphatase (inorganic); Pyrophosphatase;TM=M;SS=N; 5.03  
 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9;TM=M;SS=M; 5.03  
 436415; BE265254; Hs.343258; proliferation-associated 2G4, 38kD; Peptidase\_M24,Furin-like,pkinase,Recep\_L\_domain,efhand; 5.01  
 449674; AW444937; Hs.233482; ESTs; C2,PI-PLC-Y,PI-PLC-X,none; 5.01  
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras,arf,TK;; 5.01  
 412133; U83460; Hs.104557; solute carrier family 31 (copper transpo; none;TM=Y;SS=N; 5.01  
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;; 5.00  
 449474; AA019344; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; ThiF,UBACT,pkinase,UCH-2,UCH-1,rrm,zf-C2H2,zf-RanBP,G-patch; 5.00  
 416365; U15131; Hs.79265; suppression of tumorigenicity 5; DENN,dDENN,uDENN;TM=M;SS=N; 5.00  
 421351; AU076667; Hs.103755; receptor-interacting serine-threonine ki; CARD,pkinase;TM=M;SS=N; 4.99  
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR\_c6,Acyl-CoA\_hydro; 4.98  
 442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; rrm,IRK;; 4.95  
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT; none,none; 4.95  
 426310; NM\_000909; Hs.169266; neuropeptide Y receptor Y1; 7tm\_1;TM=Y;SS=M; 4.95  
 457718; F18572; Hs.22978; ESTs, Weakly similar to ALU4\_HUMAN ALU S; pkinase,pkinase; 4.94  
 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase;TM=M;SS=N; 4.94  
 427541; AI798983; Hs.375835; solute carrier family 35 (CMP-sialic aci; none,none; 4.94  
 452792; AB037765; Hs.30652; KIAA1344 protein; thioired;TM=M;SS=M; 4.93  
 430713; AA351647; Hs.2642; eukaryotic translation elongation factor; GTP\_EFTU,GTP\_EFTU\_D3,GTP\_EFTU\_D2;; 4.93  
 444838; AV651680; Hs.208558; ESTs; integrin\_A,FG-GAP,none; 4.93  
 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin (neuronal; HNH,cadherin,Cadherin\_C\_term;TM=M;SS=N; 4.92  
 421302; T34462; Hs.103291; neuritin; none;TM=M;SS=Y; 4.91  
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisi; pkinase;TM=M;SS=N; 4.91  
 408657; AA782601; Hs.378649; ESTs; B56,none; 4.91  
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH\_C,IMPDH\_N,CBS,integrin\_B,Ricin\_B\_lectin; 4.91  
 421462; AF016495; Hs.104624; aquaporin 9; MIP;TM=Y;SS=M; 4.90  
 424503; NM\_002205; Hs.149609; integrin, alpha 5 (fibronectin receptor;; integrin\_A,FG-GAP;TM=Y;SS=N; 4.89

- 438564; AA381553; Hs.198253; major histocompatibility complex, class ; ig,MHC\_II\_alpha,none; 4.89
- 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST\_C,EF1G\_domain,GST\_N,S1,Fz,Frizzled,calreticulin,7tm\_2,rm,PAP\_assoc;TM=Y;SS=M; 4.88
- 434521; NM\_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo\_seg,IBB;TM=M;SS=N; 4.88
- 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig;TM=Y;SS=M; 4.88
- 424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosp; perlipin;; 4.88
- 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; DEAD,helicase\_C,PRK,Alp3;TM=M;SS=N; 4.87
- 417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone H; voltage\_CLC,CBS,none; 4.86
- 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C; Phosphodiester,Somatomedin\_B,Endonuclease,none; 4.86
- 417666; A1345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4;TM=M;SS=N; 4.86
- 453864; AW021407; Hs.21068; hypothetical protein; none,none; 4.86
- 453082; H18835; Hs.31608; hypothetical protein FLJ20041; ion\_trans;TM=Y;SS=M; 4.85
- 413407; A1356293; Hs.75339; inositol polyphosphate phosphatase-like ; SH2,SAM,Exo\_endo\_phos;; 4.85
- 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin\_G,CorA;; 4.85
- 435652; N32388; Hs.334370; uncharacterized hypothalamus protein HBE; none;TM=M;SS=N; 4.84
- 419355; AA428520; Hs.90061; progesterone binding protein; heme\_1;TM=Y;SS=M; 4.83
- 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 4.83
- 408983; NM\_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC\_tran,ABC\_membrane,PRK,Bac\_export\_3;TM=Y;SS=N; 4.83
- 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG\_PE-bind,pkinase\_C,OPR;TM=M;SS=N; 4.82
- 435232; NM\_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank;TM=M;SS=N; 4.81
- 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,pkinase;TM=M;SS=N; 4.81
- 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.81
- 453354; W55946; Hs.234863; Homo sapiens cDNA FLJ12082 fis, clone HE; transmembrane4,none; 4.81
- 450883; NM\_001348; Hs.25619; death-associated protein kinase 3; pkinase;TM=M;SS=N; 4.79
- 429736; AF125304; Hs.212680; tumor necrosis factor receptor superfam; TNFR\_c6;TM=M;SS=M; 4.79
- 431183; NM\_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER\_lumen\_recept;TM=M;SS=M; 4.79
- 409960; BE261944; Hs.355264; hexokinase 1; none,none; 4.78
- 422795; AB033109; Hs.375610; KIAA1283 protein; 7tm\_1,kazal,A2M,A2M\_N;TM=Y;SS=M; 4.78
- 423619; T48691; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm\_1,7tm\_2;TM=Y;SS=M; 4.78
- 429305; AF095727; Hs.287832; myelin protein zero-like 1; ig,transmembrane4;TM=Y;SS=M; 4.78
- 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSpc;TM=M;SS=N; 4.77
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 4.76
- 444672; Z95636; Hs.11669; laminin, alpha 5; laminin\_EGF,laminin\_G,EGF,TNFR\_c6,laminin\_B,laminin\_Nterm,metalthio,Tropomyosin,DUF164,p450;TM=M;SS=N; 4.76
- 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; pfbK;TM=M;SS=N; 4.75
- 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 4.75
- 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl\_Oxidase;; 4.75
- 411165; NM\_000169; Hs.69089; galactosidase, alpha; Melibiase;; 4.75
- 425548; AA890023; Hs.1906; prolactin receptor; fn3;TM=Y;SS=M; 4.73
- 434158; T86534; Hs.14372; ESTs; adenylatekinase,none; 4.73
- 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypotheti; none,SH3,myosin\_head,IQ; 4.73
- 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 4.73
- 434503; T96231; Hs.17762; ESTs; SH3,Sorb,none; 4.73
- 446342; BE298665; Hs.14846; solute carrier family 7 (cationic amino ; none;TM=M;SS=N; 4.72
- 427418; AA402587; Hs.356667; LAT1-3TM protein; none,none; 4.71
- 449433; A1672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-bind; Frizzled,Fz,Frizzled,Fz; 4.71
- 418910; Z25821; Hs.89466; Homo sapiens, Similar to dodecenoyl-Coen; ECH;; 4.70
- 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal\_L37ae,pkinase,POLO\_box,tRNA-synt\_1b,dynamin,dynamin\_2,GED,bZIP,M;; 4.70
- 442199; BE277633; Hs.372542; etoposide-induced mRNA; none;TM=Y;SS=M; 4.69
- 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm\_1,7tm\_2;TM=Y;SS=M; 4.69
- 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 ; none;; 4.69
- 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domai; death,DED;; 4.68
- 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;SS=N; 4.68
- 443323; BE560621; Hs.9222; estrogen receptor binding site associate; none;TM=M;SS=M; 4.68
- 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor;; integrin\_A,FG-GAP;TM=Y;SS=N; 4.68
- 418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodi; Phosphodiester;TM=Y;SS=M; 4.67
- 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin\_EGF,laminin\_Nterm,integrin\_B;; 4.67
- 425976; C75094; Hs.334514; NG22 protein; voltage\_CLC;TM=Y;SS=M; 4.66
- 407844; AW073716; Hs.8037; ESTs; transmembrane4,none; 4.66
- 450656; AA010539; Hs.18912; unnamed protein product; zf-C2H2;; 4.66
- 420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-530115; none,none; 4.65
- 404287; ; FGENESH predicted novel CUB-domain conta; none,none; 4.64
- 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd\_glycop;TM=Y;SS=M; 4.63
- 426680; AA320160; Hs.171811; adenylate kinase 2; adenylatekinase;TM=M;SS=N; 4.63
- 430397; A1924533; Hs.105607; bicarbonate transporter related protein ; HCO3\_cotransp;TM=Y;SS=N; 4.63
- 447656; NM\_003726; Hs.19126; src kinase-associated phosphoprotein of ; SH3,PH;TM=M;SS=N; 4.63
- 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M;SS=N; 4.62
- 429126; AW172356; Hs.99083; ESTs; 7tm\_1,none; 4.61
- 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; COX8,SHMT,MIF,GST\_C,EF1G\_domain,GST\_N,S1,Fz,Frizzled,calreticulin,7tm\_2,rm,PAP\_assoc;TM=Y;SS=M; 4.60
- 409220; BE243323; Hs.51233; tumor necrosis factor receptor superfam; TNFR\_c6,death,Lipoprotein\_5,TIL;TM=Y;SS=M; 4.60
- 421921; H83363; Hs.355993; translocase of inner mitochondrial membr; zf-Tim10\_DDP,efhand,CH,spectrin,serpin;TM=M;SS=N; 4.60
- 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 4.59
- 400290; H18836; Hs.31608; hypothetical protein FLJ20041; none,Cys\_knot; 4.59
- 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion\_trans;TM=Y;SS=M; 4.59
- 409645; A1142265; Hs.55498; geranylgeranyl diphosphate synthase 1; polyprenyl\_synt;TM=M;SS=N; 4.59
- 427373; AB007972; Hs.130760; myosin phosphatase, target subunit 2; ank;TM=M;SS=N; 4.58
- 437212; A1765021; Hs.210775; ESTs; UDPGT,none; 4.58
- 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;; 4.57
- 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 4.56
- 416041; AA345547; Hs.53263; hypothetical protein FLJ13287; WD40;; 4.55
- 434511; R28982; Hs.18106; ESTs; pkinase,Glyco\_hydro\_39; 4.55
- 410174; AA306007; Hs.59461; DKFZP434C245 protein; none,DSpc; 4.55
- 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M;SS=N; 4.55
- 451367; AA923729; Hs.26322; cell cycle related kinase; pkinase;TM=M;SS=N; 4.54

417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR,LRRNT,LRRCT;TM=Y;SS=M; 4.54  
 411296; BE207307; Hs.10114; growth suppressor 1; ZOG-Fell\_Oxy;TM=M;SS=M; 4.53  
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph); Ham1p\_like;TM=M;SS=N; 4.53  
 431992; NM\_002742; Hs.2891; protein kinase C, mu; pkinase,DAG\_PE-bind,PH;TM=M;SS=M; 4.53  
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE\_p10,ICE\_p20;TM=M;SS=M; 4.53  
 428005; AW302245; Hs.181390; casein kinase 1, gamma 2; pkinase;TM=M;SS=N; 4.52  
 407775; NM\_004914; Hs.38772; RAB36, member RAS oncogene family; ras,arf;TM=M;SS=N; 4.52  
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 4.51  
 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HE; none,none; 4.51  
 405484; ; C3002124;gij12737280[ref]XP\_006682.2] k; none;; 4.50  
 443605; H06865; Hs.134131; ESTs; efhand,ion\_trans,none; 4.50  
 431738; AW237726; Hs.288549; hypothetical protein FLJ14710; 7tm\_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B\_box;TM=Y;SS=M; 4.50  
 422112; BE540240; Hs.111783; Lsm1 protein; Sm,BAG;; 4.49  
 418869; AW516555; ; gb:xq01d05.x1 Soares\_NHCeC\_cervical\_tumo; none,RasGAP,WW,IQ; 4.48  
 447898; AW969638; Hs.112318; 6.2 kd protein; none,none; 4.48  
 450607; AL050373; Hs.25213; hypothetical protein; SH3;TM=M;SS=N; 4.48  
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; ig;TM=Y;SS=M; 4.48  
 424823; NM\_006226; Hs.153322; phospholipase C, epsilon; C2,PH,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 4.48  
 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chlo; none;TM=Y;SS=N; 4.47  
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase,Recep\_L\_domain,YLP,none; 4.47  
 435615; Y15065; Hs.4975; potassium voltage-gated channel, KQT-like; ion\_trans,KCNQ1\_channel;TM=Y;SS=N; 4.47  
 427557; NM\_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR\_LY6,ET,PLA2\_inh;; 4.47  
 428727; AF078847; Hs.78452; general transcription factor IIH, polype; PHO4,LIM;TM=M;SS=N; 4.46  
 412760; AW379030; Hs.41324; ESTs; Cbl\_N,Cbl\_N2,Cbl\_N3,UBA,zf-C3HC4,none; 4.46  
 409093; BE243834; Hs.50441; CGI-04 protein; Ribosomal\_L37ae, pkinase,POLO\_box,tRNA-synt\_1b,dynamin,dynamin\_2,GED,bZIP,M;; 4.46  
 434375; BE277910; Hs.3833; 3-phosphoadenosine 5'-phosphosulfate aps; APS\_kinase,ATP-sulfurylase,PRK,Thymidylate\_kin;; 4.46  
 447434; R16890; Hs.137135; ESTs; pkinase,fn3,ig, pkinase,fn3; 4.45  
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar\_lr; 4.45  
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol\_BP, pkinase;TM=M;SS=N; 4.44  
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone\_rec,zf-C4,Metallothio\_5;TM=M;SS=N; 4.44  
 409686; AK000002; Hs.55879; Homo sapiens mRNA; cDNA DKFZp434L0827 (f; ABC\_tran,ABC\_membrane;TM=M;SS=M; 4.44  
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm\_3,none; 4.44  
 436823; AW749865; Hs.117077; ESTs, Weakly similar to I38022 hypotheti; aa\_permeases,zf-C2H2,KRAB,pyridoxal\_deC,bromodomain,PHD,MBD,AT\_hook,DDT,PI3\_Pi4\_kinase,FAT,FATC,BolA,RUN,TFIIS;TM=M;SS=N; 4.44  
 450505; NM\_004572; Hs.25051; plakophilin 2; Armadillo\_seg;TM=M;SS=N; 4.43  
 437915; AI637993; Hs.202312; Homo sapiens clone N11 Ntera2D1 teratoca; none,none; 4.43  
 417412; X16896; Hs.82112; interleukin 1 receptor, type I; ig,TIR;TM=M;SS=M; 4.43  
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank;; 4.43  
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor; ; inositol\_P,ig;TM=M;SS=N; 4.43  
 452124; AA454220; Hs.61170; ESTs; pkinase,none; 4.43  
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) ; NDK,PH,Oxysterol\_BP;; 4.42  
 416202; AW964492; Hs.169624; ESTs; none;TM=M;SS=N; 4.42  
 441518; AW161697; Hs.294150; ESTs; Y\_phosphatase,DSPc,none; 4.42  
 441680; AW444598; Hs.7940; RAP1, GTP-GDP dissociation stimulator 1; Armadillo\_seg;TM=M;SS=N; 4.42  
 431429; AF072813; Hs.252831; reticulon 3; Reticulon,Fz,ig,kringle, pkinase;TM=Y;SS=N; 4.42  
 453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 fis, clone L; FG-GAP,integrin\_A,NIF; 4.41  
 421242; AW161386; Hs.13561; hypothetical protein MGC4692; none;NA;NA; 4.41  
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M;SS=N; 4.41  
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death,ZU5;; 4.41  
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY\_C;TM=M;SS=N; 4.41  
 413367; NM\_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar\_tr;TM=Y;SS=N; 4.41  
 458097; AW341135; Hs.58104; ESTs; none,SH3,PID; 4.40  
 458246; BE407379; Hs.108082; ESTs, Weakly similar to T31636 hypotheti; C1q,Collagen;TM=M;SS=Y; 4.40  
 427681; AB018263; Hs.284232; tumor necrosis factor receptor superfam; death,TNFR\_c6,PH,Xlink,RhoGEF,Metallothio\_5;TM=M;SS=M; 4.40  
 443693; AI344782; Hs.9683; DnaJ (Hsp40) homolog, subfamily C, membe; rrm,DnaJ,TPR;TM=M;SS=N; 4.40  
 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating pr; bromodomain;TM=M;SS=N; 4.39  
 453891; AB037751; Hs.301242; Homo sapiens mRNA full length insert cDN; none,none; 4.39  
 442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 4.39  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig;TM=Y;SS=M; 4.37  
 445817; NM\_003642; Hs.13340; histone acetyltransferase 1; none;TM=M;SS=N; 4.37  
 444895; AI674383; Hs.22891; solute carrier family 7 (cationic amino ; ASC,death,TNFR\_c6; 4.37  
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo\_seg;TM=M;SS=M; 4.37  
 432108; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3,PDZ,Guanylate\_kin,none; 4.37  
 418283; S79895; Hs.83942; cathepsin K (pyncodysostosis); Peptidase\_C1;; 4.37  
 445826; BE313754; Hs.13350; Homo sapiens mRNA; cDNA DKFZp586D0918 (f; ig,lsp\_1,ZU5,Nucleoside\_tran; 4.37  
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y\_phosphatase;TM=Y;SS=N; 4.36  
 400257; ; Hs.76366; ENSP00000000452:BAD protein (BCL-2 bindi; none;TM=M;SS=N; 4.36  
 431476; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT;; 4.36  
 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none;TM=M;SS=N; 4.36  
 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase\_c,zf-C2H2,PHD,none; 4.36  
 427716; L38951; Hs.180446; karyopherin (importin) beta 1; Armadillo\_seg,HEAT;TM=M;SS=N; 4.35  
 425843; BE313280; Hs.159627; death associated protein 3; myb\_DNA-binding,PAH,BAH,bromodomain,PHD,SET;TM=M;SS=N; 4.35  
 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms; pkinase,ig, pkinase,ig,p450,SET,PWWP; 4.35  
 445926; AF054284; Hs.334826; splicing factor 3b, subunit 1, 155kD; none;TM=M;SS=N; 4.35  
 410726; AI623859; Hs.15936; ESTs; pkinase,pro\_isomerase,none; 4.35  
 433996; AW135357; Hs.192374; ESTs; HSP90,HATPase\_c,UDG; 4.34  
 433592; NM\_004642; Hs.3436; deleted in oral cancer (mouse, homolog) ; none;TM=M;SS=N; 4.34  
 437103; AW139408; Hs.152940; ESTs; Choline\_kinase,none; 4.34  
 410068; AI633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3;TM=M;SS=N; 4.34  
 427349; AA360154; Hs.177415; Finkel-Biskis-Reilly murine sarcoma viru; ubiquitin;TM=M;SS=N; 4.33  
 439807; AA376417; Hs.374608; hypothetical protein MGC5244; ; abhydrolase\_2;TM=M;SS=M; 4.33  
 453308; AW959731; Hs.323099; ESTs; none, pkinase,Activin\_recp; 4.33  
 424893; AW295112; Hs.153648; Homo sapiens cDNA FLJ13303 fis, clone OV; SAM;; 4.33

	444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-S; DSPc;TM=M;SS=N; 4.33
	429655; U48959; Hs.211582; myosin, light polypeptide kinase; pkinase,fn3,ig,none; 4.32
	409121; AA902256; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR,none; 4.32
5	430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 4.32
	423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbon; HCO3_cotransp;TM=Y;SS=M; 4.29
	425654; AB033022; Hs.158654; KIAA1196 protein; zf-C2H2;TM=M;SS=N; 4.29
	457500; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm,pkinase;TM=M;SS=N; 4.29
10	427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 4.29
	447191; NM_014521; Hs.17667; SH3-domain binding protein 4; SH3;TM=M;SS=N; 4.29
	408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc;TM=M;SS=N; 4.29
	441130; AI160734; Hs.267604; Homo sapiens PNAS-129 mRNA, complete cds; BTB,Kelch,K_tetra,DSPc;TM=M;SS=N; 4.28
	430057; AW450303; Hs.2534; bone morphogenetic protein receptor, typ; Activin_rec,pkinase;TM=Y;SS=M; 4.28
	430250; NM_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;SS=N; 4.28
15	406774; AW518383; Hs.177592; ribosomal protein, large, P1; 60s_ribosomal; 4.28
	413809; L25851; Hs.851; integrin, alpha E (antigen CD103, human; vwa,integrin_A,FG-GAP;TM=M;SS=Y; 4.27
	443960; AI093577; Hs.255416; hypothetical protein FLJ21986; TTL;TM=M;SS=N; 4.27
	427378; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE;TM=M;SS=N; 4.27
	412204; AI125507; Hs.24937; ESTs; ig,rm,none; 4.26
20	439506; AI361238; Hs.41136; ESTs; MAM,pkinase,Nucleoplasmin,none; 4.26
	451295; AI557212; Hs.17132; ESTs; Moderately similar to I54374 gene; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.26
	452488; N74921; Hs.184389; ESTs; none;TM=M;SS=N; 4.26
	450973; AF012072; Hs.25732; eukaryotic translation initiation factor; W2,MA3,MIF4G;TM=M;SS=N; 4.26
	452437; AA026237; Hs.181272; ESTs; efhand,ion_trans,none; 4.26
25	438204; AI589645; Hs.128690; ESTs; none,7tm_1; 4.25
	424756; AW504657; Hs.152931; lamin B receptor; ERG4_ERG24,FKBP;TM=Y;SS=N; 4.25
	430570; AI417881; Hs.292464; ESTs; 7tm_2,Fz,Frizzled,none; 4.25
	445709; H02592; Hs.74280; ESTs; PDZ,none; 4.25
	428134; AA421773; Hs.161008; ESTs; Armadillo_seg,none; 4.24
30	434149; Z43829; Hs.244624; hypothetical protein MGC5469; none;TM=M;SS=M; 4.24
	425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M;SS=N; 4.24
	433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 4.24
	447818; W79940; Hs.355279; Homo sapiens clone 24670 mRNA sequence; none,pkinase; 4.24
35	450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig;TM=Y;SS=M; 4.23
	435542; AA687376; Hs.351226; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 4.23
	426224; BE085860; Hs.374468; karyopherin (importin) beta 2; Armadillo_seg,HEAT;TM=M;SS=N; 4.23
	413284; AU077055; Hs.289107; baculoviral IAP repeat-containing 2; zf-C3HC4,CARD,BIR,death,ig;TM=M;SS=N; 4.22
	421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P14_kinase,PI3Ka;TM=M;SS=N; 4.22
40	431239; AL039971; Hs.251216; hypothetical protein DKFZp434A196; SH2,ank,WH2; 4.22
	419685; W76083; Hs.134185; ESTs; none;TM=M;SS=N; 4.22
	431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha; FG-GAP,Rhabd_glycop,integrin_A;TM=Y;SS=M; 4.22
	425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none; 4.21
	422219; AW978073; Hs.1010; regulator of mitotic spindle assembly 1; pkinase,none; 4.21
45	450746; D82673; Hs.278589; general transcription factor II, i; none,SH3,PX; 4.21
	428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone L; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 4.21
	416907; W60909; ; gb:zd29g10.s1 Soares_fetal_heart_NbHH19W; ion_trans,none; 4.21
	411768; NM_013371; Hs.71979; interleukin 19; IL10; 4.21
50	425262; D87119; Hs.155418; GS3955 protein; pkinase; 4.21
	430035; NM_003463; Hs.227777; protein tyrosine phosphatase type IVA, m; Y_phosphatase,DSPc;TM=M;SS=N; 4.21
	411789; AF245505; Hs.72157; Adican; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 4.15
	416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none,none; 4.14
	419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 4.13
55	431745; AW972448; Hs.163425; Novel FGENESH predicted cadherin repeat; none,none; 4.10
	416965; N26223; Hs.160436; MDAC1; none;NA;NA; 3.94
	426890; AA393167; Hs.41294; ESTs; none,none; 3.88
	442438; AA995998; Hs.370007; gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens; none,DNA_pol_B,DNA_pol_B_exo; 3.86
	412314; AA825247; Hs.356084; downstream of: G protein-coupled recepto; 7tm_1;TM=Y;SS=M; 3.84
60	448243; AW369771; Hs.367688; integrin, beta 8; integrin_B,none; 3.64
	439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2,CytC_asm,GPS;TM=Y;SS=M; 3.61
	415999; AA172179; Hs.294029; ESTs; none,none; 3.60
	429466; M85835; Hs.12827; ESTs; none,none; 3.45
	407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none;TM=M;SS=Y; 3.34
	400517; ; lengsin; none;TM=M;SS=N; 3.17
65	439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.88
	426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.84
	414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 2.81
	424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C; 2.70
70	438167; R28363; Hs.24286; chemokine binding protein 2 (CCBP2), mRNA; none;TM=Y;SS=M; 2.68
	418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestin; cadherin;TM=Y;SS=M; 2.17

TABLE 23B

75	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
80	Pkey	CAT Number Accession
	409745	MH1944_5 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
	417886	1031334_1 AA210987 D57294 AA214584 AA207006 D56572
	438993	2580163_1 AI926361 AA834879 AA828995

418869 12789\_14 AA229762 AA230035  
416907 1112245\_1 W60909 W61051 M78905 BG959483

TABLE 23C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
406400	9256298	Plus	1553-1712, 1878-2140, 4252-4385, 5922-6077
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404287	2326514	Plus	53134-53281
405484	5922025	Plus	199214-199579, 199672-199920, 200262-20049
400517	9796686	Minus	49996-50346

TABLE 24A: 571 GENES UP-REGULATED IN HEAD AND NECK TUMORS COMPARED WITH NORMAL BODY TISSUES

Table 24A lists about 571 genes up-regulated in head and neck tumors compared with normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UnigenelD: Unigene number  
Unigene Title: Unigene gene title  
R1: 70th percentile of AI for head and neck cancer samples vs. the 80th percentile of the AI for normal body tissues

Pkey	ExAccn	UnigenelD	Unigene Title	R1
421155	H87879	Hs.102267	lysyl oxidase	166.00
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	156.00
434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	80.00
438274	AI918906	Hs.55080	ESTs	28.00
401486				121.00
446999	AA151520	Hs.334822	hypothetical protein MGC4485	126.00
423887	AL080207	Hs.134585	DKFZP434G232 protein	13.00
419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	98.00
428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00
420602	AF060877	Hs.99236	regulator of G-protein signalling 20	35.00
445019	AI205540	Hs.281295	ESTs	93.00
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	270.62
449722	BE280074	Hs.23960	cyclin B1	9.81
423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	373.00
424086	AI351010	Hs.102267	lysyl oxidase	200.00
447078	AW885727	Hs.301570	ESTs	184.00
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	177.00
409506	NM_006153	Hs.54589	NCK adaptor protein 1	170.00
426471	M22440	Hs.170009	transforming growth factor, alpha	158.00
413268	AL039079	Hs.75256	regulator of G-protein signalling 1	155.00
419948	AB041035	Hs.93847	NADPH oxidase 4	140.00
451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	139.00
442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	111.00
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	109.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	106.00
416283	NM_005429	Hs.79141	vascular endothelial growth factor C	95.00
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	92.00
449101	AA205847	Hs.23016	G protein-coupled receptor	92.00
442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	86.00
438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothe	85.68
414132	AI801235	Hs.48480	ESTs	85.00
447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	83.00
402047	AK001921	Hs.169575	hypothetical protein MGC2550	80.00
414972	BE263782	Hs.77695	KIAA0008 gene product	74.00
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	74.00
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	71.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	70.19
449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	66.25
418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	66.00
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	64.00
414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	63.00
432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypothe	60.00
431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	58.00
411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	57.00
418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	57.00
438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	54.00
452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypothe	54.00
423020	AA383092	Hs.1608	replication protein A3 (14kD)	49.00

	422426	W79117	Hs.58559	ESTs	49.00
	406747	AI925153	Hs.217493	annexin A2	46.00
	445828	F05802	Hs.81907	ESTs	46.00
5	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	44.00
	452909	NM_015368	Hs.30985	pannexin 1	43.95
	432226	AW182766	Hs.273558	phosphate cytidyltransferase 1, cholin	43.00
	458027	L49054	Hs.85195	myeloid leukemia factor 1	43.00
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	43.00
10	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	42.00
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	40.00
	433859	AW896758	Hs.273789	ESTs	38.00
	426753	T89832	Hs.170278	ESTs	37.00
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	36.00
	402034				35.00
15	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	34.00
	458424	AI084049	Hs.206761	ESTs	34.00
	435159	AA668879	Hs.116649	ESTs	33.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	32.00
20	444361	W76027	Hs.23920	hypothetical protein FLJ11105	31.00
	439128	AI949371	Hs.153089	ESTs	29.20
	420795	AA323037	Hs.128645	sorting nexin 16	26.00
	422505	AL120862	Hs.124165	ESTs	25.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	24.00
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	22.10
25	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	19.00
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	19.00
	414869	AA157291	Hs.21479	ubiquitin 1	17.37
	453049	BE537217	Hs.30343	ESTs	16.00
30	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	14.00
	435243	AW292886	Hs.261373	hypothetical protein dJ434O14.3	13.00
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	10.80
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	10.00
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	9.60
35	414231	AI468004	Hs.278956	hypothetical protein FLJ12929	9.00
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	8.09
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	8.07
	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.07
	417791	AW965339	Hs.111471	ESTs	8.04
40	436486	AA742221	Hs.120633	ESTs	7.23
	432731	R31178	Hs.287820	fibronectin 1	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	5.18
	435039	AW043921	Hs.130526	ESTs	5.00
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	4.25
45	457001	J03258	Hs.2062	vitamin D (1,25-dihydroxyvitamin D3) re	4.24
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	3.74
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	3.19
	458531	AA367718	Hs.159083	ESTs	3.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	2.53
50	411388	X72925	Hs.69752	desmocollin 1	1.00
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	1.00
	429370	C19097	Hs.89709	glutamate-cysteine ligase, modifier subu	1.00
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	1.00
	449467	AW205008	Hs.197042	ESTs	1.00
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00
	453637	NM_002589	Hs.34073	BH-protocadherin (brain-heart)	1.00
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	517.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	616.00
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	226.00
60	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	278.00
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	56.11
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	264.00
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	124.00
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.00
65	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	1.00
	415511	AI732617	Hs.182362	ESTs	1.00
	406467				141.00
	422330	D30783	Hs.115263	epiregulin	98.00
	452461	N78223	Hs.108106	transcription factor	159.00
70	415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypotheti	1.00
	413324	V00571	Hs.75294	corticotropin releasing hormone	1.00
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (	7.60
	443211	AI128388	Hs.143655	ESTs	99.00
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00
75	441877	AW273802	Hs.11340	hypothetical protein FLJ23047	3.00
	439926	AW014875	Hs.137007	ESTs	2.79
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	94.00
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	1.22
	448062	AW295923	Hs.255472	KIAA1843 protein	1.00
80	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.27
	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	1.00
	421187	NM_014721	Hs.102471	KIAA0680 gene product	5.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	89.00
	437214	BE092336		gb:IL2-BT0734-240400-072-A12 BT0734 Homo	1.00

	449773	R76294	Hs.302383	ESTs	1.00
	443054	A1745185	Hs.8939	yes-associated protein 65 kDa	90.00
	432097	X51730	Hs.2905	progesterone receptor	1.00
5	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	0.38
	430184	AB013802	Hs.234790	contactin 5	1.00
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.23
	415025	AW207091	Hs.72307	ESTs	1.00
	416575	W02414	Hs.38383	ESTs	1.00
10	443171	BE281128	Hs.9030	TONDU	0.92
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	20.30
	400844				0.60
	409402	AF208234	Hs.695	cystatin B (stefin B)	1.96
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.38
15	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.60
	400751				1.34
	436361	AA825814	Hs.149065	ESTs	0.92
	455612	BE042896	Hs.274848	ESTs	0.81
	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	1.55
	404148				0.77
20	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	1.00
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.47
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.92
	442994	AI026718	Hs.16954	ESTs	0.40
25	415327	H22769		gb:ym54c02.r1 Soares infant brain 1NIB H	0.47
	418624	AI734080	Hs.104211	ESTs	1.90
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-lin	0.54
	401747			Homo sapiens keratin 17 (KRT17),	7.22
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	5.10
30	418259	AA215404	Hs.137289	ESTs	1.28
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	8.13
	403381				21.00
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	0.00
	418216	AA662240	Hs.283099	AF15q14 protein	11.29
35	444649	AW207523	Hs.197628	ESTs	0.10
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	4.64
	402230				1.64
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.97
40	447334	AA515032	Hs.91109	ESTs	0.62
	432829	W60377	Hs.57772	ESTs	0.86
	418686	Z36830	Hs.87268	annexin A8	8.44
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.68
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	2.22
45	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	78.00
	425721	AC002115	Hs.159309	uoplakin 1A	0.86
	420370	Y13645	Hs.97234	uoplakin 2	0.87
	417720	AA205625	Hs.208067	ESTs	5.83
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.07
	431753	X76029	Hs.2841	neuromedin U	7.00
50	402075				286.00
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	363.00
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.81
	405064				1.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	2.00
55	441233	AA972965	Hs.135568	ESTs	1.00
	456034	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCL_CGAP_Su	1.23
	414221	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCL_CGAP_Su	0.65
	412296	AW936233		gb:QV0-DT0020-090200-107-a06 DT0020 Homo	1.00
	405494				1.00
60	407189	AA598927		gb:ae37e03.s1 Gessler Wilms tumor Homo s	1.00
	403085				1.00
	408633	AW963372	Hs.46677	PRO2000 protein	2.46
	435257	AA677026	Hs.191217	ESTs	1.00
	410044	BE586742	Hs.58169	highly expressed in cancer, rich in leuc	1.00
65	445182	AW189787	Hs.147474	ESTs	0.50
	417275	X63578	Hs.295449	parvalbumin	1.00
	418406	X73501	Hs.84905	cytokeratin 20	1.00
	421110	AJ250717	Hs.1355	cathepsin E	1.00
	406081				2.13
70	449448	D60730	Hs.57471	ESTs	123.00
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.37
	408243	Y00787	Hs.624	interleukin 8	3.35
	436246	AW450963	Hs.119991	ESTs	51.00
	440304	BE159984	Hs.125395	ESTs	1.00
75	402778				1.00
	406117				1.00
	406360				71.00
	435347	AW014873	Hs.116963	ESTs	1.00
	445550	AI242754	Hs.137306	ESTs	1.00
80	451359	H85334	Hs.336623	ESTs	1.00
	419559	Y07828	Hs.91096	ring finger protein	1.00
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	58.00
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00
	402901				0.85

	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	0.87
	417715	AW969587	Hs.86366	ESTs	5.12
	442577	AA292998	Hs.163900	ESTs	2.19
5	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.54
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	1.11
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	1.27
	414683	S78296	Hs.76888	hypothetical protein MGC12702	0.67
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	0.03
10	403903				0.87
	405033				0.13
	422282	AF019225	Hs.114309	apolipoprotein L	2.13
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.05
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.59
15	430168	AW968343	Hs.24255	DKFZP434I1735 protein	1.69
	459702	AI204995			1.00
	446082	AI274139	Hs.156452	ESTs	0.60
	400843				0.76
	417409	BE272506	Hs.82109	syndecan 1	1.78
20	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	1.20
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	0.50
	404875				0.80
	436293	AI601188	Hs.120910	ESTs	1.40
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.03
25	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	0.94
	404977			Insulin-like growth factor 2 (somatomedi	0.99
	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.10
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	0.85
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.20
	420876	AA918425	Hs.177744	ESTs	0.85
30	422119	AI277829	Hs.111862	KIAA0590 gene product	0.71
	400846			sortilin-related receptor, L(DLR class)	0.75
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	4.01
	430152	AB001325	Hs.234642	aquaporin 3	1.74
	402777				0.70
35	417151	AA194055	Hs.293858	ESTs	0.99
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.48
	405034	AL035754	Hs.2474	toll-like receptor 1	1.00
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	18.68
40	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.94
	453134	AA032211	Hs.118493	ESTs	0.70
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.19
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	0.25
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	2.74
45	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.07
	438315	R56795	Hs.82419	ESTs	0.65
	418937	T71508	Hs.13861	ESTs, Weakly similar to T42383 probable	1.18
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	0.85
	444444	AI149332	Hs.14855	ESTs	0.59
50	407581	R48402	Hs.173508	P3ECSL	0.82
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	0.92
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	0.62
	446024	AB040946	Hs.284227	KIAA1513 protein	0.92
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.42
55	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.68
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptiona	1.57
	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	0.08
	446009	AI989885	Hs.231926	ESTs	1.00
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	0.98
60	415949	H10562	Hs.21691	ESTs	0.61
	420281	AI623693	Hs.191533	ESTs	7.01
	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	0.72
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.21
	414792	BE314949	Hs.87128	hypothetical protein FLJ23309	0.99
65	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	0.54
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.06
	426900	AW163564	Hs.142375	ESTs	0.48
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	0.83
	402305				0.89
70	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	0.04
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.49
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	0.65
	423916	AW993496	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	0.63
	405932				1.76
	401760				2.61
75	452240	AI591147	Hs.61232	ESTs	453.00
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	1.04
	421373	AA808229	Hs.167771	ESTs	17.00
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.16
80	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	1.68
	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.19
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.73
	453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal ki	1.00
	454789	BE156314		gb:QV0-HT0367-150200-114-d02 HT0367 Homo	1.00



	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	0.06
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.45
	418067	AI127958	Hs.83393	cystatin E/M	1.41
5	441801	AW242799	Hs.86366	ESTs	140.00
	423536	L22075	Hs.1666	guanine nucleotide binding protein (G pr	2.45
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	58.00
	400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	1.17
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	0.86
10	427587	BE348244	Hs.202628	ESTs, Weakly similar to I78885 serine/th	0.91
	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	1.00
	453204	R10799	Hs.191990	ESTs	1.13
	437240	AA747537		gb:bx85c05.s1 NCL_CGAP_GCB1 Homo sapiens	1.00
	405531				0.92
15	440249	AI246590	Hs.337275	ESTs	1.32
	426783	Z19084	Hs.172210	MUF1 protein	1.17
	434192	AW387314	Hs.34371	ESTs	1.00
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	87.14
	402001				37.00
20	433967	AF113018	Hs.284302	PRO1621 protein	1.00
	451592	AI805416	Hs.213897	ESTs	10.00
	422170	AI791949	Hs.112432	anti-Mullerian hormone	0.67
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	1.00
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	0.99
25	441940	AW298115	Hs.128152	ESTs	0.88
	425048	H05468	Hs.164502	ESTs	0.33
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.01
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.06
	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	0.45
30	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	0.62
	410348	AW182663	Hs.95469	ESTs	1.00
	419078	M93119	Hs.89584	insulinoma-associated 1	0.04
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.04
	441795	N58115	Hs.21137	AD024 protein	10.00
35	418583	AA604379	Hs.86211	hypothetical protein	1.22
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	106.67
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.30
	441495	AW294603	Hs.127039	ESTs	0.44
	417933	X02308	Hs.82962	thymidylate synthetase	2.48
40	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	1.00
	411880	AW872477		gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens	1.00
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	1.44
	430034	X60155	Hs.227767	zinc finger protein 41	1.00
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.87
45	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	0.54
	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	2.27
	417599	AA204688	Hs.136201	ESTs	1.01
	438366	AA805760	Hs.303567	ESTs	1.00
	438746	AI885815	Hs.184727	ESTs	1.47
50	409691	T89983	Hs.246042	Homo sapiens, clone MGC:5437, mRNA, comp	1.00
	408827	AW275730	Hs.254825	ESTs	1.00
	414735	BE468016	Hs.281904	ESTs	1.00
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	5.21
	412719	AW016610	Hs.129911	ESTs	494.00
55	417034	NM_006183	Hs.80962	neurotensin	1.00
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	23.36
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	6.98
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	7.50
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	9.77
60	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	445.00
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	13.93
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	12.77
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	45.00
	418663	AK001100	Hs.41690	desmocollin 3	10.89
65	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.29
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	0.88
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	38.31
	421948	L42583	Hs.334309	keratin 6A	36.81
	431846	BE019924	Hs.271580	uroplakin 1B	1.37
70	424098	AF077374	Hs.139322	small proline-rich protein 3	8.85
	453964	AI961486	Hs.12744	ESTs	0.40
	446856	AI814373	Hs.164175	ESTs	1.16
	443648	AI085377	Hs.143610	ESTs	2.15
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	4.39
75	431384	BE158000		gb:MR2-HT0377-150200-202-e03 HT0377 Homo	1.18
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.22
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	164.00
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	9.85
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	5.59
80	441020	W79283	Hs.35962	ESTs	5.76
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.97
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.09
	444371	BE540274	Hs.239	forkhead box M1	2.44
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.39

5	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.53
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	1.67
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	2.30
	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.04
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.11
10	401781				11.07
	401780				9.54
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.62
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	1.12
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	947.00
15	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.79
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.16
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.08
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	5.20
	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	2.53
20	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	72.00
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	19.96
	409103	AF251237	Hs.112208	XAGE-1 protein	0.47
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	0.66
	428471	X57348	Hs.184510	stratifin	3.39
25	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	1.61
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.31
	451541	BE279383	Hs.26557	plakophilin 3	1.82
	418203	X54942	Hs.83758	CDC28 protein kinase 2	5.60
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.78
30	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.01
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.18
	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.58
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.63
	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.25
35	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	11.88
	430677	Z26317	Hs.94560	desmoglein 2	1.38
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.09
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.09
	422963	M79141	Hs.13234	ESTs	2.28
40	418462	BE001596	Hs.85266	integrin, beta 4	1.40
	450832	AW970602	Hs.105421	ESTs	13.31
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.25
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.89
	458933	AI638429	Hs.24763	RAN binding protein 1	1.54
45	439394	AA149250	Hs.56105	ESTs	3.89
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.77
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.52
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.11
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.10
50	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.84
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	0.61
	439606	W79123	Hs.58561	G protein-coupled receptor 87	303.00
	453884	AA359925	Hs.36232	KIAA0186 gene product	10.55
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.38
55	451743	AW074266	Hs.23071	ESTs	2.90
	413129	AF292100	Hs.104613	RP42 homolog	2.38
	406974	M57293		gb:Human parathyroid hormone-related pep	1.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	5.92
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	2.18
60	416819	U77735	Hs.80205	pim-2 oncogene	1.01
	451320	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	0.67
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.19
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.55
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	3.06
65	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	1.64
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	7.04
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	203.00
	435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33
	430337	M36707	Hs.239600	calmodulin-like 3	1.32
70	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	81.00
	448993	AI471630	Hs.8127	KIAA0144 gene product	1.03
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	28.00
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.24
	425245	AI751768	Hs.155314	KIAA0095 gene product	1.40
75	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.55
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00
	418678	NM_001327	Hs.167379	cancer/testis antigen	0.82
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00
	427335	AA448542	Hs.251677	G antigen 7B	0.91
80	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	6.53
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	1.35
	421917	AB028943	Hs.109445	KIAA1020 protein	0.94
	404440				38.57
	409582	R27430	Hs.271565	ESTs	3.19
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	2.45
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.61
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	1.95

	408380	AF123050	Hs.44532	diubiquitin	7.23
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.35
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	0.81
5	446102	AW168067	Hs.252956	ESTs	1.03
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	137.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.91
	423761	NM_006194	Hs.132576	paired box gene 9	36.00
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.35
10	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	207.00
	440659	AF134160	Hs.7327	claudin 1	3.06
	434360	AW015415	Hs.127780	ESTs	3.89
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	1.28
	438898	AI819863	Hs.106243	ESTs	1.73
	441553	AA281219	Hs.121296	ESTs	1.47
15	418379	AA218940	Hs.137516	fidgetin-like 1	40.42
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	14.25
	429413	NM_014058	Hs.201877	DESC1 protein	5.17
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.95
20	415380	F07953	Hs.16085	putative G-protein coupled receptor	0.18
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.09
	429538	BE182592	Hs.11261	small proline-rich protein 2A	6.14
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00
25	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	44.00
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	149.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	127.00
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	20.00
	404996				147.00
30	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	54.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	139.00
	430563	AA481269	Hs.108650	ATP-binding cassette, sub-family C (CFTR	22.00
	438702	AI879064	Hs.54618	ESTs	1.00
35	444378	R41339	Hs.12569	ESTs	1.00
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	41.00
	407839	AA045144	Hs.161566	ESTs	7.50
	439223	AW238299	Hs.250618	UL16 binding protein 2	3.39
	409041	AB033025	Hs.50081	KIAA1199 protein	245.00
40	429228	AI553633	Hs.337139	ESTs	10.89
	409757	NM_001898	Hs.123114	cystatin SN	3.19
	411089	AA456454	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	0.78
	436511	AA721252	Hs.291502	ESTs	0.23
	449207	AL044222	Hs.23255	nucleoporin 155kD	1.68
45	453331	AI240665	Hs.8895	ESTs	5.21
	409935	AW511413	Hs.278025	ESTs	0.75
	428969	AF120274	Hs.194689	artemin	1.17
	445443	AV653838	Hs.322971	ESTs	1.00
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	11.42
50	401785				2.76
	412723	AA648459	Hs.335951	hypothetical protein AF301222	107.00
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	2.17
	405770				2.42
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.24
55	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	4.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.95
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.44
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00
	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.33
60	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	1.11
	427441	AA412605	Hs.178053	SPANX family, member C	5.00
	403478				0.78
	400842				0.16
	441525	AW241867	Hs.127728	ESTs	0.79
65	452865	AI924046	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	1.50
	405646				1.05
	427260	AA663848		gb:ae70b06.s1 Stratagene schizo brain S1	0.79
	431413	AA504777	Hs.105293	ESTs	1.00
	401994				3.25
70	402420				0.05
	404298				0.64
	404927				88.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	0.96
	436961	AW375974	Hs.156704	ESTs	3.58
75	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	0.92
	426067	AW664691	Hs.97053	ESTs	0.97
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	0.66
	426897	AW976570	Hs.97387	ESTs	1.29
	443892	AI889572	Hs.134791	ESTs	1.00
80	413223	AI732182	Hs.191866	ESTs	0.79
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	1.51
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	2.59
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.39
	420758	AW297536	Hs.33053	ESTs	0.89

5	423816	AL031985	Hs.133034	hypothetical protein	1.00
	447534	AW953935	Hs.30837	ESTs	1.88
	451919	W05086	Hs.114256	ESTs, Weakly similar to 178885 serine/th	0.11
	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell	0.92
	403715				0.89
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	37.00
	436839	AA767346	Hs.291614	ESTs	1.00
10	413582	AW295647	Hs.71331	hypothetical protein MGC5350	59.00
	413573	AI733859	Hs.149089	ESTs	78.00
	430686	NM_001942	Hs.2633	desmoglein 1	127.08
	438993	AA828995		gb:rod77b08.s1 NCI_CGAP_Ov2 Homo sapiens	1.00
	448243	AW369771	Hs.52620	integrin, beta 8	133.00
15	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	232.00
	426427	M86699	Hs.169840	TTK protein kinase	66.00
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	148.00
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	40.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	13.00
20	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	106.00
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	159.00
	415989	AI267700	Hs.317584	ESTs	196.00
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	32.44
	453160	AI263307	Hs.239884	H2B histone family, member L	7.00
25	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.13
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	45.00

TABLE 24B

30 Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accessions: Genbank accession numbers

35	Pkey	CAT number	Accessions
	411880	1263110_1	AW872477 BE088101 T05990
	412296	1288043_1	AW936233 AW936272
	413804	1390710_1	T64682 BE168190 BE168256
40	414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363
	415327	1534137_1	H22769 R35182 Z43545 F05783 N92089 H71928
	427260	276598_1	AA663848 AA400100 AA401424
	431322	331543_1	AW970622 AA503009 AA502998 AA502805 T92188
45	431384	33264_1	BE158000 BE157999 H75671 H70965 C18895 BE386512 BE385815 BE390298 AI341995 BE074534 AA055592 AA132265 AI733757
			AA134504 BE145037 AA055887 BE070191 R66492 AW858018 AW858058 AW817057 AW862031 AW861688 AW862029 AW858805 AW858792
			AW862028 AW858017 AW819164 AW853698 AI522161 AW854789 AW817408 BE152005 AI732411 AA133084
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
	437214	434730_1	BE092336 BE092259 BE092497 BE092051 AA746882 AI336378
50	437240	435139_1	AA747537 BE089068 BE089070
	438993	467651_1	AA828995 AA834879 AI926361
	439780	47673_1	AL109688 R23665 R26578
	444163	593658_1	AI126098 AI184746 AI148521
	451844	888230_1	T61430 AI820546 AI821336
55	453823	982526_1	AL137967 BE064160 BE064186
	454789	1234742_1	BE156314 BE156316 AW820750
	456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 24C

60 Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 65 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

70	Pkey	Ref	Strand	Nt_position
	400751	7331445	Minus	35395-35533
	400842	1927148	Plus	90462-90673
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
	400844	9188605	Plus	24746-24872,25035-25204
75	400846	9188605	Plus	39310-39474
	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
80	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
	402001	9501818	Plus	68052-68223

402034	7684482	Minus	86227-86451
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
402305	7328724	Plus	40832-41362
402420	9796339	Plus	129750-129919
402777	9588235	Plus	126786-126948
402778	9588235	Plus	128560-128702
402901	8894222	Minus	175426-175667
403085	8954241	Plus	165035-165334,165420-165713
403381	9438267	Minus	26009-26178
403478	9958258	Plus	116458-116564
403715	7239669	Plus	85128-85292
403903	7710671	Minus	101165-102597
404148	9863703	Plus	78218-78418,79571-79709
404298	9944263	Minus	73591-73723
404440	7528051	Plus	80430-81581
404875	9801324	Plus	96588-96732,97722-97831
404927	7342002	Plus	68690-69563
404977	3738341	Minus	43081-43229
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405033	7107731	Minus	142358-142546
405064	7658416	Plus	81207-81416
405494	8050952	Minus	70284-70518
405531	9665194	Plus	35602-35803
405646	4914350	Plus	741-969
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713
406081	9123861	Minus	38115-38691
406117	9142932	Plus	54304-54584
406360	9256107	Minus	7513-7673
406467	9795551	Plus	182212-182958

TABLE 25A: 691 genes upregulated in head and neck cancer relative to normal body tissues

Table 25A lists about 691 genes upregulated in head and neck cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar accession number, GenBank accession number  
 UniGeneID: UniGene number  
 Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).  
 UniGene Title: UniGene gene title  
 R1 85th percentile of head and neck cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prot.Domains; R1

422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psorias; efhand,S\_100;TM=M;SS=N; 46.25  
 408522; AI541214; Hs.46320; Small proline-rich protein SPRK [human; none;Cornifin; 40.37  
 417366; BE185289; Hs.1076; small proline-rich protein 1B (cornifin); Cornifin;TM=M;SS=N; 38.94  
 401781; ; Target Exon; filament;TM=M;SS=N; 29.74  
 422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap;TM=M;SS=Y; 29.54  
 401780; ; NM\_005557; Homo sapiens keratin 16 (foca; filament;filament; 28.58  
 424098; AF077374; Hs.139322; small proline-rich protein 3; Cornifin;TM=M;SS=N; 28.55  
 421948; L42583; Hs.334309; keratin 6A; filament;RhoGAP,DUF286,bZIP,Tropomyosin,tubulin,DUF164,TBCA,Collagen;TM=M;SS=N; 25.74  
 428471; X57348; Hs.184510; stratifin; 14-3-3;TM=M;SS=N; 23.65  
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; 21.02  
 421574; AJ000152; Hs.105924; defensin, beta 2; Defensin\_beta;TM=M;SS=M; 20.83  
 409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyperkeratosis); filament,bZIP,UvrD-helicase,TBCA;TM=M;SS=N; 20.72  
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR\_LY6,toxin,Activin\_recpt;TM=M;SS=Y; 19.63  
 446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium\_transp,FecCD;TM=Y;SS=M; 19.53  
 420783; AI659838; Hs.99923; lectin, galactoside-binding, soluble, 7; Gal-bind\_lectin;TM=M;SS=N; 19.12  
 407788; BE514982; Hs.38991; S100 calcium-binding protein A2; efhand,S\_100,S\_100,efhand; 17.93  
 416091; AF295370; Hs.283082; defensin, beta 3; Defensin\_beta;TM=M;SS=M; 17.63  
 431211; M86849; Hs.323733; gap junction protein, beta 2, 26kD (conn; connexin;TM=Y;SS=M; 16.94  
 429259; AA420450; Hs.380088; Plakophilin; none;none; 14.92  
 417515; L24203; Hs.82237; ataxia-telangiectasia group D-associated; zf-B\_box,zf-UBR1;TM=M;SS=N; 14.75  
 423634; AW959908; Hs.1690; heparin-binding growth factor binding pr; none;TM=M;SS=M; 14.45  
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (interstitial; hemopexin,Peptidase\_M10,Astacin,PG\_binding\_1; 13.02  
 409632; W74001; Hs.55279; serine (or cysteine) proteinase inhibitor; serpin; 12.82  
 406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 12.81  
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin,Cadherin\_C\_term;TM=Y;SS=M; 12.45  
 446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL8; 11.71  
 401760; ; Target Exon; none;bromodomain; 11.68  
 407839; AA045144; Hs.161566; ESTs; cadherin,cadherin; 11.65  
 454034; NM\_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh; 11.56  
 444781; NM\_014400; Hs.11950; GPI-anchored metastasis-associated prote; UPAR\_LY6,lactamase\_B; 11.31

453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none; TM=Y; SS=M; 11.03  
 424012; AW368377; Hs.137569; tumor protein 63 kDa with strong homolog; SAM, P53; TM=M; SS=N; 10.75  
 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin; TM=M; SS=N; 10.58  
 5 419693; AA133749; Hs.301350; FXYD domain-containing ion transport reg; ATP1G1\_PLM\_MAT8; TM=Y; SS=M; 10.30  
 411274; NM\_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 10.25  
 441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none; TM=M; SS=M; 9.84  
 446989; AK001898; Hs.16740; hypothetical protein FLJ11036; none; TM=Y; SS=N; 9.74  
 402075; ; ENSP00000251056; Plasma membrane calcium; none; 9.50  
 10 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 9.50  
 431009; BE149762; Hs.48956; gap junction protein, beta 6 (connexin 3; connexin; TM=Y; SS=M; 9.48  
 439310; AF086120; Hs.102793; ESTs; casein\_kappa, pkinase, ig, none; 9.43  
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M; SS=N; 9.33  
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh; TM=M; SS=M; 9.14  
 15 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); efhand, spectrin, GAS2, SH3, Plectin, RA, Xylose\_isom, FliD, bZIP, Tropomyosin, Myc-  
 LZ\_M, Idh\_C, CH, AIP3; TM=M; SS=N; 9.12  
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo\_seg; TM=M; SS=N; 9.11  
 425650; NM\_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin; TM=M; SS=M; 8.66  
 452240; AI591147; Hs.61232; ESTs; none, none; 8.57  
 20 429228; AI553633; Hs.356828; ESTs; none, none; 8.46  
 400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin, Peptidase\_M10, Astacin; 8.44  
 425071; NM\_013989; Hs.154424; deiodinase, iodothyronine, type II; T4\_deiodinase; TM=M; SS=Y; 8.15  
 407242; M18728; ; gb:Human nonspecific crossreacting antig; ig; TM=M; SS=M; 8.05  
 407944; R34008; Hs.239727; desmocollin 2; cadherin, Cadherin\_C\_term, Hanta\_G2; TM=Y; SS=M; 7.90  
 25 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 7.82  
 428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase\_M10; 7.82  
 417308; H60720; Hs.81892; KIAA0101 gene product; none; TM=M; SS=N; 7.77  
 413753; U17760; Hs.75517; laminin, beta 3 (nicein (125kD), kalinin; laminin\_EGF, laminin\_Nterm; 7.76  
 423217; NM\_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolys; Kunitz\_BPT1, fn3, vwa, Collagen, beta-lactamase; TM=M; SS=M; 7.71  
 30 430686; NM\_001942; Hs.2633; desmoglein 1; cadherin, Cadherin\_C\_term; TM=Y; SS=M; 7.69  
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha, arf; TM=M; SS=N; 7.54  
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ;  
 aa\_permeases, pyridoxal\_deC, bromodomain, PHD, MBD, AT\_hook, DDT, PI3\_P14\_kinase, FAT, FATC, BoA, RUN; TM=M; SS=N; 7.53  
 35 418663; AK001100; Hs.41690; desmocollin 3; cadherin, Cadherin\_C\_term, none; 7.30  
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb\_propeptide, TGF-beta, none; 7.28  
 429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin; TM=Y; SS=M; 7.26  
 412719; AW016610; Hs.816; ESTs; none, none; 7.17  
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin; 7.10  
 423961; D13666; Hs.136348; periostin (OSF-2os); Fasciclin; TM=M; SS=M; 7.09  
 40 427666; A1791495; Hs.180142; calmodulin-like skin protein (CLSP); efhand; TM=M; SS=N; 7.08  
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 7.06  
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin, Peptidase\_M10; TM=M; SS=M; 7.03  
 401747; ; ; Homo sapiens keratin 17 (KRT17); none, bromodomain; 7.01  
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM\_PNT, none; 6.98  
 45 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo\_seg; TM=M; SS=N; 6.96  
 432239; X81334; Hs.2936; matrix metalloproteinase 13 (collagenase; hemopexin, Peptidase\_M10; 6.87  
 417715; AW969587; Hs.86366; ESTs; none, none; 6.72  
 422440; NM\_004812; Hs.116724; aldo-keto reductase family 1, member B10; aldo\_ket\_red, ROK; TM=M; SS=N; 6.50  
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-in; hemopexin, Peptidase\_M10; TM=M; SS=M; 6.39  
 50 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase, PLAT; TM=M; SS=N; 6.38  
 420039; NM\_004605; Hs.376147; sulfotransferase family, cytosolic, 2B, ; Sulfotransfer; 6.38  
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA\_gyraseB, DNA\_topoisolV, HATPase\_c; 6.35  
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3, ank; TM=M; SS=N; 6.30  
 409420; Z15008; Hs.54451; laminin, gamma 2 (nicein (100kD), kalini; laminin\_B, laminin\_EGF; 6.28  
 55 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 atrophin-; ras; TM=M; SS=N; 6.27  
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 6.23  
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin, Peptidase\_M10; 6.22  
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none; TM=M; SS=N; 6.21  
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm\_3; TM=Y; SS=M; 6.12  
 423017; AW178761; Hs.227948; serine (or cysteine) proteinase inhibitor; serpin; 6.08  
 60 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none, none; 6.08  
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar\_tr; TM=Y; SS=M; 6.04  
 439335; AA742697; Hs.62492; NM\_052863; Homo sapiens secretoglobulin, fa; none; 5.81  
 439223; AW238299; Hs.250618; UL16 binding protein 2; ldi\_recept\_a, PKD, MHC\_1; TM=M; SS=Y; 5.77  
 65 418054; NM\_002318; Hs.83354; lysyl oxidase-like 2; SRCR, Lysyl\_oxidase; TM=M; SS=M; 5.72  
 454098; W27953; Hs.217493; Plakophilin; none, none; 5.71  
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevi; WD40; TM=M; SS=N; 5.70  
 435505; AF200492; Hs.211238; interleukin-1 homolog 1; IL1; TM=M; SS=N; 5.69  
 406685; M18728; ; gb:Human nonspecific crossreacting antig; ig; TM=M; SS=M; 5.67  
 70 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3, none; 5.63  
 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none; TM=Y; SS=M; 5.61  
 449722; BE280074; Hs.23960; cyclin B1; cyclin, cyclin\_C; TM=M; SS=N; 5.61  
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm\_1; TM=Y; SS=M; 5.60  
 452862; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like and metallo; Pep\_M12B\_propep, tsp\_1, Reprolysin, none; 5.58  
 75 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras, ABC, MHC\_tran, arf; TM=M; SS=M; 5.57  
 411296; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell\_Oxy; TM=M; SS=M; 5.55  
 433848; AF095719; Hs.93764; carboxypeptidase A4; Zn\_carbOpept, Propep\_M14; 5.54  
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase; 5.48  
 428368; BE440042; Hs.83326; matrix metalloproteinase 3 (stromelysin ; hemopexin, Peptidase\_M10, Astacin; 5.47  
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig, Rhabd\_glycop; TM=Y; SS=M; 5.46  
 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase, abhydrolase\_2; TM=Y; SS=M; 5.42  
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; 5.35  
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 5.28  
 80 418462; BE001596; Hs.85266; integrin, beta 4; fn3, integrin\_B, Calx-beta, EGF; TM=M; SS=M; 5.26

- 429554; NM\_012275; Hs.207224; interleukin 1, delta; IL1; TM=M; SS=N; 5.14  
 421508; NM\_004833; Hs.105115; absent in melanoma 2; PAAD\_DAPIN; HIN; TM=M; SS=N; 5.13  
 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none; TM=M; SS=N; 5.11  
 427099; AB032953; Hs.173560; odd Oz/ten-m homolog 2 (Drosophila, mous; NHL; TM=M; SS=N; 5.11  
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 5.08  
 436396; AI683487; Hs.152213; wingless-type MMTV integration site fami; wnt; none; 5.07  
 406690; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; ig; TM=M; SS=M; 5.05  
 453905; NM\_002314; Hs.36566; LIM domain kinase 1; pkinase, LIM, PDZ, zf-PARP; TM=M; SS=N; 5.04  
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor; serpin; 5.00  
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH, death, TNFR\_c6, Acyl-CoA\_hydro; 4.96  
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK; TM=M; SS=N; 4.93  
 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like (rabkines; kinesin, Tropomyosin; TM=M; SS=N; 4.92  
 445537; AJ245671; Hs.12844; EGF-like domain, multiple 6; EGF, MAM; 4.91  
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily; 60s\_ribosomal, Ribosomal\_L10, TNFR\_c6, DEAD; 4.90  
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig; HSP70, Ppx-GppA; TM=M; SS=N; 4.89  
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none, none; 4.84  
 430024; AI808780; Hs.227730; integrin, alpha 6; integrin\_A, FG-GAP; TM=Y; SS=M; 4.81  
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1\_HUMAN DEATH; none, none; 4.80  
 444371; BE540274; Hs.239; forkhead box M1; Fork\_head; TM=M; SS=N; 4.75  
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 4.74  
 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPc; 4.69  
 431630; NM\_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha; FG-GAP, Rhabd\_glycop, integrin\_A; TM=Y; SS=M; 4.69  
 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none, pkinase, fn3, ig; 4.68  
 418067; AI127958; Hs.83393; cystatin E/M; cystatin; 4.66  
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle, trypsin, plant\_thionins; 4.64  
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM, PDZ, pkinase; 4.62  
 410418; D31382; Hs.63325; transmembrane protease, serine 4; Idl\_recept\_a, trypsin; TM=Y; SS=M; 4.60  
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen, COLFI, TSPN, laminin\_G, CorA; 4.60  
 438113; AI467908; Hs.8882; ESTs; 7tm\_1, none; 4.60  
 418140; BE613836; Hs.83551; microfibrillar-associated protein 2; none; TM=M; SS=M; 4.57  
 408380; AF123050; Hs.44532; diubiquitin; ubiquitin; TM=M; SS=N; 4.55  
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC\_tran, ABC\_membrane, GTP\_EFTU; TM=M; SS=M; 4.50  
 425247; NM\_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin, Peptidase\_M10; 4.50  
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domain; death, DED; 4.49  
 408482; NM\_000676; Hs.45743; adenosine A2b receptor; 7tm\_1; TM=Y; SS=M; 4.48  
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD, helicase\_C, rrm, Ndr, Cys\_knot, TIL, vwa, vwc, vwd, IQ, RIIa, abhydrolase, TGF-beta, DUF139, TPR, DSPc, tsp\_1, Ribosomal\_S21, rvp; TM=M; SS=N; 4.47  
 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.47  
 411789; AF245505; Hs.72157; Adican; ig, LRR, LRRNT, LRRCT; TM=M; SS=M; 4.47  
 414561; AI064813; Hs.195155; Homo sapiens amino acid transport system; Aa\_trans; TM=Y; SS=N; 4.47  
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR; TM=M; SS=N; 4.45  
 427557; NM\_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR\_LY6, ET, PLA2\_inh; 4.43  
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y\_phosphatase, DSPc; TM=M; SS=N; 4.42  
 409041; AB033025; Hs.50081; Hypothetical protein, XP\_051850 (KIAA119; none; TM=M; SS=M; 4.41  
 406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gen; none, none; 4.40  
 450701; H39960; Hs.288467; hypothetical protein XP\_098151 (leucine-; none, LRRCT, LRR; 4.40  
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2, SH3, pkinase; TM=M; SS=N; 4.38  
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cytactin); EGF, fn3, fibrinogen\_C, toxin\_2, Keratin\_B2; TM=M; SS=Y; 4.38  
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT\_bind, STAT\_prot; TM=M; SS=N; 4.32  
 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; none; TM=M; SS=N; 4.32  
 411573; AB029000; Hs.70823; KIAA1077 protein; Sulfatase; TM=M; SS=N; 4.31  
 408243; Y00787; Hs.624; interleukin 8; HLH, PAS, IL8; TM=M; SS=N; 4.31  
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 4.30  
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC; none; 4.29  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, ig, FAD\_Synth, Idh, Idh\_C, pkinase; 4.29  
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 4.29  
 404996; ; ; Target Exon; Peptidase\_C1; TM=M; SS=M; 4.29  
 416539; Y07909; Hs.79368; epithelial membrane protein 1; PMP22\_Claudin, oxidored\_g5\_N; TM=Y; SS=M; 4.28  
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC\_tran, M\_SMC, N\_SMC, C\_DUF164, none; 4.25  
 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo\_seg, HEAT; TM=M; SS=N; 4.25  
 424503; NM\_002205; Hs.149609; integrin, alpha 5 (fibronectin receptor; integrin\_A, FG-GAP; TM=Y; SS=N; 4.24  
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y; SS=N; 4.24  
 439720; AI935202; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF, sugar\_tr; 4.23  
 437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none; TM=M; SS=M; 4.23  
 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta, TGFb\_propeptide, Tub; 4.20  
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA, ABC\_tran, CoaE; TM=M; SS=N; 4.20  
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN\_MK; TM=M; SS=Y; 4.19  
 407137; T97307; ; gb:ye53h05.s1 Soares fetal liver spleen ; GDA1\_CD39, none; 4.18  
 419235; AW470411; Hs.288433; neurotrimin; none, none; 4.18  
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema, PSI, TIG, integrin\_B; TM=Y; SS=M; 4.18  
 456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4, Cbl\_N, Cbl\_N2, Cbl\_N3; TM=M; SS=N; 4.17  
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moi; NUDIX; TM=M; SS=M; 4.17  
 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor; integrin\_A, FG-GAP; TM=Y; SS=N; 4.14  
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; SS=N; 4.13  
 445417; AK001058; Hs.12680; a disintegrin-like and metalloprotease w; tsp\_1, Reprolysin, Pep\_M12B\_propep, none; 4.12  
 433895; AI287912; Hs.3628; mitogen-activated protein kinase kinase ; pkinase, zf-C4, CNH, ERM; TM=M; SS=N; 4.12  
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M; SS=N; 4.09  
 419121; AA374372; Hs.89626; parathyroid hormone-like hormone; none, none; 4.08  
 416602; NM\_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF, vwc, TSPN; 4.07  
 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm\_1; TM=Y; SS=M; 4.07  
 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase; TM=M; SS=N; 4.06  
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M; SS=N; 4.03  
 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PSI, integrin\_B; TM=Y; SS=N; 4.02

414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 4.02  
 413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic; sugar\_tr; TM=Y; SS=M; 4.01  
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 4.01  
 406906; Z25424; ; gb:H.sapiens protein-serine/threonine ki; none,none; 3.98  
 450375; AA009647; Hs.352537; a disintegrin and metalloproteinase doma; Reprolysin,Pep\_M12B\_propep,disintegrin,Reprolysin,Pep\_M12B\_propep,disintegrin; 3.98  
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl\_Oxidase;; 3.96  
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM; TM=Y; SS=M; 3.95  
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated kinase; pkinase,pkinase\_C; TM=M; SS=M; 3.95  
 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR,LRRNT,LRRCT; TM=Y; SS=M; 3.95  
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfam; SRP14,TNFR\_c6;; 3.93  
 407792; AI077715; Hs.39384; putative secreted ligand homologous to f; none; TM=M; SS=Y; 3.91  
 424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD\_NFYB\_HMF;; 3.91  
 415989; AI267700; Hs.351201; ESTs; none,none; 3.90  
 423189; M59371; Hs.171596; EphA2; fn3.pkinase,SAM,EPH\_lbd; TM=Y; SS=M; 3.90  
 443859; NM\_013409; Hs.9914; follistatin; kazal;; 3.89  
 429612; AF062649; Hs.252587; pituitary tumor-transforming 1; none;; 3.89  
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death,ZU5;; 3.88  
 450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig; TM=Y; SS=M; 3.88  
 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase; TM=M; SS=N; 3.86  
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2,SH3; TM=M; SS=N; 3.84  
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP,pkinase,DAG\_PE-bind,RBD; 3.83  
 436291; BE568452; Hs.344037; protein regulator of cytokinesis 1; none; TM=M; SS=N; 3.82  
 417512; X76534; Hs.82226; glycoprotein (transmembrane) nmb; PKD; TM=Y; SS=M; 3.81  
 427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20653 fis, clone KA; none,pkinase; 3.80  
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none; TM=M; SS=Y; 3.80  
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside\_tra2,none; 3.80  
 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfam; IL2;; 3.79  
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 3.78  
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD,helicase\_C,CARD; TM=M; SS=N; 3.78  
 417720; AA205625; Hs.208067; ESTs; none,none; 3.77  
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,pkinase,Recep\_L\_domain,YLP,none; 3.77  
 449029; M28989; Hs.22891; solute carrier family 7 (cationic amino ; aa\_permeases; TM=Y; SS=M; 3.76  
 413436; AF238083; Hs.68061; sphingosine kinase 1; DAGKc; TM=M; SS=N; 3.75  
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated; ig,ITAM,Zn\_clus; TM=Y; SS=M; 3.74  
 413281; AA861271; Hs.222024; transcription factor BMAL2; HLH,PAS;; 3.74  
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ\_con; TM=M; SS=N; 3.74  
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,integrin\_A,FG-GAP; TM=Y; SS=M; 3.74  
 424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosp; perlipin;; 3.73  
 426471; M22440; Hs.170009; transforming growth factor, alpha; EGF; TM=M; SS=M; 3.72  
 422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; EGF,vwd,AMOP;; 3.72  
 450125; AA005418; Hs.158186; ESTs; CIDE-N,7tm\_1,none; 3.71  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 3.70  
 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; ldl\_recept\_a,PKD,MHC\_I; TM=M; SS=Y; 3.70  
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar\_lr; 3.70  
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; SS=N; 3.69  
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-l; fn3,Y\_phosphatase,carb\_anhydrase; TM=Y; SS=M; 3.68  
 443759; BE390832; Hs.134729; FYD domain-containing ion transport reg; ATP1G1\_PLM\_MAT8; TM=Y; SS=M; 3.68  
 452344; AI264357; Hs.55405; hypothetical protein MGC16212; Sulfate\_transp,STAS;; 3.68  
 439625; AF086453; Hs.58611; ESTs; Fork\_head,glycolytic\_enz,Na\_sulph\_symp; 3.66  
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm\_1; TM=Y; SS=M; 3.66  
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement comp; C1q,Collagen;; 3.65  
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor ( ; SH3,PH,RhoGEF; TM=M; SS=N; 3.64  
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos; TM=M; SS=M; 3.64  
 438707; L08239; Hs.5326; amino acid system N transporter 2; porcu; ACAT,MBOAT; TM=Y; SS=M; 3.64  
 422596; AF063611; Hs.118633; 2'-5'-oligoadenylate synthetase-like; ubiquitin;; 3.63  
 449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN cDNA 5730; none; TM=M; SS=N; 3.62  
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanylate\_kin,PDZ,SH3; 3.62  
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M; SS=Y; 3.62  
 452696; AI826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate\_kin,PDZ,SH3; 3.60  
 407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc; Galactosyl\_T; TM=M; SS=Y; 3.59  
 423575; C18863; Hs.163443; intron of periostin (OSF-2os); Fasciclin,none; 3.59  
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor tran; ig,none; 3.58  
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase; TM=Y; SS=M; 3.58  
 419912; AF249745; Hs.6066; Rho guanine nucleotide exchange factor ( ; SH3,PH,RhoGEF; TM=M; SS=N; 3.58  
 431457; NM\_012211; Hs.256297; integrin, alpha 11; FG-GAP,vwa; TM=Y; SS=M; 3.57  
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion\_trans; TM=Y; SS=M; 3.55  
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none; TM=Y; SS=M; 3.55  
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E coli Re; none; 3.53  
 426500; NM\_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y; TM=M; SS=N; 3.53  
 429556; AW139399; Hs.314807; ESTs; none; TM=M; SS=N; 3.52  
 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm\_1; TM=Y; SS=M; 3.52  
 432636; AA340864; Hs.278562; claudin 7; PMP22\_Claudin; TM=Y; SS=M; 3.51  
 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none; TM=Y; SS=M; 3.51  
 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC\_tran,ABC\_membrane,SRP54,Thymidylate\_kin; TM=Y; SS=M; 3.49  
 425566; AW162943; Hs.250618; UL16 binding protein 2; ldl\_recept\_a,PKD,MHC\_I; TM=M; SS=Y; 3.48  
 402447; ; C1000201.gij204416[gb]AA02627.1j (L0519; none; TM=Y; SS=M; 3.48  
 431183; NM\_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER\_Jumen\_recept; TM=M; SS=M; 3.48  
 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A recepto; Neur\_chan\_LBD,Neur\_chan\_memb; TM=Y; SS=M; 3.48  
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR; TM=M; SS=N; 3.48  
 425003; AF119046; Hs.154149; apurinic/aprimidinic endonuclease(APEX ; Troponin,Exo\_endo\_phos,IQ; TM=M; SS=N; 3.47  
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese;; 3.44  
 446051; BE048061; Hs.37054; ephrin-A3; Ephrin,A\_deamin,dsm,z-alpha; 3.43  
 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin,Reprolysin,Pep\_M12B\_propep,EGF; TM=Y; SS=M; 3.42



417426; NM\_002291; Hs.82124; laminin, beta 1; laminin\_EGF,laminin\_Nterm,integrin\_B;; 3.42  
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-asso; kinesin;TM=M;SS=N; 3.42  
 430044; AA464510; Hs.152812; ESTs; none,none; 3.42  
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD\_DAPIN,HIN;; 3.39  
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm\_1;TM=Y;SS=M; 3.39  
 428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino a; eIF6,SDF;TM=M;SS=N; 3.39  
 443648; AI085377; Hs.143610; ESTs; Fork\_head,none; 3.39  
 418869; AW516565; ; gb:xq01d05.x1 Soares\_NHCeC\_cervical\_tumo; none,RasGAP,WW,IQ; 3.38  
 432179; X75208; Hs.2913; EphB3; EPH\_lbd,fn3,ptkinase,SAM;TM=Y;SS=M; 3.38  
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; ig;TM=Y;SS=M; 3.38  
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 3.37  
 408716; AI567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein, ; UvrD-helicase,RNB,Runt;TM=M;SS=N; 3.37  
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone\_rec,zf-C4,Metallothio\_5;TM=M;SS=N; 3.37  
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 3.37  
 421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC\_tran,ABC\_membrane,GTP\_EFTU;TM=M;SS=M; 3.36  
 400298; AA032279; Hs.61635; six transmembrane epithelial antigen of ; none;TM=Y;SS=N; 3.35  
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;; 3.33  
 400261; ; Hs.1802; Eos Control; ig,MHC\_II\_beta;TM=Y;SS=M; 3.33  
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3;TM=M;SS=N; 3.32  
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none,lectin\_c; 3.32  
 416065; BE267931; Hs.78996; proliferating cell nuclear antigen; PCNA,PCNA\_C;TM=M;SS=N; 3.31  
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo\_seg,UQ\_con,none; 3.31  
 426840; BE244217; Hs.172890; diacylglycerol kinase, alpha (80kD); ehand,DAG\_PE-bind,DAGKa,DAGKc,DC1;TM=M;SS=N; 3.31  
 434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPc;TM=M;SS=N; 3.31  
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M;SS=N; 3.31  
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 3.31  
 423973; AF038461; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase,PLAT;TM=M;SS=N; 3.30  
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; ig,pkinase;TM=Y;SS=M; 3.30  
 449027; AJ271216; Hs.22880; dipeptidylpeptidase II; Peptidase\_M49,EGF,ig,Neuregulin;TM=M;SS=N; 3.28  
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr\_redox;TM=Y;SS=M; 3.28  
 426457; AW894667; Hs.380138; chimerin (chimaerin) 1; DAG\_PE-bind,RhoGAP,SH2;TM=M;SS=N; 3.28  
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 3.27  
 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M;SS=N; 3.27  
 430397; AI924533; Hs.105607; bicarbonate transporter related protein ; HCO3\_cotransp;TM=Y;SS=N; 3.27  
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3\_PI4\_kinase,FAT,FATC;TM=M;SS=N; 3.26  
 446006; NM\_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 3.26  
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH,none; 3.25  
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm\_2;TM=Y;SS=M; 3.25  
 405932; ; C15000305:gil3806122[gb]AAC69198.1| (AF0; ras;TM=M;SS=N; 3.25  
 400205; ; Hs.81848; NM\_006265; Homo sapiens RAD21 (S. pombe); DUF173; 3.25  
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3;TM=M;SS=Y; 3.24  
 412942; AL120344; Hs.76074; mitogen-activated protein kinase-activat; pkinase;TM=M;SS=N; 3.23  
 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; ig;TM=M;SS=M; 3.22  
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 3.22  
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 3.22  
 427318; AF186081; Hs.175783; zinc transporter; Zip;TM=Y;SS=M; 3.22  
 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 3.22  
 428698; AA852773; Hs.334838; KIAA1866 protein; none;NA;NA; 3.22  
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M;SS=N; 3.22  
 415149; X12451; Hs.78056; cathepsin L; Peptidase\_C1; 3.21  
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD;TM=M;SS=N; 3.21  
 424618; L29472; Hs.1802; major histocompatibility complex, class ; ig,MHC\_II\_beta;TM=Y;SS=M; 3.20  
 438564; AA381553; Hs.198253; major histocompatibility complex, class ; ig,MHC\_II\_alpha,none; 3.20  
 456181; L36463; Hs.1030; ras inhibitor; RA,SH2,VPS9;TM=M;SS=N; 3.20  
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase ; pkinase,CNH;TM=M;SS=N; 3.19  
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin,bZIP;TM=M;SS=N; 3.18  
 415010; NM\_004203; Hs.77783; membrane-associated tyrosine- and threon; ank,pkinase,UPF0073;; 3.16  
 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8;; 3.16  
 450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin,ld\_recept\_a,none; 3.16  
 426395; BE151985; Hs.355669; hypothetical protein FLJ23316; pkinase,none; 3.15  
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor; none,none; 3.15  
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE\_p10,ICE\_p20;; 3.15  
 410668; BE379794; Hs.159651; hypothetical protein; death,TNFR\_c6;TM=Y;SS=M; 3.15  
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 3.15  
 432251; AW972983; Hs.232165; polycythemia rubra vera 1; cell surface ; none;TM=M;SS=M; 3.15  
 407844; AW073716; Hs.8037; ESTs; transmembrane4,none; 3.14  
 408634; AW407254; Hs.356216; calmodulin 2 (phosphorylase kinase, delt; none,none; 3.14  
 423061; AI290473; Hs.44807; ESTs; integrin\_B,Sema,PSI,TIG,none; 3.14  
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ;; 3.13  
 431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 3.13  
 425394; AA356730; Hs.323949; kangai 1 (suppression of tumorigenicity ; transmembrane4,none; 3.13  
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIII (25-hy; p450;; 3.13  
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; ig,isodh,Ribosomal\_L6,F-box;TM=Y;SS=M; 3.13  
 429305; AF095727; Hs.287832; myelin protein zero-like 1; ig,transmembrane4;TM=Y;SS=M; 3.12  
 419034; NM\_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M;SS=N; 3.12  
 417386; AL037228; Hs.301957; D123 gene product; NUDIX,secY,E1\_dehydrog,transket\_pyr;TM=Y;SS=M; 3.11  
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion\_trans,SPRY,RYDR,ITPR,RyR,MIR;TM=Y;SS=N; 3.11  
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-li; AAA,NB-ARC,PAAD\_DAPIN;NA;NA; 3.10  
 406467; ; Target Exon; ehand,Acyltransferase,none; 3.10  
 422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell transformi; BRCT,RhoGEF;TM=M;SS=N; 3.10  
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 3.09  
 437016; AU076916; Hs.5398; guanine monophosphate synthetase; PHD,SET,zf-  
 CXXC,EGF,ank,notch,WW,FCH,GATase,GMP\_synt\_C,Occludin,YEATS,metalthio,EB,heme\_1,RCC1,ZZ,FeThRed\_A,ENTH,Band\_41,HECT;TM=M;SS=N; 3.09

441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm\_3,none; 3.09  
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none,none; 3.09  
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion\_trans;TM=Y;SS=M; 3.09  
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;SS=N; 3.08  
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 3.08  
 402233; ; NM\_030760; Homo sapiens endothelial diff; 7tm\_1;TM=Y;SS=M; 3.07  
 430066; A1929659; Hs.237825; signal recognition particle 72kD; TPR,AIRC,SAICAR\_synt; 3.07  
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 3.06  
 434263; N34895; Hs.79187; ESTs; ig,none; 3.06  
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 3.05  
 409378; U42387; Hs.54428; pancreatic polypeptide receptor 1; 7tm\_1;TM=Y;SS=M; 3.05  
 410165; BE560228; Hs.71869; apoptosis-associated speck-like protein ; PAAD\_DAPIN,CARD;TM=M;SS=N; 3.05  
 440270; NM\_015986; Hs.7120; cytokine receptor-like molecule 9; fn3; 3.05  
 449003; X76342; Hs.389; alcohol dehydrogenase 7 (class IV), mu o; adh\_zinc;TM=M;SS=N; 3.05  
 420189; AW296380; Hs.95821; osteoclast stimulating factor 1; SH3,ank; 3.05  
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 doma; SH2;; 3.05  
 421541; NM\_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase, pkinase\_C;TM=M;SS=N; 3.04  
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M;SS=N; 3.03  
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb\_DNA-  
 binding, THF\_DHG\_CYH, THF\_DHG\_CYH\_C, CAP\_GLY, AAA, LON, Peptidase\_C9, bZIP, M, xan\_ur\_permease, HCO3\_cotransp;TM=M;SS=N; 3.03  
 449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp;TM=M;SS=M; 3.03  
 413869; NM\_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 3.02  
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K\_tetra,DUF51,none; 3.02  
 436576; A1458213; Hs.77542; ESTs; 7tm\_1,DnaJ; 3.02  
 446269; AW263155; Hs.14559; hypothetical protein FLJ10540; none;TM=M;SS=N; 3.02  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm\_1,7tm\_2;TM=Y;SS=M; 3.01  
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 3.00  
 421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, polyp; pkinase, pkinase\_C;TM=M;SS=N; 3.00  
 409705; M37762; Hs.56023; brain-derived neurotrophic factor; NGF;; 2.99  
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory su; CDK5\_activator,none; 2.99  
 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 2.98  
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin\_B,EGF,PSI;TM=Y;SS=M; 2.97  
 410026; A1912061; Hs.55016; hypothetical protein FLJ21935; none,none; 2.97  
 448733; NM\_005629; Hs.187958; solute carrier family 6 (neurotransmitte; SNF;TM=Y;SS=N; 2.97  
 432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2;TM=M;SS=N; 2.97  
 453035; AW581943; Hs.334; Rho guanine nucleotide exchange factor (; none,none; 2.97  
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 2.97  
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase,Furin-like,Recep\_L\_domain,none; 2.96  
 441389; AF134838; Hs.7835; endocytic receptor (macrophage mannose r; fn2,lectin\_c;TM=Y;SS=M; 2.95  
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (; MIF,sugar\_tr,none; 2.94  
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm\_1,none; 2.94  
 402558; ; C1000201.gij204416[gbl]AA02627.1 (L0519; none;TM=Y;SS=M; 2.94  
 425852; AK001504; Hs.159551; death receptor 6, TNF superfamily member; death,TNFR\_c6;TM=Y;SS=M; 2.94  
 442080; AW444761; Hs.72901; ESTs; ank;; 2.94  
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 2.93  
 444809; BE207568; Hs.208219; occludin; transmembrane4;TM=Y;SS=N; 2.93  
 449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none;TM=Y;SS=M; 2.93  
 416110; Z42262; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin\_B;TM=Y;SS=M; 2.93  
 453768; BE382670; Hs.198511; Homo sapiens mRNA; cDNA DKFZp7611177 (fr; arf, G-alpha,none; 2.92  
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian ; Furin-like,pkinase,Recep\_L\_domain;TM=M;SS=M; 2.92  
 421429; NM\_014922; Hs.104305; death effector filament-forming Ced-4-li; LRR,PAAD\_DAPIN,AAA,CARD,NB-ARC;NA;NA; 2.92  
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 2.91  
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;SS=N; 2.91  
 422127; AW504286; Hs.112049; SET binding factor 1; dDENN,DENN,GRAM,PH;; 2.91  
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC\_tran,ABC\_membrane;TM=Y;SS=M; 2.90  
 430451; AA83644; Hs.297939; calthepsin B; Peptidase\_C1,pro\_isomerase;; 2.90  
 424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibitor; serpin;TM=M;SS=N; 2.89  
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal\_L37ae,pkinase,POLO\_box,tRNA-synt\_1b,dynamin,dynamin\_2,GED,bZIP,M;; 2.89  
 429619; AL120751; Hs.211568; eukaryotic translation initiation factor; none,none; 2.89  
 413879; AA132961; Hs.212533; Homo sapiens cDNA: FLJ22572 fis, clone H; none,none; 2.89  
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2,SH3,pkinase;TM=M;SS=N; 2.89  
 422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, s; IRK;TM=Y;SS=N; 2.89  
 405556; ; homeodomain-interacting protein kinase 3; trypsin;TM=M;SS=N; 2.89  
 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 2.89  
 425262; D87119; Hs.155418; GS3955 protein; pkinase;; 2.88  
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) ; NDK,PH,Oxysterol\_BP;; 2.88  
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 2.88  
 414703; BE243877; Hs.380063; ATPase, Na? transporting, beta 3 polypep; Na\_K-ATPase;TM=Y;SS=M; 2.87  
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2,none; 2.86  
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF;TM=Y;SS=M; 2.86  
 458039; AA835884; Hs.130685; leukotriene b4 receptor (chemokine recep; CIDE-N,none; 2.86  
 434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp586F2224 (f; DSPc,none; 2.86  
 425802; Y14838; ; chemokine-like receptor 1; 7tm\_1,none; 2.86  
 403112; ; Target Exon; efhand,C2,PH,PI-PLC-Y,PI-PLC-X;; 2.86  
 435563; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar\_tr;TM=Y;SS=N; 2.85  
 442117; AW664964; Hs.128899; ESTs; hypothetical protein for IMAGE:447; none,none; 2.84  
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein FLJ20522; none,none; 2.84  
 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase\_c,zf-C2H2,PHD,none; 2.83  
 408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delt; none,none; 2.83  
 446947; AF146747; Hs.232165; polycythemia rubra vera 1; cell surface ; none;TM=M;SS=M; 2.83  
 448386; AB037750; Hs.21061; KIAA1329 protein; PKD,BNR;TM=Y;SS=M; 2.82  
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin\_head,IQ,zf-MYND;TM=M;SS=M; 2.82  
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC;TM=Y;SS=M; 2.82

- 5 459707; AA631362; Hs.120866; gb:np86b01.s1 NCI\_CGAP\_Thy1 Homo sapiens; 7tm\_1,none; 2.82  
 422699; BE410590; Hs.119257; ems1 sequence (mammary tumor and squamous); SH3,HS1\_rep;TM=M;SS=N; 2.82  
 438108; A1471795; Hs.287776; vanilloid receptor-related osmotically a; ank,ion\_trans;TM=Y;SS=N; 2.82  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y\_phosphatase;TM=M;SS=N; 2.82  
 448595; AB014544; Hs.21572; KIAA0644 gene product; LRR,LRRCT;TM=Y;SS=M; 2.81  
 423598; BE247600; Hs.377968; ESTs; 7tm\_1;TM=Y;SS=M; 2.81  
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPC; 2.81  
 414198; AW505308; Hs.75812; phosphoenolpyruvate carboxykinase 2 (mit; PEPCK; 2.81  
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 2.81  
 10 432314; AA533447; Hs.285173; ESTs; Xlink,none; 2.81  
 416207; NM\_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, comp; none;TM=Y;SS=M; 2.80  
 446985; AL038704; Hs.156827; ESTs, Weakly similar to ALU1\_HUMAN ALU S; SAM,SH3,HS1\_rep; 2.80  
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone L;  
 15 aa\_permeases,pyridoxal\_deC,bromodomain,PHD,MBD,AT\_hook,DDT,PI3\_P14\_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 2.80  
 432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M;SS=N; 2.80  
 426006; R49031; Hs.22627; ESTs; pkinase,TBC; 2.79  
 414217; A1309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 2.79  
 411165; NM\_000169; Hs.69089; galactosidase, alpha; Melibiase; 2.79  
 20 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheti; ABC\_tran,ABC\_membrane,ig,MHC\_II\_beta,SRP54,proteasome,ABC\_membrane,ABC\_tran; 2.78  
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 2.78  
 421448; AF033850; Hs.104519; phospholipase D2; PH,PLDc,PX;TM=M;SS=N; 2.78  
 410226; A1831958; Hs.61053; hypothetical protein; SH3,TPR;TM=M;SS=N; 2.78  
 433535; AF111106; Hs.3382; protein phosphatase 4, regulatory subunit; HEAT;TM=M;SS=N; 2.78  
 25 442503; AF147078; Hs.375031; p53-responsive gene 5; K\_tetra,ion\_trans,none; 2.77  
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/i; TPR,PDZ,WW,Guanylate\_kin;TM=M;SS=N; 2.77  
 454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M;SS=N; 2.77  
 440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK;TM=M;SS=N; 2.77  
 449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep\_L\_domain,none; 2.76  
 422667; H25642; Hs.132821; ESTs; FMO-like,FMO-like; 2.76  
 30 415012; NM\_004383; Hs.77793; c-src tyrosine kinase; SH2,SH3,pkinase;TM=M;SS=N; 2.76  
 402316; ; NM\_013447;Homo sapiens egf-like module c; 7tm\_2,GPS;TM=M;SS=M; 2.75  
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG\_PE-bind,pkinase\_C,OPR;TM=M;SS=N; 2.75  
 447250; A1878909; Hs.17883; protein phosphatase 1G (formerly 2C); ma; PP2C;TM=M;SS=N; 2.75  
 35 438629; A1187380; Hs.257170; ESTs, Weakly similar to T12515 hypotheti; TNFR\_c6,none; 2.75  
 451144; AW956103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme; HATPase\_c,none; 2.74  
 408543; N78098; Hs.44289; ESTs; none;TM=M;SS=N; 2.74  
 429345; R11141; Hs.199695; hypothetical protein; K\_tetra,SAM; 2.74  
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; ptkB;TM=M;SS=N; 2.73  
 420602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS;TM=M;SS=N; 2.73  
 407217; AA477136; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase\_C;TM=M;SS=N; 2.73  
 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPC,Y\_phosphatase;TM=M;SS=N; 2.73  
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 2.73  
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 2.73  
 438022; AW517524; Hs.135201; NOD2 protein; LRR,CARD,GTP\_CDC,Viral\_helicase1;TM=M;SS=N; 2.72  
 45 420929; A1694143; Hs.326248; programmed cell death 4; MA3;TM=M;SS=N; 2.72  
 421155; H87879; Hs.102267; lysyl oxidase; Lysyl\_oxidase,Aldose\_epim,Epimerase; 2.72  
 448564; AL044962; Hs.21453; inositol 1,4,5-trisphosphate 3-kinase C; IPK; 2.71  
 449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep\_L\_domain,none; 2.71  
 50 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ig;TM=Y;SS=M; 2.71  
 412259; A1560292; Hs.279909; protein phosphatase 2 (formerly 2A), reg; WD40;TM=M;SS=N; 2.71  
 419569; A1971651; Hs.91143; jagged 1 (Alagille syndrome); DSL,EGF,laminin\_EGF\_vwc,metalthio;TM=M;SS=M; 2.71  
 452401; NM\_007115; Hs.29352; tumor necrosis factor, alpha-induced pro; Xlink,CUB; 2.71  
 458190; BE561793; Hs.21446; KIAA1716 protein; ASC,Galactosyl\_T,none; 2.70  
 432126; AA865239; Hs.37196; ESTs; 7tm\_1;TM=Y;SS=M; 2.70  
 55 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS\_C;TM=M;SS=N; 2.70  
 424717; H03754; Hs.152213; wingless-type MMTV integration site faml; wnt,none; 2.70  
 414108; A1267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol\_BP,pkinase;TM=M;SS=N; 2.70  
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1\_rep;TM=M;SS=N; 2.70  
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none,none; 2.69  
 60 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;SS=N; 2.69  
 404891; ; Target Exon; none,none; 2.69  
 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 2.69  
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2,SH3,pkinase;TM=M;SS=N; 2.68  
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; ig,kringle,pkinase,Fz;TM=Y;SS=M; 2.68  
 65 414443; AU077268; Hs.76144; platelet-derived growth factor receptor,; ig,pkinase;TM=Y;SS=N; 2.68  
 427274; NM\_005211; Hs.174142; colony stimulating factor 1 receptor, fo; ig,pkinase;TM=Y;SS=M; 2.68  
 436856; A1469355; Hs.127310; ESTs; pkinase,rrm;TM=M;SS=N; 2.68  
 437429; H79981; Hs.5613; Homo sapiens mRNA; cDNA DKFZp564E2222 (f; SH2,SH3,BTB; 2.67  
 70 450690; AA296696; Hs.333418; FXD domain-containing ion transport reg; ATP1G1\_PLM\_MAT8;TM=Y;SS=M; 2.67  
 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 2.67  
 445330; R52656; Hs.21691; ESTs; 7tm\_1,none; 2.67  
 452698; NM\_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm\_1;TM=Y;SS=M; 2.67  
 419754; H52299; Hs.308467; Homo sapiens mRNA; cDNA DKFZp586i0523 (f; none;TM=M;SS=N; 2.67  
 75 434237; AF119908; Hs.235516; hypothetical protein PRO2955; none; 2.67  
 445826; BE313754; Hs.13350; Homo sapiens mRNA; cDNA DKFZp586D0918 (f; ig,isp\_1,ZU5,Nucleoside\_tran; 2.66  
 446696; AF279265; Hs.298476; solute carrier family 26, member 6; Sulfate\_transp,STAS,xan\_ur\_permease;TM=Y;SS=N; 2.66  
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH\_C,IMPDH\_N,CBS,integrin\_B,Ricin\_B\_lectin; 2.66  
 413745; AW247252; Hs.75514; nucleoside phosphorylase; Mtap\_PNP; 2.66  
 80 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 2.66  
 449523; NM\_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm\_1;TM=Y;SS=M; 2.66  
 449030; A1365582; Hs.57100; Homo sapiens mRNA for FLJ00016 protein, ; transmembrane4;TM=Y;SS=M; 2.66  
 434979; A1953054; Hs.89643; transketolase (Wernicke-Korsakoff syndro; ASC,transketolase,transket\_pyr,transketolase\_C,pkinase; 2.66  
 406137; ; NM\_000179;Homo sapiens mutS (E. coli) h; MutS\_C,PWWP,MutS\_N;TM=M;SS=N; 2.66

- 412935; BE267045; Hs.75064; tubulin-specific chaperone c; none;; 2.66  
 408633; AW963372; Hs.222088; PRO2000 protein; bromodomain,AAA,Sigma54\_activat;; 2.66  
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subu; PC\_rep; TM=M;SS=N; 2.65  
 452682; AA456193; Hs.374574; progesterone membrane binding protein; homeobox; none; 2.65  
 401752; ; RAN binding protein 3; SH2,STAT,STAT\_bind,STAT\_prot,ion\_trans,PAC,PAS,Orexin; 2.65  
 450747; AI064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm,zf-RanBP,GAS2; 2.65  
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm\_2,HRM; TM=Y;SS=M; 2.64  
 452701; NM\_005110; Hs.30332; glutamine-fructose-6-phosphate transamin; GATase\_2,SIS; TM=M;SS=N; 2.64  
 433933; AI754389; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none;NA;NA; 2.64  
 421677; H64092; Hs.38282; ESTs; A1pp,Armadoillo\_seg,IBB; 2.64  
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none;; 2.64  
 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese; none; 2.64  
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH; TM=M;SS=N; 2.64  
 437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor, ; Tropomyosin,pkinase,LRR,LRRCT,Hydantoinase\_B,Hydantoinase\_A; TM=M;SS=N; 2.63  
 458946; AA009716; Hs.42311; ESTs; none,DSPc,Y\_phosphatase; 2.63  
 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5\_F8\_type\_C; TM=M;SS=M; 2.63  
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 2.63  
 425075; AA506324; Hs.1852; acid phosphatase, prostate; acid\_phosphat; TM=Y;SS=M; 2.63  
 405588; ; NM\_000299; Homo sapiens plakophilin 1 (e; Armadoillo\_seg; TM=M;SS=N; 2.63  
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH; none; 2.63  
 448243; AW369771; Hs.367688; integrin, beta 8; integrin\_B; none; 2.63  
 452012; AA307703; Hs.279766; kinesin family member 4A; kinesin,DNA\_topoisolV,K-box; TM=M;SS=N; 2.63  
 412182; AA205588; Hs.73737; Splicing factor, arginine/serine-rich, 4; rrm,hormone\_rec,zf-C4,sugar\_tr; 2.63  
 423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC\_tran; TM=Y;SS=N; 2.63  
 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4; TM=Y;SS=M; 2.62  
 413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like ; SH2,SAM,Exo\_endo\_phos;; 2.62  
 414998; NM\_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin\_c; TM=Y;SS=M; 2.62  
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin\_c,sushi; TM=M;SS=M; 2.62  
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker\_histone; TM=M;SS=N; 2.62  
 401812; ; sorting nexin 14; AAA,NB-ARC,APS\_kinase,cdc48\_N,cdc48\_2; none; 2.61  
 417886; AA214584; ; ESTs; SPRY,7tm\_3,ANF\_receptor; none; 2.61  
 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substra; SH3; TM=M;SS=N; 2.61  
 428512; AI018187; Hs.375624; Human DNA sequence from clone RP11-243J1; none;; 2.61  
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Pribosyltran,OMPdecase; TM=M;SS=N; 2.61  
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT; none; 2.61  
 421077; AK000061; Hs.101590; hypothetical protein; ank,pkinase,death,SPRY,SAP,Ribosomal\_L24e,SRP54,dDENN,DENN,uDENN; TM=M;SS=N; 2.60  
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase; TM=M;SS=N; 2.60  
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain,rrm; TM=M;SS=N; 2.60  
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin\_ADF;; 2.60  
 411133; AW819204; ; gb:CM1-ST0283-071299-061-h03 ST0283 Homo; ANF\_receptor; none; 2.60  
 405602; ; Target Exon; pkinase;; 2.60  
 400440; X83957; Hs.83870; nebulin; SH3,Nebulin;; 2.60  
 424848; AI263231; Hs.327090; EST; SH3,PDZ,Guanylate\_kin; none; 2.59  
 432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate sy; APS\_kinase,ATP-sulfurylase; TM=M;SS=N; 2.59  
 452690; AI536070; Hs.15085; ESTs; pou,homeobox,lig\_chan,ANF\_receptor; 2.59  
 422753; AI928995; Hs.1575; small nuclear ribonucleoprotein D3 polyp; Srm;; 2.59  
 428028; U52112; Hs.182018; interleukin-1 receptor-associated kinase; death,pkinase; TM=M;SS=N; 2.58  
 433573; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G-type rece; 7tm\_2,EGF,cadherin,laminin\_EGF,laminin\_G,Trypan\_glycop,GPS,HRM; TM=Y;SS=M; 2.58  
 422785; AI824114; Hs.289088; heat shock 90kD protein 1, alpha; zf-C2H2; none; 2.58  
 418685; U76376; Hs.87247; harakiri, BCL2-interacting protein (cont; none; TM=M;SS=M; 2.58  
 452329; N36626; Hs.29106; mitogen-activated protein kinase phosphatase; DSPc; TM=M;SS=N; 2.58  
 428405; Y00762; Hs.2266; cholinergic receptor, nicotinic, alpha p; Neur\_chan\_LBD,Neur\_chan\_memb; TM=Y;SS=M; 2.58  
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ; 2.57  
 407245; X90568; Hs.172004; titin; tn3,ig,SGXXSG,pkinase; TM=M;SS=N; 2.57  
 422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic; sugar\_lr; TM=Y;SS=M; 2.57  
 401751; ; RAN binding protein 3; Orexin,SH2,STAT,STAT\_bind,STAT\_prot,ion\_trans,PAC,PAS; none; 2.57  
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE\_p10,ICE\_p20,DED; TM=M;SS=N; 2.57  
 422282; AF019225; Hs.114309; apolipoprotein L; MotA\_ExbB; TM=Y;SS=M; 2.57  
 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; lipoxigenase,PLAT,lipoxigenase,PLAT; 2.57  
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2; TM=Y;SS=N; 2.57  
 401218; ; eukaryotic translation elongation factor; ion\_trans; TM=Y;SS=N; 2.57  
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L OR; PLDc; TM=M;SS=N; 2.57  
 444743; AA045648; Hs.301957; nudix (nucleoside diphosphate linked moi; NUDIX,secY,E1\_dehydrog,transkeL\_pyr; TM=Y;SS=M; 2.56  
 429782; NM\_005754; Hs.220689; Ras-GTPase-activating protein SH3-domain; rrm,NTF2; TM=M;SS=N; 2.56  
 442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal\_S14; 2.56  
 456602; AA411607; Hs.118964; ESTs, Weakly similar to KIAA1150 protein; none,pkinase; 2.56  
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3,PX; TM=M;SS=N; 2.56  
 441699; AW511126; Hs.127572; ESTs; none,Aa\_trans; 2.56  
 447912; AW576549; Hs.165728; ESTs, Weakly similar to I38022 hypotheti; none,GSHPx,ABC\_tran; 2.56  
 442945; AI024849; Hs.131853; ESTs; pkinase; none; 2.56  
 453199; AI336266; Hs.32353; mitogen-activated protein kinase kinase ; pkinase; TM=M;SS=N; 2.56  
 451477; AI798425; Hs.42710; ESTs; SH3; none; 2.56  
 415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-Coenzyme A sy; HMG\_CoA\_synt;; 2.55  
 413529; U11874; Hs.846; interleukin 8 receptor, beta; 7tm\_1; TM=Y;SS=N; 2.55  
 425345; AU077297; Hs.155894; protein tyrosine phosphatase, non-recept; Y\_phosphatase,DSPc; TM=M;SS=M; 2.55  
 401321; ; receptor tyrosine kinase-like orphan rec; none; TM=M;SS=N; 2.55  
 446999; AA151520; Hs.351416; hypothetical protein MGC4485; none; none; 2.55  
 401057; ; eukaryotic translation elongation factor; ion\_trans,IQ; TM=Y;SS=N; 2.55  
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4; TM=Y;SS=M; 2.55  
 408204; AA454501; Hs.43666; protein tyrosine phosphatase type IVA, m; Y\_phosphatase; TM=M;SS=N; 2.54  
 424539; L02911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK; pkinase,Activin\_rec; TM=M;SS=M; 2.54  
 459060; H89244; Hs.303627; heterogeneous nuclear ribonucleoprotein ; rrm,pkinase; TM=M;SS=N; 2.54  
 450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2; TM=M;SS=N; 2.54

- 425966; NM\_001761; Hs.1973; cyclin F; cyclin,F-box,cyclin\_C;TM=M;SS=N; 2.54  
 446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 2.54  
 412834; R77123; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm\_1,none; 2.54  
 457255; AL133011; Hs.253920; Homo sapiens mRNA; cDNA DKFZp434P201 (fr; none,none; 2.54  
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit.; proteasome;TM=M;SS=N; 2.53  
 417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2,PID,zf-C2H2,SCAN,AMP-binding,KRAB;TM=M;SS=N; 2.53  
 414570; Y00285; Hs.76473; insulin-like growth factor 2 receptor; fn2,C1MR;TM=M;SS=M; 2.53  
 444838; AV651680; Hs.208558; ESTs; integrin\_A,FG-GAP,none; 2.53  
 422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR,SH2,SH3,pkinase;TM=Y;SS=M; 2.53  
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none,none; 2.53  
 400702; ; Target Exon; lig\_chan,SBP\_bac\_3,ANF\_receptor;TM=Y;SS=M; 2.53  
 432336; NM\_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm,pkinase;TM=M;SS=N; 2.53  
 442643; U82756; Hs.374973; PRP4/STK/WD splicing factor; WD40;; 2.52  
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN2; ABC\_tran,IRK,SWIB; 2.52  
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22\_Claudin,none; 2.52  
 428975; NM\_004672; Hs.194694; mitogen-activated protein kinase kinase ; pkinase;; 2.52  
 407608; AI928218; Hs.380063; ATPase, Na? transporting, beta 3 polypep; none,none; 2.51  
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm\_1;TM=Y;SS=M; 2.51  
 410293; AK000047; Hs.61960; hypothetical protein; K\_tetra;TM=M;SS=N; 2.51  
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, ; C2,PLA2\_B;TM=M;SS=N; 2.51  
 425424; NM\_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;SS=N; 2.51  
 457013; AA037145; Hs.172865; cleavage stimulation factor, 3' pre-RNA; WD40;TM=M;SS=N; 2.51  
 439221; AA737106; Hs.32250; ESTs, Moderately similar to I78885 serin; adh\_short,Bcl-2,BH4,none; 2.51  
 405429; ; Target Exon; Y\_phosphatase,none; 2.51  
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible Ik; pkinase,RIO1;TM=M;SS=N; 2.51  
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 2.50  
 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 2.50  
 414419; F06829; Hs.76090; tumor necrosis factor, alpha-induced pro; K\_tetra;TM=M;SS=N; 2.50  
 405369; ; NM\_005569; Homo sapiens LIM domain kinase; pkinase,LIM,PDZ;; 2.50  
 418216; AA662240; Hs.283099; AF15q14 protein; Hemagglutinin,squash;TM=Y;SS=N; 2.50  
 404321; ; C7001741;gij4299629[sp]Q63932[MPK2\_MOUSE; none,none; 2.50  
 430900; U91939; Hs.248123; G protein-coupled receptor 25; 7tm\_1;TM=Y;SS=M; 2.49  
 440861; BE244115; Hs.7482; KIAA0682 gene product; rrm,Guanylate\_kin;TM=M;SS=N; 2.49  
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; ig;TM=Y;SS=N; 2.49  
 418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosom; pkinase,Activin\_recp,pkinase,Activin\_recp; 2.49  
 417034; NM\_006183; Hs.80962; neurotensin; none;; 2.49  
 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none,none; 2.49  
 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase;TM=M;SS=N; 2.49  
 418255; AW135405; Hs.37251; ESTs; pkinase,none; 2.49  
 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase;TM=M;SS=N; 2.44  
 417791; AW965339; Hs.44269; ESTs; none,fer2,FAD\_binding\_5,Ald\_Xan\_dh\_C,fer2\_2,Ald\_Xan\_dh\_C2,CO\_deh\_flav\_C; 2.44  
 453941; U39817; Hs.36820; Bloom syndrome; DEAD,helicase\_C,HRDC;TM=M;SS=N; 2.41  
 417849; AW291587; Hs.82733; nidogen 2; EGF,Idl\_recept\_b,thyroglobulin\_1;TM=M;SS=M; 2.39  
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;; 2.32  
 428513; BE220806; Hs.184697; plexin C1; PSI,none; 2.31  
 426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 2.31  
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q,Collagen;; 2.28  
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M;SS=N; 2.28  
 452461; N78223; Hs.108106; transcription factor; zf-C3HC4,ubiquitin,PHD,YDG\_SRA;TM=M;SS=N; 2.26  
 429547; AW009166; Hs.99376; FGENESH predicted novel secreted protein; none,none; 2.15  
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; SNF2\_N,helicase\_C;TM=M;SS=N; 2.15  
 401486; ; C4000647;gij4758508[ref]NP\_004253.1[ ai; none;TM=Y;SS=M; 2.15  
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient, yeast, h; HORMA;TM=M;SS=N; 2.14  
 424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 BT095 Homo ; none;TM=M;SS=M; 2.14  
 423761; NM\_006194; Hs.132576; paired box gene 9; PAX;TM=M;SS=N; 2.13  
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC004858 3 U1 sm; none,none; 2.13  
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm\_2,CytC\_asm,GPS;TM=Y;SS=M; 2.03  
 445019; AI205540; Hs.281295; ESTs; none,none; 2.00  
 443211; AI128388; Hs.143655; ESTs; none,none; 1.98  
 449448; D60730; Hs.57471; ESTs; none,none; 1.92  
 435243; AW292886; Hs.348932; hypothetical protein dJ434O14.3; IRF,none; 1.85  
 406360; ; Target Exon; WD40;TM=M;SS=N; 1.84  
 411388; X72925; Hs.69752; desmocollin 1; cadherin;TM=Y;SS=N; 1.84  
 453102; NM\_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm\_2;TM=Y;SS=M; 1.79  
 419183; U60669; Hs.89663; cytochrome P450, subfamily XXIV (vitamin; p450;; 1.78  
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf\_5;TM=Y;SS=M; 1.77  
 432842; AW674093; Hs.334822; hypothetical protein MGC4485; Ribosomal\_L4;TM=M;SS=N; 1.76  
 419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA sequence; none,none; 1.73  
 426427; M86699; Hs.169840; TTK protein kinase; pkinase;; 1.62  
 437915; AI637993; Hs.202312; Homo sapiens clone N11 Ntera2D1 teratoca; none,none; 1.58  
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz,NTR;; 1.50  
 434377; AW137148; Hs.306593; intron of periostin (OSF-2os); Fasciclin,none; 1.47  
 451592; AI805416; Hs.213897; ESTs; none,none; 1.47  
 404927; ; Target Exon; Galactosyl\_T;TM=M;SS=Y; 1.28  
 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;; 1.27  
 427335; AA448542; Hs.278444; G antigen 7B; none;; 1.25  
 431808; M30703; Hs.270833; amphiregulin (schwannoma-derived growth ; EGF;TM=Y;SS=M; 1.24  
 447993; AW139525; Hs.170362; ESTs; none,none; 1.21  
 428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1\_HUMAN G ANT; none;TM=M;SS=N; 1.18  
 453637; NM\_002589; Hs.34073; BH-protocadherin (brain-heart); cadherin;TM=Y;SS=M; 1.14  
 438274; AI918906; Hs.55080; ESTs; PAX,none; 1.14  
 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin,Idl\_recept\_a,none; 1.10  
 413268; AL039079; Hs.75256; regulator of G-protein signalling 1; RGS;TM=M;SS=N; 1.07

429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen, COLFI, TSPN, laminin\_G, CorA;; 1.00  
452795; AW392555; Hs.18878; hypothetical protein FLJ21620; 2OG-Fell\_Oxy; TM=M; SS=N; 1.00

TABLE 25B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
406685	0_0	M18728
418869	12789_14	AA229762 AA230035
425802	8884_3	AA122298 AA360788
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
411133	1070995_1	AW819203 AW819204 AW819197 AW819202 AW819211 BE158469 AW819221 BE158473 AW819235 AW819207 AW819220 AW819208 AW819238
AW819198	AW819234	

TABLE 25C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
405932	7767812	Minus	123525-123713
406467	9795551	Plus	182212-182958
402233	7690102	Plus	90281-91477
402558	9863760	Plus	19047-19145,21133-21293,33968-34069
405556	1552511	Plus	163497-163623,164715-164968,165369-16550
403112	8980973	Minus	113051-113195
402316	7527774	Minus	10751-10919,18817-19052,22131-22328
404891	7329392	Plus	84974-85125
406137	9166422	Minus	30487-31058
401752	9828651	Plus	144600-144794
405588	5002511	Plus	46180-46366
401812	7407975	Minus	55084-55391
405602	4753260	Plus	44647-44778
401751	9828651	Plus	139165-139322
401218	9929301	Minus	40793-41031
401321	9863631	Minus	104278-104748
401057	8117645	Plus	158309-159238
400702	8118856	Minus	11457-11585,26311-26536,27902-28067,3204
405429	7321905	Minus	51577-51723
405369	2078469	Minus	34183-34357,35686-35751
404321	9665209	Minus	76594-77805
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
406360	9256107	Minus	7513-7673
404927	7342002	Plus	68690-69563

TABLE 26A: 834 GENES UP-REGULATED IN EWING'S SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 26A lists about 834 genes up-regulated in Ewing's sarcoma compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 1.5. The "average" kidney cancer level was set to the 75<sup>th</sup> percentile amongst Ewing sarcomas. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 7.5<sup>th</sup> percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UniGeneID: UniGene number  
UniGene Title: UniGene gene title  
R1: Ratio of Ewing sarcoma to normal tissue

Pkey	ExAccn	UniGeneID	UniGene Title	R1
101447	M21305		gb:Human alpha satellite and satellite 3	38.4
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	34.2
110278	AF061573	Hs.19492	protocadherin 8	32.2
121362	AF050147	Hs.97932	chondromodulin I precursor	30.3
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	26.3

	121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	24.4
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	23.4
	104659	AW969769	Hs.105201	ESTs	20.2
5	106533	AL134708	Hs.145998	ESTs	16.9
	124006	AI147155	Hs.270016	ESTs	15.0
	110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	14.8
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	14.6
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	14.5
10	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	13.7
	121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	12.3
	129526	S69681	Hs.177582	surfactant, pulmonary-associated protein	12.1
	119791	AA554907	Hs.58291	ESTs	11.7
	116301	AW969706	Hs.293332	ESTs	11.2
15	123308	C14187	Hs.103538	ESTs	10.9
	127742	AW293496	Hs.180138	ESTs	10.8
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	10.7
	127489	AA650250	Hs.272076	ESTs	10.6
	115909	AW872527	Hs.58761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.6
20	101063	D54745	Hs.80247	cholecystokinin	10.6
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	10.5
	100299	D49493	Hs.2171	growth differentiation factor 10	10.1
	127987	AI022103	Hs.124511	ESTs	10.1
	131313	R96290	Hs.336629	ribosomal protein L44	9.2
25	126799	AW753865	Hs.74376	olfactomedin related ER localized protei	8.5
	125847	AW161885	Hs.249034	ESTs	7.0
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	6.9
	114837	BE244930	Hs.166895	ESTs	6.6
	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	6.6
30	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.5
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous r	6.5
	125186	AA610620	Hs.181244	major histocompatibility complex, class	6.4
	118644	AA443241	Hs.336629	ribosomal protein L44	6.3
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	6.3
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	6.1
	113003	AW292315	Hs.7215	ESTs	5.8
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.7
	101050	AU077324	Hs.1832	neuropeptide Y	5.7
	116790	AW161357	Hs.101174	microtubule-associated protein tau	5.5
40	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	5.1
	132315	AF091086	Hs.44563	hypothetical protein	5.0
	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	4.9
	126077	M78772	Hs.210836	ESTs	4.7
	126426	AA125984		gb:zn27h06.r1 Stralagene neuroepithelium	4.6
45	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	4.5
	123619	AA602964		gb:no97c02.s1 NCL_CGAP_Pr2 Homo sapiens	4.4
	128361	AW172570	Hs.130246	ESTs	4.3
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	4.3
	100020				4.2
50	125556	AB033064	Hs.334806	KIAA1238 protein	4.2
	105316	AI671245	Hs.24835	hypothetical protein FLJ14594	4.0
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.0
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	3.9
	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	3.9
55	129012	R81936	Hs.336629	ribosomal protein L44	3.9
	125447	AI582222	Hs.128686	ESTs	3.8
	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	3.6
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	3.6
	128391	AW188326	Hs.170652	ESTs	3.5
60	123829	AF251237	Hs.112208	XAGE-1 protein	3.4
	123949	AA621665	Hs.208957	EST	3.4
	126872	AW450979		gb:U1-H-BI3-ala-a-12-0-UI.s1 NCL_CGAP_Su	3.4
	101266	L36645	Hs.73964	EphA4	3.3
	121309	AA293834	Hs.97312	ESTs	3.3
65	130637	AA356764	Hs.17109	integral membrane protein 2A	3.2
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	3.2
	135175	M91463	Hs.95958	solute carrier family 2 (facilitated glu	3.2
	107599	AW664072	Hs.60136	ESTs	3.2
	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.2
70	131688	AI935413	Hs.30692	p21 (CDKN1A)-activated kinase 2	3.1
	120147	AI917116	Hs.155376	hemoglobin, beta	3.1
	110343	AW136703	Hs.17268	ESTs	3.1
	127664	AA806164	Hs.116502	ESTs	3.0
	103076	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	3.0
75	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	3.0
	125558	R59305		gb:yh16c10.r1 Soares infant brain 1NIB H	3.0
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.9
	133421	AF134160	Hs.7327	claudin 1	2.8
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.8
80	113577	AI300699	Hs.278937	PRO0470 protein	2.8
	118397	BE139479	Hs.161492	ESTs	2.8
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	2.8
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	2.8
	127262	AA828125		gb:od71a09.s1 NCL_CGAP_Ov2 Homo sapiens	2.8

	106472	AI207162	Hs.3815	stathmin-like-protein RB3	2.7
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	2.7
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	2.7
5	126600	AA699949	Hs.191385	ESTs	2.7
	120325	AA195651	Hs.104106	ESTs	2.7
	127256	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN	2.7
	117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	2.7
	126735	M69113	Hs.226795	glutathione S-transferase pi	2.7
10	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	2.7
	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (	2.6
	129706	AA443241	Hs.336629	ribosomal protein L44	2.6
	107731	AA016086	Hs.272106	ESTs, Weakly similar to I38022 hypotheti	2.6
	128283	AI076570	Hs.134053	ESTs	2.6
15	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	2.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
	105577	AW852257	Hs.171391	C-terminal binding protein 2	2.6
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	2.6
	130262	D63216	Hs.153684	frizzled-related protein	2.6
20	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.6
	102479	NM_001991	Hs.194669	enhancer of zeste (Drosophila) homolog 1	2.6
	128531	H03721	Hs.2953	ribosomal protein S15a	2.6
	126165	AI741816	Hs.125897	ESTs	2.6
	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	2.5
25	118967	AI668670	Hs.216756	ESTs	2.5
	120830	AI568170	Hs.96886	ESTs	2.5
	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.5
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	2.5
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	2.5
30	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	2.5
	133761	AF041430	Hs.75922	brain protein I3	2.5
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.5
	126693	C05723		gb:C05723 Human pancreatic islet Homo sa	2.5
35	126021	AA775894	Hs.187516	ESTs	2.5
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	2.5
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	2.5
	125743	H17151		gb:ym37a05.r1 Soares infant brain 1NIB H	2.5
	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	2.5
40	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	2.4
	123110	AA486256	Hs.193510	EST	2.4
	113283	T66813	Hs.12947	EST	2.4
	107711	W96141	Hs.220687	ESTs	2.4
	128992	H04150	Hs.107708	ESTs	2.4
	106111	AW875398	Hs.6451	PRO0659 protein	2.4
45	129948	AI537162	Hs.263988	ESTs	2.4
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	2.4
	116728	F13687	Hs.227976	EST	2.4
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	2.4
	124971	T23800	Hs.151001	hypothetical protein FLJ14728	2.4
50	131019	W28614	Hs.306155	chorionic somatomammotropin hormone 1 (p	2.4
	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory s	2.4
	111795	AI435437	Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCL	2.4
	119127	AA708035	Hs.12248	ESTs	2.4
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	2.4
55	111898	R38944	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.4
	131916	AA025976	Hs.34569	ESTs	2.4
	130850	AB040922	Hs.20237	DKFZP566C134 protein	2.4
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	2.4
	126722	N66148	Hs.11125	HSPC033 protein	2.4
60	123720	AA609734	Hs.112755	EST	2.4
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovir	2.4
	131136	AB033099	Hs.23413	KIAA1273 protein	2.4
	129001	AA443323	Hs.107812	BPOZ protein	2.4
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	2.4
65	107593	AI093688	Hs.60051	ESTs	2.4
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	2.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	2.4
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	2.4
	128367	AW611791	Hs.150742	ESTs	2.4
70	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	2.4
	112342	AW410273	Hs.92614	longevity assurance (LAG1, S. cerevisiae	2.3
	114721	D61939	Hs.103822	ESTs	2.3
	127768	AW085002	Hs.156187	ESTs	2.3
	127706	AI174238	Hs.186982	ESTs	2.3
75	126029	AA704253	Hs.169359	ESTs	2.3
	124250	AA350256	Hs.323875	EST, Weakly similar to 2109260A B cell	2.3
	117265	AA451966	Hs.43005	RAB9-like protein	2.3
	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	2.3
	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	2.3
80	127252	AI049545	Hs.94	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
	129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	2.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.3
	109252	BE440157	Hs.85944	ESTs	2.3
	127889	AI147408	Hs.144941	ESTs	2.3



	121292	AA401807		gb:zv65f11.s1 Soares_total_fetus_Nb2HFB_	2.3
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte sec	2.3
	132985	AL045579	Hs.62113	KIAA0717 protein	2.3
5	125174	W51835	Hs.231082	EST	2.3
	125401	AI204637	Hs.337585	ESTs, Highly similar to KIAA0350 [H.sapi	2.3
	135278	AA399542	Hs.229671	EST, Moderately similar to PEPTIDYL-PROL	2.3
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN	2.3
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	2.3
10	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	2.3
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	2.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC	2.3
	101086	AA382524	Hs.250959	histatin 1	2.3
	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	2.3
	126879	D90391	Hs.1265	branched chain keto acid dehydrogenase E	2.3
15	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	2.3
	124691	R05835	Hs.110153	ESTs	2.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	2.3
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	2.2
20	129052	BE275031	Hs.158210	hypothetical protein MGC2555	2.2
	129248	W04606	Hs.171637	hypothetical protein MGC2628	2.2
	100780	BE561958	Hs.302063	immunoglobulin heavy constant mu	2.2
	135416	BE281018	Hs.99969	fusion, derived from t(12;16) malignant	2.2
	129928	AI338993	Hs.134535	ESTs	2.2
25	103319	X83492	Hs.82359	tumor necrosis factor receptor superfam	2.2
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	2.2
	120734	AA299948		gb:EST12544 Uterus tumor I Homo sapiens	2.2
	111777	AK001100	Hs.41690	desmocollin 3	2.2
	128963	J03890	Hs.1074	surfactant, pulmonary-associated protein	2.2
30	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	2.2
	134964	AI803516	Hs.272891	hippocalcin-like protein 4	2.2
	127248	AA364195		gb:EST75015 Pineal gland II Homo sapiens	2.2
	125761	R68351		gb:yh99b03.r1 Soares placenta Nb2HP Homo	2.2
	101358	M10058	Hs.12056	asialoglycoprotein receptor 1	2.2
35	101613	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.2
	107121	AB015427	Hs.250493	zinc finger protein 219	2.2
	118751	N74210	Hs.50454	ESTs	2.2
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	2.2
	126581	W73306	Hs.306668	Homo sapiens cDNA FLJ14089 fis, clone MA	2.2
40	127634	AA633469	Hs.193283	ESTs, Weakly similar to unnamed protein	2.2
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	2.2
	132867	AF226667	Hs.58553	CTP synthase II	2.2
	126323	N77584	Hs.68644	Homo sapiens microsomal signal peptidase	2.2
	111790	AW769683	Hs.6734	ESTs, Weakly similar to S26650 DNA-bind	2.2
45	125549	R20215		gb:ygl8b09.r1 Soares infant brain 1N1B H	2.2
	128059	AA972446	Hs.145096	ESTs	2.2
	132342	AW162758	Hs.45232	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.2
	125722	H29796	Hs.269622	ESTs	2.2
	106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	2.2
50	127644	N88858	Hs.155101	ATP synthase, H+ transporting, mitochond	2.2
	128179	AW293689	Hs.127116	ESTs	2.2
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	2.2
	126962	R12014	Hs.20976	ESTs	2.2
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	2.2
55	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	2.2
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypothet	2.2
	108743	AI580150	Hs.71074	ESTs	2.2
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	2.2
	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	2.2
60	109929	AA773187	Hs.294027	ESTs	2.2
	129059	AW069534	Hs.279583	CGI-81 protein	2.2
	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	2.2
	116962	H79677		gb:yu76g10.s1 Soares fetal liver spleen	2.2
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	2.2
65	106711	BE390125	Hs.143187	hypothetical protein	2.2
	135191	X16866	Hs.301086	cytochrome P450, subfamily IID (debrisoq	2.2
	125822	H03162	Hs.268768	ESTs	2.2
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	2.2
	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	2.2
70	126250	AL050391	Hs.321247	Homo sapiens mRNA; cDNA DKFZp586A181 (fr	2.2
	103392	X94563		gb:H.sapiens dbi/acbp gene exon 1 & 2.	2.2
	129794	AF161399	Hs.23259	hypothetical protein FLJ13433	2.2
	100253	D38024	Hs.157425	double homeobox, 2	2.2
	130743	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.2
75	125466	R08234	Hs.180461	ESTs	2.2
	122682	AA984531	Hs.159293	ESTs	2.2
	133347	BE257758	Hs.71475	acid cluster protein 33	2.2
	104455	AL110261	Hs.157211	DKFZP586B0621 protein	2.2
	116332	AA491208	Hs.62620	chromosome 6 open reading frame 1	2.2
80	131163	AA099524	Hs.23754	ESTs	2.2
	109592	AI198059	Hs.26370	ESTs	2.2
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.1
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	2.1
	128434	AI190914	Hs.143880	ESTs	2.1

	103163	AU077018	Hs.3235	keratin 4	2.1
	112379	AK001713	Hs.17860	hypothetical protein FLJ10851	2.1
	127507	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	2.1
5	133097	W03512	Hs.6479	hypothetical protein MGC13272	2.1
	126153	H85692	Hs.40730	ESTs	2.1
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	2.1
	100554	M95923		gb:Human 12-lipoxygenase mRNA, partial c	2.1
	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	2.1
10	132664	AI740461	Hs.54542	ESTs	2.1
	114620	AA642974		gb:nr60h01.s1 NCL_CGAP_Lym3 Homo sapiens	2.1
	115348	AA281562	Hs.292100	ESTs	2.1
	133231	AK000517	Hs.6844	hypothetical protein FLJ20510	2.1
	133160	N54968	Hs.66309	hypothetical protein MGC11061	2.1
15	124656	AW297702	Hs.102915	ESTs	2.1
	133576	M19650	Hs.150741	2',3'-cyclic nucleotide 3' phosphodiester	2.1
	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypothet	2.1
	126505	AA282881	Hs.190057	ESTs	2.1
	118865	AA736405	Hs.54530	ESTs	2.1
20	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	2.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	2.1
	133493	AW998046	Hs.194369	arginine-glutamic acid dipeptide (RE) re	2.1
	112853	T02843		gb:FB11H5 Fetal brain, Stratagene Homo s	2.1
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU	2.1
25	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	2.1
	134869	AL157518	Hs.90421	PRO2463 protein	2.1
	128869	AA768242	Hs.80618	hypothetical protein	2.1
	129179	AW969025	Hs.109154	ESTs	2.1
30	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	2.1
	101651	AL037111	Hs.75641	galactose-1-phosphate uridylyltransferas	2.1
	129726	H15474	Hs.132898	fatty acid desaturase 1	2.1
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	126271	AI250773	Hs.270012	ESTs	2.1
	116925	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-ce	2.1
35	128468	T23625	Hs.150580	putative translation initiation factor	2.1
	116031	AA452239	Hs.103329	KIAA0970 protein	2.1
	130724	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	2.1
	121897	AA427419	Hs.229162	EST, Weakly similar to ZN91_HUMAN ZINC	2.1
	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	2.1
40	122333	AA625872	Hs.98977	ESTs, Moderately similar to T34561 hypot	2.1
	127841	AW136558	Hs.125246	ESTs	2.1
	100023				2.1
	113002	BE243513	Hs.7212	hypothetical protein PP1044	2.1
	111567	F12628	Hs.334786	hypothetical protein MGC16040	2.1
45	113697	T97183	Hs.17992	Homo sapiens mRNA; cDNA DKFZp434J1726 (f	2.1
	128033	AI248705	Hs.149321	ESTs	2.1
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	2.1
	112370	AF052095	Hs.167344	Homo sapiens clone 23911 mRNA sequence	2.1
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	2.1
50	113226	AI821008	Hs.10697	ESTs	2.1
	117997	N52090	Hs.47420	EST	2.1
	116996	H83935	Hs.40535	ESTs	2.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	2.1
	122591	AI188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	2.1
55	107279	S57296	Hs.323910	v-erb-b2 avian erythroblastic leukemia	2.1
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	2.1
	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	2.1
	127447	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	2.1
	128352	AW137413	Hs.169942	ESTs	2.1
60	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.0
	128275	AI218235	Hs.131240	ESTs	2.0
	125976	AA436760		gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_	2.0
	120820	AA347417	Hs.96869	EST	2.0
	134937	AI251449	Hs.171939	ESTs	2.0
65	129602	AI282193	Hs.198298	v-src avian sarcoma (Schmidt-Ruppin A-2)	2.0
	129535	AA397972	Hs.169965	chimerin (chimaerin) 1	2.0
	106095	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.0
	128538	R44214	Hs.101189	ESTs	2.0
	105593	AA279341	Hs.174151	aldehyde oxidase 1	2.0
70	105788	AB009698	Hs.23965	solute carrier family 22 (organic anion	2.0
	128148	AA918175	Hs.126637	ESTs	2.0
	125982	R98091		gb:yr30e11.r1 Soares fetal liver spleen	2.0
	125746	AL137506	Hs.274256	hypothetical protein FLJ23563	2.0
	127835	AA748762	Hs.163113	ESTs, Weakly similar to I38022 hypotheti	2.0
75	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	2.0
	124282	AA018408	Hs.110287	ESTs	2.0
	126926	AA179472	Hs.832	ESTs, Highly similar to A41029 integrin	2.0
	100221	D28383		gb:Human mRNA for ATP synthase B chain,	2.0
	126053	H64450		gb:yu62d01.r1 Weizmann Olfactory Epithel	2.0
80	100944	L07518	Hs.159593	mucin 6, gastric	2.0
	125581	AI272848	Hs.75309	eukaryotic translation elongation factor	2.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.0
	114612	AI124557	Hs.95456	ESTs	2.0
	130453	U80735	Hs.173854	PAX transcription activation domain inte	2.0

	135060	AK001887	Hs.259842	protein kinase, AMP-activated, gamma 2 n	2.0
	114419	AI248013	Hs.106532	ESTs, Weakly similar to I38588 reverse t	2.0
	126283	N40359	Hs.271896	ESTs	2.0
5	112003	AW978731	Hs.301824	hypothetical protein PRO1331	2.0
	127391	AW380893	Hs.11039	hypothetical protein MGC2722	2.0
	127717	F12209	Hs.173380	CK2 interacting protein 1; HQ0024c prote	2.0
	126893	AJ252060	Hs.26320	TRABID protein	2.0
	106798	BE252749	Hs.20558	hypothetical protein FLJ20345	2.0
10	103760	AA642973	Hs.183842	ubiquitin B	2.0
	118922	AW206193	Hs.91065	hypothetical protein DKFZp761B2423	2.0
	133195	AI434760	Hs.279949	KIAA1007 protein	2.0
	133424	AA350994	Hs.20281	KIAA1700	2.0
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	2.0
15	132347	BE271016	Hs.169850	ESTs, Weakly similar to T21554 hypothe	2.0
	125599	H13295	Hs.106135	ESTs	2.0
	114459	AW445217	Hs.103362	ESTs	2.0
	128478	AA708205	Hs.100343	ESTs	2.0
	127271	H96820		gb:yy99b03.r1 Soares melanocyte 2NbHM Ho	2.0
20	111122	N63753	Hs.16492	DKFZP564G2022 protein	2.0
	130695	T97205	Hs.17998	ESTs, Weakly similar to 2109260A B cell	2.0
	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	2.0
	119244	AW407564	Hs.275865	ribosomal protein S18	2.0
	127603	AI016798	Hs.9925	hypothetical protein FLJ20772	2.0
25	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	2.0
	128115	AI435590	Hs.130168	ESTs	2.0
	117639	AA377165	Hs.44833	ESTs	2.0
	127033	AF169301	Hs.9098	sulfate transporter 1	2.0
	112411	R43090	Hs.271510	ESTs, Moderately similar to ALU1_HUMAN A	2.0
30	114601	AA075566		gb:zm88f06.s1 Stratagene ovarian cancer	2.0
	127573	AA594196	Hs.269464	ESTs, Weakly similar to S65657 alpha-1C-	2.0
	125500	AW952654	Hs.244624	ESTs	2.0
	119416	T97186		gb:ye50h09.s1 Soares fetal liver spleen	2.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	2.0
35	128902	AA036637	Hs.107052	ESTs	2.0
	127684	AA668631	Hs.32556	KIAA0379 protein	2.0
	126288	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	2.0
	122059	AA431737	Hs.98749	EST, Moderately similar to T42671 hypoth	2.0
	125486	AI023895	Hs.190587	ESTs	2.0
40	128895	AW467000	Hs.106985	ESTs	2.0
	105301	AW352357	Hs.7457	MAGE1 protein	2.0
	125536	F08266	Hs.77948	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	121387	AA405854		gb:zu66g08.s1 Soares_testis_NHT Homo sap	2.0
	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	2.0
45	126860	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.0
	102907	BE409861	Hs.202833	heme oxygenase (decycling) 1	2.0
	127804	AA740634	Hs.292084	ESTs	2.0
	130566	R85474	Hs.16073	ESTs	1.9
	113782	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	1.9
50	124119	AA040123	Hs.248953	solute carrier family 27 (fatty acid tra	1.9
	132490	NM_001290	Hs.4980	LIM domain binding 2	1.9
	125494	AU077029	Hs.177543	antigen identified by monoclonal antibod	1.9
	100237	D30715	Hs.306333	Human PAP (pancreatitis-associated prot	1.9
	127687	AW772383	Hs.300635	ESTs	1.9
55	103136	AF087917	Hs.247936	olfactory receptor, family 1, subfamily	1.9
	125704	R55094	Hs.26239	Human DNA sequence from clone RP11-438B2	1.9
	126208	N22588	Hs.288548	Homo sapiens cDNA FLJ12368 fis, clone MA	1.9
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	1.9
	128660	AA011597	Hs.177398	ESTs	1.9
60	118049	N53145		gb:yy55f09.s1 Soares fetal liver spleen	1.9
	134624	AF035119	Hs.8700	deleted in liver cancer 1	1.9
	127432	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.9
	126414	AI363157	Hs.24756	hepatocyte growth factor-regulated tyros	1.9
	120861	AA350394	Hs.96952	ESTs	1.9
65	124669	AI571594	Hs.102943	hypothetical protein MGC12916	1.9
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	1.9
	103891	NM_007212	Hs.124186	ring finger protein 2	1.9
	128727	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.9
	126831	AI929107	Hs.79933	cyclin I	1.9
70	125360	AW898892	Hs.189741	ESTs	1.9
	124276	H83465		gb:ys91a11.s1 Soares retina N2b5HR Homo	1.9
	126524	Z45455	Hs.182447	heterogeneous nuclear ribonucleoprotein	1.9
	126647	AK000283	Hs.270502	hypothetical protein FLJ20276	1.9
	125957	H41694		gb:yo06b06.r1 Soares adult brain N2b5HB5	1.9
75	121782	AW452957	Hs.334698	Homo sapiens, clone MGC:15203, mRNA, com	1.9
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	1.9
	130945	U20582	Hs.2149	actin like protein	1.9
	126348	T16243	Hs.6473	Homo sapiens cDNA FLJ13992 fis, clone Y7	1.9
	103558	BE616547	Hs.2785	keratin 17	1.9
80	126982	AA211419		gb:zn55g05.s1 Stratagene muscle 937209 H	1.9
	125613	AA765957	Hs.21077	KIAA0532 protein	1.9
	129601	AB032964	Hs.115726	KIAA1138 protein	1.9
	126007	H51097	Hs.143261	ESTs	1.9
	123627	AA909619	Hs.112668	ESTs	1.9

	111587	AI125867	Hs.20734	ESTs	1.9
	135231	BE613615	Hs.74280	hypothetical protein FLJ22237	1.9
	128897	AW979134	Hs.10700	hypothetical protein	1.9
5	109891	H04757	Hs.323176	ESTs	1.9
	127704	AA679609		gb:ag72c02.s1 Gessler Wilms tumor Homo s	1.9
	129340	H75334	Hs.11050	F-box only protein 9	1.9
	126502	T10077	Hs.13453	hypothetical protein FLJ14753	1.9
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	1.9
10	127136	R36277	Hs.7773	Homo sapiens ubiquitin conjugating enzyme	1.9
	110636	H72868	Hs.19110	ESTs	1.9
	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	1.9
	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.9
	130829	BE262530	Hs.2006	glutathione S-transferase M3 (brain)	1.9
	125768	AI557486	Hs.119122	ribosomal protein L13a	1.9
15	123613	AA609158	Hs.291166	EST	1.9
	127506	T61039	Hs.252574	ribosomal protein L10a	1.9
	123546	AA608817	Hs.112597	EST	1.9
	126516	R95872	Hs.117572	chemokine binding protein 2	1.9
20	103973	AA305729	Hs.18272	amino acid transporter system A1	1.9
	127426	AA854756	Hs.124076	ESTs	1.9
	112339	R56570	Hs.50547	ESTs	1.9
	129101	NM_013403	Hs.108665	zinedin	1.9
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	1.9
25	118103	AA401733	Hs.184134	ESTs	1.9
	125752	AW136622	Hs.206673	ESTs	1.9
	102926	W28363	Hs.239752	nuclear receptor subfamily 2, group F, m	1.9
	133975	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.9
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.9
30	127329	AW160551	Hs.124021	soggy-1 gene	1.8
	126659	T16245		gb:NIB1005R Normalized infant brain, Ben	1.8
	127297	AW629485	Hs.140720	GSK-3 binding protein FRAT2	1.8
	127640	AI557486	Hs.119122	ribosomal protein L13a	1.8
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	1.8
35	127964	F06298		gb:HSC13F081 normalized infant brain cDN	1.8
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	1.8
	128193	AJ224442	Hs.155020	putative methyltransferase	1.8
	115173	BE612940	Hs.88252	ESTs	1.8
	125532	AJ734146	Hs.271800	ESTs, Weakly similar to alternatively sp	1.8
40	126541	AJ271671	Hs.7854	zinc/iron regulated transporter-like	1.8
	127309	AI669765	Hs.133184	ESTs	1.8
	129062	AA452970	Hs.155218	E1B-55kDa-associated protein 5	1.8
	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	1.8
	127775	AA128808	Hs.179902	transporter-like protein	1.8
45	126994	AA455265	Hs.86686	ESTs, Moderately similar to I54374 gene	1.8
	130734	AW137091	Hs.18624	KIAA1052 protein	1.8
	114461	AA531187	Hs.126705	ESTs	1.8
	100842	U05597		gb:Human anion exchanger 3 cardiac isofo	1.8
	127389	T65126	Hs.12743	carnitine O-octanoyltransferase	1.8
50	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	1.8
	107736	AA016239	Hs.60715	ESTs	1.8
	125669	R51308	Hs.333256	ESTs, Weakly similar to ALU8_HUMAN ALU	1.8
	100370	D79989	Hs.184884	KIAA0167 gene product	1.8
	113479	AI023133	Hs.10739	ESTs	1.8
55	105165	BE280787	Hs.16079	hypothetical protein FLJ10233	1.8
	120602	AA808018	Hs.109302	ESTs	1.8
	112399	R60920	Hs.296770	KIAA1719 protein	1.8
	123474	AA599209		gb:ag34b11.s1 Jia bone marrow stroma Hom	1.8
	134212	AA654353	Hs.17719	EBP50-PDZ interactor of 64 kD	1.8
60	104204	AK001691	Hs.57655	hypothetical protein FLJ10829	1.8
	127464	AW971875	Hs.292071	ESTs	1.8
	116715	AL117440	Hs.170263	tumor protein p53-binding protein, 1	1.8
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	1.8
	132380	AW373665	Hs.46853	ESTs	1.8
65	120087	AF186780	Hs.79219	RalGDS-like gene; KIAA0959 protein	1.8
	116356	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	1.8
	125499	H10543		gb:ym04c06.r1 Soares infant brain 1NIB H	1.8
	128846	AA730767	Hs.285753	SCG10-like-protein	1.8
	123869	AA620924	Hs.112923	EST	1.8
70	108889	AA135722	Hs.61481	ESTs	1.8
	126528	Z24895		gb:HSB67F122 STRATAGENE Human skeletal m	1.8
	127629	AA293279	Hs.29173	hypothetical protein FLJ20515	1.8
	130004	AA703684	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN A	1.8
	130847	AI672483	Hs.20220	lipase protein	1.8
75	111620	R14853	Hs.307478	EST, Weakly similar to I39058 hypotheti	1.8
	131971	BE567100	Hs.154938	hypothetical protein MDS025	1.8
	121360	AA405635	Hs.96854	ESTs, Weakly similar to DYLLX_HUMAN CYTOP	1.8
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	1.8
	124687	AA833902	Hs.270745	ESTs	1.8
80	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	1.8
	126730	AA442429		gb:zv70g02.r1 Soares_totai_fetus_Nb2HF8_	1.8
	127916	AI239950	Hs.294111	ESTs, Moderately similar to B34087 hypo	1.8
	128408	AI183407	Hs.143704	EST	1.8
	128440	AW090340	Hs.14337	Homo sapiens cDNA FLJ14407 fis, clone HE	1.8

	123783	AA610112		gb:af19g05.s1 Soares_tetal_fetus_Nb2HF8_	1.8
	109152	AW380723	Hs.73451	ESTs, Weakly similar to S55024 nebulin,	1.8
	107242	AB020672	Hs.175411	KIAA0865 protein	1.8
5	132804	AI805943	Hs.326067	hypothetical protein MGC5178	1.8
	125387	AJ243669	Hs.8127	KIAA0144 gene product	1.8
	121578	AA398791	Hs.178185	ESTs	1.8
	132944	T96641	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	1.8
	126295	AI281459	Hs.270114	ESTs	1.8
10	133335	BE251012	Hs.263812	nuclear distribution gene C (A.nidulans)	1.8
	129879	AK001696	Hs.13109	Ran binding protein 11	1.7
	125175	W52355	Hs.303030	EST	1.7
	126919	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	1.7
	127773	AA725863	Hs.120508	ESTs	1.7
15	126495	AB029021	Hs.137732	KIAA1098 protein	1.7
	126948	AW968535	Hs.14328	hypothetical protein FLJ20071	1.7
	126671	C03105	Hs.285847	CGI-19 protein	1.7
	115428	AA284112	Hs.94680	ESTs, Weakly similar to I78885 serine/t	1.7
	128232	AI830319	Hs.334641	hypothetical protein DKFZp43411916	1.7
20	126082	H81188	Hs.269571	ESTs	1.7
	120467	AW292562	Hs.187628	ESTs	1.7
	124041	AW590171	Hs.101413	ESTs	1.7
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	1.7
	123951	AB012922	Hs.173043	metastasis-associated 1-like 1	1.7
25	126449	AF223944	Hs.325443	breast cell glutaminase	1.7
	124554	N65961		gb:za27d03.s1 Soares fetal liver spleen	1.7
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2	1.7
	126780	R12421	Hs.5811	chromosome 21 open reading frame 59	1.7
	125661	AA491830	Hs.25689	ESTs	1.7
30	125888	H18298		gb:yn48b09.r1 Soares adult brain N2b5HB5	1.7
	127245	AA323958		gb:EST26810 Cerebellum II Homo sapiens c	1.7
	111223	AA852773	Hs.334838	KIAA1866 protein	1.7
	115611	R44789	Hs.33191	Homo sapiens, Similar to transmembrane r	1.7
	124846	R59977	Hs.158196	transcriptional adaptor 3 (ADA3, yeast	1.7
	100397	D84424	Hs.57697	hyaluronan synthase 1	1.7
35	127180	T27097	Hs.22790	ESTs	1.7
	102598	BE250742	Hs.106673	eukaryotic translation initiation factor	1.7
	134076	AF086215		gb:Homo sapiens full length insert cDNA	1.7
	115659	W99382	Hs.283709	lipopolysaccharide specific response-7 p	1.7
40	125555	R19382	Hs.117869	ESTs	1.7
	128382	AI138886	Hs.143243	ESTs	1.7
	127710	AA682867	Hs.191901	ESTs	1.7
	125445	AI452722	Hs.7709	WW domain binding protein 1	1.7
	129951	AL110282	Hs.268024	Homo sapiens, clone IMAGE:3873720, mRNA	1.7
45	119898	R93325	Hs.58690	ESTs	1.7
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	1.7
	133531	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.7
	119726	AF086289	Hs.234766	skin-specific protein	1.7
	125198	W69474	Hs.323140	ESTs	1.7
50	121414	AW291477	Hs.188763	testis expressed sequence 13A	1.7
	112542	AI458867	Hs.24276	ESTs	1.7
	101368	M13058	Hs.73952	proline-rich protein HaeIII subfamily 2	1.7
	125820	AA730136	Hs.75561	teratocarcinoma-derived growth factor 1	1.7
	129091	AA056483	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	1.7
55	132609	U20165	Hs.53250	bone morphogenetic protein receptor, typ	1.7
	119447	W31714	Hs.122656	ESTs, Highly similar to formin 2-like pr	1.7
	113675	T81034	Hs.14841	ESTs	1.7
	113701	T97301	Hs.18026	ESTs	1.7
	116180	AA463902	Hs.13522	ESTs, Weakly similar to I38022 hypothet	1.7
60	127133	AA280740	Hs.292072	ESTs, Moderately similar to A46010 X-lin	1.7
	113316	T70318	Hs.268581	ESTs	1.7
	123316	AI290561	Hs.155361	ESTs	1.7
	122638	AL137476	Hs.123609	Homo sapiens mRNA; cDNA DKFZp43410623 (f	1.7
	105053	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.7
65	103305	X82279		gb:H.sapiens Fas, Apo-1 gene (promoter a	1.7
	110384	H45282	Hs.268798	ESTs	1.7
	115626	AW630870	Hs.86674	ESTs, Weakly similar to hypothetical pro	1.7
	126905	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	1.7
	130820	AL353934	Hs.288798	hypothetical protein FLJ21012	1.7
70	112394	AK000373	Hs.8358	hypothetical protein FLJ20366	1.7
	129589	AW504292	Hs.11517	ESTs	1.7
	126446	NM_015670	Hs.118926	sentrin/SUMO-specific protease 3	1.7
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3	1.7
	120287	AF219946	Hs.102237	tubby super-family protein	1.7
75	129991	R28386	Hs.179925	ESTs, Weakly similar to ALU8_HUMAN ALU	1.7
	123912	AA621283	Hs.332855	EST	1.7
	102071	AL120051	Hs.144700	ephrin-B1	1.7
	121046	AB033083	Hs.97377	KIAA1257 protein	1.7
	128403	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	1.7
80	104268	AL043864	Hs.70604	ATPase, Class II, type 9A	1.7
	111598	R11505	Hs.268912	ESTs	1.7
	128109	AW269421	Hs.128093	ESTs	1.7
	125435	R08480	Hs.272138	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.7
	133104	AI091195	Hs.65029	growth arrest-specific 1	1.7

	126826	AA099764		gb:zn61f12.r1 Stratagene muscle 937209 H	1.7
	106483	NM_006548	Hs.30299	IGF-II mRNA-binding protein 2	1.7
	129765	M86933	Hs.1238	amelogenin (Y chromosome)	1.7
5	115904	AI167560	Hs.61297	ESTs	1.7
	125514	AB040912	Hs.191098	hypothetical protein FLJ11598	1.7
	125797	H03117	Hs.111497	similar to mouse neuronal protein 15.6	1.7
	133179	U81599	Hs.66731	homeo box B13	1.7
	115167	AA749209	Hs.43728	hypothetical protein	1.7
10	118036	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.7
	124540	N63232		gb:yz39a12.s1 Morton Fetal Cochlea Homo	1.7
	126183	BE018708	Hs.81972	SHC (Src homology 2 domain-containing) t	1.7
	127897	AA773681		gb:af77b12.r1 Soares_NhHMPu_S1 Homo sapi	1.7
	126680	F07097	Hs.133865	transmembrane 6 superfamily member 1	1.7
15	126972	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	1.7
	130605	BE514362	Hs.306024	FK506-binding protein 3 (25kD)	1.7
	127541	AA573449	Hs.171515	ESTs	1.7
	127392	AI816736	Hs.14896	DHHC1 protein	1.7
	106879	AI190785	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA,	1.7
20	128303	AI096444	Hs.7187	hypothetical protein FLJ10707	1.7
	126469	BE384361	Hs.182885	ESTs, Weakly similar to JC5024 UDP-galac	1.7
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	1.7
	132332	AW978906	Hs.45005	hypothetical protein FLJ12960	1.6
	127142	AW452942	Hs.130393	ESTs	1.6
25	128416	F13165	Hs.12549	ESTs, Weakly similar to 2109260A B cell	1.6
	103790	AL122044	Hs.331633	hypothetical protein DKFZp566N034	1.6
	134578	AL110193	Hs.224137	hypothetical protein	1.6
	110023	AW294701	Hs.31040	ESTs	1.6
	125511	AJ271379	Hs.76194	ribosomal protein S5	1.6
30	111483	R06569	Hs.269534	ESTs	1.6
	127363	AF064104	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	1.6
	126231	AA991766	Hs.300793	ESTs	1.6
	106181	AI803651	Hs.191608	ESTs	1.6
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	1.6
35	119929	W86464	Hs.304825	ESTs	1.6
	132542	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f	1.6
	127155	AA284993		gb:zt23e10.r1 Soares ovary tumor NbHOT H	1.6
	125956	AK000214	Hs.129014	hypothetical protein FLJ20207	1.6
	126854	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.6
40	131330	D13969	Hs.184669	zinc finger protein 144 (Mel-18)	1.6
	129445	W52452	Hs.29797	ribosomal protein L10	1.6
	113427	T85105	Hs.15471	ESTs	1.6
	106124	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	1.6
45	128135	AA954381	Hs.269721	ESTs, Moderately similar to ALU1_HUMAN	1.6
	111460	R02728	Hs.117331	ESTs	1.6
	125636	H12382	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	1.6
	134118	BE336680	Hs.182877	KIAA0116 protein	1.6
	111570	AF059203	Hs.20580	sterol O-acyltransferase 2	1.6
	113511	T89578	Hs.189740	ESTs	1.6
50	113296	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	1.6
	109875	H03260	Hs.30385	ESTs	1.6
	105930	AF016371	Hs.9880	peptidyl prolyl isomerase H (cyclophilin	1.6
	105564	BE616694	Hs.288042	hypothetical protein FLJ14299	1.6
	128063	AI377750	Hs.167177	ESTs	1.6
55	109779	AB029396	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur	1.6
	125334	T86569	Hs.182118	ESTs	1.6
	127206	AW816490	Hs.337508	ESTs	1.6
	108845	AW362901	Hs.68864	ESTs, Weakly similar to phosphatidylseri	1.6
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.6
60	114062	AI560984	Hs.27283	ESTs	1.6
	122550	AA451859	Hs.99253	ESTs	1.6
	113413	R08872	Hs.186512	ESTs	1.6
	127019	AI929355	Hs.286128	hypothetical protein FLJ23329	1.6
	106251	R12607	Hs.35101	proline-rich Gla (G-carboxyglutamic acid	1.6
65	112670	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	1.6
	114913	AI435199	Hs.58940	ESTs, Weakly similar to I38022 hypotheti	1.6
	126604	AI023299	Hs.269806	ESTs	1.6
	125324	R07785		gb:yf15c06.r1 Soares fetal liver spleen	1.6
	121438	AW445024	Hs.139389	ESTs	1.6
70	127289	AI041014	Hs.220752	ESTs, Weakly similar to unnamed protein	1.6
	126935	AI198535	Hs.89463	potassium large conductance calcium-acti	1.6
	132430	AW973652	Hs.283105	ESTs	1.6
	133541	H75334	Hs.11050	F-box only protein 9	1.6
	102612	U65402	Hs.248124	G protein-coupled receptor 31	1.6
75	120228	AI192528	Hs.164537	ESTs	1.6
	122652	AA454641		gb:zx99d05.s1 Soares_NhHMPu_S1 Homo sapi	1.6
	103456	AA496425	Hs.9629	papillary renal cell carcinoma (transloc	1.6
	105355	AL031447	Hs.26938	Homo sapiens, clone IMAGE:4053044, mRNA,	1.6
	108043	AA042873	Hs.160412	ESTs	1.6
80	128695	NM_003478	Hs.101299	cullin 5	1.6
	127984	AA846377	Hs.193706	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.6
	124405	AA228137	Hs.25005	hypothetical protein MGC3329	1.6
	103934	BE278111	Hs.134200	DKFZP564C186 protein	1.6
	124195	H83034		gb:yq48e07.r1 Soares fetal liver spleen	1.6

	110938	N48982	Hs.38034	Homo sapiens cDNA FLJ12924 fis, clone NT	1.6
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.6
	121226	AA364109	Hs.177990	ESTs	1.6
5	120415	AA235810		gb:zs41a03.s1 Soares_NhHMPu_S1 Homo sapi	1.6
	123864	AA620882		gb:at95g01.s1 Soares_testis_NHT Homo sap	1.6
	125045	AI114630	Hs.208334	Homo sapiens cDNA: FLJ21874 fis, clone H	1.6
	133425	AA444390	Hs.155482	hydroxyacyl glutathione hydrolase	1.6
	126578	AF151861	Hs.107528	androgen induced protein	1.6
10	102406	U43177		(NONE)	1.6
	114126	BE566962	Hs.7063	Homo sapiens cDNA: FLJ20913 fis, clone A	1.6
	125233	W85713	Hs.110092	ESTs	1.6
	109635	F04296	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.6
	125675	BE294972	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	1.6
15	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	1.6
	127569	AI765107	Hs.274422	hypothetical protein FLJ20550	1.6
	113302	T66919	Hs.268575	ESTs	1.6
	119705	AI984203	Hs.57874	ESTs	1.6
	127226	AL036559	Hs.3463	ribosomal protein S23	1.6
20	123489	AA599708		gb:ag11a10.s1 Gessler Wilms tumor Homo s	1.6
	107468	AA740979	Hs.91389	ESTs	1.6
	115916	AI052731	Hs.91910	ESTs	1.6
	127815	AA743490	Hs.255015	ESTs	1.6
	100364	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.6
25	125568	AW615396	Hs.105613	ESTs	1.6
	105260	N81201	Hs.31755	ESTs	1.6
	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	1.6
	111275	N70970	Hs.35006	ESTs	1.6
	106542	AA339541	Hs.24956	hypothetical protein FLJ22056	1.6
30	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.6
	124770	AA984414	Hs.120429	ESTs	1.6
	117936	AI382904	Hs.47213	ESTs	1.6
	134385	M14660	Hs.169274	ESTs, Highly similar to IFT2_HUMAN INTER	1.6
	108367	AW410478	Hs.104019	transforming, acidic coiled-coil contain	1.6
35	131143	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	1.6
	105441	N28522	Hs.8935	quinolinate phosphoribosyltransferase (n	1.6
	128215	AA973310		gb:op91e06.s1 Soares_NFL_T_GBC_S1 Homo s	1.6
	127344	AI003929	Hs.80624	hypothetical protein MGC2560	1.6
	126478	BE541249	Hs.109697	ESTs	1.6
40	122053	AI637498	Hs.98745	ESTs	1.5
	111760	BE551929	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE	1.5
	112401	R61279	Hs.237536	ESTs, Weakly similar to AF151067 1 HSPC2	1.5
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	1.5
	125575	H14983		gb:ym19h09.r1 Soares infant brain 1NIB H	1.5
45	128765	AF073310	Hs.143648	insulin receptor substrate 2	1.5
	108935	AA147848	Hs.67991	hypothetical protein DKFZp434G0522	1.5
	121221	AI140708	Hs.97461	ESTs	1.5
	120091	AW024672	Hs.59558	EST	1.5
	107375	BE011845	Hs.251064	high-mobility group (nonhistone chromoso	1.5
50	125803	AW876115	Hs.29852	ESTs	1.5
	115132	AA811762	Hs.71433	ESTs	1.5
	113346	AF143876	Hs.14318	Homo sapiens clone IMAGE:113399 mRNA seq	1.5
	107357	U63973	Hs.103501	rhodopsin kinase	1.5
	125443	BE251057	Hs.177592	ribosomal protein, large, P1	1.5
55	133803	M24461	Hs.76305	surfactant, pulmonary-associated protein	1.5
	113378	T80738	Hs.14757	ESTs	1.5
	105540	BE391690	Hs.9265	hypothetical protein FLJ20917	1.5
	127446	F13008		gb:HSC3HE011 normalized infant brain cDN	1.5
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	1.5
60	127585	AA604144	Hs.190632	ESTs	1.5
	125824	Z45258	Hs.286013	short coiled-coil protein	1.5
	127606	AA621135	Hs.136552	ESTs	1.5
	125585	AW298113	Hs.92909	SON DNA binding protein	1.5
	107757	BE621721	Hs.280792	hypothetical protein FLJ12387 similar to	1.5
65	109978	H09356	Hs.22528	ESTs	1.5
	132297	BE272446	Hs.265317	hypothetical protein MGC2562	1.5
	115784	AW402151	Hs.54673	tumor necrosis factor (ligand) superfami	1.5
	127880	W39735	Hs.73818	ubiquinol-cytochrome c reductase hinge p	1.5
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	1.5
70	102868	X02419	Hs.77274	plasminogen activator, urokinase	1.5
	133457	J04948	Hs.333509	alkaline phosphatase, placental-like 2	1.5
	130339	AA435746		gb:zt79e03.s1 Soares_testis_NHT Homo sap	1.5
	125444	N28476	Hs.159161	Rho GDP dissociation inhibitor (GDI) alp	1.5
	123470	AW303285	Hs.303632	Human DNA sequence from clone RP11-110H4	1.5
75	100025				1.5
	127063	AI276526	Hs.331564	Homo sapiens mRNA; cDNA DKFZp434H1215 (f	1.5
	127945	AA815031	Hs.123598	ESTs	1.5
	111557	R09510	Hs.20373	EST	1.5
	116009	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	1.5
80	119858	W01370	Hs.46824	ESTs	1.5
	106509	AI042309	Hs.64552	hypothetical protein MGC15563	1.5
	124124	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clone HE	1.5
	126713	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypothi	1.5
	126475	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	1.5

	126851	R40611	Hs.137565	ESTs	1.5
	104820	AW162768	Hs.22620	ESTs	1.5
	127235	AI817309	Hs.225583	ESTs, Weakly similar to 2004399A chromos	1.5
5	126552	AF168711	Hs.159397	x 010 protein	1.5
	127523	AA617637		gb:np34h12.s1 NCI_CGAP_Lu1 Homo sapiens	1.5
	131692	BE559681	Hs.30736	KIAA0124 protein	1.5
	112974	AL353965	Hs.101174	microtubule-associated protein tau	1.5
	118921	N91914	Hs.54751	ESTs	1.5
10	100676	X02761	Hs.287820	fibronectin 1	1.5
	127721	T59578	Hs.188440	ESTs, Weakly similar to ALUF_HUMAN !!!!	1.5
	115254	AA279024	Hs.269316	ESTs, Weakly similar to S65657 alpha-1C	1.5
	128173	AI457242	Hs.127024	ESTs	1.5
	126846	AA663527	Hs.116910	ESTs	1.5
15	125294	R40025	Hs.106551	ESTs	1.5
	127494	AW978730	Hs.291956	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.5
	134191	W26632	Hs.7979	KIAA0736 gene product	1.5
	107394	AA864798	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	1.5
	131562	NM_003512	Hs.28777	H2A histone family, member L	1.5
20	127310	AW450671	Hs.189284	ESTs	1.5
	122359	AA523486		gb:ni67f11.s1 NCI_CGAP_Pr12 Homo sapiens	1.5
	100524	M80902	Hs.183704	ubiquitin C	1.5
	128422	T77794		gb:yd20d09.r1 Soares fetal liver spleen	1.5
	129902	AA076278	Hs.13277	hypothetical protein FLJ22054	1.5
25	126784	T81887	Hs.108854	HSPC163 protein	1.5
	123343	AI761902	Hs.99597	ESTs	1.5
	105458	AW954377	Hs.26412	ring finger protein 26	1.5
	112266	AI652534	Hs.25934	ESTs, Weakly similar to HSHU11 histone H	1.5
	127622	AA628222	Hs.97883	ESTs	1.5
30	113659	R06545	Hs.189781	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.5
	116892	AI573283	Hs.38458	ESTs	1.5
	126995	NM_014351	Hs.189810	sulforanferase family 4A, member 1	1.5
	111657	R07364	Hs.268667	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
	100243	AB028125	Hs.77854	regucalcin (senescence marker protein-30	1.5
35	116153	AF107203	Hs.57937	ataxin 2-binding protein 1	1.5
	108892	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	1.5
	113294	AI037922	Hs.11000	leptin receptor overlapping transcript-l	1.5
	126691	W03046	Hs.283664	aspartate beta-hydroxylase	1.5
	106979	AW015227	Hs.289053	hypothetical protein FLJ14733	1.5
40	125546	H09950		gb:ym01d12.r1 Soares infant brain 1NIB H	1.5
	113990	AI497945	Hs.83097	hypothetical protein FLJ22955	1.5
	129295	U63127	Hs.110121	SEC7 homolog	1.5
	125431	AW851639	Hs.75584	polymyositis/scleroderma autoantigen 2 (	1.5
	112558	AK001621	Hs.15921	hypothetical protein FLJ10759	1.5
45	122046	AI560456	Hs.107319	ESTs	1.5
	122472	AA448509	Hs.128652	ESTs	1.5
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	1.5
	131714	AA642831	Hs.31016	putative DNA binding protein	1.5
	101233	AL135173	Hs.878	sorbitol dehydrogenase	1.5
50	109501	AF047437	Hs.90436	sperm associated antigen 7	1.5
	126984	AA213820	Hs.256533	ESTs, Weakly similar to S11998 finger pr	1.5
	125765	BE243877	Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly	1.5
	127693	AA676727		gb:zj68b11.s1 Soares fetal_liver_spleen_	1.5
	128453	X02761	Hs.287820	fibronectin 1	1.5
55	119418	T97590	Hs.221711	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr	1.5
	116708	F10528	Hs.70001	ESTs, Moderately similar to JC6169 nucl	1.5
	122420	AA446971		gb:zw85f11.s1 Soares_total_fetus_Nb2HF8_	1.5
	100238	L24959	Hs.348	calcium/calmodulin-dependent protein kin	1.5
60	109710	D20044	Hs.12929	hypothetical protein FLJ20721	1.5
	105704	AI282341	Hs.75431	fibrinogen, gamma polypeptide	1.5
	112712	R91060	Hs.330761	ESTs	1.5
	100098	AF003743		gb:Homo sapiens delayed rectifier potass	1.5
	114122	R46128	Hs.12751	ESTs	1.5
65	132397	AA021160	Hs.4750	hypothetical protein DKFZp564K0822	1.5
	107881	AI568350	Hs.61273	hypothetical protein MGC2650	1.5
	106302	AA398859	Hs.18397	hypothetical protein FLJ23221	1.5
	125898	AK001823	Hs.92287	Homo sapiens mRNA; cDNA DKFZp564C2478 (f	1.5
	104957	AI359009	Hs.10026	mitochondrial ribosomal protein L17	1.5
70	102909	NM_005269	Hs.2693	glioma-associated oncogene homolog (zinc	1.5
	125559	BE297488	Hs.279877	cell division protein FtsJ	1.5
	109634	H17063	Hs.183646	ESTs	1.5
	116607	W05238	Hs.94316	ESTs, Weakly similar to T31613 hypotheti	1.5
	127175	R11937		gb:yf54b08.r1 Soares infant brain 1NIB H	1.5
75	110617	W93231	Hs.285901	Homo sapiens, clone IMAGE:3948563, mRNA,	1.5
	125988	W27648		gb:37e10 Human retina cDNA randomly prim	1.5
	115093	AI241932	Hs.3542	hypothetical protein FLJ11273	1.5
	121207	AA705799	Hs.183714	ESTs	1.5
80	112652	BE269699	Hs.235782	solute carrier family 21 (organic anion	1.5
	125213	AB014554	Hs.109299	protein tyrosine phosphatase, receptor t	1.5
	125912	AW867467	Hs.278712	eukaryotic translation initiation factor	1.5
	133046	R96881	Hs.63609	Hpal1 tiny fragments locus 9C	1.5
	122791	AL122055	Hs.129836	KIAA1028 protein	1.5



Table 26B

5	Pkey:		Unique Eos probeset identifier number
	CAT number:		Gene cluster number
10	Accession:		Genbank accession numbers
	Pkey	CAT number	Accession
10	108451	13766_27	AA079195 AA084955 AA126308 AA084956
	124195	2606_3	H83034 H52379
	123619	371681_1	AA602964 AA609200
	125165	1852047_1	W45350 W45406
	125324	1692163_1	R07785 T85948 T86972
15	126053	1601238_1	H64450 H64464
	126086	1606216_1	H75681 H70975
	126098	1629789_1	M79088 N88221
	125464	168460_1	N71807 AA203399
	125499	1562851_1	H10543 R11878
20	126127	1205826_1	N95428 W24040 AW751366 H81987
	125546	356478_1	H09950 R18413 AA570553 AW973425
	125549	1702179_1	R20215 R18767
	125558	1703083_1	R59305 R19748
	125575	1566885_1	H14983 R21554
25	125743	5025_5	H17151 H11956
	125761	1744008_1	R68351 R68364
	126426	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017
			AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
			AA284993 AA478122 AA477923
30	127175	1695805_1	R11937 Z45532
	126528	1276201_1	Z24895 AW891336 R01294
	125957	1583542_1	H41694 H45213
	125976	296453_1	AA436760 AW237453 BE327496 N47347 N56967
	125982	1766315_1	R98091 W92898
35	125988	1365728_1	W27648 R99193 BE090398
	127245	226662_1	AA323958 AA370268
	127248	227560_1	AA364195 AA325029 AW962050
	127262	231725_1	AA828125 AA834883 AA330555
	126659	1541209_1	T16245 R19694 F13545 H10299 T66048 T65279 H18006
40	126693	87363_1	C05723 AA018342
	127315	37938_1	AF116622 AI114507 AA640834 AA377999
	126730	297653_1	AA442429 T19477
	103898	187213_-3	AA248884
	127446	16001_2	F13008 T75435
45	126826	127356_1	AA099764 AA112950
	126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073, BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363
	128132	177108_1	AA225632 AI820970 AI820952 AA226472 AI732140 AI732059 AA226307
			AA225500
50	127523	351071_1	AA617637 AA554963
	126982	171753_1	AA211419 AA211566
	128215	530345_-1	AA973310
	127704	405690_1	AA679609 AA694592
	127705	966283_2	AJ003322 AJ003324
55	128422	1811283_1	T77794 T85681
	127897	446527_1	AA773681 AA773857
	120734	208882_1	AA299948 AA299949
	100098	25117_-13	AF003743
	114620	32062_8	AA642974 AA084223
60	122652		26401_-30 AA454641
	100842		tigr_HT4398 U05597
	123783		genbank_AA610112
	125032		genbank_T74884
	123808		genbank_AA620552
65	123864		genbank_AA620882
	118049		genbank_N53145
	102406		entrez_U43177
	116962		genbank_H79677
	134076	40321_1	AF086215 W02702 AA284288 W25655
70	125888	266863_1	H18298 H46830
	127271	321389_1	H96820 H79463
	113119		genbank_T47910 T47910
	104799		genbank_AA029703 AA029703
	127693	790317_1	AA676727 AA704704
75	120415		genbank_AA235810 AA235810
	127964	135151_1	F06298 R18057
	122359		681003_1 AA523486 AW026780 AI821660 AA443898
	122420		genbank_AA446971
	124276		genbank_H83465
80	101447		entrez_M21305
	124540		genbank_N63232
	124554		genbank_N65961
	117357		genbank_N24829
	103305		entrez_X82279

103392 entrez\_X94563  
 119416 genbank\_T97186  
 105225 genbank\_AA211777  
 121292 genbank\_AA401807  
 112853 genbank\_T02843  
 121387 genbank\_AA405854  
 114601 genbank\_AA075566  
 100221 entrez\_D28383  
 130339 genbank\_AA435746  
 100554 tigr\_HT2241  
 123423 genbank\_AA598484  
 123474 genbank\_AA599209  
 123489 genbank\_AA599708

TABLE 27A: ABOUT 895 GENES UP-REGULATED IN COMBINED LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 27A lists about 895 genes that are upregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with the normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90<sup>th</sup> percentile amongst fibrosis samples. The "average" normal adult tissue level was set to the 95<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15<sup>th</sup> percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of fibrosis to normal body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	56.0
424917	AI636208	Hs.96901	Homo sapiens cDNA: FLJ23049 fis, clone L	26.5
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	25.5
457200	U33749	Hs.197764	thyroid transcription factor 1	22.2
414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	21.1
429272	W25140	Hs.110667	ESTs	19.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	19.1
442006	AW975183	Hs.292663	ESTs	18.8
445885	AI734009	Hs.127699	KIAA1603 protein	18.0
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	17.8
422426	W79117	Hs.58559	ESTs, Weakly similar to rhotekin [M.musc	17.4
444929	AI685841	Hs.161354	ESTs	16.5
440807	AW269421	Hs.128093	ESTs	16.3
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	14.2
446967	AI699629	Hs.156781	ESTs	13.3
417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	12.3
437119	AI379921	Hs.177043	ESTs	12.3
451103	R52804	Hs.25956	DKFZP564D206 protein	11.5
443450	N66045	Hs.133529	ESTs	11.4
411880	AW872477		gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens	11.3
432519	AI221311	Hs.130704	ESTs	11.3
414142	AW368397	Hs.150042	ESTs	11.0
433283	BE041135	Hs.175622	ESTs	10.1
441082	AW444804	Hs.202655	ESTs	10.1
452039	AI922988	Hs.172510	ESTs	10.0
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	9.9
421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	9.8
412372	R65998	Hs.118615	ESTs	9.8
426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfam	9.7
431007	AF039564	Hs.248211	retinoblastoma-binding protein 9	9.4
443709	AI082692	Hs.134662	ESTs	9.3
446232	AI281848	Hs.165547	ESTs	9.2
448253	H25899	Hs.201591	ESTs	9.2
432133	AB033088	Hs.272567	KIAA1262 protein	9.1
409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	9.0
431353	AA828032	Hs.189076	ESTs	8.8
450050	AI681268	Hs.257883	ESTs	8.8
458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	8.8
414968	C16096	Hs.297777	ESTs	8.7
425664	AJ006276	Hs.159003	transient receptor potential channel 6	8.7
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	8.6
453672	U73531	Hs.34526	G protein-coupled receptor	8.5
429420	AK001679	Hs.202289	hypothetical protein FLJ10376	8.5
421478	AI683243	Hs.97258	ESTs	8.4
404916				8.4
444396	T65213	Hs.4257	ESTs	8.3
442275	AW449467	Hs.54795	ESTs	8.3
437479	R61866	Hs.101277	ESTs	8.2
432203	AA305746	Hs.49	macrophage scavenger receptor 1	8.2
431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	7.9
406747	AI925153	Hs.217493	annexin A2	7.8

	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	7.7
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	7.6
	421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	7.5
5	421155	H87879	Hs.102267	lysyl oxidase	7.5
	446917	AI347863	Hs.156672	ESTs	7.5
	422798	R92347	Hs.34574	ESTs	7.4
	426830	AA385751	Hs.160392	ESTs	7.4
	437157	BE048860	Hs.120655	ESTs	7.4
10	433231	AB040926	Hs.143552	KIAA1493 protein	7.3
	451561	N52812	Hs.177403	ESTs	7.1
	430656	AA482900	Hs.162080	ESTs	7.1
	448206	BE622585	Hs.3731	ESTs	7.1
	420209	AA256444	Hs.32295	Homo sapiens cDNA FLJ12604 fis, clone NT	7.0
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	6.9
15	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.9
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	6.8
	443324	R44013	Hs.164225	ESTs	6.8
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	6.8
20	427356	AW023482	Hs.97849	ESTs	6.7
	418735	N48769	Hs.44609	ESTs	6.7
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	6.6
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.6
	430099	AW194988	Hs.20537	Homo sapiens cDNA FLJ13942 fis, clone Y7	6.6
25	441835	AB036432	Hs.184	advanced glycosylation end product-speci	6.5
	428508	BE252383	Hs.184668	SBBI31 protein	6.5
	438202	AW169287	Hs.22588	ESTs	6.5
	441233	AA972965	Hs.135568	ESTs	6.4
	433384	AI021992	Hs.124244	ESTs	6.3
	427043	AA397679	Hs.298460	ESTs	6.3
30	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	6.3
	438909	AF085839		gb:Homo sapiens full length insert cDNA	6.3
	433365	AF026944	Hs.293797	ESTs	6.3
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.2
35	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.2
	431337	N48107	Hs.292593	ESTs	6.1
	434819	AA650099	Hs.291541	ESTs	6.0
	458219	H22195	Hs.31874	ESTs	6.0
	434377	AW137148	Hs.136348	osteoblast specific factor 2 (fascinlin	5.9
40	435933	AA805520	Hs.192075	ESTs	5.9
	436954	AA740151	Hs.130425	ESTs	5.9
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	5.8
	449108	AI140683	Hs.98328	ESTs	5.8
	410334	AW979261	Hs.291993	ESTs	5.7
45	447112	H17800	Hs.7154	ESTs	5.7
	447700	AI420183	Hs.171077	ESTs, Weakly similar to similar to serin	5.7
	449208	AW263635	Hs.48643	ESTs	5.7
	445657	AW612141	Hs.279575	ESTs	5.7
	421554	AW137676	Hs.97775	ESTs, Weakly similar to Testis-specific	5.7
50	435299	AI745458	Hs.122614	ESTs, Weakly similar to apoptotic protea	5.6
	416769	AI339257	Hs.115436	ESTs	5.6
	433527	AW235613	Hs.133020	ESTs	5.6
	452771	T05477		gb:EST03366 Fetal brain, Stratagene (cat	5.6
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	5.5
55	411514	AW850178	Hs.18995	KIAA1304 protein	5.5
	424084	AI940675	Hs.20914	Homo sapiens cDNA: FLJ23056 fis, clone L	5.5
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.4
	429710	AI337113	Hs.146025	Homo sapiens cDNA: FLJ23594 fis, clone L	5.4
	432113	AA935065	Hs.152385	ESTs	5.4
60	447997	H00656	Hs.29792	ESTs	5.4
	449328	AI962493	Hs.197647	ESTs	5.3
	416575	W02414	Hs.38383	ESTs	5.3
	432009	AL137424		gb:Homo sapiens mRNA; cDNA DKFZp761G2123	5.3
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	5.3
65	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	5.2
	414299	AA142989	Hs.71730	ESTs	5.2
	431041	AA490967	Hs.105276	ESTs	5.2
	448104	AI674818	Hs.178391	ribosomal protein L44	5.2
	445279	R41900	Hs.22245	ESTs	5.1
70	408978	AL133617	Hs.49421	Homo sapiens mRNA; cDNA DKFZp434M0728 (f	5.1
	415094	D59513		gb:HUM042H10B Clontech human fetal brain	5.1
	428244	AI564123	Hs.42500	ADP-ribosylation factor-like 5	5.1
	452784	BE463857	Hs.151258	Homo sapiens cDNA: FLJ21062 fis, clone C	5.1
	455431	AW938484	Hs.80738	sialophorin (gpl115, leukosialin, CD43)	5.1
75	449416	AI651016	Hs.246311	ESTs	5.1
	421659	NM_014459	Hs.106511	protocadherin 17	5.1
	407638	AJ404672	Hs.288693	Homo sapiens cDNA FLJ11667 fis, clone HE	5.0
	446164	AW273539	Hs.199329	Homo sapiens cDNA: FLJ23577 fis, clone L	5.0
	413048	M93221	Hs.75182	mannose receptor, C type 1	5.0
80	446608	N75217	Hs.257846	ESTs	4.9
	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo	4.9
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	4.9
	442652	AI005163	Hs.201378	ESTs, Weakly similar to KIAA0944 protein	4.9
	429496	AA453800	Hs.192793	ESTs	4.8

	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	4.8
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	4.8
	425509	AF079363	Hs.158213	sperm associated antigen 6	4.8
5	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.8
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	4.8
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	4.7
	453382	AA709285	Hs.5997	Homo sapiens cDNA FLJ13078 fis, clone NT	4.7
	447033	AI357412	Hs.157601	ESTs	4.7
10	417235	AA810278	Hs.24250	ESTs	4.7
	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	4.7
	427652	AI673025	Hs.43874	ESTs	4.7
	431255	AA497043	Hs.115685	ESTs	4.7
	441143	AI027604	Hs.159650	ESTs	4.7
15	452293	AI871833		gb:wm51h09.x1 NCI_CGAP_Ui2 Homo sapiens	4.7
	443903	AI220547	Hs.135223	ESTs	4.7
	422352	AA766296	Hs.99200	ESTs	4.7
	424105	AI142336	Hs.43977	ESTs	4.6
	439759	AI359055	Hs.67709	Homo sapiens mRNA full length insert cDN	4.6
20	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.6
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.6
	425804	BE501698	Hs.258189	ESTs	4.6
	435347	AW014873	Hs.116963	ESTs	4.6
	446002	AI346468	Hs.145789	ESTs	4.6
25	452883	X80031	Hs.150318	ESTs	4.6
	442176	AA983764	Hs.128910	ESTs	4.6
	443253	AI041212	Hs.132117	ESTs	4.5
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	4.5
	439920	H05430	Hs.144455	ESTs	4.5
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	4.5
30	434424	AI811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone L	4.4
	408625	AW243323	Hs.266785	ESTs	4.4
	449299	AA299919		gb:EST12592 Uterus tumor I Homo sapiens	4.4
	450656	AA010539	Hs.18912	ESTs	4.4
35	433815	AI696602	Hs.112757	ESTs	4.4
	416879	H98899	Hs.42599	ESTs	4.3
	432182	AW607789	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.3
	445386	AI422005	Hs.160380	ESTs	4.3
	450478	AW451709	Hs.271200	ESTs	4.3
40	453080	AI423056	Hs.23921	Homo sapiens cDNA FLJ12482 fis, clone NT	4.3
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	4.3
	443257	AI334040	Hs.11614	Homo sapiens cDNA: FLJ23555 fis, clone L	4.3
	453921	AI824009	Hs.44577	ESTs	4.3
	419721	NM_001650	Hs.288650	aquaporin 4	4.2
45	432316	AW973235	Hs.293697	ESTs	4.2
	435202	AI971313	Hs.170204	KIAA0551 protein	4.2
	440320	AA879294		gb:nw86e09.s1 NCI_CGAP_Pr12 Homo sapiens	4.2
	438796	W67821	Hs.109590	genethonin 1	4.2
	400269				4.2
50	447724	AW298375	Hs.24477	ESTs	4.1
	446509	AF169693	Hs.132892	prolactin 20	4.1
	451620	AW449888	Hs.257224	ESTs	4.1
	451963	AI825440	Hs.224952	ESTs	4.1
	456408	AI288348	Hs.23450	mRNA for FLJ00023 protein	4.1
55	425895	AI269484	Hs.161427	zinc finger protein 215	4.1
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	4.1
	454024	AA993527	Hs.16281	hypothetical protein FLJ23403	4.0
	415929	AA724373	Hs.295306	ESTs, Highly similar to unnamed protein	4.0
	426625	T78300	Hs.171409	serologically defined colon cancer antig	4.0
60	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	4.0
	437138	AI935622	Hs.271245	ESTs	4.0
	455024	AW851309		gb:IL3-CT0220-170200-067-C11 CT0220 Homo	4.0
	436246	AW450963	Hs.119991	ESTs	4.0
	416030	H15261	Hs.21948	ESTs	4.0
65	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA	3.9
	445122	AW241632	Hs.147377	Homo sapiens cDNA: FLJ23598 fis, clone L	3.9
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.9
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	3.9
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.9
70	429208	AA447990	Hs.190478	ESTs	3.9
	442957	AI949952	Hs.49397	ESTs	3.9
	444050	AW138295	Hs.135024	ESTs	3.9
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.9
	451024	AA442176		gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_	3.9
75	442832	AW206560	Hs.253569	ESTs	3.9
	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	3.9
	451895	T93573	Hs.16970	ESTs	3.9
	442353	BE379594	Hs.49136	ESTs	3.8
	421464	AA291553	Hs.190086	ESTs	3.8
80	404043				3.8
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	3.8
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	3.8
	410247	AF181721	Hs.61345	RU2S	3.8
	417461	R38403	Hs.13305	ESTs	3.8

	423609	AA328348	Hs.218289	ESTs	3.8
	440444	AA885221	Hs.156984	ESTs	3.8
	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone NT	3.8
5	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	3.8
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	3.8
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	3.8
	444271	AW452569	Hs.149804	ESTs	3.8
	434217	AW014795	Hs.23349	ESTs	3.8
10	452571	W31518	Hs.34665	ESTs	3.7
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	3.7
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	3.7
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	3.7
	445034	AW293376	Hs.160323	ESTs	3.7
15	438842	AA827176	Hs.124316	ESTs	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	415025	AW207091	Hs.72307	ESTs	3.7
	420313	AB023230	Hs.96427	KIAA1013 protein	3.7
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone CO	3.7
20	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo	3.7
	434636	AA083764	Hs.241334	ESTs	3.7
	435747	AI079519	Hs.134398	ESTs	3.7
	458158	AW296778	Hs.300357	ESTs, Highly similar to dJ416F21.2 [H.sa	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
25	410060	NM_001448	Hs.58367	glypican 4	3.7
	426116	AA868729	Hs.144694	ESTs	3.7
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	3.7
	414259	W44633	Hs.25044	Homo sapiens cDNA: FLJ23131 fis, clone L	3.7
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	3.6
30	431889	AA521277	Hs.124946	ESTs	3.6
	430414	AW365665	Hs.120388	ESTs	3.6
	433426	H69125	Hs.133525	ESTs	3.6
	421764	AI681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN CALCI	3.6
35	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	3.6
	455235	AW875951		gb:CM1-PT0013-131299-067-f09 PT0013 Homo	3.6
	408399	NM_005426	Hs.44585	tumor protein p53-binding protein, 2	3.6
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	3.6
40	432231	AA339977	Hs.274127	CLST 11240 protein	3.6
	432837	AA310693	Hs.279512	HSPC072 protein	3.6
	452166	AI948607	Hs.264680	ESTs	3.5
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234 Homo	3.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	3.5
	424202	BE350295	Hs.15032	ESTs, Weakly similar to RAN binding prot	3.5
45	410658	AW105231	Hs.192035	ESTs	3.5
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	419503	AA243642	Hs.137422	ESTs	3.5
	439479	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.5
50	424268	AA397653	Hs.144339	Human DNA sequence from clone 495010 on	3.5
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	3.5
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.5
	428927	AA441837	Hs.90250	ESTs	3.5
	422544	AB018259	Hs.118140	KIAA0716 gene product	3.4
55	431207	AA495925	Hs.9394	ESTs	3.4
	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13658 fis, clone PL	3.4
	441484	AA935481	Hs.58972	ESTs	3.4
	425916	NM_006786	Hs.162200	urotensin 2	3.4
	401793				3.4
60	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	3.4
	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	3.4
	439619	AW975998	Hs.58595	ESTs	3.4
	446577	AB040933	Hs.15420	KIAA1500 protein	3.4
	450445	AW974636	Hs.194563	ESTs	3.4
65	459482	AA625339	Hs.237052	EST, Weakly similar to ALU1_HUMAN ALU SU	3.4
	445495	BE622641	Hs.38489	ESTs	3.4
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.4
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.4
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	3.3
70	419235	AW470411	Hs.288433	neurotrimin	3.3
	429703	T93154	Hs.28705	ESTs	3.3
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	3.3
	406182				3.3
	417307	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ	3.3
75	430140	AW296771	Hs.221999	ESTs	3.3
	436111	AI803082	Hs.157212	ESTs	3.3
	449729	R72032	Hs.29235	ESTs	3.3
	457620	AA602711		gb:np03h06.s1 NCI_CGAP_Pr2 Homo sapiens	3.3
80	428434	AW363590	Hs.65551	ESTs, Weakly similar to AF172993 1 PLUNC	3.3
	406554				3.3
	451381	BE241831		gb:TCAAP2E0011 Pediatric acute myelogeno	3.3
	443113	AI040686	Hs.132908	ESTs	3.3
	421470	R27496	Hs.1378	annexin A3	3.3
	446428	AW082270	Hs.210617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3

	435031	AI632091	Hs.116877	ESTs	3.3
	413136	BE066941		gb:PMO-BT0340-091299-002-a11 BT0340 Homo	3.2
	429228	AI553633	Hs.104985	ESTs	3.2
5	420252	AW270404	Hs.193161	ESTs	3.2
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.2
	444339	T96555	Hs.31562	ESTs	3.2
	434164	AW207019	Hs.148135	ESTs	3.2
	404599				3.2
10	426920	AA393351	Hs.132121	ESTs	3.2
	453736	AL118674	Hs.34871	KIAA0569 gene product	3.2
	408923	H73881	Hs.255436	ESTs	3.2
	430919	AA489041	Hs.295448	ESTs	3.2
	431622	AW979271	Hs.293184	ESTs	3.2
15	433584	AW295399		gb:UI-H-BI2-ahv-h-03-0-UI.s1 NCL_CGAP_Su	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
	438394	BE379623	Hs.27693	CGI-124 protein	3.2
	446242	N66336	Hs.7360	ESTs	3.2
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	3.2
20	454009	AW015927	Hs.233071	ESTs	3.2
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN AL	3.2
	415652	T79213	Hs.272073	ESTs	3.2
	453931	AL121278	Hs.25144	ESTs	3.2
	439382	BE247684	Hs.103070	ESTs	3.2
25	420077	AW512260	Hs.87767	ESTs	3.2
	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.2
	446745	AW118189	Hs.156400	ESTs	3.1
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	3.1
	450320	AW291775	Hs.213793	ESTs	3.1
30	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.1
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.1
	451110	AI955040	Hs.301584	ESTs	3.1
	431745	AW972448	Hs.163425	ESTs	3.1
	410781	AI375672	Hs.165028	ESTs	3.1
35	419546	AA244199		gb:nc06c05.s1 NCL_CGAP_Pr1 Homo sapiens	3.1
	444330	AI597655	Hs.49265	ESTs	3.1
	408761	AA057264	Hs.238936	ESTs	3.1
	409026	AL137554	Hs.49927	Homo sapiens mRNA; cDNA DKFZp434H1720 (f	3.1
	432055	AW972359	Hs.293334	ESTs	3.1
40	432441	AW292425	Hs.163484	ESTs	3.1
	408045	AW138959	Hs.245123	ESTs	3.1
	427191	BE221825	Hs.97691	ESTs	3.1
	416965	N26223	Hs.160436	ESTs	3.1
	441594	AL041080	Hs.208765	ESTs	3.1
45	406992	S82472		gb:beta-pol=DNA polymerase beta [exon a	3.0
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.0
	438323	AI985394	Hs.123369	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	424296	AI631874	Hs.169391	ESTs	3.0
50	450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.0
	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	3.0
	417991	AA731452	Hs.190008	ESTs	3.0
	422589	AA312735	Hs.179725	ESTs	3.0
	437583	AA761190	Hs.244627	ESTs	3.0
55	452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.0
	449494	AW237014	Hs.288650	aquaporin 4	3.0
	444188	AI393165	Hs.19175	ESTs	3.0
	400297	AI127076	Hs.288381	hypothetical protein DKFZp564O1278	3.0
	410811	AW805687	Hs.300648	ESTs	3.0
60	450584	AA040403	Hs.60371	ESTs	3.0
	428043	T92248	Hs.2240	uteroglobin	3.0
	436120	AI248193	Hs.119860	ESTs	3.0
	442324	R63578	Hs.28426	ESTs	2.9
	448693	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	2.9
65	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.9
	431385	BE178536	Hs.11090	high affinity immunoglobulin epsilon rec	2.9
	408427	AW194270	Hs.177236	ESTs	2.9
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to U4/U6 small nucl	2.9
70	408938	AA059013	Hs.22607	ESTs	2.9
	419276	BE165909	Hs.134682	Homo sapiens cDNA: FLJ23161 fis, clone L	2.9
	422022	AA302420	Hs.200442	ESTs	2.9
	426890	AA393167	Hs.41294	ESTs	2.9
	427374	AI150033	Hs.143686	ESTs	2.9
75	434208	T92641	Hs.127648	hypothetical protein PRO2176	2.9
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	2.9
	451229	AW967707	Hs.48473	ESTs	2.9
	415511	AI732617	Hs.182362	ESTs	2.9
	408776	AA057365	Hs.63356	ESTs	2.9
80	421110	AJ250717	Hs.1355	cathepsin E	2.9
	453636	R67837	Hs.169872	ESTs	2.9
	436578	AI091435	Hs.134859	ESTs	2.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	2.9
	419231	AL046294	Hs.136245	ESTs, Weakly similar to dJ202121.4 [H.sa	2.8

	408171	AA301228	Hs.43299	Homo sapiens cDNA FLJ12890 fis, clone NT	2.8
	445189	AI936450	Hs.147482	ESTs	2.8
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.8
5	427457	AW779105	Hs.164682	ESTs, Weakly similar to ORF2 consensus s	2.8
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	2.8
	446932	AA961459	Hs.125644	ESTs	2.8
	439140	W85737	Hs.290830	ESTs	2.8
	405041				2.8
10	421306	AA806207	Hs.125889	ESTs	2.8
	427514	AA640773	Hs.209224	ESTs	2.8
	427939	T92459	Hs.16886	ESTs	2.8
	429127	AA749382	Hs.107233	ESTs	2.8
	429590	AI219490	Hs.44445	ESTs, Weakly similar to Kelch motif cont	2.8
15	433163	R40468	Hs.163582	ESTs	2.8
	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone H	2.8
	448015	AI458065	Hs.23196	ESTs	2.8
	456761	D59899	Hs.127842	CGI-142	2.8
	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
20	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	2.8
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	2.8
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.8
	433515	AA595800	Hs.190246	ESTs	2.8
	424450	AL137526	Hs.147472	dynein intermediate chain 2	2.8
25	438122	AI620270	Hs.129837	ESTs	2.8
	424086	AI351010	Hs.102267	lysyl oxidase	2.8
	438885	AI886558	Hs.184987	ESTs	2.8
	412903	BE007967	Hs.155795	ESTs	2.8
	454111	AW081681	Hs.269064	ESTs	2.8
30	439398	AA284267	Hs.221504	ESTs	2.8
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	2.8
	434812	AA649860	Hs.189496	ESTs	2.8
	432583	AW023624	Hs.162282	ESTs	2.8
	428104	AA421350	Hs.191604	ESTs	2.8
35	408217	AI433201	Hs.279860	hypothetical protein FLJ20030	2.8
	438016	AI949638	Hs.109150	SH3-domain binding protein 5 (BTK-associ	2.8
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	2.7
	430887	N66801	Hs.260287	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
	446311	AW007294	Hs.149795	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
40	416185	AW975861	Hs.291995	ESTs	2.7
	408613	AW242086	Hs.253967	ESTs	2.7
	442510	AF150179	Hs.249890	ESTs	2.7
	433293	AF007835	Hs.32417	ESTs	2.7
	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.7
	404488				2.7
45	408936	AL138043	Hs.293549	ESTs	2.7
	431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fis, clone C	2.7
	436738	AW102613	Hs.152913	ESTs	2.7
	451797	AW663858	Hs.56120	ESTs	2.7
50	452163	AI863140		gb:tz43h12.x1 NCL_CGAP_Brn52 Homo sapien	2.7
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.7
	459366	AA129703		gb:zn92b05.r1 Stratagene lung carcinoma	2.7
	431448	AL137517	Hs.288381	hypothetical protein DKFZp56401278	2.7
	430733	AW975920	Hs.283361	ESTs	2.7
55	453652	AW009640	Hs.28368	ESTs	2.7
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	2.7
	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	2.7
	408729	AA195764	Hs.72639	ESTs	2.7
	450726	AW204600	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.7
60	447720	AL038765	Hs.161304	ESTs	2.7
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	2.7
	442074	C17511	Hs.128430	ESTs	2.7
	424115	AA335497	Hs.293965	ESTs	2.7
	417728	AW138437	Hs.24790	KIAA1573 protein	2.7
65	433803	AI823593	Hs.27688	ESTs	2.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	2.7
	424310	AA338648	Hs.50334	ESTs	2.6
	438504	AW665281	Hs.224625	ESTs	2.6
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	2.6
70	430417	AA461045	Hs.50701	ESTs	2.6
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	422505	AL120862	Hs.124165	ESTs	2.6
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-tyr	2.6
	428667	AI375550	Hs.74407	nucleolar protein p40; homolog of yeast	2.6
75	431750	AA514986	Hs.283705	ESTs	2.6
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.6
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.6
	403903				2.6
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.6
80	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	2.6
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	2.6
	436645	AW023424	Hs.156520	ESTs	2.6
	408380	AF123050	Hs.44532	diubiquitin	2.6
	402629				2.6

	406594			2.6
	415122	D60708	Hs.22245	ESTs
	416747	AW876523	Hs.15929	Homo sapiens cDNA FLJ12910 fis, clone NT
5	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C
	444361	W76027	Hs.23920	Homo sapiens cDNA FLJ13124 fis, clone NT
	446609	BE395090	Hs.15535	Human gene from PAC 886K2, chromosome 1
	449260	AA741180	Hs.29879	ESTs
	452311	AW304029	Hs.252744 <sup>1</sup>	ESTs
10	413802	AW964490	Hs.32241	ESTs
	417318	AW953937	Hs.12891	ESTs
	440028	AW473675	Hs.125843	ESTs
	437960	AI669586	Hs.222194	ESTs
	433687	AA743991		gb:ny57g01.s1 NCL_CGAP_Pr18 Homo sapiens
15	430573	AA744550	Hs.136345	ESTs
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN
	453204	R10799	Hs.191990	ESTs
	436751	AA732217	Hs.294054	ESTs
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f
20	431120	AA492588		gb:ng99c08.s1 NCL_CGAP_Thy1 Homo sapiens
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f
	438458	AW975186	Hs.162875	ESTs, Weakly similar to ALU1_HUMAN ALU S
	446063	AI720140	Hs.151079	ESTs
	430499	AW969408	Hs.231991	ESTs
25	450496	AW449251	Hs.257131	ESTs
	441330	AI692984	Hs.129354	ESTs
	424433	H04607	Hs.9218	ESTs
	434677	AW444575	Hs.130834	ESTs
	445779	AI253104	Hs.189267	ESTs
30	444649	AW207523	Hs.197628	ESTs
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1
	404288			
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A
35	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912
	410095	AW589638	Hs.258947	ESTs
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298
	418343	AA216372	Hs.159501	ESTs
40	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto
	428637	AW979268		gb:EST391378 MAGE resequences, MAGP Homo
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy
	432507	BE391093		gb:601286042F1 NIH_MGC_44 Homo sapiens c
	433858	N69243	Hs.192974	Homo sapiens cDNA FLJ12735 fis, clone NT
45	438651	H64500	Hs.123646	ESTs
	443830	AI142095	Hs.143273	ESTs
	446800	AI341635	Hs.156486	ESTs
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN A
	451343	AW975057	Hs.293353	ESTs
50	451539	AA059467	Hs.218933	ESTs
	452412	AA029608	Hs.61373	ESTs
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap
	445745	AB007924	Hs.13245	KIAA0455 gene product
	424943	ALU077260	Hs.153924	death-associated protein kinase 1
55	440106	AA864968	Hs.127699	KIAA1603 protein
	458429	AV646559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C
	415261	T40928	Hs.8346	ESTs
	420026	AI831190	Hs.166676	ESTs
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam
60	458722	AA741545	Hs.282832	ESTs
	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S
	433644	AW342028	Hs.256112	ESTs
	419172	AW338625	Hs.22120	ESTs
65	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti
	443348	AW873596	Hs.57572	ESTs
	417218	AA005247	Hs.285754	met proto-oncogene (hepalcocyte growth fa
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE
	448030	N30714	Hs.20161	HDCME31P protein
70	417203	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE
	449275	AW450848	Hs.205457	KIAA1620 protein
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL
	442191	W95186	Hs.8136	endothelial PAS domain protein 1
75	428571	NM_006531	Hs.2291	Probe hTg737 polycystic kidney disease,
	453142	AA033648	Hs.7473	ESTs
	425657	T89839	Hs.119471	ESTs
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone H
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf
80	458332	AI000341	Hs.220491	ESTs
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor
	459644			
	429125	AA446854	Hs.271004	ESTs
	448337	AW206453	Hs.3782	ESTs



	427778	AA412323	Hs.105323	ESTs	2.4
	425371	D49441	Hs.155981	mesothelin	2.4
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.4
5	447610	AW296286	Hs.255534	ESTs	2.4
	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.4
	441006	AW605267	Hs.7627	CGI-60 protein	2.4
	440817	AI341423	Hs.270165	ESTs	2.4
	420020	BE295866	Hs.94382	adenosine kinase	2.4
10	435395	AA729235	Hs.117907	ESTs	2.4
	424144	AA454033	Hs.41644	Homo sapiens cDNA: FLJ23003 fis, clone L	2.4
	405494				2.4
	458145	AI239457	Hs.130794	ESTs	2.4
	408547	AA574291	Hs.57837	ESTs	2.4
15	408941	AI452469	Hs.165221	ESTs	2.4
	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276 Homo	2.4
	417137	U46265	Hs.81281	hypothetical protein	2.4
	418950	T78517	Hs.13941	ESTs	2.4
	420756	AA411800	Hs.189900	ESTs	2.4
20	428316	AI860775	Hs.98506	ESTs	2.4
	432896	NM_014097	Hs.279778	PRO1693 protein	2.4
	436148	BE005252		gb:CM1-BN0116-030400-171-g02 BN0116 Homo	2.4
	436284	AA708016	Hs.190389	ESTs	2.4
	437327	AL353942		gb:Homo sapiens mRNA; cDNA DKFZp761L2312	2.4
25	442611	BE077155	Hs.177537	ESTs	2.4
	456062	AI866286	Hs.71962	ESTs	2.4
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.4
	401335				2.4
30	428771	AB028992	Hs.193143	KIAA1069 protein	2.4
	419140	AI982647	Hs.215725	ESTs	2.4
	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	2.4
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.4
	407339	AA777542	Hs.132670	ESTs	2.4
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	2.4
35	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	2.4
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.4
	452561	AI692181	Hs.49169	KIAA1634 protein	2.4
	427878	C05766	Hs.181022	CGI-07 protein	2.4
	419752	AA249573	Hs.152618	ESTs	2.4
40	430073	U86136	Hs.232070	telomerase-associated protein 1	2.4
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	2.4
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.3
	407905	AW103655	Hs.252905	ESTs	2.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.3
45	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3 (G	2.3
	453049	BE537217	Hs.30343	ESTs	2.3
	438568	R98865	Hs.11135	major histocompatibility complex, class	2.3
	453445	AL036532	Hs.91453	ESTs	2.3
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.3
50	446346	AI290205		gb:q179g06.x1 Soares_NhHMPu_S1 Homo sapi	2.3
	441974	AI683782	Hs.128245	ESTs	2.3
	444805	AB007899	Hs.12017	KIAA0439 protein; homolog of yeast ubiqu	2.3
	424027	AW337575	Hs.201591	ESTs	2.3
	419606	AW294795	Hs.198529	ESTs, Weakly similar to similar to acyl-	2.3
55	428613	AB037749	Hs.186928	KIAA1328 protein	2.3
	434340	AI193043	Hs.128685	ESTs	2.3
	450297	AW901347	Hs.38592	Homo sapiens cDNA: FLJ23342 fis, clone H	2.3
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.3
	433650	AA603472	Hs.28456	ESTs	2.3
60	419086	NM_000216	Hs.89591	Kalman syndrome 1 sequence	2.3
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PL	2.3
	430153	AW968128		gb:EST380338 MAGE resequences, MAGJ Homo	2.3
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.3
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	2.3
65	400610				2.3
	402222				2.3
	407162	N63855	Hs.142634	zinc finger protein	2.3
	415250	F02614	Hs.27319	ESTs	2.3
	421751	AW813731	Hs.159153	ESTs	2.3
70	428552	AW274560	Hs.129520	ESTs	2.3
	432658	AW973769	Hs.162319	ESTs	2.3
	434742	AA648302	Hs.291695	ESTs	2.3
	436586	AI308862	Hs.167028	ESTs	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
75	442039	AW276240	Hs.128352	ESTs, Weakly similar to p80 [R.norvegicu	2.3
	443160	AI467915	Hs.36053	ESTs	2.3
	448764	AI568607	Hs.182112	ESTs	2.3
	449579	AW207260	Hs.134014	prostate cancer associated protein 6	2.3
	439810	AL109710	Hs.85568	EST	2.3
80	413714	AI560944	Hs.71428	ESTs	2.3
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	2.3
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	2.3
	438670	AI275803	Hs.123428	ESTs	2.3
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	2.3

	459702				2.3
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	2.3
	438474	AW865818	Hs.6232	KIAA0764 gene product	2.3
5	453037	AA045175	Hs.177552	ESTs	2.3
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	2.3
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	2.3
	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	2.3
	415083	Al632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	2.3
10	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.3
	406506				2.3
	448330	AL036449	Hs.207163	ESTs	2.3
	409719	Al769160	Hs.108681	ESTs	2.3
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.3
15	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.3
	427961	AW293165	Hs.143134	ESTs	2.3
	447357	Al375922	Hs.159367	ESTs	2.3
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	2.3
	453716	AA037675	Hs.152675	ESTs	2.3
20	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.2
	407949	W21874	Hs.247057	ESTs	2.2
	427972	AA864870	Hs.181304	putative gene product	2.2
	453313	BE005771	Hs.153746	Homo sapiens cDNA: FLJ22490 fis, clone H	2.2
	426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	2.2
25	424238	AA337401	Hs.137635	ESTs	2.2
	452930	AW195285	Hs.194097	ESTs	2.2
	424527	AW138558	Hs.267158	ESTs	2.2
	453095	AW295660	Hs.252756	ESTs	2.2
	449161	N53431	Hs.47647	ESTs, Weakly similar to KIAA0423 [H.sapi	2.2
30	429586	T73510	Hs.209153	angiotensin-like 3	2.2
	423782	Al472209	Hs.288369	ESTs	2.2
	458124	AW005548	Hs.124590	ESTs	2.2
	450109	Al539295	Hs.17967	ESTs	2.2
	421461	AW291023	Hs.97255	ESTs	2.2
35	412222	AA528283	Hs.292737	ESTs	2.2
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	441736	AW292779	Hs.169799	ESTs	2.2
	401049				2.2
	440727	Al073991	Hs.134268	ESTs	2.2
40	419751	AW195581	Hs.93121	KIAA0761 protein	2.2
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.2
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.2
	410292	AA843087	Hs.124194	ESTs	2.2
45	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	2.2
	449695	AA164569	Hs.34550	ESTs	2.2
	429399	AA452244	Hs.16727	ESTs	2.2
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	2.2
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.2
50	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	2.2
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.2
	445268	Al218358	Hs.175048	ESTs	2.2
	402481				2.2
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.2
55	416521	H60929	Hs.44197	hypothetical protein DKFZp564D0462	2.2
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
	421211	AA284966	Hs.266308	ESTs, Weakly similar to AF216312 1 type	2.2
	427541	Al798983	Hs.97961	ESTs	2.2
60	432013	Al796879	Hs.162102	ESTs	2.2
	436461	AW511956	Hs.293261	ESTs	2.2
	438002	Al560246	Hs.201648	ESTs, Weakly similar to ZN42_HUMAN ZINC	2.2
	440312	AW614597	Hs.72475	ESTs	2.2
	440479	AA886461	Hs.208161	ESTs	2.2
65	441178	W90789	Hs.153976	ESTs	2.2
	441235	Al884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	2.2
	443314	AW771701	Hs.54646	ESTs	2.2
	422165	AL041199	Hs.1481	histidine decarboxylase	2.2
	450696	Al654223	Hs.16026	Homo sapiens cDNA: FLJ23191 fis, clone L	2.2
70	432974	BE348793		gb:ht70g02.x1 NCI_CGAP_Lu24 Homo sapiens	2.2
	404200				2.2
	435990	Al015862	Hs.131793	ESTs	2.2
	421309	Al222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.2
75	416642	T96118	Hs.226313	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	406672	M26041	Hs.198253	major histocompatibility complex, class	2.2
	417819	Al253112	Hs.133540	ESTs	2.2
	417355	D13168	Hs.82002	endothelin receptor type B	2.2
	459574	Al741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	2.2
80	404274				2.2
	415086	Al597963	Hs.118726	ESTs	2.2
	418210	R54575	Hs.13337	ESTs, Weakly similar to unnamed protein	2.2
	419220	AA811938	Hs.291759	ESTs	2.2
	444314	Al140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.2

	451050	AW937420	Hs.69662	ESTs	2.2
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	2.2
	428414	AL049980	Hs.184216	DKFZP564C152 protein	2.2
5	412925	AI089319	Hs.179243	ESTs	2.2
	438192	AI859065	Hs.16808	ESTs, Weakly similar to paraplegin-like	2.2
	410976	R36207	Hs.25092	ESTs	2.2
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.2
	449677	AA002071		gb:zh85d01.s1 Soares_fetal_liver_spleen_	2.2
10	449321	AA001150	Hs.132937	ESTs	2.2
	418557	BE140602	Hs.246645	ESTs	2.2
	416320	H47867	Hs.34024	ESTs	2.2
	426384	AI472078		gb:tj85h03.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.2
	414140	AA281279	Hs.23317	ESTs	2.2
	419520	AB009303	Hs.297790	Human clone 23734 mRNA sequence	2.2
15	446999	AA151520	Hs.279525	hypothetical protein PRO2605	2.2
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	2.2
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.1
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	2.1
20	410048	W76467	Hs.274550	proline oxidase homolog	2.1
	400880				2.1
	418092	R45154	Hs.106604	ESTs	2.1
	428780	AI478578	Hs.50636	ESTs	2.1
	431067	AW574823	Hs.200413	ESTs	2.1
25	432803	AA565398		gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	2.1
	412104	AW205197	Hs.240951	ESTs	2.1
	422819	AL122084	Hs.121073	hypothetical protein FLJ10466	2.1
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	2.1
	424806	AA382523	Hs.105689	ESTs	2.1
30	434445	AI349306	Hs.11782	ESTs	2.1
	442994	AI026718	Hs.16954	ESTs	2.1
	410371	AA084482	Hs.115850	ESTs	2.1
	450232	BE300815	Hs.201326	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.1
35	430899	BE018217	Hs.183528	ESTs, Weakly similar to Bem46-like prote	2.1
	431814	BE256242	Hs.270847	delta-tubulin	2.1
	417543	AA203620	Hs.110153	ESTs, Weakly similar to BCGF_HUMAN B-CEL	2.1
	444542	AI161293	Hs.146862	ESTs, Weakly similar to KIAA0525 protein	2.1
	404593				2.1
40	434803	AW974640		gb:EST386744 MAGE resequences, MAGM Homo	2.1
	451623	H77818	Hs.268991	ESTs	2.1
	452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on	2.1
	402046				2.1
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.1
45	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	2.1
	401987				2.1
	423119	AA322201	Hs.131976	EST	2.1
	427112	Z32887	Hs.290951	ESTs	2.1
	414464	AI870175	Hs.13957	ESTs	2.1
50	447829	AI433029	Hs.164104	ESTs	2.1
	449679	AI823951	Hs.296668	Homo sapiens cDNA FLJ11846 fis, clone HE	2.1
	405472				2.1
	413621	AI808648	Hs.184156	ESTs	2.1
	432212	AW137742	Hs.293451	ESTs	2.1
55	404289				2.1
	415362	F06735		gb:HSC1JB091 normalized infant brain cDN	2.1
	427739	AW196755	Hs.98105	ESTs	2.1
	427772	AA412289	Hs.98123	ESTs	2.1
60	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.1
	434335	AA630107	Hs.213220	ESTs	2.1
	436052	AI021983	Hs.271432	ESTs	2.1
	442773	AB037722	Hs.8707	Homo sapiens mRNA; cDNA DKFZp434N1131 (f	2.1
	446799	AW978373	Hs.49221	ESTs, Weakly similar to zinc finger prot	2.1
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.1
65	455673	BE065939		gb:RC3-BT0319-100100-012-c11 BT0319 Homo	2.1
	458624	AI362790	Hs.181801	ESTs	2.1
	405095				2.1
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	2.1
	433589	AA886530	Hs.188912	ESTs	2.1
70	438398	AA806526	Hs.130277	ESTs	2.1
	447233	AW246333	Hs.17901	Homo sapiens cDNA: FLJ21974 fis, clone H	2.1
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.1
	431087	H12723	Hs.290791	ESTs	2.1
	409064	AA062954	Hs.141883	ESTs	2.1
75	427558	D49493	Hs.2171	growth differentiation factor 10	2.1
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	2.1
	438118	AW753311	Hs.259415	ESTs	2.1
	427621	BE621182	Hs.179882	Homo sapiens cDNA FLJ12437 fis, clone NT	2.1
	452114	N22687	Hs.8236	ESTs	2.1
80	448782	AL050295	Hs.301550	KIAA0758 protein	2.1
	403937				2.1
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	2.1
	452416	AA026115	Hs.114777	ESTs	2.1
	451609	AL046019	Hs.209276	ESTs	2.1

	435934	R19382	Hs.117869	ESTs	2.1
	445158	AI992108	Hs.127206	ESTs	2.1
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.1
5	439335	AA742697	Hs.62492	ESTs, Weakly similar to S59856 collagen	2.1
	443949	AW827419	Hs.235070	ESTs	2.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.1
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	2.1
	438676	AA813745	Hs.123446	ESTs	2.1
	405848				2.1
10	416940	N75620	Hs.43157	ESTs	2.1
	442381	AI185136	Hs.48650	ESTs	2.1
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp5861823 (f	2.1
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	2.1
15	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	2.1
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	2.1
	439425	AF086244	Hs.114659	ESTs	2.1
	421168	AF182277	Hs.1360	cytochrome P450, subfamily IIB (phenobar	2.1
	449611	AI970394	Hs.197075	ESTs	2.1
	404548				2.1
20	416734	H81213	Hs.14825	ESTs	2.1
	435865	AA883552	Hs.16810	ESTs	2.1
	439072	AF085930	Hs.269123	ESTs	2.1
	447482	AB033059	Hs.18705	KIAA1233 protein	2.1
	457292	AI921270	Hs.214178	Homo sapiens cDNA FLJ14251 fis, clone OV	2.1
25	444974	AI203500	Hs.151612	ESTs	2.1
	456034	AW450979		gb:U1-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	2.1
	430634	AI860651	Hs.26685	ESTs	2.1
	426782	R14614	Hs.191254	ESTs	2.0
30	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.0
	445326	AI220072	Hs.165893	ESTs	2.0
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.0
	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	2.0
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.0
	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.0
35	417321	N68722	Hs.191368	ESTs	2.0
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.0
	404323				2.0
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
40	421047	AW514772	Hs.104473	ESTs	2.0
	425497	AA524596	Hs.188844	ESTs	2.0
	444623	AI183829	Hs.202111	ESTs	2.0
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.0
	433563	AI732637	Hs.277901	ESTs	2.0
	406485				2.0
45	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.0
	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.0
	425465	L18964	Hs.1904	protein kinase C, iota	2.0
	449424	AW448937	Hs.197030	ESTs	2.0
50	427940	AA417812	Hs.38775	ESTs	2.0
	411502	AW946605	Hs.250154	Homo sapiens cDNA FLJ12973 fis, clone NT	2.0
	411365	M76477	Hs.278242	tubulin, alpha, ubiquitous	2.0
	412369	H80456	Hs.285243	Homo sapiens cDNA: FLJ22029 fis, clone H	2.0
	452959	AI933416	Hs.189674	ESTs	2.0
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.0
55	428775	AA434579	Hs.143691	ESTs	2.0
	420000	AB036063	Hs.180726	Homo sapiens cDNA FLJ13543 fis, clone PL	2.0
	408321	AW405882	Hs.44205	cortistatin	2.0
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	2.0
	411050	AW814902		gb:MR1-ST0206-120400-022-f08 ST0206 Homo	2.0
60	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.0
	428978	AA442784	Hs.125445	ESTs	2.0
	458562	N34128	Hs.145268	ESTs	2.0
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	2.0
	403760				2.0
65	424368	AB037766	Hs.146085	KIAA1345 protein	2.0
	421229	AI056590	Hs.7086	Homo sapiens cDNA: FLJ23000 fis, clone L	2.0
	436304	AA339622	Hs.108887	ESTs	2.0
	453498	BE181412	Hs.23245	Homo sapiens cDNA FLJ11767 fis, clone HE	2.0
70	439018	AW300887	Hs.26638	ESTs, Weakly similar to unnamed protein	2.0
	453280	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFZp761C082 (fr	2.0
	420193	AI460080	Hs.202869	ESTs	2.0
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.0
	401575				2.0
75	419092	J05581	Hs.89603	mucin 1, transmembrane	2.0
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.0
	410763	AF279145	Hs.8966	tumor endothelial marker 8	2.0
	414783	AW069569	Hs.75839	zinc finger protein 6 (CMPX1)	2.0
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.0
	405963				2.0
80	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.0
	420831	AA280824	Hs.190035	ESTs	2.0
	424152	AL133591	Hs.301405	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.0
	424641	AB001106	Hs.151413	glia maturation factor, beta	2.0

	427616	AI698684	Hs.98028	ESTs	2.0
	435115	AI821726	Hs.116603	ESTs	2.0
	437636	AA764781	Hs.291844	ESTs	2.0
5	438295	AI394151	Hs.37932	ESTs	2.0
	439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	2.0
	445388	AI925280	Hs.236842	EST	2.0
	447101	N72185	Hs.44189	ESTs	2.0
	448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.0
10	449623	C00719	Hs.120440	ESTs	2.0
	450159	AI702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN CALPA	2.0
	456613	R19992	Hs.106620	Homo sapiens clone 23950 mRNA sequence	2.0
	457233	AI355009	Hs.221698	ESTs	2.0
	457384	AA501760	Hs.18075	chromosome 9 open reading frame 3	2.0
15	457471	AW971364		gb:EST383453 MAGE resequenes, MAGL Homo	2.0

TABLE 27B

20	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
25	Pkey	CAT number	Accession
	409457	1132521_1	AW818081 AW392887 AW514700 AW392881
	409519	113722_1	AA075368 AA075369
	410008	116812_1	AA079552 BE142525 BE142527
	410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
	411050	1230330_1	AW814902 BE156656 BE156667 BE156590 BE156441 BE156447
30	411880	1263110_1	AW872477 BE088101 T05990
	411905	1265181_1	BE265067 BE264978 AW875420
	412303	1288130_1	AW936336 AW936339
	413136	1350379_1	BE066941 BE066911 BE066929 BE066925
	413499	1373910_1	BE144884 H97942
35	413875	1396766_1	BE176776 H85072
	415094	1522103_1	D59513 D59515 D80174 D59514
	415362	1534980_1	F06735 R55896 R12110 H08697
	416624	1604694_1	H69044 T47567 H75691 T50292
40	418378	174656_1	AW962081 AA218925 AA354237
	419546	185766_1	AA244199 AA244272 H57440
	419807	188252_1	R77402 AA262462 AA250988 R06794
	420637	195241_1	AW976153 AA278945 AA747691
	422429	216469_1	AA310527 AW962295 Z4865 H06641
45	423377	22769_1	AL049377 AL079930 AL047223 AW885968 AA385235
	426384	266211_1	AI472078 AA377209 AA865807
	428637	293660_1	AW979268 AA878419 AA431342 AA431628
	430153	313709_1	AW968128 AA468102 AA468165
	430844	324570_1	T94960 AA487679 T95013
50	431120	328264_1	AA492588 AA492498 AA492571
	431169	328799_1	AW971240 AA493843 AA493723
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
	432009	34025_1	AL137424 BE007148 T52277
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
55	432507	348711_1	BE391093 AA551334 BE389643
	432779	354024_1	AW979241 AA565006 AA847102
	432803	354267_1	AA565398 AW894072 H97930
	432869	355475_1	AW974094 AA569074 AA602574
	432974	356950_1	BE348793 AA573118 N79366
60	433492	367934_1	AW605849 AW262898 N41060 AA594852
	433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
	433687	373061_1	AA743991 AA604852 AW272737
	434803	393471_1	AW974640 AA649516 N75626
	436148	41500_1	BE005252 AK000786
	437327	43610_1	AL353942 AW994305
65	438909	46684_1	AF085839 R69137 AW188788 R69254
	440320	491930_1	AA879294 N67538 AI474541
	444314	600667_1	AI140497 AW749625 AW749626 AW749644
	444610	612257_1	AI174783 R83569 R12271
70	446346	673545_1	AI290205 AW235762 AI651268
	447197	711623_1	R36075 AI366546 R36167
	448404	761515_1	BE089973 AI498612 AW805032
	449299	80436_1	AA299919 AW957012 AA001107 T83631 BE156389
	449540	80945_2	AA001713 H63836
	449677	81270_1	AA002071 AA002232 T99209
75	450522	837264_1	AI698839 AI909260 AI909259
	451024	85565_1	AA442176 AA259181
	451381	867770_1	BE241831 AW249135 BE548847 AW250245
	452163	902067_1	AI863140 W80703 R43474
	452293	909195_1	AI871833
80	452453	918300_1	AI902519 AI902518 AI902516
	452542	921410_1	AW812256 AW812257 AI906423 AI906422
	452771	930983_1	T05477 T07855 AI917711
	454359	1130674_1	N71277 AW390764

454693 1229132\_1 AW813428 AW813444 AW813367 AW813368 AW813429 AW813424  
 455024 1249196\_1 AW851309 AW850888 AW851419 AW851412 AW851299  
 455226 1262534\_1 AW902103 AW869012 AW869139  
 455235 1265634\_1 AW875951 AW875950 AW875936 AW875948 AW875939 AW875957  
 455673 1349656\_1 BE065939 BE066079 BE065956  
 455807 1370914\_1 BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108  
 456034 142696\_1 AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367  
 BE011368 BE011362 BE011215 BE011365 BE011363  
 457471 340916\_1 AW971364 AA525021 AA570759  
 457620 371514\_1 AA602711 BE078290  
 458154 491768\_1 AW816379 AA888282 AA879046 AA879195  
 459267 966605\_1 AJ003631 AJ003650 AJ003651

TABLE 27C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source: 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400610	9887671	Minus	117606-117928,124040-124147
400880	9931121	Plus	29235-29336,36363-36580
401049	7232177	Plus	149157-150692
401335	9884881	Plus	15736-16352
401575	7229804	Minus	76253-76364
401793	7263888	Minus	102945-103083
401987	4406829	Minus	72893-73021,76938-77049
402046	8072415	Plus	166394-166556,168167-168395
402222	9958106	Plus	3261-3834,3939-4269
402481	9797406	Plus	87891-88991
402629	9931216	Plus	33641-33775,34182-34372,36003-36084,40343-40612
403760	7712202	Minus	45910-46260,47563-47824
403903	7710671	Minus	101165-102597
403937	7711761	Minus	12609-12773
404043	9558573	Plus	29042-29135,46597-46699
404200	6010176	Minus	7066-7210
404274	9885189	Plus	104127-104318
404288	2769644	Plus	3512-3691
404289	2769644	Plus	15049-15286,30267-30457
404323	9719753	Minus	31913-32219
404488	8113286	Minus	64835-64994
404548	8570305	Minus	83896-84162
404593	9944086	Minus	74922-75788
404599	8705107	Plus	110443-110733
404916	7341826	Plus	91057-91188
405041	7547195	Plus	121230-121714
405095	8072599	Plus	138877-139066
405472	8439781	Plus	106297-106447,108462-108596
405494	8050952	Minus	70284-70518
405848	7651809	Minus	28135-28244
405963	8247786	Plus	4056-4699
406182	5923650	Minus	28256-28935
406485	7711305	Plus	125036-125422
406506	7711374	Minus	6843-8077
406554	7711566	Plus	106956-107121
406594	8248611	Minus	35543-35845

TABLE 28A: ABOUT 796 GENES DOWN-REGULATED IN LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 28A lists of about 796 genes that are downregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues sample expression was less than or equal to 0.1. The "average" normal lung tissue level was set to the 75<sup>th</sup> percentile amongst normal lung tissues. The "average" fibrosis expression level was set to the 95<sup>th</sup> percentile amongst fibrosis samples. In order to remove gene-specific background levels of non-specific hybridization, the 15<sup>th</sup> percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of normal lung to fibrosis

Pkey	ExAccn	Unigene ID	Unigene Title	R1
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	18.18
421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	9.39
404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	8.30
404795				5.56

	403211				5.46
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	5.43
	400489				5.19
5	425571	AJ007292	Hs.158306	ephrin-A2	5.19
	406357				5.08
	407979	AA046306	Hs.62927	ESTs	5.08
	452378	AA025855	Hs.19597	ESTs	4.78
	408053	AW139474	Hs.246862	ESTs	4.62
10	421770	AA374192	Hs.108124	ribosomal protein L41	4.52
	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	4.49
	402386				4.39
	402448				4.37
	448245	AI923551	Hs.170843	ESTs	4.31
15	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	4.29
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	4.24
	447768	X86400	Hs.19520	FXFD domain-containing ion transport reg	4.21
	405163				4.19
	437120	AI356125	Hs.157767	ESTs, Weakly similar to human HOXA2 [H.s	4.19
20	409020	AA062549	Hs.21162	ESTs	4.09
	431073	BE254470	Hs.249186	cone-rod homeobox	4.07
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	4.05
	403716				3.99
	424969	AW950928	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.94
25	404348				3.90
	407070	Y10209		gb:H.sapiens mRNA for CD30L protein	3.82
	412919	AI368680	Hs.816	SRY (sex determining region Y)-box 2	3.81
	402409				3.80
	456150	Z42308		gb:HSC0FB121 normalized infant brain cDN	3.79
30	427030	AA397600	Hs.97531	ESTs	3.76
	426328	AW631296		gb:hh83c09.y1 NCL_CGAP_GU1 Homo sapiens	3.74
	429307	AU076592	Hs.198951	jun B proto-oncogene	3.71
	400172				3.70
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	3.68
35	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 proline-r	3.68
	446850	R71245	Hs.174303	ESTs	3.67
	405147				3.64
	406821	AA977896	Hs.128873	ESTs, Highly similar to ALFA_HUMAN FRUCT	3.57
	402762				3.55
40	401496				3.50
	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	3.50
	402911				3.49
	425330	D25216	Hs.155650	KIAA0014 gene product	3.49
	438004	AA774984	Hs.220649	ESTs, Weakly similar to FCE2 MOUSE LOW A	3.46
45	448185	AI633040	Hs.172730	ESTs	3.46
	433367	AA584930	Hs.269451	ESTs, Weakly similar to XAP-5-like prote	3.43
	416596	H67669	Hs.38564	ESTs	3.41
	400545				3.39
	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB5	3.37
50	426507	AA380285		gb:EST93491 Supt cells Homo sapiens cDNA	3.35
	403479				3.34
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (iso	3.34
	401919				3.33
	449031	AI867502	Hs.271462	ESTs	3.33
55	400116				3.31
	401590				3.29
	401007				3.28
	404610	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	3.25
	408641	AW245207	Hs.5555	Homo sapiens cDNA FLJ13170 fis, clone NT	3.25
60	407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma viru	3.23
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-bi	3.23
	433232	AI658621	Hs.127769	ESTs	3.23
	457937	AW976930	Hs.128760	ESTs	3.23
	406101				3.18
	407080	Z38133	Hs.113973	myosin, heavy polypeptide 8, skeletal mu	3.18
65	419947	AW298744	Hs.118894	ESTs	3.16
	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H	3.16
	454019	D31846	Hs.37025	aquaporin 2 (collecting duct)	3.16
	428674	AA431734	Hs.104915	ESTs	3.14
70	402056				3.06
	425182	AF041259	Hs.155040	zinc finger protein 217	3.06
	425393	NM_000218	Hs.156115	potassium voltage-gated channel, KQT-IIk	3.06
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	3.05
	402158				3.03
75	404938				3.02
	403376				3.01
	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-ty	3.00
	402423				2.99
	416253	BE250659	Hs.15463	ESTs	2.99
80	435265	AA779958	Hs.185932	ESTs	2.99
	425655	BE614551	Hs.158675	ribosomal protein L14	2.98
	428704	AA432007	Hs.249484	ESTs	2.98
	425439	D38024	Hs.157425	double homeobox, 2	2.97
	445613	BE550889	Hs.158491	ESTs	2.97

	402714			2.96	
	403526			2.96	
	403605			2.95	
5	441852	AB028968	Hs.7989	KIAA1045 protein	2.95
	417629	T76945	Hs.64211	ESTs, Weakly similar to similar to acyl-	2.94
	447744	AA313230	Hs.19413	S100 calcium-binding protein A12 (calgr	2.91
	419821	AW967486	Hs.189119	ESTs	2.90
	446993	AI570964	Hs.164257	ESTs	2.89
10	414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	2.88
	423379	AI985349	Hs.157492	Homo sapiens cDNA FLJ14079 fis, clone HE	2.88
	440206	AI762232	Hs.46794	ESTs	2.88
	402212	AW502761	Hs.30909	KIAA0430 gene product	2.87
	406059				2.86
15	423548	AF007194	Hs.129782	mucin 3A, intestinal	2.86
	402051				2.85
	415196	AK000150	Hs.78185	MAX-like bHLHZIP protein	2.85
	455446	AW947749		gb:RC0-MT0005-130300-031-b01 MT0005 Homo	2.85
	442428	BE464988	Hs.298302	ESTs	2.84
	403247				2.83
20	404825				2.83
	459184	L35001	Hs.95669	ESTs	2.83
	402968				2.82
	417575	R00382	Hs.191199	ESTs	2.82
	404668				2.81
25	420619	AF130255	Hs.99430	testis zinc finger protein	2.81
	447241	BE382838	Hs.19322	ESTs	2.80
	448793	AI864581	Hs.215477	ESTs	2.79
	453014	AI937242	Hs.176590	ESTs	2.79
	446775	AI792836	Hs.232273	ESTs	2.78
30	455075	AW854850		gb:QV2-CT0261-201099-011-h03 CT0261 Homo	2.78
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	2.75
	457546	AA568484	Hs.153632	ESTs	2.75
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.74
35	433677	AI791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN A	2.74
	405703				2.73
	408840	AW277132	Hs.254880	ESTs	2.73
	413958	BE277913	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	2.73
	454421	BE409759	Hs.59563	Homo sapiens mRNA for FLJ00007 protein,	2.73
40	406702	Z20656	Hs.278432	myosin, heavy polypeptide 6, cardiac mus	2.72
	408664	R56362		gb:yg93c07.r1 Soares infant brain 1N1B H	2.72
	402457				2.71
	403612				2.71
	407049	X72632		(NONE)	2.71
45	415423	AA164743	Hs.187617	Homo sapiens cDNA FLJ13941 fis, clone Y7	2.70
	402862				2.69
	403540				2.69
	431465	AW293178	Hs.180086	ESTs	2.69
	406563				2.68
50	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.68
	426220	AI383475	Hs.171697	ESTs, Weakly similar to immunoglobulin s	2.68
	446707	AI591214	Hs.156336	ESTs	2.68
	447557	AW028809	Hs.229570	ESTs	2.68
	413529	U11874	Hs.846	interleukin 8 receptor, beta	2.67
55	403997				2.66
	408704	AA056635	Hs.5366	Homo sapiens cDNA: FLJ21522 fis, clone C	2.66
	407005	U20230		gb:Human guanyl cyclase C gene, partial	2.65
	405075				2.64
	430728	AW968522		gb:EST380598 MAGE resequences, MAGJ Homo	2.64
60	405327				2.63
	409419	BE207219	Hs.20474	ESTs, Highly similar to S17112 interfero	2.63
	434300	AA740944	Hs.116295	ESTs	2.63
	405895				2.62
	431929	AW294163	Hs.146127	ESTs	2.61
65	405217				2.60
	437569	AA760849	Hs.294052	ESTs	2.60
	419822	AW966864	Hs.255780	ESTs	2.59
	445918	AW014139	Hs.145656	ESTs	2.59
	446149	BE242960	Hs.203181	ESTs	2.59
70	457829	AI742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [H.sa	2.58
	404282				2.53
	409778	AW499705		gb:UI-HF-BR0p-ajk-b-05-0-UI.r1 NIH_MGC_5	2.53
	445353	BE551465	Hs.175211	ESTs	2.53
	458764	BE619386		gb:601473204F1 NIH_MGC_68 Homo sapiens c	2.53
75	402195				2.52
	404247				2.52
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.52
	402588				2.50
	432301	U34249	Hs.167075	ring finger protein 9	2.50
80	424958	AA984420	Hs.283659	ESTs	2.49
	442197	AW837912		gb:QV3-LT0048-260100-068-c02 LT0048 Homo	2.49
	415003	M11437	Hs.77741	kininogen	2.48
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	2.48
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1	2.47



	440424	AI991125	Hs.189109	Homo sapiens cDNA: FLJ21458 fis, clone C	2.47
	402153				2.46
	432152	AK000245	Hs.272790	Homo sapiens cDNA FLJ20238 fis, clone CO	2.46
5	454414	R55574	Hs.164675	ESTs	2.45
	401603				2.44
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.44
	408513	AW206468	Hs.103118	ESTs	2.43
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	2.42
10	400672				2.41
	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	2.41
	449748	H23963	Hs.32043	ESTs	2.41
	453756	AW139415	Hs.61906	ESTs	2.41
	400624				2.40
	403125				2.40
15	406118				2.39
	402165				2.38
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	2.38
	425515	W26609		gb:35f12 Human retina cDNA randomly prim	2.38
	402951				2.37
20	427886	AA417083	Hs.104789	ESTs	2.37
	447173	AW449385	Hs.157294	ESTs	2.37
	448703	BE613942	Hs.170890	Homo sapiens cDNA: FLJ21129 fis, clone C	2.37
	426344	H41821	Hs.169393	transcriptional activator of the c-fos p	2.36
25	401840				2.35
	403731				2.34
	405378				2.34
	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	2.34
	416559	AI039195	Hs.128060	ESTs, Weakly similar to cDNA EST yk481g5	2.34
30	438216	Z83952	Hs.252815	ESTs	2.34
	448427	BE395260		gb:601311130F1 NIH_MGC_44 Homo sapiens c	2.34
	451588	AW072057		gb:ws58g05.x1 NCL_CGAP_Brn25 Homo sapien	2.34
	423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA	2.33
	451172	AW206465	Hs.207423	ESTs	2.33
35	401015				2.32
	414705	BE464157	Hs.281455	ESTs	2.32
	439894	AA853077		gb:NHTBCae03a05f1 Normal Human Trabecula	2.31
	446305	AW270149	Hs.254515	ESTs, Moderately similar to AF248953 1 g	2.31
	453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker pr	2.29
40	418556	T02850		gb:FB12A9 Fetal brain, Stralagene Homo s	2.28
	457197	AB016092	Hs.197114	RNA binding protein; AT-rich element bin	2.28
	457275	AA463422	Hs.209431	ESTs	2.28
	458766	AW183618	Hs.188417	ESTs, Weakly similar to ZnT-3 [H.sapiens	2.28
	414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	2.27
45	430210	AL157426	Hs.235390	Homo sapiens mRNA; cDNA DKFZp761B101 (fr	2.27
	442614	AI269030		gb:qj73c12.x1 NCL_CGAP_Kid3 Homo sapiens	2.27
	402538				2.26
	439891	AL389940	Hs.109968	ESTs	2.26
	440056	BE294828	Hs.13323	hypothetical protein FLJ22059	2.26
50	406150				2.25
	426880	AA453482		gb:zx47a11.r1 Soares_testis_NHT Homo sap	2.25
	447129	AW014123	Hs.161402	ESTs	2.25
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.25
	456778	AI458309	Hs.117406	ESTs	2.24
55	401728				2.23
	404139				2.23
	414095	BE293546		gb:601186671F1 NIH_MGC_15 Homo sapiens c	2.23
	432037	AW450592	Hs.300459	ESTs	2.23
	451965	AA021163	Hs.22287	ESTs	2.23
60	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	2.22
	427586	AA609661	Hs.190592	ESTs	2.22
	454108	AA161071	Hs.71465	squalene epoxidase	2.22
	429749	AI685174	Hs.22293	ESTs	2.21
	434507	AW511138	Hs.256581	ESTs	2.21
65	436652	AA724543	Hs.168824	ESTs	2.21
	437433	R74016	Hs.121581	ESTs	2.21
	401688				2.20
	441748	R14439	Hs.209194	ESTs	2.19
	453072	BE251845	Hs.221516	ESTs, Weakly similar to tetraspan TM4SF	2.19
70	400635				2.18
	417176	AW974475	Hs.143467	ESTs	2.18
	427858	NM_001971	Hs.21	elastase 1, pancreatic	2.18
	454886	AW837063		gb:QV1-LT0037-150200-069-g08 LT0037 Homo	2.18
	458232	BE217872	Hs.279537	ESTs	2.18
75	408922	R87388		gb:ym88g04.r1 Soares adult brain N2b4HB5	2.17
	423668	Y10148	Hs.131138	neurotensin receptor 2	2.17
	440338	R62431	Hs.12758	ESTs	2.17
	403115				2.16
	409125	R17268	Hs.301560	ESTs	2.16
80	426887	AI971975	Hs.212892	ESTs	2.16
	413811	BE168828		gb:QV1-HT0517-020400-145-f04 HT0517 Homo	2.15
	442962	AI025315	Hs.131615	ESTs	2.15
	403921				2.14
	413140	T06607	Hs.6846	hypothetical protein FLJ13055	2.14

	421996	AW583807	Hs.1460	glucagon	2.14
	436130	AA341497	Hs.31408	ESTs	2.14
	407243	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	2.13
5	407708	AF019968	Hs.37936	suppressor of variegation 3-9 (Drosophil	2.13
	442792	AI352340	Hs.131194	ESTs	2.12
	454406	AA213605	Hs.267861	ESTs	2.12
	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	2.11
	433963	AI218808	Hs.187778	ESTs	2.11
10	400736				2.10
	406343				2.10
	409702	AI752244	Hs.285749	Human DNA from chromosome 19-specific co	2.10
	432092	AF135026		gb:Homo sapiens kallikrein-like protein	2.10
	441915	AI566116	Hs.207066	ESTs, Weakly similar to FOG [M.musculus]	2.10
15	453147	AA733098	Hs.279909	CGI-05 protein	2.10
	415604	Z44177	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.08
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.08
	401211	AJ004832	Hs.5038	neuropathy target esterase	2.07
	413808	J00287	Hs.182183	caldesmon 1	2.07
20	414433	BE407755	Hs.169100	Homo sapiens cDNA FLJ12529 fis, clone NT	2.07
	421978	AJ243662	Hs.110196	NICE-1 protein	2.07
	431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	2.07
	433605	AI378012	Hs.147953	ESTs	2.06
	449383	AW444712	Hs.196573	ESTs	2.06
25	455652	BE064675		gb:RC1-BT0313-301299-012-h11 BT0313 Homo	2.05
	402382				2.04
	407282	AI345597	Hs.254727	ESTs	2.04
	457273	AI167145	Hs.165538	ESTs	2.04
	459073	AW968616	Hs.296234	ESTs, Highly similar to mitogen-activate	2.04
30	402394				2.03
	428875	AW451624	Hs.178202	ESTs	2.03
	456634	AA609911	Hs.109012	ESTs	2.03
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.02
	439281	AA100768	Hs.48485	ESTs	2.02
35	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	2.02
	401122				2.01
	444340	AI143198	Hs.143561	ESTs	2.01
	455104	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	2.01
	415011	AW963085		gb:EST375158 MAGE resequences, MAGH Homo	2.00
40	440144	AW082297	Hs.88523	ESTs	2.00
	403183				1.99
	409802	AW500732		gb:UI-HF-BN0-akm-h-07-0-UI.r1 NIH_MGC_50	1.98
	430144	AI732722	Hs.187694	ESTs	1.98
	444580	AI168365	Hs.268663	ESTs	1.98
45	401704				1.97
	401810				1.97
	424473	AK001405	Hs.148584	Homo sapiens cDNA FLJ10543 fis, clone NT	1.97
	438573	AW135084	Hs.299865	ESTs	1.97
	412921	BE009345	Hs.128942	ESTs	1.96
50	422233	AB002058	Hs.113275	purinergic receptor P2X-like 1, orphan r	1.96
	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin	1.96
	410285	AA083609		gb:zm63d05.r1 Stratagene fibroblast (937	1.95
	414323	NM_014759	Hs.239500	KIAA0273 gene product	1.94
	428119	AW298211	Hs.255737	ESTs	1.94
55	424510	AK001841	Hs.149797	hypothetical protein FLJ10979	1.92
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	1.92
	429785	H82114	Hs.301769	ESTs	1.92
	437344	R90921	Hs.6846	hypothetical protein FLJ13055	1.92
	451819	AI819096	Hs.249260	ESTs	1.92
60	459060	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein	1.92
	422664	AA315933	Hs.120879	ESTs	1.91
	432247	AA531287	Hs.105805	ESTs	1.91
	453820	R77494	Hs.75416	DAZ associated protein 2	1.91
	400675				1.90
65	405556	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	1.90
	407099	M94891	Hs.278423	pregnancy specific beta-1-glycoprotein 4	1.90
	440297	BE560553	Hs.205450	Homo sapiens cDNA: FLJ22570 fis, clone H	1.90
	443104	AA088470	Hs.83135	p53-responsive gene 6	1.90
	444329	W73753	Hs.58330	ESTs	1.90
70	402690				1.89
	432354	AW137262	Hs.192713	ESTs	1.89
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.88
	443322	AI825817	Hs.143272	ESTs	1.88
	458185	AI762757	Hs.129869	ESTs, Weakly similar to AF113685 1 PRO09	1.88
75	459072	AI815978	Hs.160427	ESTs	1.88
	402534				1.87
	409689	AA078492		gb:7P04D11 Chromosome 7 Placental cDNA L	1.87
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	1.87
	430176	AL161995	Hs.234775	neurturin	1.87
80	430631	AJ003147	Hs.278464	olfactory receptor, family 1, subfamily	1.87
	433114	AA121579		gb:zn77f02.r1 Stratagene NT2 neuronal pr	1.87
	439254	U57352	Hs.6517	amiloride-sensitive cation channel 1, ne	1.87
	448461	AW166358	Hs.124979	ESTs	1.87
	450675	AA010662	Hs.188639	ESTs	1.87

	401767				1.86
	449891	N64867	Hs.37848	ESTs	1.85
	400527				1.84
5	428581	AA430570	Hs.104881	ESTs	1.84
	443647	AV653846	Hs.126251	Homo sapiens Chromosome 16 BAC clone CIT	1.84
	444785	AV651441	Hs.282475	ESTs	1.84
	449566	AA001778	Hs.288156	Homo sapiens cDNA: FLJ21819 fis, clone H	1.84
	436752	AW298529	Hs.255774	ESTs	1.83
10	437405	AA338837	Hs.42547	Homo sapiens cDNA FLJ13975 fis, clone Y7	1.83
	449174	T66136	Hs.12880	ESTs	1.83
	449887	AW080843	Hs.200275	ESTs	1.83
	453261	AA034116	Hs.118494	ESTs	1.83
	454243	AW241901	Hs.250683	ESTs	1.83
15	459188	AA216382	Hs.30002	SH3-containing protein SH3GLB2	1.83
	424334	AA393460		gb:z171e05.r1 Soares_testis_NHT Homo sap	1.82
	432150	AK000224	Hs.272789	hypothetical protein FLJ20217	1.82
	408123	AW163377		gb:au94e02.y1 Schneider fetal brain 0000	1.81
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	1.80
20	442196	AI902646	Hs.31844	Homo sapiens cDNA FLJ12586 fis, clone NT	1.80
	421419	M99587	Hs.104134	homeo box (H6 family) 1	1.79
	405420				1.78
	405737				1.78
	414016	AA134594	Hs.71528	ESTs	1.78
25	415744	AW964850	Hs.279307	ESTs	1.78
	420375	AF182077	Hs.97244	glioma tumor suppressor candidate region	1.78
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	1.78
	421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila) homolog 1	1.77
	401743				1.75
	405187				1.75
30	442763	AI017037	Hs.131121	ESTs	1.75
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	1.75
	413248	T64858	Hs.21433	ESTs	1.74
	423913	NM_016436	Hs.301055	hepatocellular carcinoma-associated anti	1.74
35	439999	AA115811	Hs.6838	ras homolog gene family, member E	1.74
	440185	AW104546	Hs.270929	ESTs	1.74
	450482	AI697844	Hs.221720	ESTs	1.74
	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYD	1.73
	420476	AW575863	Hs.136232	ESTs	1.73
40	428748	AW593206	Hs.98785	ESTs	1.73
	431148	AA502653	Hs.28621	ESTs	1.73
	447205	BE617015	Hs.11006	ESTs	1.73
	455994	BE179190		gb:RC0-HT0613-210300-032-f07 HT0613 Homo	1.73
	401039				1.72
	403251				1.72
45	409762	AW498884	Hs.257970	ESTs	1.72
	440914	AA909552	Hs.143884	ESTs	1.72
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	1.72
	409605	AW444477	Hs.258507	ESTs	1.71
50	441212	AW242447	Hs.146182	ESTs, Weakly similar to lactase phlorizi	1.71
	445624	AW140103	Hs.78880	ilvB (bacterial acetolactate synthase)-I	1.71
	458619	AA872064	Hs.301218	ESTs, Weakly similar to Unknown gene pro	1.71
	401969				1.70
	403327				1.70
55	407245	X90568	Hs.172004	titin	1.70
	417361	NM_000275	Hs.82027	oculocutaneous albinism II (pink-eye dil	1.70
	436034	AF282693	Hs.150185	inflammation-related G protein-coupled r	1.70
	442682	AI014545	Hs.231027	EST	1.70
	458494	AI380906	Hs.158436	ESTs	1.70
	404682				1.69
60	407402	AF035303		gb:Homo sapiens clone 23943 mRNA sequenc	1.69
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	1.69
	440362	AA883812	Hs.125508	ESTs	1.69
	448866	BE297743	Hs.284203	myogenic factor 3	1.69
	402201				1.68
65	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.68
	403186				1.67
	409543	AW410200		gb:fh05b12.x1 NIH_MGC_17 Homo sapiens cD	1.67
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate di	1.67
70	450391	AI694522	Hs.202280	ESTs	1.67
	408919	AW295352	Hs.251836	ESTs	1.66
	416136	H45027	Hs.181770	ESTs	1.66
	416865	H97863	Hs.42456	ESTs	1.66
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	1.66
75	437237	BE513073		gb:601171435F1 NIH_MGC_15 Homo sapiens c	1.66
	429134	AA446953	Hs.99004	ESTs	1.65
	445041	T64183	Hs.11398	ESTs	1.65
	453240	AI969564	Hs.284249	Homo sapiens cDNA: FLJ22334 fis, clone H	1.65
	405243				1.64
80	426039	BE265133	Hs.217493	annexin A2	1.64
	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate	1.64
	435942	R06285	Hs.191215	ESTs	1.64
	448106	AI800470	Hs.171941	ESTs	1.64
	408591	AF015224	Hs.46452	mammaglobin 1	1.63

	410881	AW809157		gb:RC0-ST0118-041099-031-c07_1 ST0118 Ho	1.63
	417743	R14738	Hs.8312	ESTs, Weakly similar to AF170723 1 prote	1.62
	430632	AC004597	Hs.248088	olfactory receptor, family 10, subfamily	1.62
5	448651	BE246440	Hs.93728	pre-B-cell leukemia transcription factor	1.62
	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, c	1.62
	459499	AW402653	Hs.28355	Homo sapiens cDNA: FLJ22402 fis, clone H	1.62
	412374	X01388	Hs.73849	apolipoprotein C-III	1.61
	419113	AI446586	Hs.21835	ESTs	1.61
10	426795	AI810474	Hs.196945	ESTs	1.61
	426998	BE274360		gb:601121068F1 NIH_MGC_20 Homo sapiens c	1.61
	428407	NM_003963	Hs.184194	transmembrane 4 superfamily member 5	1.61
	444475	C75571		gb:C75571 Human pancreatic islet Homo sa	1.61
	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	1.61
15	456275	AW976183	Hs.88414	ESTs, Weakly similar to dJ512E2.1 [H.sap	1.61
	414060	BE246327		gb:TCBAP1E1967 Pediatric pre-B cell acut	1.60
	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	1.60
	428651	AF196478	Hs.188401	annexin A10	1.60
	443853	AI089064	Hs.250644	ESTs	1.60
	407007	U22961		gb:Human mRNA clone with similarity to L	1.59
20	412067	N45697		gb:yy78d01.r1 Soares_multiple_sclerosis_	1.59
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	1.59
	448619	AI867182	Hs.202255	ESTs	1.59
	403665				1.58
25	407524	X64985		gb:H.sapiens mRNA HTPCRX11 for olfactory	1.58
	424286	AA338285	Hs.90744	proteasome (prosome, macropain) 26S subu	1.58
	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	1.57
	430218	AW998865	Hs.186703	ESTs	1.57
	431882	NM_001426	Hs.271977	engrailed homolog 1	1.57
30	450797	AI761930	Hs.205127	ESTs	1.57
	455366	AW947563		gb:RC0-MT0004-140300-031-g11 MT0004 Homo	1.57
	408421	AW193734	Hs.253067	ESTs	1.56
	421907	BE018556	Hs.109358	ATPase, Class V, type 10B	1.56
	432742	AA564453	Hs.162339	ESTs	1.56
35	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	1.56
	439543	W75935	Hs.146083	ESTs	1.56
	443317	AI051601	Hs.200191	ESTs	1.56
	449097	BE271708	Hs.95110	ESTs, Weakly similar to PIP6_HUMAN 1-PHO	1.56
	457127	AA194554	Hs.183434	ATPase, H+ transporting, lysosomal (vacu	1.56
40	407387	AB000895		gb:Homo sapiens mRNA for cadherin FIB1,	1.55
	418837	U48263	Hs.89040	prepronociceptin	1.55
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.55
	458475	AI650322	Hs.143249	ESTs	1.55
	402561				1.54
45	411187	AW821291		gb:PM3-ST0307-241299-002-f03 ST0307 Homo	1.54
	419224	NM_012189	Hs.252716	fibrousheathin II	1.54
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	1.53
	415426	Z41991	Hs.23197	ESTs	1.53
	421428	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	1.53
50	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.53
	428489	AI807459	Hs.98582	ESTs	1.53
	437728	AA766719		gb:aa39c09.s1 NCL_CGAP_GCB1 Homo sapiens	1.53
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.52
	414932	C14577	Hs.194517	ESTs	1.52
55	433500	AF064255	Hs.111401	very long-chain acyl-CoA synthetase homo	1.52
	439688	AW445181	Hs.209637	Homo sapiens cDNA FLJ12921 fis, clone NT	1.52
	453391	AW600302	Hs.232655	ESTs	1.52
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	1.51
	436895	AF037335	Hs.5338	carbonic anhydrase XII	1.51
60	443012	AI566813	Hs.132278	ESTs	1.51
	415824	D42039	Hs.78871	mesoderm development candidate 2	1.50
	445152	AI214667	Hs.283597	ESTs	1.50
	455941	BE160011	Hs.129998	Homo sapiens cDNA FLJ14267 fis, clone PL	1.50
	457889	AL035864	Hs.69517	ESTs, Highly similar to differentially e	1.50
65	458503	AL133933	Hs.64310	interleukin 11 receptor, alpha	1.50
	400694				1.49
	420937	AW966719	Hs.1340	collpase, pancreatic	1.49
	426752	X69490	Hs.172004	titin	1.49
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.49
70	428874	W32133	Hs.194366	transthyretin (prealbumin, amyloidosis t	1.49
	444287	AI033077	Hs.10755	dihydropyrimidinase	1.49
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.49
	425747	AI457620	Hs.205360	ESTs	1.48
	432378	AI493046	Hs.146133	ESTs	1.48
75	447999	AW138840	Hs.201778	ESTs	1.48
	453888	AW450670	Hs.252819	ESTs	1.48
	406667	M12523	Hs.75442	albumin	1.47
	418129	X52997	Hs.1144	glycoprotein IX (platelet)	1.47
	426309	AI912555	Hs.157195	peptide YY, 2 (seminalplasmin)	1.47
80	426755	BE253469		gb:601108143F1 NIH_MGC_16 Homo sapiens c	1.47
	414258	AA203285	Hs.294141	ESTs, Weakly similar to dJ733D15.1 [H.sa	1.46
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	1.46
	420562	AI345569	Hs.190046	ESTs	1.46
	425011	T51986	Hs.283108	hemoglobin, gamma G	1.46

	443050	AI612788	Hs.132348	ESTs, Weakly similar to diaphanous 1 [H.	1.46
	411074	XG0435	Hs.68137	adenylate cyclase activating polypeptide	1.45
	434680	T11738	Hs.127574	ESTs	1.45
5	454771	AW819939	Hs.273629	ESTs	1.45
	415672	N53097	Hs.193579	ESTs	1.44
	418141	AW845738	Hs.171118	Homo sapiens mRNA for FLJ00026 protein,	1.44
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.43
	418197	AA214253		gb:zn58g02.r1 Stratagene muscle 937209 H	1.43
10	431821	AW452256	Hs.271221	hypothetical protein FLJ20064	1.43
	455433	AW939463		gb:QV1-DT0072-310100-056-g02 DT0072 Homo	1.43
	407743	AW814118		gb:MR3-ST0203-151199-011-d09 ST0203 Homo	1.42
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	1.42
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	1.42
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.42
15	452456	BE080763		gb:QV1-BT0631-150200-071-f09 BT0631 Homo	1.42
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit Vb	1.42
	408349	BE546947	Hs.44276	homeo box C10	1.41
	420391	AA456891	Hs.79123	KIAA0084 protein	1.41
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	1.41
20	449329	AW752783		gb:IL3-CT0219-221199-029-F03 CT0219 Homo	1.41
	453615	AA195712	Hs.132696	ESTs	1.41
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	1.40
	420287	AA740907	Hs.88297	ESTs	1.40
25	427583	M82962	Hs.179704	meprin A, alpha (PABA peptide hydrolase)	1.40
	418787	AW296134	Hs.86999	ESTs	1.39
	422072	AB018255	Hs.111138	KIAA0712 gene product	1.39
	425988	BE045897	Hs.274454	ESTs	1.39
	428087	AA100573	Hs.182421	troponin C2, fast	1.39
30	438136	NM_002390	Hs.6088	a disintegrin and metalloproteinase doma	1.39
	455579	BE011320		gb:PM3-BN0218-090500-002-d09 BN0218 Homo	1.39
	402316				1.38
	417084	H08370	Hs.33067	ESTs	1.38
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	1.38
35	433787	AI472951	Hs.173688	ESTs	1.38
	413830	BE263439	Hs.13144	HSPC160 protein	1.37
	423576	NM_000383	Hs.129829	autoimmune regulator (automimmune polyen	1.37
	401886				1.36
	412688	AW583062	Hs.74502	chymotrypsinogen B1	1.36
40	401238				1.34
	421511	AA488940	Hs.105216	hypothetical protein FLJ11125	1.34
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11	1.34
	425450	U14755	Hs.157449	LIM homeobox protein 1	1.34
	427333	AF067797	Hs.176658	aquaporin 8	1.34
45	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	1.34
	445204	AW135523	Hs.245853	ESTs	1.34
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (f	1.34
	456379	W22206		gb:63E10 Human retina cDNA Tsp5091-cleav	1.34
	457416	BE142052		gb:CM3-HT0137-150999-011-b05 HT0137 Homo	1.34
50	415741	AI902761	Hs.272087	ESTs	1.33
	422260	AA315993	Hs.105484	ESTs, Weakly similar to LITB_HUMAN LITHO	1.33
	429188	AB011171	Hs.198037	KIAA0599 protein	1.33
	442776	AW959498	Hs.8709	chymotrypsin C (caldecrin)	1.33
	454748	AW862014		gb:RC3-CT0347-160200-013-d09 CT0347 Homo	1.33
55	437744	AW290905	Hs.300288	ESTs, Weakly similar to CGHU2E collagen	1.32
	451997	AA021351	Hs.158497	KIAA0724 gene product	1.32
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	1.32
	411879	BE145354	Hs.273758	Homo sapiens cDNA: FLJ23112 fis, clone L	1.31
	424304	NM_001395	Hs.144879	dual specificity phosphatase 9	1.31
60	401442				1.30
	403942				1.30
	443687	F13040	Hs.182937	peptidylprolyl isomerase A (cyclophilin	1.30
	401624				1.29
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	1.29
65	418575	AA225313	Hs.222886	ESTs	1.29
	419818	AI657122	Hs.301931	ESTs	1.29
	429845	AB020337	Hs.225943	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	1.29
	447586	AI081980	Hs.285829	solute carrier family 25 (mitochondrial	1.29
	407013	U35637		gb:Human nebulin mRNA, partial cds	1.28
70	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	1.28
	429780	AL137518	Hs.300388	ESTs	1.28
	453539	AW731886	Hs.95196	ESTs, Weakly similar to T20B12.3 [C.eleg	1.28
	400846				1.27
	420257	AA257035	Hs.190042	ESTs	1.27
75	429184	AF095735	Hs.198003	sarcosine dehydrogenase	1.27
	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	1.27
	444412	AI147652	Hs.216381	Homo sapiens clone HH409 unknown mRNA	1.27
	451139	AW293316	Hs.205558	ESTs	1.27
	431284	AA570148	Hs.126783	Homo sapiens cDNA: FLJ22610 fis, clone H	1.26
80	431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	1.26
	406158				1.25
	419648	T73661	Hs.91877	ESTs, Highly similar to THIH_HUMAN THYRO	1.25
	430681	AW969675	Hs.291232	ESTs	1.25
	434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.25

	436217	T53925	Hs.107	fibrinogen-like 1	1.25
	440089	AA064468	Hs.135646	ESTs	1.25
	446787	U67167	Hs.315	mucin 2, intestinal/tracheal	1.25
5	448207	AI475490	Hs.170577	ESTs	1.25
	454869	AW836004		gb:PM0-LT0019-170200-001-d11 LT0019 Homo	1.25
	413271	AA127873	Hs.114949	ESTs	1.24
	422619	AA313322		gb:EST185218 Colon carcinoma (HCC) cell	1.24
	422796	AW897265		gb:CM0-NN0057-150400-335-a04 NN0057 Homo	1.24
10	427530	AA405093	Hs.126519	ESTs	1.24
	437727	AA766707	Hs.153039	ESTs	1.24
	426435	AI827946	Hs.189118	ESTs	1.23
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	1.22
	407964	AW130334	Hs.281111	ESTs	1.21
	430828	AI763257	Hs.86327	Homo sapiens cDNA: FLJ22431 fis, clone H	1.21
15	432029	D31628	Hs.2899	4-hydroxyphenylpyruvate dioxygenase	1.21
	457843	AW138211	Hs.128746	ESTs	1.21
	413242	BE074165		gb:PM3-BT0564-030300-002-e12 BT0564 Homo	1.20
	446057	AI420227	Hs.149358	ESTs	1.20
	447198	D61523	Hs.283435	ESTs	1.20
20	449513	AI653232	Hs.195059	EST	1.20
	415566	F12119		gb:HSC35H091 normalized infant brain cDN	1.19
	423315	R54109	Hs.26096	ESTs	1.19
	455817	BE142384		gb:CM2-HT0144-210999-011-d04 HT0144 Homo	1.19
25	459354	BE514778		gb:601317094F1 NIH_MGC_9 Homo sapiens cD	1.19
	408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	1.18
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.18
	419251	NM_001486	Hs.89771	glucokinase (hexokinase 4) regulatory pr	1.18
	456702	AI684534		gb:wa72f10.x1 Soares_NFL_T_GBC_S1 Homo s	1.18
30	458009	AI221409	Hs.144983	ESTs	1.18
	410193	AJ132592	Hs.59757	zinc finger protein 281	1.17
	417779	AA829526	Hs.124977	ESTs	1.17
	435101	AI743156	Hs.131064	ESTs	1.17
	445360	AI798776	Hs.156029	ESTs	1.17
	414160	BE257021		gb:601117426F1 NIH_MGC_16 Homo sapiens c	1.15
35	418078	AA521268	Hs.86508	ESTs	1.15
	425133	NM_002613	Hs.154729	3-phosphoinositide dependent protein kin	1.15
	437935	AW939591	Hs.5940	hypothetical protein FLJ20063	1.15
	446377	AW014022	Hs.170953	ESTs	1.15
40	420097	AA700127	Hs.190504	ESTs	1.13
	446591	H44186	Hs.15456	PDZ domain containing 1	1.13
	451477	AI798425	Hs.42710	ESTs	1.13
	459197	BE244587		gb:TCBAP2E0851 Pediatric pre-B cell acut	1.13
	428934	AF039401	Hs.194659	chloride channel, calcium activated, fam	1.12
45	431191	AW972118	Hs.100002	HSPC162 protein	1.12
	424403	F05183	Hs.1799	CD1D antigen, d polypeptide	1.11
	433546	AI075877	Hs.125461	Homo sapiens cDNA FLJ11539 fis, clone HE	1.11
	451179	W05469	Hs.31818	ESTs	1.11
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	1.10
50	420774	AA280209	Hs.165270	ESTs	1.10
	428887	AA437009	Hs.98984	ESTs	1.10
	430582	AI215509	Hs.143964	ESTs	1.10
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	1.10
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.09
55	417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo	1.09
	456387	W28876		gb:52h7 Human retina cDNA randomly prime	1.09
	427965	D00306	Hs.183864	elastase 3B	1.08
	447388	AW630534	Hs.76277	ESTs, Weakly similar to TB2 [H.sapiens]	1.08
	413841	M34276	Hs.75576	plasminogen	1.07
60	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.07
	433313	W20128	Hs.296039	ESTs	1.07
	439450	R51613	Hs.125304	ESTs	1.07
	458963	AI701393	Hs.278728	Rad and Gem-related 2 (rat homolog)	1.07
	405161				1.06
65	406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	1.06
	424294	BE299311		gb:601119256F1 NIH_MGC_17 Homo sapiens c	1.06
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.06
	444687	AW972109	Hs.135107	ESTs	1.06
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	1.06
70	421243	AW873803	Hs.102876	pancreatic lipase	1.05
	444290	AA262496	Hs.29280	ESTs	1.05
	407984	AW134708	Hs.243569	ESTs	1.04
	439706	AW872527	Hs.59761	ESTs	1.04
	402194				1.03
75	427506	AK000134	Hs.179100	hypothetical protein FLJ20127	1.03
	428819	AL135623	Hs.193914	KIAA0575 gene product	1.03
	434590	T47232		gb:yb64b08.s1 Stralagene ovary (937217)	1.03
	416378	AW044467	Hs.73708	ESTs, Weakly similar to A57291 cytokine	1.02
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	1.02
80	443316	AI478463	Hs.18443	ESTs	1.02
	428585	AB007863	Hs.185140	KIAA0403 protein	1.01
	400440	X83957	Hs.83870	nebulin	1.00
	404619	BE514535	Hs.77171	minichromosome maintenance deficient (S.	1.00
	407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB H	1.00

	408052	AW501117	Hs.283585	ESTs	1.00
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	1.00
5	410234	NM_003837	Hs.61255	fructose-1,6-bisphosphatase 2	1.00
	410319	R23413	Hs.71935	putative zinc finger protein from EUOIM	1.00
	411000	N40449	Hs.201619	ESTs, Weakly similar to SEB4B [H.sapiens	1.00
	412098	AI493054	Hs.158968	ESTs	1.00
	412446	AI768015	Hs.92127	ESTs	1.00
10	412637	AA115097	Hs.261313	ESTs	1.00
	413147	BE067271		gb:PM2-BT0349-161299-001-b05 BT0349 Homo	1.00
	413597	AW302885	Hs.117183	ESTs	1.00
	414117	W88559	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	1.00
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	1.00
15	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	1.00
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	1.00
	419768	T72104	Hs.93194	apolipoprotein A-I	1.00
	420182	Z44245	Hs.22999	ESTs	1.00
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	1.00
20	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.00
	421204	AW081587	Hs.165051	ESTs	1.00
	422189	AF252292	Hs.112933	Tax interaction protein 40	1.00
	422792	AI951548	Hs.135163	ESTs	1.00
	423371	AU076819	Hs.1650	solute carrier family 26, member 3	1.00
25	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.00
	424922	BE386547	Hs.217112	ESTs, Weakly similar to Similarity to Ye	1.00
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	1.00
	425545	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	1.00
	425983	AK000226	Hs.165619	mucin and cadherin-like	1.00
30	426004	AW600300	Hs.124123	ESTs, Weakly similar to syncollin [R.nor	1.00
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	1.00
	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	1.00
	429027	AL022314	Hs.194750	Human DNA sequence from clone 1170K4 on	1.00
	429231	AA813214		gb:aj32e09.s1 Soares_testis_NHT Homo sap	1.00
35	429441	AJ224172	Hs.204096	lipophilin B (uterglobin family member)	1.00
	429930	AI580809	Hs.99569	ESTs	1.00
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1.00
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	1.00
	431845	AA516469	Hs.270554	ESTs	1.00
40	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	1.00
	433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00
	434452	AA634333	Hs.116822	ESTs	1.00
	435499	R89344	Hs.14148	ESTs	1.00
	438433	AB018274	Hs.6214	KIAA0731 protein	1.00
45	442403	AW207724	Hs.129516	ESTs	1.00
	442803	AI675298	Hs.199917	ESTs	1.00
	443266	AI277101	Hs.25890	ESTs, Weakly similar to transducin [H.sa	1.00
	444656	AI277924	Hs.145199	ESTs	1.00
	445573	AI439646	Hs.157494	ESTs, Weakly similar to KIAA0676 protein	1.00
50	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00
	447359	NM_012093	Hs.18268	adenylate kinase 5	1.00
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac mus	1.00
	448657	BE147857	Hs.293841	ESTs, Weakly similar to KIAA0672 protein	1.00
	449238	AA428229	Hs.85524	muscle-specific RING-finger protein homo	1.00
55	450085	AW293791	Hs.60162	Homo sapiens cDNA: FLJ21528 fis, clone C	1.00
	450390	N93227	Hs.98403	ESTs	1.00
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	1.00
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	1.00
	452528	AA742457	Hs.291479	ESTs	1.00
60	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	1.00
	453754	AW972580	Hs.172753	ESTs	1.00
	453991	AW014915	Hs.273741	ESTs	1.00
	454517	AW803340		gb:IL2-UM0079-090300-050-D02 UM0079 Homo	1.00
	459367	BE148877		gb:CM4-HT0244-111199-040-h12 HT0244 Homo	1.00
65	408021	AW137133	Hs.245867	ESTs	0.99
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	0.99
	437206	AW975934	Hs.283382	ESTs, Weakly similar to Protein sequence	0.99
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial	0.98
	425878	AW964806	Hs.38085	ESTs, Weakly similar to putative glycine	0.98
70	441888	AI733306	Hs.128071	hypothetical protein FLJ21302	0.98
	423068	M25629	Hs.123107	kallikrein 1, renal/pancreas/salivary	0.97
	453534	NM_014796	Hs.33187	KIAA0748 gene product	0.97
	457787	AA683268		gb:ae92b04.s1 Stratagene schizo brain S1	0.97
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	0.96
75	422069	AJ010063	Hs.111110	titin-cap (telethonin)	0.96
	425260	L47726	Hs.1870	phenylalanine hydroxylase	0.96
	418406	X73501	Hs.84905	cytokeratin 20	0.95
	425670	AW968536	Hs.190146	ESTs	0.95
	416373	AA195845	Hs.73680	ESTs, Weakly similar to AF198455 1 epith	0.94
80	452243	AL355715	Hs.28555	programmed cell death 9	0.94
	411908	L27943	Hs.72924	cytidine deaminase	0.93
	415067	AI264969	Hs.929	myosin, heavy polypeptide 7, cardiac mus	0.93
	437156	AI916600	Hs.121194	Homo sapiens cDNA: FLJ21569 fis, clone C	0.93
	450685	L15533	Hs.423	pancreatitis-associated protein	0.92

	427450	AB014526	Hs.178121	KIAA0626 gene product	0.91
	432440	X63597	Hs.2996	sucrase-isomaltase	0.91
	426651	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.90
5	414910	X12662	Hs.29679	cofactor required for Sp1 transcriptiona	0.89
	423317	AJ272204	Hs.64616	chromosome 12 open reading frame 3	0.89
	424735	U31875	Hs.152677	Homo sapiens cDNA FLJ20338 fis, clone HE	0.89
	439751	AA196090	Hs.50794	Homo sapiens mRNA full length insert cDN	0.89
	452689	F33868	Hs.284176	transferrin	0.89
10	446240	AI535736	Hs.170165	ESTs	0.88
	449110	H56112	Hs.277053	ESTs	0.88
	453817	AW755253	Hs.61920	ESTs	0.88
	428221	U96781	Hs.183075	ESTs, Highly similar to Ca2+ ATPase of f	0.87
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	0.87
15	446525	AW967069	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone H	0.87
	453341	AI758912	Hs.296341	adenylyl cyclase-associated protein 2	0.87
	403740				0.86
	420156	AW449258	Hs.6187	ESTs	0.86
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFp434H1235 (f	0.86
20	421142	AW503944	Hs.130822	ESTs	0.85
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	0.85
	419415	AW451692	Hs.192036	ESTs	0.84
	423321	AB013885	Hs.126926	beta-ureidopropionase	0.84
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	0.84
25	433447	U29195	Hs.3281	neuronal pentraxin II	0.84
	403047				0.83
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	0.81
	407782	AA608956	Hs.112619	ESTs, Weakly similar to PQ0109 Purkinje	0.81
	405232				0.80
30	437776	AA768037	Hs.291671	ESTs	0.80
	415505	R39870	Hs.12548	ESTs	0.79
	444436	N25871	Hs.177337	ESTs	0.78
	409096	AA194412	Hs.50550	sarcomeric muscle protein	0.77
	432134	AI816782	Hs.122583	Homo sapiens cDNA: FLJ21934 fis, clone H	0.76
35	437066	AA743570	Hs.200935	ESTs	0.76
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	0.75
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	0.73
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	0.71
	420567	AK000812	Hs.98874	similar to proline-rich protein 48	0.71
40	447145	AA761073	Hs.192943	ESTs	0.71
	452103	R42764	Hs.3248	mutS (E. coli) homolog 6	0.71
	410929	H47233	Hs.30643	ESTs	0.70
	400301	X03635	Hs.1657	estrogen receptor 1	0.69
	415702	F28877		gb:HSPD18414 HM3 Homo sapiens cDNA clone	0.67
45	411396	C04646	Hs.85428	ESTs	0.65
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	0.65

TABLE 28B

50	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
55	Pkey	CAT number
	407743	1012151_1
	408123	1040435_1
	408432	1058667_1
60	408664	1073340_1
	408922	109017_1
	409368	112377_1
	409543	1138723_1
	409689	114833_1
65	409778	1154206_1
	409802	1155179_1
	410285	119128_1
	410881	1225682_1
	411187	1235092_1
	412067	1275641_1
70	413147	1350637_1
	413242	1355323_1
	413811	1391117_1
	414060	1413697_1
	414095	1416521_1
75	414160	1422273_1
	414580	1463848_1
	415011	151328_1
	415566	1539861_1
80	415702	1547874_1
	417998	171375_1
	418197	172864_1
	418464	1759038_-2
	418556	1767866_-1



	422619	218670_1	AA313322 BE408282 AA465612 BE073382
	422796	221500_1	AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361 T06241 AA326794 AL138130
5	424294	237907_1	BE299311 AA338954 AA338468 AW960907
	424334	238221_1	AA393460 AA338940 AW966277 AA419006
	424648	241947_1	AA344576 AA732430 AA344601
	425515	252721_1	W26609 W27360 AA358818
	426328	264901_1	AW631296 AA375484
10	426507	268382_1	AA380285 AW934727 AW934914
	426755	271382_1	BE253469 BE176417 BE176415 AA384133
	426880	273277_2	AA453482 AF012388
	426998	274259_1	BE274360
	429231	301463_1	AA813214 AI936567 AI743529 AA448279 AA994476 AI807452 AI218180 AA972858
15	430728	322706_1	AW968522 AA485112 AA485162 AW968698
	432092	34124_1	AF135026 AA583908
	433114	35904_1	AA121579 AB005217
	434590	38931_1	T47232 AF147365 T47231
	437237	43506_2	BE513073
20	437728	441520_1	AA766719 AA767041 AW977440
	439894	478738_1	AA853077 AA852175
	442197	535550_1	AW837912 AW837934 AA984475 AW997490
	442614	547073_1	AI269030 AI204085 AI004047
	444475	607874_1	C75571 AI150469 T10778
25	448427	762970_1	BE395260 AW291036 AI500420
	449329	80484_1	AW752783 H38266 AA001166
	451588	87667_1	AW072057 AI225096 AA018702
	452456	918391_1	BE080763 T96699 BE081135 AI902630 H49182 AI904021 AI902697
	454517	1221063_1	AW803340 AW803280 AW803275 AW803415 AW803343 AW803422
30	454748	1233013_1	AW862014 AW858740 AW858735 AW818542 AW858765 AW862027 AW858775 AW858771 AW858763
	454869	1238137_1	AW836004 AW836087 AW836163 AW836162 AW836085 AW836084 AW836079 AW836083 AW836086 AW836088 AW836166 AW836164
			AW836002 AW836078 AW836161 AW862135 AW836165 AW836003
	454886	1238987_1	AW837063 AW935882 AW935957
	455075	1252389_1	AW854850 AW854848
35	455104	1253737_1	BE064863 BE153698 AW856751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AW856622 BE155079 BE064651 BE153665
			BE064650 BE064691
	455366	1284685_1	AW947563 AW947543 AW947553 AW947549 AW947717 AW902859 AW902927 BE011032
	455433	1290311_1	AW939463 AW939484 AW939480 AW939459 AW939546 AW939593 AW939548 AW939595 AW939106
	455446	1291969_1	AW947749 AW947746 AW947754 AW946636 AW946674
40	455579	1333944_1	BE011320 BE006381 BE006361 BE011180 BE011328 BE011325 BE011157 BE006384 BE006387 BE006385 BE011160 BE011319 BE011346
			BE006370 BE006386 BE011173 BE006389 BE006376 BE006375 BE006364 BE011321 BE006379
	455652	1348736_1	BE064675 BE064761 BE064809 BE064673 BE064672 BE064674
	455817	1371986_1	BE142384 BE142387
	455994	1398737_1	BE179190 BE179206 BE179182 BE179185 BE179186 BE179194
45	456150	1574395_1	Z42308 H23514
	456379	1839113_2	W22206 W22498 W26922
	456387	1842730_1	W28876 W26158
	456702	219191_1	AI684534 BE262411 AA314031 AW752724
	457416	334503_1	BE142052 AW265588 AA506741
50	457787	407235_1	AA683268 BE002903 BE002672
	458764	73207_1	BE619386 AA300687
	459197	924229_1	BE244587 AW938684 AW176490 AI940102 AW844995 AW938670 AI909850 AI909885 AI940079 AI909873
55	TABLE 28C		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.	
60	Strand:	Indicates DNA strand from which exons were predicted.	
	Nt_position:	Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand Nt_position
65	400489	8954013	Plus 131475-131652
	400527	9796886	Plus 160750-161007
	400545	9800107	Minus 124618-124881
	400624	7228177	Minus 94097-94756
	400635	8567750	Minus 102800-102932,107482-107689
70	400672	8118724	Minus 148067-148503
	400675	8118750	Plus 11223-11816
	400694	8118802	Plus 94288-94442
	400736	8118985	Plus 143447-143851
	400846	9188605	Plus 39310-39474
75	401007	8117333	Minus 140821-141050
	401015	8117441	Plus 72260-72369
	401039	7232177	Plus 6588-6884
	401122	8570296	Plus 68256-68444
	401238	9954455	Minus 49473-49644
80	401442	8346725	Minus 85674-85910
	401496	7381769	Minus 82790-83002
	401590	9966320	Minus 33547-33649
	401603	7689963	Minus 116659-116780
	401624	8575907	Plus 168318-168444,172964-173647

	401688	2347081	Plus	22016-22624
	401704	3097841	Plus	24712-25374
	401728	8134856	Minus	82117-82920
5	401743	2865207	Plus	115475-115640
	401767	9958312	Plus	156823-156921,157364-157554
	401810	7342191	Plus	129063-129476
	401840	7684597	Plus	56283-56439
	401886	7229913	Minus	79215-79393
10	401919	9502466	Plus	67536-67666
	401969	3126777	Plus	44863-45366
	402051	8082020	Minus	19346-19480,20041-20119
	402056	8084234	Plus	207002-207288
	402153	8247879	Minus	122580-122987
15	402158	8516165	Minus	148298-148429,148566-148677
	402165	8569830	Minus	65064-65979
	402194	8576113	Plus	70917-71191
	402195	7689778	Minus	147901-148884
	402201	8576119	Plus	655-951
20	402316	7527774	Minus	10751-10919,18817-19052,22131-22328
	402382	9690314	Minus	155331-155528
	402386	9799769	Plus	22069-22303
	402394	9929690	Plus	33308-33482
	402409	9796255	Minus	8571-10061
25	402423	9796344	Minus	62487-62664
	402448	9796640	Plus	112942-113069,114303-114521
	402457	9796782	Minus	16513-16577,16838-16926
	402534	9801061	Plus	58989-59457
	402538	9801137	Minus	96314-96539
30	402561	9864675	Plus	72967-73163
	402588	9908948	Minus	33027-33183,59060-59198
	402690	8348058	Plus	13368-13998
	402714	8969253	Minus	18811-18886,19105-19328,19525-19764
	402762	9230904	Minus	123298-124035
35	402862	2956660	Minus	18518-18656
	402911	7263904	Plus	142689-142979
	402951	9408717	Plus	73252-73329,73718-73877,76217-76299,78195-78401
	402968	9581763	Minus	58658-58924
	403047	3540153	Minus	59793-59968
40	403115	7331404	Minus	142952-143094,145474-145653,146269-146445,152816-152998
	403125	9180936	Minus	197548-197712
	403183	9838273	Plus	109930-110074
	403186	9838287	Minus	117513-117856
	403211	7630841	Minus	159211-159369
45	403247	7656833	Minus	76626-77140
	403251	7677983	Plus	100391-100652
	403327	8440025	Minus	174311-174451,174587-174705,175523-175592
	403376	9369545	Minus	108698-108830
	403479	7329292	Minus	148369-148533,150678-150809
50	403526	8017144	Plus	55367-55483
	403540	8077057	Minus	56315-56450
	403605	6862654	Plus	91614-91718
	403612	8469060	Minus	94723-94859
	403665	7249278	Plus	69027-69375
55	403716	7239669	Plus	86899-87122
	403731	7543752	Minus	144000-144618
	403740	7630882	Plus	86504-87227
	403921	7711590	Minus	3297-3536
	403942	7711825	Minus	99606-99757
60	403997	7708819	Plus	134427-134593
	404139	9838113	Plus	76707-76891
	404247	7406725	Minus	83949-84214,84312-84415,84499-84677,84878-85114
	404282	2276311	Plus	61503-62205
	404348	7630858	Minus	28895-29062
65	404668	9797204	Minus	11332-11546,12584-12718
	404682	9797231	Minus	40977-41150
	404795	4826439	Plus	147501-147780
	404825	6478944	Plus	210382-210494
	404938	7381808	Minus	165838-165950
70	405075	7770506	Minus	124680-125321
	405147	9438278	Minus	158996-159557
	405161	9966260	Plus	157607-157785
	405163	9966267	Minus	161171-161299
	405187	7229826	Plus	117025-117170,118567-118736
75	405217	7239551	Plus	32646-33138
	405232	7249042	Plus	125904-126063
	405243	7249201	Minus	22312-23197
	405327	6094661	Minus	120550-120750
	405378	6491714	Plus	91139-91440
80	405420	7211837	Minus	13428-13582
	405703	4240388	Minus	15850-16061
	405737	9943984	Minus	104275-104508,104755-104877
	405895	7677903	Minus	66990-67484
	406059	9103984	Minus	13856-14004

406101	9124019	Plus	125325-125831
406118	9143818	Plus	53997-54629
406150	9886026	Minus	59331-59701
406158	7144874	Plus	62393-63016,65012-65578
406343	9255974	Plus	17284-17440,18489-18646,18917-19004,19384-19538
406357	9256093	Minus	77181-77415
406563	7711604	Plus	34401-34538

TABLE 29A: 2286 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO NORMAL BODY

Table 29A lists about 2286 genes that are up regulated in idiopathic pulmonary fibrosis samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis expression level to "average" normal adult tissues sample expression was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90<sup>th</sup> percentile amongst idiopathic pulmonary fibrosis samples. The "average" normal adult tissue level was set to the 95<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15<sup>th</sup> percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of IPF to normal body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	211.8
442275	AW449467	Hs.54795	ESTs	189.7
431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	134.1
441835	AB036432	Hs.184	advanced glycosylation end product-speci	130.4
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	116.8
421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	92.1
406964	M21305		gb:Human alpha satellite and satellite 3	80.7
443709	AI082692	Hs.134662	ESTs	67.1
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	61.4
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	57.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	54.6
457200	U33749	Hs.197764	thyroid transcription factor 1	44.9
432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	42.7
443324	R44013	Hs.164225	ESTs	39.8
414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	27.3
442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypotheti	27.1
444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	27.1
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	26.9
424084	AI940675	Hs.20914	hypothetical protein FLJ23056	22.2
421659	NM_014459	Hs.106511	protocadherin 17	21.0
450478	AW451709	Hs.271200	ESTs	20.2
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	19.7
447033	AI357412	Hs.157601	ESTs	19.4
445885	AI734009	Hs.127699	KIAA1603 protein	18.9
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	17.9
432437	W07088	Hs.293685	ESTs	17.8
424105	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1	17.3
431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	17.2
440807	AW269421	Hs.128093	ESTs	16.7
424917	AI636208	Hs.96901	hypothetical protein FLJ23049	16.4
433365	AF026944	Hs.293797	ESTs	16.4
445279	R41900	Hs.22245	ESTs	16.4
417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	16.4
405654				16.1
449328	AI962493	Hs.197647	ESTs	16.1
449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	15.7
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	15.5
417728	AW138437	Hs.24790	KIAA1573 protein	15.0
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	14.8
452039	AI922988	Hs.172510	ESTs	14.4
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	14.3
421464	AA291553	Hs.190086	ESTs	14.1
421554	AW137676	Hs.97775	ESTs	13.8
431889	AA521277	Hs.124946	ESTs, Weakly similar to A46010 X-linked	13.2
434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	13.2
431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	12.9
459702				12.7
421110	AJ250717	Hs.1355	cathepsin E	12.6
407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	12.6
423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	12.5
423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	12.2
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	12.1
436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	12.1
451561	N52812	Hs.177403	ESTs	12.0
424086	AI351010	Hs.102267	lysyl oxidase	12.0
435299	AI745458	Hs.122614	ESTs, Weakly similar to T20593 hypotheti	12.0
429496	AA453800	Hs.192793	ESTs	11.9

	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	11.2
5	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	10.9
	421470	R27496	Hs.1378	annexin A3	10.8
	440209	H05049	Hs.22269	neurexin 3	10.8
	428927	AA441837	Hs.90250	ESTs	10.7
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	10.5
10	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	10.4
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	10.4
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.4
	442176	AA983764	Hs.128910	ESTs	10.4
	439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
15	452883	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture	10.3
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	10.3
	422022	AA302420	Hs.200442	ESTs	10.3
	447724	AW298375	Hs.24477	ESTs	10.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	10.0
20	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	9.9
	446232	AI281848	Hs.194691	retinoic acid induced 3	9.9
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	9.9
	453382	AA709285	Hs.5997	hypothetical protein FLJ13078	9.8
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	9.8
25	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H	9.8
	407568	AA740964	Hs.62699	ESTs	9.8
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	9.6
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	9.5
	441484	AA935481	Hs.58972	ESTs	9.5
30	422426	W79117	Hs.58559	ESTs	9.4
	406747	AI925153	Hs.217493	annexin A2	9.4
	450050	AI681268	Hs.257883	ESTs	9.4
	431337	N48107	Hs.292593	ESTs	9.3
	408427	AW194270	Hs.177236	ESTs	9.3
35	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	9.3
	453636	R67837	Hs.169872	ESTs	9.3
	443450	N66045	Hs.133529	ESTs	9.2
	418735	N48769	Hs.44609	ESTs	9.2
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	9.1
40	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	9.1
	441233	AA972965	Hs.135568	ESTs	9.1
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	9.0
	436246	AW450963	Hs.119991	ESTs	9.0
	445189	AI936450	Hs.147482	ESTs	8.9
45	410781	AI375672	Hs.165028	ESTs	8.9
	446868	AV660737	Hs.135100	ESTs	8.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	8.8
	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	8.8
50	410334	AW979261	Hs.291993	ESTs	8.8
	442510	AF150179	Hs.249890	ESTs	8.8
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	8.7
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	8.7
	444929	AI685841	Hs.161354	ESTs	8.7
55	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	8.6
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	8.6
	412719	AW016610	Hs.129911	ESTs	8.6
	453445	AL036532	Hs.91453	ESTs	8.5
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	8.5
60	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	8.5
	433815	AI696602	Hs.112757	ESTs	8.3
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	8.3
	451103	R52804	Hs.25956	DKFZP564D206 protein	8.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	8.3
65	424989	AA985520	Hs.23575	ESTs	8.3
	433231	AB040926	Hs.143552	KIAA1493 protein	8.2
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	8.1
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	8.1
	436751	AA732217	Hs.294054	ESTs	8.0
70	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	8.0
	413048	M93221	Hs.75182	mannose receptor, C type 1	8.0
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	7.9
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	7.8
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	7.8
75	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.7
	421013	M62397	Hs.1345	mutated in colorectal cancers	7.7
	437479	R61866	Hs.101277	ESTs	7.6
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	7.6
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	7.6
80	444396	T65213	Hs.4257	ESTs	7.6
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	7.6
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.6
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	7.6
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	7.6

	449108	AI140683	Hs.98328	hypothetical protein MGC13040	7.5
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.5
	416030	H15261	Hs.21948	ESTs	7.5
5	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	7.4
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	7.4
	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	7.3
	432133	AB033088	Hs.272567	KIAA1262 protein	7.3
	447112	H17800	Hs.7154	ESTs	7.3
10	446917	AI347863	Hs.156672	ESTs	7.3
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.3
	431761	AW002846	Hs.105468	hypothetical protein FLJ22690	7.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	7.2
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	7.2
15	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	7.2
	438122	AI620270	Hs.129837	ESTs, Weakly similar to Z263_HUMAN ZINC	7.2
	449611	AI970394	Hs.197075	ESTs	7.2
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	7.2
	410060	NM_001448	Hs.58367	glypican 4	7.2
20	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
	452571	W31518	Hs.34665	ESTs	7.2
	453736	AL118674	Hs.34871	zinc finger homeobox 1B	7.2
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	7.2
	405494				7.2
25	442832	AW206560	Hs.253569	ESTs	7.1
	420193	AI460080	Hs.202869	ESTs	7.1
	434217	AW014795	Hs.23349	ESTs	7.0
	427356	AW023482	Hs.97849	ESTs	7.0
30	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.9
	408308	AL033337	Hs.44197	hypothetical protein DKFZp564D0462	6.9
	442377	AA993807	Hs.167367	ESTs	6.9
	441143	AI027604	Hs.159650	ESTs	6.9
	445122	AW241632	Hs.147377	hypothetical protein FLJ23598	6.9
	431353	AA828032	Hs.189076	ESTs	6.9
35	407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.8
	426753	T89832	Hs.170278	ESTs	6.8
	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.8
	451963	AI825440	Hs.224952	ESTs	6.8
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	6.8
40	433426	H69125	Hs.133525	ESTs	6.8
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	6.8
	416236	R41400		gb:yr94b12.s1 Soares infant brain 1NIB H	6.8
	409031	AA376836	Hs.76728	ESTs	6.7
	427558	D49493	Hs.2171	growth differentiation factor 10	6.7
45	437259	AI377755	Hs.120695	ESTs	6.7
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	6.7
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	6.7
	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	6.7
	422475	AL359938	Hs.117313	Meis (mouse) homolog 3	6.7
50	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.7
	424750	D29956	Hs.152818	ubiquitin specific protease 8	6.6
	403574				6.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	6.6
	415025	AW207091	Hs.72307	ESTs	6.5
55	448104	AI674818	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HE	6.5
	444271	AW452569	Hs.149804	ESTs	6.5
	437157	BE048860	Hs.120655	ESTs	6.5
	444050	AW138295	Hs.135024	ESTs	6.5
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	6.5
60	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	6.5
	424433	H04607	Hs.9218	ESTs	6.4
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	6.4
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	6.4
	422544	AB018259	Hs.118140	KIAA0716 gene product	6.4
65	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	6.3
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	6.3
	417246	AI760098	Hs.21411	ESTs	6.3
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	6.3
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	6.3
70	438909	AF085839		gb:Homo sapiens full length insert cDNA	6.3
	446002	AI346468	Hs.145789	ESTs	6.3
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	6.3
	424202	BE350295	Hs.15032	RAN binding protein 17	6.3
75	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	6.2
	415511	AI732617	Hs.182362	ESTs	6.2
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.2
	416879	H98899	Hs.42599	ESTs	6.2
	432803	AA566398		gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	6.2
80	442862	BE080429	Hs.15738	ESTs	6.2
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	6.2
	441082	AW444804	Hs.202655	ESTs	6.2
	404599				6.1
	453931	AL121278	Hs.25144	ESTs	6.1

	420252	AW270404	Hs.193161	ESTs	6.1
	431622	AW979271	Hs.293184	ESTs	6.1
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.1
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.0
	424693	BE169810	Hs.47557	ESTs	6.0
	419172	AW338625	Hs.22120	ESTs	6.0
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.0
	453037	AA045175	Hs.177552	ESTs	6.0
10	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	6.0
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	6.0
	422352	AA766296	Hs.99200	ESTs	5.9
	433527	AW235613	Hs.133020	ESTs	5.9
	420077	AW512260	Hs.87767	ESTs	5.9
15	429703	T93154	Hs.28705	ESTs	5.9
	433098	AW190593	Hs.151143	ESTs	5.9
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	5.9
	449416	AI651016	Hs.246311	ESTs	5.9
	459023	AW968226	Hs.60798	ESTs	5.9
20	450584	AA040403	Hs.60371	ESTs	5.9
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	5.9
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	5.9
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	5.9
	433479	AW511459	Hs.249972	ESTs	5.8
25	443113	AI040686	Hs.132908	ESTs	5.8
	430414	AW365665	Hs.120388	ESTs	5.8
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	5.8
	435420	AI928513	Hs.59203	ESTs	5.8
	404916				5.8
30	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.8
	448253	H25899	Hs.201591	ESTs	5.8
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.8
	446967	AI699629	Hs.156781	ESTs	5.8
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	5.7
35	438842	AA827176	Hs.124316	ESTs	5.7
	437260	AA747807	Hs.149500	ESTs	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	428043	T92248	Hs.2240	uteroglobin	5.7
	408045	AW138959	Hs.245123	ESTs	5.7
40	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	5.7
	428508	BE252383	Hs.184668	SBB131 protein	5.7
	453393	AW956392	Hs.110376	ESTs	5.6
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	5.6
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.6
45	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	5.6
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	5.6
	416575	W02414	Hs.38383	ESTs	5.5
	404043				5.5
	415094	D59513	Hs.330778	ESTs	5.5
50	453049	BE537217	Hs.30343	ESTs	5.5
	430153	AW968128	Hs.336679	ESTs	5.5
	410811	AW805687	Hs.300648	ESTs	5.5
	443903	AI220547	Hs.135223	ESTs	5.5
	429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	5.5
55	444471	AB020684	Hs.11217	KIAA0877 protein	5.5
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	5.5
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	5.5
	432113	AA935065	Hs.152385	ESTs	5.5
	446608	N75217	Hs.257846	ESTs	5.5
60	419945	AW290975	Hs.118923	ESTs	5.5
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	5.4
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	5.4
	439382	BE247684	Hs.103070	ESTs	5.4
	428895	AA437124	Hs.187247	ESTs	5.4
65	446577	AB040933	Hs.15420	KIAA1500 protein	5.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	427778	AA412323	Hs.105323	ESTs	5.4
	437138	AI935622	Hs.271245	ESTs	5.4
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	5.4
70	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	5.4
	435202	AI971313	Hs.170204	KIAA0551 protein	5.4
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	5.3
	434992	AA658501	Hs.283358	ESTs	5.3
	454039	AW079064	Hs.245540	ESTs	5.3
75	456408	AI288348	Hs.23450	mitochondrial ribosomal protein S25	5.3
	406554				5.3
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	5.3
	416769	AI339257	Hs.115436	ESTs, Moderately similar to I54374 gene	5.3
	414299	AA142989	Hs.71730	ESTs	5.3
80	420362	U79734	Hs.97206	huntingtin interacting protein 1	5.3
	459664				5.3
	425509	AF079363	Hs.158213	sperm associated antigen 6	5.3
	401497				5.3
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	5.2

	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.2
	408776	AA057365	Hs.63356	ESTs, Weakly similar to I38022 hypotheti	5.2
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	5.2
5	451050	AW937420	Hs.69662	ESTs	5.2
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	5.2
	404957				5.2
	452771	T05477	Hs.333265	ESTs	5.2
	438885	AI886558	Hs.184987	ESTs	5.2
10	428244	AI564123	Hs.42500	ADP-ribosylation factor-like 5	5.2
	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	5.2
	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.2
	408729	AA195764	Hs.72639	ESTs	5.1
	457100	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A	5.1
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.1
15	417154	AI674701	Hs.21388	ESTs	5.1
	411869	W20027	Hs.23439	ESTs	5.1
	427043	AA397679	Hs.3991	ESTs	5.1
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
20	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	5.1
	422063	BE156476		gb:QV0-HT0368-040100-082-c05 HT0368 Homo	5.1
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	5.1
	408677	AI279892	Hs.46801	sorting nexin 14	5.0
	404097				5.0
25	437636	AA764781	Hs.291844	ESTs	5.0
	452822	X85689	Hs.288617	hypothetical protein FLJ22621	5.0
	410733	D84284	Hs.66052	CD38 antigen (p45)	5.0
	439140	W85737	Hs.290830	ESTs	5.0
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	5.0
30	405547				5.0
	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	5.0
	449168	NM_016206	Hs.23142	colon carcinoma related protein	5.0
	455431	AW938484		gb:CM0-DT0057-290200-253-d06 DT0057 Homo	5.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.0
35	411149	N68715	Hs.269128	ESTs	5.0
	432441	AW292425	Hs.163484	ESTs	5.0
	419807	R77402		gb:yi75f11.s1 Soares placenta Nb2HP Homo	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
	450109	AI539295	Hs.115740	KIAA0210 gene product	5.0
40	449695	AA164569	Hs.34550	ESTs	5.0
	421764	AI681535	Hs.148135	serine/threonine kinase 33	4.9
	404593				4.9
	423607	AA328329	Hs.6591	ESTs	4.9
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (f	4.9
45	419235	AW470411	Hs.288433	neurotrimin	4.9
	436304	AA339622	Hs.108887	ESTs	4.9
	434613	AI821826		gb:ms92b10.x5 NCL_CGAP_Pr3 Homo sapiens	4.9
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	4.9
	415245	N59650	Hs.27252	ESTs	4.9
50	428780	AI478578	Hs.50636	ESTs	4.9
	406333				4.9
	445034	AW293376	Hs.143659	ESTs	4.8
	440202	AW516211	Hs.125300	ring finger protein 21, interferon-respo	4.8
	424638	AI472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HE	4.8
55	451497	H83294	Hs.284122	Wnt inhibitory factor-1	4.8
	427652	AI673025	Hs.43874	ESTs, Moderately similar to I54374 gene	4.8
	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.8
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
60	415261	T40928	Hs.8346	ESTs	4.8
	453543	AA485425	Hs.48919	Homo sapiens cDNA FLJ11508 fis, clone HE	4.8
	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HE	4.8
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	4.8
	441006	AW605267	Hs.7627	CGI-60 protein	4.8
65	412222	AA528283	Hs.292737	ESTs	4.8
	424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypotheti	4.8
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	4.8
	439398	AA284267	Hs.221504	ESTs	4.8
	436397	AA715013	Hs.169835	ESTs	4.8
70	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	425916	NM_006786	Hs.162200	urotensin 2	4.8
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	4.8
	427457	AW779105	Hs.164682	ESTs	4.7
75	451620	AW449888	Hs.257224	ESTs	4.7
	408938	AA059013	Hs.22607	ESTs	4.7
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	4.7
	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13658 fis, clone PL	4.7
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	4.7
80	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	4.7
	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	435347	AW014873	Hs.116963	ESTs	4.7
	425458	H89317	Hs.182889	ESTs	4.7
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	4.7

	436594	AI419982	Hs.156189	ESTs	4.7
	421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	4.7
	432731	R31178	Hs.287820	fibronectin 1	4.7
5	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	4.7
	426320	W47595	Hs.169300	transforming growth factor, beta 2	4.7
	419751	AW195581	Hs.93121	KIAA0761 protein	4.6
	433515	AA595800	Hs.190246	ESTs	4.6
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	4.6
10	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	4.6
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	4.6
	406992	S82472		gb:beta-pol=DNA polymerase beta [exon a	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	435933	AA805520	Hs.192075	ESTs	4.6
	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	4.6
15	445657	AW612141	Hs.279575	Homo sapiens G-protein coupled receptor	4.6
	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypotheti	4.6
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapi	4.6
20	424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.6
	416258	N45661	Hs.90011	adenylosuccinate synthase	4.6
	410011	AB020641	Hs.57856	PFTAIRe protein kinase 1	4.6
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	4.5
	422977	AA631498		gb:np83h04.s1 NCL_CGAP_Thy1 Homo sapiens	4.5
25	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
	450192	AA263143	Hs.24596	RAD51-interacting protein	4.5
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	4.5
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	4.5
	409041	AB033025	Hs.50081	KIAA1199 protein	4.5
30	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.5
	452526	W38537	Hs.280740	hypothetical protein MGC3040	4.5
	403271				4.5
	450656	AA010539	Hs.18912	ESTs	4.5
	446096	AI276454		gb:q171a12.x1 Soares_NhHMPu_S1 Homo sapi	4.5
35	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.5
	437960	AI669586	Hs.222194	ESTs	4.5
	440862	H39048	Hs.127432	ESTs	4.5
	410615	AW772721		gb:hl95c01.x1 NCL_CGAP_Thy8 Homo sapiens	4.5
	413583	AL120806	Hs.5888	ESTs	4.5
40	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL	4.5
	442324	R63578	Hs.28426	ESTs	4.4
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	4.4
	435747	AI079519	Hs.134398	ESTs	4.4
	446509	AF169693	Hs.132892	protocadherin 20	4.4
45	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.4
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	4.4
	448089	AI467945	Hs.173696	ESTs	4.4
	434367	AB020700	Hs.3830	KIAA0893 protein	4.4
	434757	AI038997	Hs.132921	ESTs	4.4
50	413453	AA129640	Hs.128065	ESTs	4.4
	454438	AA224053	Hs.172405	cell division cycle 27	4.4
	458154	AW816379	Hs.335018	ESTs	4.4
	430417	AA461045	Hs.50701	ESTs	4.4
	434819	AA650099	Hs.291541	ESTs, Weakly similar to ALUB_HUMAN !!!!	4.4
55	438796	W67821	Hs.109590	genethonin 1	4.4
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.4
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.4
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.4
	451895	T93573	Hs.16970	ESTs	4.4
60	435434	AA680387	Hs.187850	ESTs	4.4
	449623	C00719	Hs.120440	EST	4.4
	433563	AI732637	Hs.277901	ESTs	4.3
	444649	AW207523	Hs.197628	ESTs	4.3
	441594	AL041080	Hs.208765	ESTs, Moderately similar to ALU7_HUMAN A	4.3
65	443314	AW771701	Hs.54646	ESTs	4.3
	400292	AA250737	Hs.72472	ESTs	4.3
	427972	AA864870	Hs.181304	putative gene product	4.3
	446932	AA961459	Hs.125644	ESTs	4.3
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.3
70	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	4.3
	400608				4.3
	411156	AW819939	Hs.273629	ESTs	4.3
	435772	AA700019	Hs.132992	ATP-binding cassette, sub-family G (WHIT	4.3
75	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	4.3
	455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	4.3
	443257	AI334040	Hs.11614	HSPC065 protein	4.3
	436033	H75391	Hs.255748	ESTs	4.3
	420214	AI146375	Hs.286073	ESTs, Moderately similar to ALU5_HUMAN A	4.3
80	410519	AW612264	Hs.131705	ESTs	4.3
	401189				4.3
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3



	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	4.3
	434677	AW444575	Hs.130834	ESTs	4.3
	403310				4.3
5	451830	H18433	Hs.21542	KIAA1035 protein	4.3
	422222	AI699372	Hs.193247	hypothetical protein DKFZp434A171	4.3
	435627	W88774	Hs.118370	ESTs	4.3
	436461	AW511956	Hs.293261	ESTs	4.3
	452166	AI948607	Hs.264680	ESTs	4.3
10	413998	AW103807	Hs.243933	ESTs	4.2
	416642	T96118	Hs.226313	ESTs	4.2
	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	4.2
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypotheti	4.2
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.2
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	4.2
15	424641	AB001106	Hs.151413	glia maturation factor, beta	4.2
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.2
	409629	AW449589	Hs.279724	ESTs	4.2
	458771	AW295151	Hs.163612	ESTs	4.2
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	4.2
20	436645	AW023424	Hs.156520	ESTs	4.2
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	4.2
	445268	AI218358	Hs.175048	ESTs	4.2
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.2
25	431917	D16181	Hs.2868	peripheral myelin protein 2	4.2
	443348	AW873596	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	4.2
	443151	AI827193	Hs.132714	ESTs	4.2
	419255	AA235672	Hs.87491	ESTs	4.2
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	4.2
	452561	AI692181	Hs.49169	KIAA1634 protein	4.2
30	421106	AA877124	Hs.172844	ESTs	4.2
	424268	AA397653	Hs.307438	Human DNA sequence from clone 495010 on	4.2
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.2
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	4.2
	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	4.2
35	428771	AB028992	Hs.193143	KIAA1069 protein	4.1
	445745	AB007924	Hs.13245	KIAA0455 gene product	4.1
	417009	AA191719	Hs.314714	ESTs	4.1
	436517	BE080932	Hs.135225	ESTs	4.1
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.1
	414083	AL121282	Hs.257786	ESTs	4.1
	452728	AI915676	Hs.239708	ESTs	4.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	4.1
	441802	AA968636	Hs.127877	ESTs	4.1
45	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	4.1
	413875	BE176776		gb:RC3-HT0586;110300-011-g09 HT0586 Homo	4.1
	444009	AI380792	Hs.135104	ESTs	4.1
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	4.1
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	4.1
50	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	435256	AF193766	Hs.13872	cytokine-like protein C17	4.1
	428104	AA421350	Hs.191604	ESTs	4.1
	439648	AW780192	Hs.267596	ESTs	4.1
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	4.1
55	446364	AB006624	Hs.14912	KIAA0286 protein	4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	4.0
	404561				4.0
60	401575				4.0
	419296	AA236115	Hs.120785	ESTs	4.0
	432055	AW972359	Hs.293334	ESTs	4.0
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	4.0
	450320	AW291775	Hs.213793	ESTs	4.0
65	447350	AI375572	Hs.172634	ESTs	4.0
	441974	AI683782	Hs.128245	ESTs	4.0
	453142	AA033648	Hs.7473	ESTs	4.0
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.0
	410292	AA843087	Hs.124194	ESTs	4.0
70	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	4.0
	420218	AW958037	Hs.286	ribosomal protein L4	4.0
	426625	T78300	Hs.300642	serologically defined colon cancer antig	4.0
	417708	N74392	Hs.50495	ESTs	4.0
75	451024	AA442176		gb:zw63b08.r1 Soares_total_fetus_Nb2HF8_	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0
	422058	AA862231	Hs.334443	ESTs	4.0
	439479	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	4.0
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.0
80	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.0
	453096	AW294631	Hs.11325	ESTs	4.0
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	4.0
	421002	AF116030	Hs.100932	transcription factor 17	4.0
	445414	AV653692	Hs.146105	ESTs	4.0

	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.0
	451353	N21043	Hs.42932	ESTs	4.0
	437075	AA743748	Hs.40758	ESTs	3.9
5	410505	AW752139	Hs.314323	ESTs	3.9
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	3.9
	426116	AA868729	Hs.144694	ESTs	3.9
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
10	417718	T86540	Hs.193981	ESTs	3.9
	436772	AW975688	Hs.74170	metallothionein 1E (functional)	3.9
	401045				3.9
	408767	AA057279	Hs.211928	ESTs	3.9
	407303	AA016296	Hs.165200	ESTs, Weakly similar to A56194 thromboxa	3.9
15	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	3.9
	451623	H77818	Hs.268991	ESTs	3.9
	450063	AI681509	Hs.277133	ESTs	3.9
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.9
	419276	BE165909	Hs.306881	MSTP043 protein	3.9
20	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
	436149	AI754308	Hs.159452	ESTs	3.9
	422667	H25642	Hs.133471	ESTs	3.9
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	3.9
	458219	H22195	Hs.31874	ESTs	3.9
25	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.9
	439810	AL109710	Hs.85568	EST	3.9
	436578	AI091435	Hs.134859	ESTs	3.9
	415598	AI433165	Hs.9856	ESTs	3.9
	425087	R62424	Hs.126059	ESTs	3.9
30	454111	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	3.9
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	3.9
	452466	N84635	Hs.29664	hypothetical protein DKFZp564B052	3.9
	424962	NM_012288	Hs.153954	TRAM-like protein	3.9
	435823	R07856	Hs.16355	ESTs	3.9
35	440633	AI140686	Hs.263320	ESTs	3.9
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	3.9
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.9
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.9
	417461	R38403	Hs.13305	ESTs	3.9
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.8
	419140	AI982647	Hs.215725	ESTs	3.8
	415652	T79213	Hs.272073	ESTs	3.8
	430140	AW296771	Hs.221999	ESTs	3.8
45	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	3.8
	422165	AL041199	Hs.1481	histidine decarboxylase	3.8
	417706	T90797	Hs.268623	ESTs	3.8
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.8
	450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.8
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.8
50	449729	R72032	Hs.29235	ESTs	3.8
	414700	H63202	Hs.38163	ESTs	3.8
	440899	AW449445	Hs.120021	DKFZP434I092 protein	3.8
	439335	AA742697	Hs.62492	ESTs, Weakly similar to B39066 proline-r	3.8
	408625	AW243323	Hs.266785	ESTs	3.8
55	421987	AI133161	Hs.286131	CGI-101 protein	3.8
	418915	AI474778	Hs.118977	ESTs	3.8
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.8
	442849	R10099	Hs.269805	ESTs	3.8
60	427191	BE221825	Hs.97691	ESTs	3.8
	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	3.8
	437030	AA742577	Hs.303781	EST	3.8
	427940	AA417812	Hs.38775	ESTs	3.7
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.7
65	449679	AI823951	Hs.129700	toll-like 1	3.7
	425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3.7
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	439957	AI453184	Hs.66357	ESTs	3.7
70	446999	AA151520	Hs.334822	hypothetical protein MGC4485	3.7
	428414	AL049980	Hs.184216	DKFZP564C152 protein	3.7
	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.7
	418379	AA218940	Hs.137516	fidgetin-like 1	3.7
	419720	AA249131	Hs.337778	hypothetical protein FLJ11068	3.7
75	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	3.7
	416185	AW975861	Hs.47367	KIAA1785 protein	3.7
	417235	AA810278	Hs.24250	ESTs	3.7
	441720	AI346487	Hs.28739	ESTs	3.7
80	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
	417355	D13168	Hs.82002	endothelin receptor type B	3.7
	449321	AA001150	Hs.132937	ESTs	3.7
	424806	AA382523	Hs.105689	MSTP031 protein	3.7
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	3.7
	409248	AB033035	Hs.51965	KIAA1209 protein	3.7

	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	3.7
	420026	AI831190	Hs.166676	ESTs	3.7
5	429419	AB023226	Hs.202276	KIAA1009 protein	3.7
	447410	AI470235	Hs.172698	EST	3.7
	404274				3.7
	416320	H47867	Hs.34024	ESTs	3.7
10	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	3.7
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.7
	446025	AW305075	Hs.180948	KIAA0729 protein	3.7
	450458	AA009926		gb:zi07e05.r1 Soares_fetal_liver_spleen_	3.6
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	3.6
15	438257	AW474419	Hs.224794	ESTs	3.6
	440887	AI799488	Hs.135905	ESTs	3.6
	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.6
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	408687	AL110280	Hs.301152	Homo sapiens mRNA; cDNA DKFZp434F053 (fr	3.6
	407726	AA435679	Hs.88594	ESTs	3.6
20	436026	AI349764	Hs.217081	ESTs	3.6
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
	452293	AI871833	Hs.304609	ESTs	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.6
25	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.6
	429208	AA447990	Hs.190478	ESTs	3.6
	458429	AV646559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C	3.6
	404476				3.6
	405848				3.6
30	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	3.6
	403937				3.6
	437918	AI761449	Hs.121629	ESTs	3.6
	432408	N39127	Hs.332557	ESTs, Weakly similar to A46010 X-linked	3.6
	437641	AA811452	Hs.291911	ESTs	3.6
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.6
35	446102	AW168067	Hs.252956	ESTs	3.6
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	432030	AI908400	Hs.143789	ESTs	3.6
40	446453	AV658469	Hs.188646	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	3.6
	440801	AA906366	Hs.190535	ESTs	3.6
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	440886	AW511032	Hs.190516	ESTs	3.6
	401049				3.6
45	449424	AW448937	Hs.197030	ESTs	3.6
	418076	R61388	Hs.6724	ESTs	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	3.6
50	438016	AI949638	Hs.336846	EST	3.6
	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	3.5
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	3.5
	455536	AW135986	Hs.257859	ESTs	3.5
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	3.5
55	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	435344	AA700326	Hs.190599	ESTs	3.5
	445056	AB014530	Hs.12259	KIAA0630 protein	3.5
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	3.5
	442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	3.5
60	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	3.5
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.5
	428409	AW117207	Hs.98523	ESTs	3.5
	431087	H12723	Hs.290791	ESTs	3.5
65	426920	AA393351	Hs.132121	ESTs	3.5
	427687	AW003867	Hs.1570	histamine receptor H1	3.5
	437583	AA761190	Hs.244627	ESTs	3.5
	421599	AA293655	Hs.97293	ESTs	3.5
	433687	AA743991		gb:ny57g01.s1 NCL_CGAP_Pr18 Homo sapiens	3.5
70	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	3.5
	430499	AW969408	Hs.231991	ESTs	3.5
	451531	AA018311	Hs.114762	ESTs	3.5
	457620	AA602711	Hs.336753	EST	3.5
	410658	AW105231	Hs.192035	ESTs	3.5
75	427865	AA416931	Hs.126065	ESTs	3.5
	453390	AA862496	Hs.28482	ESTs	3.5
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	3.5
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
80	427718	AI798680	Hs.25933	ESTs	3.5
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.5
	420381	D50640	Hs.337616	phosphodiesterase 3B, cGMP-inhibited	3.5
	410908	AA121686	Hs.10592	ESTs	3.5
	442080	AW444761	Hs.44565	ESTs	3.5
	406685	M18728		gb:Human nonspecific crossreacting antig	3.5

	404200			3.5
	417976	BE565892	Hs.83077	interleukin 18 (interferon-gamma-inducin
	433285	AW975944	Hs.237396	ESTs
	432868	AW974093	Hs.292775	ESTs
5	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706
	428775	AA434579	Hs.143691	ESTs
10	410004	AI298027	Hs.5057	carboxypeptidase D
	422093	AF151852	Hs.111449	CGI-94 protein
	441736	AW292779	Hs.169799	ESTs
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor
	405970			
15	431954	AK001974	Hs.272242	hypothetical protein FLJ11112
	459482	AA625339	Hs.237052	EST, Weakly similar to I38022 hypothetic
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar
	402230			
20	436120	AI248193	Hs.119860	ESTs
	405336			
	434374	AA631439		gb:np85d02.s1 NCI_CGAP_Thy1 Homo sapiens
	428911	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1672 (f
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S
25	416057	AI927382	Hs.29857	ESTs
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r
	436088	AA704687	Hs.191294	ESTs
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp
	454076	AW204712	Hs.61957	ESTs
30	431733	AW298410	Hs.21475	ESTs
	432974	BE348793	Hs.233331	ESTs
	412576	AA447718	Hs.107057	ESTs
	446142	AI754693	Hs.145968	ESTs
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi
35	433384	AI021992	Hs.124244	ESTs
	413621	AI808648	Hs.184156	ESTs
	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens
	436111	AI803082	Hs.157212	ESTs
	421236	AI287622	Hs.151956	ESTs
40	433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D1
	403515			
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protei
	453375	AI990114	Hs.240091	ESTs
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT
45	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi
	409642	AW450809	Hs.257347	ESTs
	420092	AA814043	Hs.88045	ESTs
	453365	AA035211	Hs.17404	ESTs
50	437007	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypotheli
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT
	439024	R96696	Hs.35598	ESTs
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi
	417991	AA731452	Hs.190008	ESTs
55	403356			
	433650	AA603472	Hs.28456	ESTs
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970
	413714	AI560944	Hs.71428	ESTs
60	430887	N66801	Hs.260287	KIAA1841 protein
	413618	BE154078		gb:PMO-HT0339-200400-010-F04 HT0339 Homo
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE
	405692			
65	432809	AA565509	Hs.131703	ESTs
	433805	AA706910	Hs.112742	ESTs
	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-hergulin
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro
70	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo
	410434	AF051152	Hs.63668	toll-like receptor 2
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I
	444301	AK000136	Hs.10760	asporin (LRR class 1)
75	428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyl
	458924	BE242158	Hs.24427	DKFZP566O1646 protein
	435934	R19382	Hs.117869	ESTs
	400269			
80	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	412903	BE007967	Hs.155795	ESTs
	400889			
	449585	AI655321	Hs.197693	ESTs
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C
	418557	BE140602	Hs.246645	ESTs

5	453204	R10799	Hs.191990	ESTs	3.3
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	3.3
	427374	AI150033	Hs.143686	ESTs	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
10	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.3
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	3.3
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.3
	403895				3.2
	414899	AW975433	Hs.36288	ESTs	3.2
15	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.2
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
	427119	AW880562	Hs.114574	ESTs	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
20	443830	AI142095	Hs.143273	ESTs	3.2
	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_UI2 Homo sapiens	3.2
	417561	AW974345		gb:EST386449 MAGE resequences, MAGM Homo	3.2
	446063	AI720140	Hs.151079	ESTs	3.2
25	423609	AA328348	Hs.218289	ESTs	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.2
	435808	AA702866	Hs.113150	ESTs	3.2
	424001	W67883	Hs.137476	paternally expressed 10	3.2
30	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	3.2
	418946	AI798841	Hs.164526	ESTs	3.2
	431750	AA514986	Hs.283705	ESTs	3.2
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	3.2
	428268	AA424957	Hs.294132	ESTs	3.2
35	418878	W20090	Hs.6616	ESTs	3.2
	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	3.2
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap	3.2
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.2
	404588				3.2
40	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	444910	AI201849		gb:qs76g04.x1 NCI_CGAP_Pr28 Homo sapiens	3.2
	407339	AA777542	Hs.132670	ESTs	3.2
	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	3.2
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	3.2
45	419340	AA236590	Hs.87530	ESTs	3.2
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone CO	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	421187	NM_014721	Hs.102471	KIAA0680 gene product	3.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	3.2
50	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.2
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.2
	438839	AW297945	Hs.128490	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
	427961	AW293165	Hs.143134	ESTs	3.2
55	429228	AI553633	Hs.337139	ESTs	3.2
	431548	AI834273	Hs.9711	novel protein	3.1
	441839	AW975512	Hs.29160	ESTs	3.1
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.1
	441274	AW593781	Hs.131357	ESTs	3.1
60	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	436154	AA764950	Hs.119898	ESTs	3.1
	406752	AI285598		gb:qu49f06.x1 NCI_CGAP_Lym6 Homo sapiens	3.1
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	3.1
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.1
65	436739	BE208022	Hs.127685	KIAA1627 protein	3.1
	451674	AA019104	Hs.175483	Homo sapiens cDNA: FLJ22016 fis, clone H	3.1
	421166	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	3.1
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
70	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	3.1
	424780	U39576	Hs.153058	butyrophilin, subfamily 1, member A1	3.1
	456551	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.1
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.1
75	431814	BE256242	Hs.270847	delta-tubulin	3.1
	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	436401	AI087958	Hs.29088	ESTs	3.1
	437439	H29796	Hs.269622	ESTs	3.1
	403277				3.1
80	408547	AA574291	Hs.57837	ESTs	3.1
	424131	AA335714	Hs.199665	ESTs	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	3.1
	434636	AA083764	Hs.6101	hypothetical protein MGC3178	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.1
	407905	AW103655	Hs.252905	ESTs	3.1
	452311	AW304029	Hs.252744	ESTs	3.1

	434849	AW292765	Hs.8053	ESTs	3.1
	446770	AV660309	Hs.154986	ESTs, Weakly similar to PLLP_HUMAN PLASM	3.1
	424238	AA337401	Hs.137635	ESTs	3.1
5	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.1
	447829	AI433029	Hs.164104	ESTs	3.1
	406506				3.1
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.1
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.1
10	451229	AW967707	Hs.48473	ESTs	3.1
	401103				3.1
	433589	AA886530	Hs.188912	ESTs	3.1
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypotheti	3.1
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	3.1
	404288				3.1
15	406195				3.1
	438202	AW169287	Hs.22588	ESTs	3.1
	425516	BE000707	Hs.29567	ESTs	3.1
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.1
20	422692	AA332376	Hs.24135	transmembrane protein vezatin; hypotheti	3.1
	435414	AW270550	Hs.116957	ESTs	3.1
	418950	T78517	Hs.13941	ESTs	3.1
	426890	AA393167	Hs.41294	ESTs	3.1
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	3.1
25	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.1
	459371	R20991		gb:yg06h01.r1 Soares infant brain 1NIB H	3.1
	421823	N40850	Hs.28625	ESTs	3.1
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.1
	452896	AA831508	Hs.32553	ESTs	3.1
30	425895	AI269484	Hs.161427	zinc finger protein 215	3.1
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	3.1
	407340	AA810168	Hs.284289	vitellogenesis-associated protein VIT-1	3.1
	401862				3.1
	444325	AW152618	Hs.16757	ESTs	3.1
35	408171	AA301228	Hs.43299	hypothetical protein FLJ12890	3.1
	423949	AI014546	Hs.130912	ESTs	3.1
	419519	AI198719	Hs.176376	ESTs	3.0
	434683	AW298724	Hs.202639	ESTs	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
40	415086	AI597963	Hs.118726	ESTs	3.0
	419220	AA811938	Hs.291759	ESTs	3.0
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	3.0
45	405090				3.0
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
	443253	AI041212	Hs.132117	ESTs	3.0
	444974	AI203500	Hs.151612	ESTs	3.0
	445717	AW664658	Hs.149332	ESTs	3.0
50	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.0
	424406	D54120	Hs.146409	cell division cycle 42 (GTP-binding prot	3.0
	410371	AA084482	Hs.115850	ESTs	3.0
55	426384	AI472078	Hs.303662	ESTs	3.0
	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	3.0
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo	3.0
60	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	3.0
	455601	AI368680	Hs.816	SRX (sex determining region Y)-box 2	3.0
	447482	AB033059	Hs.18705	KIAA1233 protein	3.0
	439416	W58294	Hs.56254	ESTs	3.0
	436635	AW104325	Hs.272093	ESTs, Weakly similar to I78885 serine/th	3.0
65	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.0
	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	3.0
	415452	F09134	Hs.12839	ESTs	3.0
	427874	AA732367	Hs.98198	ESTs	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
70	454193	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	3.0
	454678	AW813089		gb:RC3-ST0186-240400-111-b05 ST0186 Homo	3.0
	415122	D60708	Hs.22245	ESTs	3.0
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.0
	400227				3.0
75	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	3.0
	419503	AA243642	Hs.137422	ESTs	3.0
	446563	BE326588	Hs.141454	ESTs	3.0
	457285	AI038858	Hs.130522	Kv channel-interacting protein 1	3.0
	434998	AW975157	Hs.26037	ESTs	3.0
80	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.0
	424539	L02911	Hs.150402	activin A receptor, type I	3.0
	449856	AA203155	Hs.18200	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN A	3.0

	442994	AI026718	Hs.16954	ESTs	3.0
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	3.0
	421072	AI215069	Hs.89113	ESTs	3.0
5	456273	AF154846	Hs.1148	zinc finger protein	3.0
	404548				3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	441519	AA972740	Hs.127092	ESTs	3.0
	445413	AA151342	Hs.12677	CGI-147 protein	3.0
10	418717	AI334430	Hs.86984	ESTs	3.0
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.0
	407758	D50915	Hs.38365	KIAA0125 gene product	3.0
	431906	AW328038	Hs.37486	ESTs	3.0
	424968	AA349086	Hs.259746	ESTs, Weakly similar to A46010 X-linked	3.0
15	431023	AI283133	Hs.297420	ESTs	3.0
	432596	AJ224741	Hs.278461	matriin 3	3.0
	452412	AA029608	Hs.61373	ESTs	3.0
	421309	AI222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to T2D4_HUMAN TRANS	2.9
20	408321	AW405882	Hs.44205	cortistatin	2.9
	439236	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN !	2.9
	400880				2.9
	417014	AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN !!!!	2.9
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.9
25	406603				2.9
	425573	AB006423	Hs.158308	serine (or cysteine) proteinase inhibito	2.9
	427878	C05766	Hs.181022	CGI-07 protein	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.9
30	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.9
	422634	NM_016010	Hs.118821	CGI-62 protein	2.9
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.9
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	2.9
	408525	AW206972	Hs.253595	ESTs	2.9
35	412248	BE176480		gb:RC3-HT0585-160300-022-c02 HT0585 Homo	2.9
	432507	BE391093	Hs.324667	ESTs	2.9
	447290	AI476732	Hs.263912	ESTs	2.9
	424188	AW954552	Hs.142634	zinc finger protein	2.9
	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	2.9
40	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119	AA322201	Hs.131976	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
45	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	2.9
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	2.9
	444339	T96555	Hs.31562	ESTs	2.9
	446745	AW118189	Hs.156400	ESTs	2.9
	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
50	430573	AA744550	Hs.136345	ESTs	2.9
	451073	AI758905	Hs.206063	ESTs	2.9
	440575	AA889870	Hs.126006	ESTs	2.9
	402046				2.9
	426882	AA393108	Hs.97365	ESTs	2.9
55	435738	AA699633	Hs.269543	ESTs, Weakly similar to A56194 thromboxa	2.9
	420656	AA279098	Hs.187636	ESTs	2.9
	438323	AI985394	Hs.123369	ESTs	2.9
	453123	AI953718	Hs.221849	ESTs	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
60	431595	AA508196		gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens	2.9
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.9
	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Brn52 Homo sapien	2.9
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	2.9
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	2.9
65	456034	AW450979		gb:UI-H-BI3-ala-a-12-O-UI.s1 NCI_CGAP_Su	2.9
	442118	AA976718	Hs.202242	ESTs	2.9
	420727	H75701	Hs.99886	complement component 4-binding protein,	2.9
	433849	BE465884	Hs.280728	ESTs	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
70	429826	N93266	Hs.40747	ESTs	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
	441330	AI692984	Hs.129354	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	2.9
75	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.9
	444631	AW995395	Hs.84520	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.9
	458186	AA904244	Hs.153205	ESTs	2.9
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	2.9
	415757	AA830854	Hs.187810	ESTs	2.9
80	449299	AA299919	Hs.84561	ESTs	2.9
	457003	S78234	Hs.172405	cell division cycle 27	2.9
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.9
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.9
	426174	AA547959	Hs.115838	ESTs	2.9

	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	2.9
	429950	AW081608	Hs.105053	ESTs	2.9
	412733	AA984472	Hs.74554	KIAA0080 protein	2.9
5	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	442655	AW027457	Hs.30323	ESTs, Weakly similar to B34087 hypotheti	2.9
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	2.9
	430447	W17064	Hs.332848	SWI/SNF related, matrix associated, acti	2.9
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	2.9
10	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.9
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	2.9
	401094				2.9
	401526				2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
15	417320	AA195667	Hs.86022	ESTs	2.9
	418282	AA215535	Hs.98133	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	450006	AI241555	Hs.60171	ESTs	2.9
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	2.8
20	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	2.8
	403329				2.8
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.8
	419038	AW134924	Hs.190325	ESTs	2.8
	440106	AA864968	Hs.127699	KIAA1603 protein	2.8
25	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.8
	431745	AW972448	Hs.163425	ESTs	2.8
	421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA,	2.8
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.8
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	2.8
30	441790	AW294909	Hs.132208	ESTs	2.8
	404443				2.8
	428129	AI244311	Hs.26912	ESTs	2.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.8
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	2.8
35	449327	AI638743	Hs.224672	ESTs	2.8
	400983				2.8
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	2.8
	411213	AA676939	Hs.69285	neuropilin 1	2.8
	420896	AW149342	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	2.8
40	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	2.8
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.8
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
45	440192	AA872282	Hs.190596	ESTs	2.8
	448466	AI522109	Hs.171066	ESTs	2.8
	414869	AA157291	Hs.21479	ubiquitin 1	2.8
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
50	439235	N45513	Hs.46608	ESTs	2.8
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	2.8
	434812	AA649860	Hs.189496	ESTs	2.8
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	2.8
	455512	AW983608		gb:RC3-HN0001-240400-012-c01 HN0001 Homo	2.8
55	408380	AF123050	Hs.44532	diubiquitin	2.8
	435990	AI015862	Hs.131793	ESTs	2.8
	410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
	432798	AA565309	Hs.194015	ESTs	2.8
	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	2.8
60	438886	AA827728	Hs.128705	ESTs, Weakly similar to AF149422 2 unkno	2.8
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.8
	416940	N75620	Hs.43157	ESTs	2.8
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	2.8
	438398	AA806526	Hs.130277	ESTs	2.8
65	435313	AI769400	Hs.189729	ESTs	2.8
	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	2.8
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	2.8
	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	2.8
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.8
70	401323				2.8
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.8
	428532	AF157326	Hs.184786	TBP-interacting protein	2.8
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	2.8
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse l	2.8
75	406970	M29994		gb:Human alpha-I spectrin gene, exon 12.	2.8
	426172	AA371307	Hs.125056	ESTs	2.8
	452114	N22687	Hs.8236	ESTs	2.8
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
80	430660	R11884	Hs.100826	ESTs	2.8
	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.8
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.8
	429881	T80112	Hs.192245	ESTs	2.8
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.8



	409435	AI810721	Hs.95424	ESTs	2.8
	442191	W95186	Hs.8136	endothelial PAS domain protein 1	2.8
	407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	2.8
5	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheli	2.8
	412189	R60982	Hs.22581	ESTs	2.8
	420976	AI924940	Hs.108082	ESTs, Weakly similar to T31636 hypotheli	2.8
	448330	AL036449	Hs.207163	ESTs	2.8
10	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
	422505	AL120862	Hs.124165	ESTs	2.8
	427752	AA470687	Hs.104772	ESTs	2.8
	433513	AI566356	Hs.171437	ESTs	2.8
	433703	AA210863	Hs.3532	nemo-like kinase	2.8
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
	405621				2.8
15	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to	2.8
	450400	AI694722	Hs.279744	ESTs	2.8
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.8
	418342	BE002723	Hs.226627	leptin receptor	2.8
20	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	440320	AA879294		gb:nw86e09.s1 NCI_CGAP_Pr12 Homo sapiens	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	439831	AW136488	Hs.25545	ESTs	2.8
25	425661	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	2.8
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	2.8
	418658	AW874263	Hs.32468	ESTs	2.8
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
	421340	F07783	Hs.1369	decay accelerating factor for complement	2.8
30	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.8
	409241	AF070602	Hs.51649	Homo sapiens clone 24504 mRNA sequence	2.8
	448219	AA228092	Hs.42656	KIAA1681 protein	2.8
	408936	AL138043	Hs.293549	ESTs	2.8
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	2.8
35	426471	M22440	Hs.170009	transforming growth factor, alpha	2.8
	454455	AW752710		gb:IL3-CT0219-281099-024-A03 CT0219 Homo	2.8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	401335				2.7
	436577	W84774	Hs.17643	ESTs	2.7
40	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.7
	436007	AI247716	Hs.232168	ESTs	2.7
45	408874	AW818091	Hs.252730	ESTs	2.7
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	2.7
	435625	H50654	Hs.113999	ESTs	2.7
	435766	R11673	Hs.186498	ESTs	2.7
	410327	T33130	Hs.301746	RAP2A, member of RAS oncogene family	2.7
50	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
	427134	AA398409	Hs.173561	EST	2.7
	428137	AA421792	Hs.170999	ESTs	2.7
55	429710	AI337113	Hs.146025	hypothetical protein FLJ23594	2.7
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.7
	441928	AI370188	Hs.211454	ESTs	2.7
	409721	AW887732	Hs.257861	ESTs	2.7
60	427112	Z32887	Hs.290951	ESTs	2.7
	403776				2.7
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
	427839	AA608823	Hs.98244	ESTs	2.7
	432837	AA310693	Hs.87329	HSPC072 protein	2.7
65	438782	AA828380	Hs.126733	ESTs	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	458043	AW979009	Hs.326108	ESTs	2.7
	438171	AW976507	Hs.293515	ESTs	2.7
	452959	AI933416	Hs.189674	ESTs	2.7
70	439556	AI623752	Hs.163603	ESTs	2.7
	446152	AI292036	Hs.150028	ESTs	2.7
	434803	AW974640	Hs.303413	ESTs	2.7
	407771	AL138272	Hs.62713	ESTs	2.7
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.7
75	417543	AA203620	Hs.110153	ESTs	2.7
	401517				2.7
	403677				2.7
	416337	H48713		gb:yq78d02.r1 Soares fetal liver spleen	2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
80	446800	AI341635	Hs.156486	ESTs	2.7
	457906	AW975939	Hs.153290	Homo sapiens cDNA FLJ14318 fis, clone PL	2.7
	452277	AL049013	Hs.28783	KIAA1223 protein	2.7
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to t38022 hypotheli	2.7

	408715	AA768873	Hs.112250	hypothetical protein FLJ23518	2.7
	410743	AA089474	Hs.272153	ESTs	2.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.7
5	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.7
	427565	AI287280	Hs.97933	ESTs, Weakly similar to T46370 hypotheti	2.7
	406092				2.7
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	2.7
	438504	AW665281	Hs.224625	ESTs	2.7
10	414783	AW069569	Hs.278270	inactive progesterone receptor, 23 kD	2.7
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	2.7
	418686	Z36830	Hs.87268	annexin A8	2.7
	413795	AL040178	Hs.142003	ESTs	2.7
	457528	AW973791	Hs.292784	ESTs	2.7
15	444230	H95537	Hs.146067	ESTs	2.7
	403760				2.7
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.7
	428904	AI312526	Hs.46640	ESTs	2.7
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	2.7
20	458638	N78553	Hs.282204	nucleosomal binding protein 1	2.7
	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA	2.7
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.7
	433906	AI167816	Hs.43355	ESTs	2.7
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	2.7
25	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.7
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	2.7
	421585	U95626	Hs.302043	chemokine (C-C motif) receptor-like 2	2.7
	445158	AI992108	Hs.127206	ESTs	2.7
	421175	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.7
30	401793				2.7
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.7
	451343	AW975057	Hs.293353	ESTs	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
35	438475	W03856	Hs.13188	ESTs, Highly similar to Gene product wit	2.7
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	2.7
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	2.7
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	2.7
40	451487	AA018072		gb:ze51g02.r1 Soares retina N2b4HR Homo	2.7
	418269	AA806113	Hs.189025	ESTs	2.7
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	441963	AI733307	Hs.128002	ESTs	2.7
45	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.7
	426902	AI125334	Hs.97408	ESTs	2.7
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	2.7
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	2.7
	445265	AI218295	Hs.144942	ESTs	2.7
50	422988	AW673847	Hs.97321	ESTs	2.7
	428613	AB037749	Hs.186928	KIAA1328 protein	2.7
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	2.7
	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	2.7
	402800				2.7
55	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.7
	414729	BE466928	Hs.281901	ESTs	2.7
	453716	AA037675	Hs.152675	ESTs	2.7
	452693	T79153	Hs.48589	zinc finger protein 228	2.7
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	2.7
60	443305	AI050693	Hs.133318	ESTs	2.7
	416709	R99369	Hs.283108	hemoglobin, gamma G	2.7
	419077	AA233885	Hs.164526	ESTs	2.7
	453878	AW964440	Hs.19025	DC32	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
65	446817	AI700684	Hs.134166	ESTs	2.7
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	2.6
	410406	AI969703	Hs.1466	glycerol kinase	2.6
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.6
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	2.6
70	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.6
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	2.6
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
75	418217	AI910647	Hs.13442	ESTs	2.6
	428667	AI375550	Hs.74407	nucleolar protein p40; homolog of yeast	2.6
	414573	AI821846	Hs.71999	ESTs	2.6
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
80	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	2.6
	428483	AI908539	Hs.321444	KIAA0344 gene product	2.6
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
	405059				2.6
	425178	H16097	Hs.161027	ESTs	2.6

	442952	AI743261	Hs.131860	ESTs	2.6
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	2.6
	456179	H75490	Hs.271930	ESTs	2.6
5	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
	459456	AA486036	Hs.190124	ESTs	2.6
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	2.6
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
10	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	438295	AI394151	Hs.37932	ESTs	2.6
	445550	AI242754	Hs.137306	ESTs	2.6
	450469	AI955049	Hs.281326	ESTs	2.6
15	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen	2.6
	429250	H56585	Hs.198308	tryptophan rich basic protein	2.6
	437906	AA771704	Hs.194626	ESTs	2.6
	426775	AA384564	Hs.108829	ESTs	2.6
20	443372	AI792557	Hs.133107	ESTs	2.6
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	425465	L18964	Hs.1904	protein kinase C, iota	2.6
	422746	NM_004484	Hs.119651	glypican 3	2.6
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	2.6
25	424527	AW138558	Hs.267158	ESTs, Weakly similar to I54374 gene NF2	2.6
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	2.6
	411402	BE297855	Hs.69855	NRAS-related gene	2.6
	445264	AI218263	Hs.323472	EST	2.6
	458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Ce	2.6
30	415227	AW821113	Hs.72402	ESTs	2.6
	435429	AW592035	Hs.254414	ESTs, Weakly similar to 1805195B RNA-bin	2.6
	434445	AI349306	Hs.11782	ESTs	2.6
	448570	AI923944	Hs.30913	ESTs	2.6
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
35	422879	AI241409	Hs.188092	ESTs	2.6
	409026	AL137554	Hs.49927	protein kinase NYD-SP15	2.6
	425717	X07282	Hs.171495	retinoic acid receptor, beta	2.6
	429127	AA749382	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	2.6
40	438298	H23542	Hs.181788	ESTs	2.6
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.6
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.6
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.6
45	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
	437939	AW298600	Hs.141840	ESTs, Weakly similar to S59501 interfero	2.6
	430719	AA488988	Hs.293796	ESTs	2.6
	452864	AA033714	Hs.287629	hypothetical protein FLJ14260	2.6
	432095	AW022273	Hs.105769	ESTs	2.6
50	431086	AI829692	Hs.211561	ESTs	2.6
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	2.6
	423952	AW877787	Hs.136102	KIAA0853 protein	2.6
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	2.6
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.6
55	430933	AW863635		gb:MR3-SN0010-270300-103-h02 SN0010 Homo	2.6
	420691	AA829433	Hs.275343	ESTs	2.6
	429761	AI276780	Hs.135173	ESTs	2.6
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
60	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.6
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	2.6
	438647	AA813118	Hs.163230	ESTs	2.6
	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.6
65	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.6
	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.6
	428170	H05530	Hs.12565	ESTs	2.6
	457343	NM_013936	Hs.247862	olfactory receptor, family 12, subfamily	2.6
70	424020	R76946	Hs.39738	ESTs	2.6
	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.6
	411965	BE467339	Hs.280115	ESTs	2.6
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.6
	455488	AA102322		gb:z190f03.r1 Stratagene colon (937204)	2.6
75	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.6
	404285				2.6
	418744	AI887288	Hs.196379	ESTs, Weakly similar to putative p150 [H	2.6
	454714	AW815098		gb:QV4-ST0212-091199-023-f10 ST0212 Homo	2.6
80	429828	AB019494	Hs.225767	IDN3 protein	2.6
	436387	AA714760	Hs.240075	Homo sapiens cDNA FLJ13234 fis, clone OV	2.6
	448587	AI539652	Hs.28338	KIAA1546 protein	2.6
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.6
	440479	AA886461	Hs.208161	ESTs	2.6
	443160	AI467915	Hs.36053	ESTs	2.6

	428978	AA442784	Hs.125445	ESTs	2.5
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.5
	453459	BE047032	Hs.257789	ESTs	2.5
5	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.5
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.5
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.5
	458760	AI498631	Hs.111334	ferritin, light polypeptide	2.5
	434131	AI858275	Hs.143659	ESTs	2.5
10	441805	AA285136	Hs.301914	neuronal specific transcription factor D	2.5
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	2.5
	417351	T90278	Hs.15049	ESTs	2.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sa	2.5
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	2.5
15	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	2.5
	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	453919	AW959912	Hs.7076	KIAA1705 protein	2.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.5
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	2.5
20	427491	R43279	Hs.22574	ESTs, Weakly similar to I38022 hypotheti	2.5
	435102	AW899053	Hs.76917	F-box only protein 8	2.5
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.5
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.5
	432887	AI926047	Hs.162859	ESTs	2.5
25	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5
	401078				2.5
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.5
	425201	AA352111		gb:EST60061 Activated T-cells XX Homo sa	2.5
	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
30	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
	444542	AI161293	Hs.280380	aminopeptidase	2.5
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	2.5
	428497	BE010877	Hs.98584	ESTs	2.5
	457336	AW969657	Hs.291029	ESTs	2.5
35	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	2.5
	423782	AI472209	Hs.323117	ESTs	2.5
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	2.5
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	2.5
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.5
40	417137	U46265	Hs.81281	mitochondrial ribosomal protein S21	2.5
	436787	AA908554	Hs.192756	ESTs	2.5
	440331	AL046412	Hs.202151	ESTs	2.5
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.5
	417169	R13550	Hs.246773	ESTs	2.5
45	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	2.5
	455286	BE144384		gb:MR0-HT0166-191199-004-c11 HT0166 Homo	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	2.5
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	2.5
50	446346	AI290205	Hs.309940	ESTs	2.5
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	2.5
	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	2.5
	425523	AB007948	Hs.158244	KIAA0479 protein	2.5
	433124	U51712	Hs.13775	hypothetical protein SMAP31	2.5
55	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.5
	425657	T89839	Hs.119471	ESTs	2.5
	401254				2.5
	426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	2.5
	449535	W15267	Hs.23672	low density lipoprotein receptor-related	2.5
60	433138	AB029496	Hs.59729	semaphorin sem2	2.5
	425804	BE501698	Hs.258189	ESTs	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	437267	AW511443	Hs.258110	ESTs	2.5
	454305	BE062633	Hs.28338	KIAA1546 protein	2.5
65	455631	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	2.5
	401878				2.5
	450350	T97817	Hs.174880	ESTs	2.5
	436532	AA721522		gb:nv54h12.r1 NCL_CGAP_Ew1 Homo sapiens	2.5
	457460	AI143312	Hs.129206	casein kinase 1, gamma 3	2.5
70	427304	AA761526	Hs.163853	ESTs	2.5
	419721	NM_001650	Hs.288650	aquaporin 4	2.5
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	2.5
	446252	AI283125	Hs.150009	ESTs	2.5
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	2.5
75	434273	AA913143	Hs.26303	ESTs	2.5
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	2.5
	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN I	2.5
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.5
	452232	AW020603	Hs.158423	radial spoke protein 3	2.5
80	433764	AW753676	Hs.39982	ESTs	2.5
	412050	H96503	Hs.109087	Homo sapiens cDNA: FLJ22845 fis, clone K	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	2.5
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.5

	408813	AI580090	Hs.48295	RNA helicase family	2.5
	414109	BE250744		gb:600943376F1 NIH_MGC_17 Homo sapiens c	2.5
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.5
5	419985	H66373	Hs.15973	ESTs, Highly similar to bA393J16.3 [H.sa	2.5
	417859	T26453		gb:AB214F6R Infant brain, LLNL array of	2.5
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.5
	448015	AI458065	Hs.23196	ESTs	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
10	445865	AI262584	Hs.145575	ESTs	2.5
	451800	AW977435	Hs.323867	ESTs	2.5
	456987	AI557290	Hs.173536	ESTs	2.5
	403568				2.5
	435209	AW027809	Hs.187698	Homo sapiens cytomegalovirus partial fus	2.5
15	430371	D87466	Hs.240112	KIAA0276 protein	2.5
	418033	W68180	Hs.259855	elongation factor-2 kinase	2.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.5
	453619	H87648	Hs.33922	Homo sapiens, clone MGC:9084, mRNA, comp	2.5
	431071	AA491379		gb:aa65f05.r1 NCL_CGAP_GCB1 Homo sapiens	2.5
20	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.5
	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	2.4
	417318	AW953937	Hs.12891	ESTs	2.4
25	413382	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.4
	406748	AW339106	Hs.217493	annexin A2	2.4
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.4
	441817	AW969706	Hs.293332	ESTs	2.4
	450551	AJ010046	Hs.25155	neuroepithelial cell transforming gene 1	2.4
30	457940	AL360159	Hs.306517	Homo sapiens TRIPartite motif protein ps	2.4
	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	2.4
	436907	AA737171	Hs.131809	ESTs	2.4
	429399	AA452244	Hs.16727	ESTs	2.4
	448782	AL050295	Hs.22039	KIAA0758 protein	2.4
35	434404	AW445034	Hs.256578	ESTs	2.4
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	2.4
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	2.4
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	2.4
	450705	U90304	Hs.25351	iroquois homeobox protein 5	2.4
40	425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1 (J	2.4
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	2.4
	458986	AI802772	Hs.208655	ESTs	2.4
	443861	AW449462	Hs.134743	ESTs	2.4
	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo	2.4
45	415250	F02614	Hs.27319	ESTs	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
	443919	AI091284	Hs.135224	ESTs, Weakly similar to A47582 B-cell gr	2.4
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.4
	400385	NM_020389	Hs.283104	putative capacitative calcium channel	2.4
50	411322	AW887330	Hs.172405	cell division cycle 27	2.4
	434638	H50758		gb:yp86e06.r1 Soares fetal liver spleen	2.4
	435559	AF209198	Hs.42636	zinc finger protein 277	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
	448005	AW207437	Hs.170378	ESTs	2.4
55	454201	AB023191	Hs.44131	KIAA0974 protein	2.4
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.4
	449486	AI652715	Hs.270811	ESTs	2.4
	421516	AI362418	Hs.105379	FT005 protein	2.4
	412167	AW897230		gb:CM0-NN0057-150400-335-a11 NN0057 Homo	2.4
60	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	2.4
	400641				2.4
	430576	AA767125	Hs.293574	ESTs	2.4
	434423	NM_006769	Hs.3844	LIM domain only 4	2.4
65	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.4
	441499	AW298235	Hs.101689	ESTs	2.4
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.4
	417819	AI253112	Hs.133540	ESTs	2.4
	431728	NM_007351	Hs.268107	multimerin	2.4
70	425025	AW953168	Hs.12407	ESTs	2.4
	421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	2.4
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.4
	408867	AA437199	Hs.656	cell division cycle 25C	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
75	445038	AI635444	Hs.143917	dJ467N11.1 protein	2.4
	450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.4
80	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.4
	453864	AW021407	Hs.21068	hypothetical protein	2.4
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.4
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.4
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	2.4

	447357	AI375922	Hs.159367	ESTs	2.4
	452631	AI188658	Hs.87496	ESTs	2.4
	405041				2.4
	405472				2.4
5	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	2.4
	433868	AA612960	Hs.337300	ESTs	2.4
	437119	AI379921	Hs.177043	ESTs	2.4
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.4
10	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.4
	434936	AI285970	Hs.183817	ESTs	2.4
	408918	BE218603	Hs.279708	ESTs	2.4
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.4
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.4
15	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	2.4
	446659	AI335361	Hs.226376	ESTs	2.4
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	2.4
	434995	AW974995		gb:EST387100 MAGE resequences, MAGN Homo	2.4
	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.4
20	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	2.4
	427131	AA448460	Hs.112017	GE36 gene	2.4
	442039	AW276240	Hs.128352	ESTs	2.4
	448595	AB014544	Hs.21572	KIAA0644 gene product	2.4
	432949	AA570749	Hs.298866	ESTs	2.4
25	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.4
	417420	T85150	Hs.268814	ESTs	2.4
	427551	T96203		gb:ye48b07.r1 Soares fetal liver spleen	2.4
	420057	AA806899	Hs.184387	ESTs	2.4
	434950	AW974892		gb:EST386997 MAGE resequences, MAGN Homo	2.4
30	425497	AA524596		gb:nh34b02.s1 NCI_CGAP_Pr3 Homo sapiens	2.4
	438214	H06076	Hs.26320	TRABID protein	2.4
	416100	H18700	Hs.268799	ESTs	2.4
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
35	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	2.4
	419179	AW275291	Hs.113009	hypothetical protein FLJ22527	2.4
	436391	AJ227892	Hs.146274	ESTs	2.4
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	2.4
	447499	AW262580	Hs.147674	protocadherin beta 16	2.4
40	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.4
	412877	BE011168		gb:PM3-BN0218-100500-003-d08 BN0218 Homo	2.4
	435985	AA703154	Hs.191934	ESTs	2.4
	440674	BE561546		gb:601347208F1 NIH_MGC_8 Homo sapiens cD	2.4
	446476	AW294072	Hs.141376	ESTs	2.4
45	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.4
	435731	AA699581	Hs.186811	ESTs	2.4
	437105	AA744554	Hs.222127	ESTs	2.4
	406091				2.4
	457024	AA397546	Hs.119151	ESTs	2.4
50	404249				2.4
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	2.4
	424943	AU077260	Hs.153924	death-associated protein kinase 1	2.4
	444229	AV648613	Hs.282397	ESTs	2.4
	404860				2.4
55	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	2.4
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.4
	420843	H96982	Hs.42321	ESTs	2.4
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.4
	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
60	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	2.4
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG	2.3
65	418782	AI792648	Hs.14665	ESTs	2.3
	447870	BE139479	Hs.161492	ESTs	2.3
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.3
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	2.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	2.3
70	424049	AB014524	Hs.138380	KIAA0624 protein	2.3
	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.3
	430702	U56979	Hs.250651	H factor 1 (complement)	2.3
	409620	AA076278	Hs.13277	hypothetical protein FLJ22054	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.3
75	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	2.3
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	2.3
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	2.3
	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
80	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	2.3
	404513				2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	448506	AI524673	Hs.38170	ESTs	2.3
	434811	AW971205	Hs.114280	ESTs	2.3

	457065	AI476318	Hs.192480	ESTs	2.3
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypep	2.3
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	2.3
5	423596	AA328195	Hs.234101	ESTs, Weakly similar to CTL1 protein [H.	2.3
	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.3
	435867	AA954229	Hs.114052	ESTs	2.3
	440196	N72847	Hs.125221	ESTs	2.3
	401213				2.3
10	407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo	2.3
	442490	AW965078	Hs.30212	thyroid receptor interacting protein 15	2.3
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.3
	438138	R98299	Hs.177502	ESTs	2.3
	440283	AI732892	Hs.190489	ESTs	2.3
15	447039	AV661798	Hs.282915	ESTs	2.3
	412777	AI335773	Hs.270123	ESTs	2.3
	421424	AW452690	Hs.258775	ESTs	2.3
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.3
	440555	D31292	Hs.6853	hypothetical protein FLJ22167	2.3
20	451516	AI800515	Hs.12024	ESTs	2.3
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	2.3
	421046	AA810854	Hs.89081	ESTs	2.3
	423604	AA486585	Hs.258901	ESTs	2.3
	409029	BE087807		gb:QV1-BT0681-290400-181-g02 BT0681 Homo	2.3
25	444206	AW301017	Hs.146492	ESTs	2.3
	451836	T63673	Hs.173220	ESTs	2.3
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.3
	436671	AW137159	Hs.146151	ESTs	2.3
30	434988	AI418055	Hs.161160	ESTs	2.3
	452862	AW378065	Hs.8687	ESTs	2.3
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	2.3
	410606	AW418779	Hs.114889	ESTs	2.3
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.3
35	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	2.3
	430217	N47863	Hs.336901	ribosomal protein S24	2.3
	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	2.3
	421253	AI188102	Hs.31028	ESTs	2.3
	438180	AA808189	Hs.272151	ESTs	2.3
40	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	2.3
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	2.3
	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	2.3
	412953	Z45794	Hs.238809	ESTs	2.3
45	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	2.3
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	423003	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	2.3
	428595	AB037795	Hs.186547	KIAA1374 protein	2.3
50	437887	AA811524	Hs.29263	hypothetical protein FLJ11896	2.3
	447720	AL038765	Hs.161304	ESTs	2.3
	452355	N54926	Hs.29202	G protein-coupled receptor 34	2.3
	408374	AW025430	Hs.155591	forkhead box F1	2.3
55	440381	AA917808	Hs.190495	ESTs	2.3
	425478	AB007953	Hs.268840	ESTs	2.3
	432231	AA339977	Hs.274127	CLST 11240 protein	2.3
	431757	AA196930	Hs.268526	Homo sapiens chromosome 21q22.1 anonymou	2.3
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.3
	452837	AL121053	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	2.3
60	417426	NM_002291	Hs.82124	laminin, beta 1	2.3
	423739	AA398155	Hs.97600	ESTs	2.3
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	2.3
	425876	AW005887	Hs.234058	ESTs	2.3
	457411	AW085961	Hs.130093	ESTs	2.3
65	413136	BE066941		gb:PM0-BT0340-091299-002-a11 BT0340 Homo	2.3
	420313	AB023230	Hs.96427	KIAA1013 protein	2.3
	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
	436331	AI239495	Hs.120189	ESTs	2.3
70	439275	AF086093	Hs.141566	ESTs	2.3
	449272	AW137656	Hs.197645	ESTs	2.3
	454352	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo	2.3
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	2.3
	407242	M18728		gb:Human nonspecific crossreacting antig	2.3
75	445326	AI220072	Hs.165893	ESTs	2.3
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.3
	452607	AI160029	Hs.61438	ESTs	2.3
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	2.3
	418851	AI417828	Hs.192435	ESTs	2.3
80	458332	AI000341	Hs.220491	ESTs	2.3
	432565	AA553477	Hs.152428	ESTs	2.3
	437511	AI807500	Hs.125247	ESTs	2.3
	430957	AI937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.3
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	2.3

	448225	AI476429	Hs.19238	ESTs	2.3
	408955	BE315170	Hs.8087	NAG-5 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
5	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothe	2.3
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	440348	AW015802	Hs.47023	ESTs	2.3
	436340	R42246	Hs.21606	ESTs	2.3
10	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	2.3
	438462	AI624122	Hs.89578	general transcription factor IIH, polype	2.3
	411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN !!!	2.3
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	2.3
	412505	AA974491	Hs.21734	ESTs	2.3
	418236	AW994005	Hs.337534	ESTs	2.3
15	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	2.3
	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.3
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.3
	433404	T32982	Hs.102720	ESTs	2.3
20	409517	X90780	Hs.120036	troponin I, cardiac	2.3
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
	445641	AI245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	2.3
25	437770	AA767881	Hs.122897	ESTs	2.3
	409064	AA062954	Hs.141883	ESTs	2.3
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.3
	449869	W57990	Hs.60059	Homo sapiens cDNA FLJ11478 fis, clone HE	2.3
	422108	AA297914	Hs.111749	postmeiotic segregation increased (S. ce	2.3
	418251	AA832123	Hs.177723	ESTs	2.3
30	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA P	2.3
	413638	H71252		gb:ys12h12.s1 Soares fetal liver spleen	2.3
	415980	R52414		gb:yg80b05.r1 Soares infant brain 1NIB H	2.3
	449232	AW192780	Hs.196080	ESTs	2.3
35	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.3
	454389	AW752571		gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.3
	438089	W05391	Hs.83623	nuclear receptor subfamily 1, group I, m	2.3
	400238				2.3
	404488				2.3
40	407809	AW082279	Hs.244106	ESTs	2.3
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp58611518 (f	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	2.3
45	426567	AA381579	Hs.182962	ESTs	2.3
	435708	AI362949	Hs.75169	ESTs	2.3
	441417	AI733297	Hs.144474	ESTs	2.3
	445117	AI208754	Hs.147369	ESTs	2.3
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.2
50	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	2.2
	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	2.2
	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	2.2
	420653	AI224532	Hs.88550	ESTs	2.2
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.2
55	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	2.2
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.2
	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
60	437637	AJ003029	Hs.65792	syntrophin, gamma 2	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	446164	AW273539	Hs.288750	hypothetical protein FLJ23577	2.2
	450232	BE300815	Hs.201326	ESTs	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	402745				2.2
65	434008	AA740878	Hs.112982	ESTs	2.2
	439492	AF086310	Hs.103159	ESTs	2.2
	436853	BE328074	Hs.148661	ESTs	2.2
	417648	R06552		gb:yf09e12.r1 Soares fetal liver spleen	2.2
70	427690	AI253134	Hs.283410	ESTs	2.2
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.2
	450229	R18717	Hs.8929	hypothetical protein FLJ11362	2.2
	400756				2.2
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	2.2
	403388				2.2
75	433643	AI821787	Hs.179586	ESTs	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
80	439920	H05430	Hs.288433	neurotrimin	2.2
	432436	AW300248	Hs.181693	ESTs	2.2
	429493	AL134708	Hs.145998	ESTs	2.2
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.2
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	2.2



	442757	AI739528	Hs.28345	ESTs	2.2
	430212	AA469153		gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens	2.2
	437146	AA730977		gb:nw55f05.s1 NCI_CGAP_Ew1 Homo sapiens	2.2
5	432101	AI918950	Hs.123642	EphA3	2.2
	459644				2.2
	453887	BE564037	Hs.36237	hypothetical protein	2.2
	431170	AW971246	Hs.291022	ESTs	2.2
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.2
10	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	2.2
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	2.2
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.2
	425810	AI923627	Hs.31903	ESTs	2.2
	433037	NM_014158	Hs.279938	HSPC067 protein	2.2
	407162	N63855	Hs.142634	zinc finger protein	2.2
15	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
	454766	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414221	AW450979		gb:UL-H-BI3-ala-a-12-0-UL.s1 NCI_CGAP_Su	2.2
20	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: hamy2)	2.2
	400639				2.2
	406149				2.2
	424027	AW337575	Hs.201591	ESTs	2.2
	427531	AA405097	Hs.97957	ESTs	2.2
	448353	BE407125	Hs.231510	ESTs	2.2
25	417669	T99898		gb:ye68g01.r1 Soares fetal liver spleen	2.2
	449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	2.2
	452335	AW188944	Hs.61272	ESTs	2.2
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
30	447748	AI422023	Hs.161338	ESTs	2.2
	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	438550	AW976002	Hs.258402	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
35	444540	AI693927	Hs.265165	ESTs	2.2
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.2
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.2
	439443	AF086261	Hs.127892	ESTs	2.2
	418824	AW751661	Hs.53542	choreoacanthocytosis gene; KIAA0986 prot	2.2
40	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.2
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.2
	432702	AW973953	Hs.293744	ESTs	2.2
	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p	2.2
	425570	AA359558		gb:EST68590 Fetal lung II Homo sapiens c	2.2
45	414935	C15671		gb:C15671 Clontech human aorta polyA+ mR	2.2
	453153	N53893	Hs.24360	ESTs	2.2
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	2.2
	439867	AA847510	Hs.161292	ESTs	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
50	433420	AI674093	Hs.293961	ESTs, Moderately similar to putative DNA	2.2
	434690	AI867679	Hs.148410	ESTs	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	431688	AA513906		gb:ng67c08.s1 NCI_CGAP_Lip2 Homo sapiens	2.2
55	403133				2.2
	414885	AA157531	Hs.269276	ESTs, Moderately similar to S65657 alpha	2.2
	432111	AW972777		gb:EST384871 MAGE resequences, MAGL Homo	2.2
	410073	AW408163	Hs.58488	catenin (cadherin-associated protein), a	2.2
	448869	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
60	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.2
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	2.2
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.2
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	2.2
	403378				2.2
65	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	2.2
	438580	AA811262	Hs.299202	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Claspin	2.2
	412282	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	2.2
	411966	AA099113	Hs.118609	ESTs	2.2
70	443915	Z40763	Hs.135292	ESTs	2.2
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.2
	446094	AK001760	Hs.13801	KIAA1685 protein	2.2
	436486	AA742221	Hs.120633	ESTs	2.2
	411139	AW819461		gb:RCS-ST0293-061299-031-C03 ST0293 Homo	2.2
75	409070	AA063003	Hs.224560	ESTs	2.2
	432713	AL118623	Hs.29494	PRO1912 protein	2.2
	419384	AA490866	Hs.39429	ESTs	2.2
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.2
	408444	AW661839	Hs.253204	ESTs	2.2
80	432128	AA127221	Hs.117037	ESTs	2.2
	418027	AB037807	Hs.83293	hypothetical protein	2.2
	446060	Z42061	Hs.27004	ESTs	2.2
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.2
	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU8_HUMAN A	2.2

	443401	AI394067	Hs.160159	ESTs	2.2
	424665	AW368576	Hs.139851	caveolin 2	2.2
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	2.2
5	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.2
	414564	AA164803	Hs.71994	ESTs, Weakly similar to I38022 hypotheti	2.2
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	2.2
	419160	AA911342	Hs.35524	KIAA1559 protein	2.2
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	2.2
10	442879	AF032922	Hs.8813	syntaxin binding protein 3	2.2
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.2
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	2.2
	432074	AA525248	Hs.149723	ESTs	2.2
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	2.2
15	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	2.2
	409723	AW885757	Hs.257862	ESTs	2.2
	425627	AF019612	Hs.297007	membrane-bound transcription factor prot	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	449369	AA001256	Hs.27260	ESTs	2.2
20	425514	AF112345	Hs.158237	integrin, alpha 10	2.2
	455821	BE143341		gb:MR0-HT0162-191099-002-d04 HT0162 Homo	2.2
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.2
	432284	AA532807	Hs.105822	ESTs	2.2
	403467				2.2
25	436032	AA150797	Hs.109276	latexin protein	2.2
	404356				2.2
	434205	AF119861	Hs.283032	hypothetical protein PRO2015	2.2
	405257				2.2
	402103				2.2
30	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.2
	432985	T92363	Hs.178703	ESTs	2.2
	417649	AW239285	Hs.82359	tumor necrosis factor receptor superfami	2.2
	431277	AA501806	Hs.249965	ESTs	2.2
	454056	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	2.2
35	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	448390	AL035414	Hs.21068	hypothetical protein	2.2
40	449939	T86420	Hs.272139	ESTs	2.2
	455678	BE060007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.2
	404555				2.2
	418186	BE541042	Hs.23240	Homo sapiens cDNA: FLJ21848 fis, clone H	2.2
	419981	AA897581	Hs.128773	ESTs	2.2
45	449581	AI989517	Hs.181605	ESTs	2.2
	419229	AI827237	Hs.282884	ESTs	2.2
	403691				2.2
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.2
	443479	AF027219	Hs.9443	zinc finger protein 202	2.2
50	425329	AI961644	Hs.145444	Homo sapiens cDNA FLJ11494 fis, clone HE	2.2
	453345	AA302862	Hs.90063	neurocalcin delta	2.2
	424335	AW021508	Hs.28170	ESTs	2.2
	451072	AA013451	Hs.117929	ESTs	2.2
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	2.2
55	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.2
	438035	AA938198	Hs.146123	poly(A) polymerase gamma	2.2
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.2
	400241				2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
60	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	2.2
	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	446009	AI989885	Hs.231926	ESTs	2.2
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	2.1
	416441	BE407197		gb:601301552F1 NIH_MGC_21 Homo sapiens c	2.1
65	414891	R27124	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE	2.1
	430172	AA468591	Hs.161889	ESTs	2.1
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.1
	422985	AU076411	Hs.1602	dihydropyrimidine dehydrogenase	2.1
70	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	2.1
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	2.1
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	2.1
	438379	N23018	Hs.171391	C-terminal binding protein 2	2.1
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
75	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.1
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	2.1
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.1
	437132	AL049353	Hs.297268	ESTs	2.1
	415304	T66079	Hs.12799	ESTs	2.1
80	450152	AI138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	2.1
	421147	AW592167	Hs.293299	ESTs	2.1
	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.1
	451750	AA280851	Hs.226930	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.1

	406945	K01383	Hs.173451	metallothionein 1A (functional)	2.1
	452449	AW068658	Hs.20943	ESTs	2.1
	436009	H57130	Hs.120925	ESTs	2.1
5	418637	T86737	Hs.193536	ESTs	2.1
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	2.1
	449203	AI634578	Hs.282121	ESTs	2.1
	437751	AA767373	Hs.35669	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	428412	AA428240	Hs.126083	ESTs	2.1
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.1
10	441967	AA972742	Hs.209786	ESTs	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.1
15	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
	431229	AA496479	Hs.259929	ESTs	2.1
	435148	AI918049	Hs.124961	ESTs	2.1
	436349	AI445255	Hs.115315	ESTs	2.1
	446895	AA166655	Hs.282803	ESTs	2.1
20	448582	AI538880	Hs.94812	ESTs	2.1
	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.1
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	2.1
	451874	AW963137	Hs.194233	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	448076	AJ133123	Hs.20196	adenylate cyclase 9	2.1
25	443484	AI091458	Hs.134559	ESTs	2.1
	430686	NM_001942	Hs.2633	desmoglein 1	2.1
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	2.1
	407624	AW157431	Hs.248941	ESTs	2.1
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.1
30	428923	BE047698	Hs.188785	ESTs	2.1
	422496	AA311301	Hs.278827	ESTs	2.1
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.1
	408418	AW963897	Hs.44743	KIAA1435 protein	2.1
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.1
35	427434	BE538374	Hs.301732	hypothetical protein MGC5306	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	459325	AW088369	Hs.282184	ESTs	2.1
	416996	W91892	Hs.59609	ESTs	2.1
40	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.1
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	2.1
	418894	W73921	Hs.50743	ESTs	2.1
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.1
	437378	AI198823	Hs.160473	ESTs	2.1
	454100	AI693231	Hs.126043	chromosome 21 open reading frame 51	2.1
45	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	2.1
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	2.1
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.1
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	2.1
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	2.1
50	424103	NM_001918	Hs.139410	dihydrolipoamide branched chain transacy	2.1
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	2.1
	449911	AI262106	Hs.12653	ESTs	2.1
	449509	AA001615	Hs.84561	ESTs	2.1
	452762	AW501435	Hs.278582	v-akt murine thymoma viral oncogene homo	2.1
55	422839	AI674784	Hs.298908	ESTs	2.1
	435040	AI932350	Hs.152825	ESTs	2.1
	401200				2.1
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.1
	442262	BE170651	Hs.8700	deleted in liver cancer 1	2.1
60	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypotheti	2.1
	453908	AW613920	Hs.282178	ESTs	2.1
	446965	BE242873	Hs.16677	WD repeat domain 15	2.1
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
65	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
	455995	BE179408		gb:IL3-HT0618-060500-125-B07 HT0618 Homo	2.1
	422411	AW749443	Hs.22511	ESTs	2.1
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	2.1
	446893	AI610818	Hs.7110	ESTs	2.1
70	442992	AI914699	Hs.13297	ESTs	2.1
	407021	U52077		gb:Human mariner1 transposase gene, comp	2.1
	436938	AW139680	Hs.161393	ESTs	2.1
	433194	AB040883	Hs.83243	KIAA1450 protein	2.1
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	2.1
75	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	2.1
	434739	AA804487	Hs.144130	ESTs	2.1
	406468				2.1
	457023	AA001732	Hs.173233	hypothetical protein FLJ10970	2.1
80	416226	N55342	Hs.34372	ESTs	2.1
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.1
	432810	AA863400	Hs.23054	ESTs	2.1
	412894	R09778	Hs.186510	ESTs	2.1
	430602	D13752	Hs.184927	cytochrome P450, subfamily XIB (steroid	2.1
	436981	AA740891	Hs.293316	ESTs	2.1

	452501	AB037791	Hs.29716	hypothetical protein FLJ10980	2.1
	449838	AB020653	Hs.24024	KIAA0846 protein	2.1
	447160	AA330310	Hs.24181	ESTs	2.1
5	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	2.1
	440137	AA866199	Hs.171397	ESTs	2.1
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	2.1
	436471	AA719813	Hs.117662	ESTs	2.1
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	2.1
10	426782	R14614	Hs.191254	ESTs	2.1
	430027	AB023197	Hs.227743	KIAA0980 protein	2.1
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.1
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	2.1
	427115	AW972853	Hs.112237	ESTs	2.1
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.1
15	400451				2.1
	435255	W87434	Hs.106015	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	418375	NM_003081	Hs.84389	synaposomal-associated protein, 25kD	2.1
	442835	AI021989	Hs.131903	ESTs	2.1
20	400196				2.1
	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.1
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	2.1
	438940	AF075045	Hs.271609	ESTs	2.1
25	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.1
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	2.1
	410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	2.1
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.1
	419088	AI538323	Hs.52620	integrin, beta 8	2.1
30	447373	AI381922	Hs.158781	ESTs	2.1
	457465	AW301344	Hs.122908	DNA replication factor	2.1
	413918	AW015898	Hs.71245	ESTs	2.1
	402820				2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
35	428552	AW274560	Hs.129520	ESTs	2.1
	435464	BE548300	Hs.192999	ESTs, Moderately similar to KIAA0961 pro	2.1
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	2.1
	420838	AW118210	Hs.5244	ESTs	2.1
40	428231	U17989	Hs.183105	nuclear autoantigen	2.1
	434933	R91095	Hs.4276	KIAA1701 protein	2.1
	444870	AI200621	Hs.148504	ESTs	2.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.1
	429183	AB014604	Hs.197955	KIAA0704 protein	2.1
45	439155	H81076	Hs.269001	ESTs	2.1
	442787	W93048	Hs.250723	hypothetical protein MGC2747	2.1
	429864	AA460039	Hs.286	ribosomal protein L4	2.1
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.1
	437140	AA312799	Hs.283689	activator of CREM in testis	2.1
50	421991	NM_014918	Hs.110488	KIAA0990 protein	2.1
	446534	AI307356	Hs.175225	ESTs	2.1
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.1
	444838	AV651680	Hs.208558	ESTs	2.1
	402318				2.1
55	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	421306	AA806207	Hs.125889	ESTs	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	429088	D61542	Hs.227716	KIAA0934 protein	2.1
60	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	2.1
	428060	AA420616	Hs.249483	ESTs	2.1
	419953	BE267154	Hs.125752	ESTs	2.1
	443718	AI083580	Hs.221373	ESTs	2.1
	444187	AW138466	Hs.151274	ESTs	2.1
65	428048	AA705745		gb:zf41b11.s1 Soares_fetal_heart_NbHH19W	2.1
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.1
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.1
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.1
	430335	D80007	Hs.239499	KIAA0185 protein	2.1
70	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.1
	434029	AA621763	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.1
	410945	AW811552		gb:QV2-ST0145-071299-017-h10 ST0145 Homo	2.1
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.1
	433374	AI821409	Hs.332789	EST	2.1
75	445644	R77766	Hs.271593	ESTs, Moderately similar to A47582 B-cel	2.1
	450271	AI693900	Hs.200920	ESTs	2.1
	448084	AI467800	Hs.271000	ESTs, Weakly similar to I38022 hypotheti	2.1
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	2.1
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	2.1
80	435542	AA687376	Hs.269533	ESTs	2.1
	443544	AI076315	Hs.16359	ESTs	2.1
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	2.1
	405759				2.1
	446242	N66336	Hs.7360	ESTs	2.1

	457938	AI373638	Hs.133900	ESTs	2.1
	433017	Y15067	Hs.279914	zinc finger protein 232	2.1
	436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	2.1
5	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.1
	439224	AW471088	Hs.145950	ESTs, Highly similar to T08692 hypotheti	2.1
	410976	R36207	Hs.25092	hypothetical protein MGC10744	2.1
	454574	AW809109		gb:MR4-ST0117-070100-027-a04 ST0117 Homo	2.1
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	2.1
10	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	2.1
	446891	AL036877	Hs.282878	ESTs	2.1
	434294	AJ271379	Hs.76194	ribosomal protein S5	2.1
	449057	AB037784	Hs.22941	KIAA1363 protein	2.1
	432769	AA620814	Hs.144959	ESTs	2.1
15	441224	AU076964	Hs.7753	calumenin	2.1
	407891	AA486620	Hs.41135	endomucin-2	2.1
	429017	AA463605	Hs.66295	multi-PDZ-domain-containing protein	2.1
	406817	AI936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
	430566	AA481282	Hs.190149	ESTs	2.1
20	449208	AW263635	Hs.48643	ESTs	2.1
	451397	AA017432	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	2.1
	452042	H38857	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	2.1
	444779	AI192105	Hs.147170	ESTs	2.0
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	2.0
25	415954	AA171850	Hs.42251	ESTs	2.0
	420273	AI652864	Hs.197257	ESTs	2.0
	411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.0
	422389	AF240635	Hs.115897	protocadherin 12	2.0
	446994	AV650435	Hs.16755	MBIP protein	2.0
30	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	2.0
	422654	AA314316	Hs.163725	ESTs	2.0
	425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	2.0
	405634				2.0
	451562	H04150	Hs.107708	ESTs	2.0
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.0
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.0
	442010	AI032680	Hs.132213	ESTs	2.0
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	2.0
	425312	AA354940	Hs.145958	ESTs	2.0
40	415191	AA190381	Hs.120810	ESTs	2.0
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	2.0
	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1	2.0
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.0
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	2.0
45	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	2.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	2.0
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
50	429418	AI381028	Hs.118769	ESTs	2.0
	445829	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.0
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	2.0
	400462				2.0
55	422003	AA361760	Hs.296326	ESTs	2.0
	444585	AW170015	Hs.6594	ESTs	2.0
	444898	AI201548	Hs.308338	ESTs	2.0
	403525				2.0
60	443031	AW134696	Hs.49418	ESTs	2.0
	430818	AI311928		gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	2.0
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PNO099 son3 prot	2.0
	440941	BE268362	Hs.7535	COBW-like protein	2.0
	409627	AW997628	Hs.313637	ESTs	2.0
65	433258	AI806626	Hs.207300	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.0
	412863	AA121673	Hs.59757	zinc finger protein 281	2.0
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.0
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	2.0
	417280	AW173116	Hs.262206	ESTs	2.0
70	423528	AB011137	Hs.300938	KIAA0565 gene product	2.0
	424800	AL035588	Hs.153203	MyoD family inhibitor	2.0
	446019	AI362520	Hs.279789	histone deacetylase 3	2.0
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.0
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	2.0
75	430473	AW130690	Hs.59962	ESTs	2.0
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	2.0
	438118	AW753311	Hs.259415	ESTs	2.0
	400859				2.0
	405829				2.0
80	415258	AW752247	Hs.293853	ESTs	2.0
	420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypotheti	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	2.0
	453118	AW195849	Hs.252757	ESTs	2.0

	430706	NM_003540	Hs.247816	H4 histone family, member C	2.0
	420568	F09247	Hs.247735	protocadherin alpha 10	2.0
	452759	AW590773	Hs.258996	ESTs	2.0
5	408496	AI683802	Hs.136182	ESTs	2.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	2.0
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	2.0
	450086	AW016343	Hs.233301	ESTs	2.0
	410853	H04588	Hs.30469	ESTs	2.0
10	438607	AW080237	Hs.252884	ESTs	2.0
	422232	D43945	Hs.113274	transcription factor EC	2.0
	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
	402490				2.0
	446551	AI308176	Hs.65636	ESTs	2.0
	438315	R56795	Hs.82419	ESTs	2.0
15	445261	T79759	Hs.282939	ESTs, Weakly similar to I38022 hypotheti	2.0
	401986				2.0
	420335	AA258771	Hs.43616	Homo sapiens mRNA for FLJ00029 protein,	2.0
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
20	435413	AI267476	Hs.46669	ESTs	2.0
	458175	AW296024	Hs.150434	ESTs	2.0
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.0
	417494	AI369494	Hs.222137	ESTs	2.0
	416045	H15990	Hs.31403	ESTs	2.0
25	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	2.0
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	2.0
	411578	AW238524		gb:xp27c05.x1 NCL_CGAP_HN10 Homo sapiens	2.0
	453116	AI276680	Hs.146086	ESTs	2.0
	426692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.0
30	435608	AW183971	Hs.250896	ESTs	2.0
	402102				2.0
	458308	AI828155	Hs.211055	ESTs	2.0
	438177	BE327015	Hs.281391	ESTs	2.0
	415205	H71616	Hs.135233	ESTs	2.0
	427244	AA402400	Hs.178045	ESTs	2.0
35	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	2.0
	438979	AW976218	Hs.32565	ESTs	2.0
	400285				2.0
	405966				2.0
40	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	427739	AW196755	Hs.98105	NYD-SP14 protein	2.0
	433584	AW295399		gb:U1-H-BI2-ahv-h-03-0-UI.s1 NCL_CGAP_Su	2.0
	448956	AK001674	Hs.22630	cofactor required for Sp1 transcriptiona	2.0
	439474	AI824060	Hs.211501	ESTs	2.0
45	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.0
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.0
	418836	AI655499	Hs.161712	ESTs	2.0
	453108	AI311457	Hs.99472	ESTs	2.0
	447101	N72185	Hs.44189	ESTs	2.0
50	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	2.0
	426226	AA769045		gb:oa80h07.s1 NCL_CGAP_GCB1 Homo sapiens	2.0
	401157				2.0
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.0
	425646	AW157044	Hs.158512	cyclin-dependent kinase-like 2 (CDC2-rel	2.0
55	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	2.0
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	2.0
	402855				2.0
	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	2.0
	445672	AI907438	Hs.282862	ESTs	2.0
60	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.0
	411941	AW876909	Hs.25201	ESTs, Weakly similar to FAT DROME CADHER	2.0
	430664	AW969834	Hs.303303	ESTs	2.0
	402812				2.0
	457434	AW628192	Hs.18851	hypothetical protein FLJ10875	2.0
65	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
	402048				2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	2.0
	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
70	437373	H67505	Hs.191979	KIAA1733 protein	2.0
	439217	AF086041	Hs.42975	ESTs	2.0
	446609	BE395090	Hs.15535	Homo sapiens clone 24582 mRNA sequence	2.0

75 TABLE 3B: List of accession numbers for primekeys lacking unigenelD's for Table 3A. For each such probeset is listed a gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

80 Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey CAT number Accession

	408690	107490_1	AW864542 AA056567 AW882724
	409029	1095422_1	BE087807 AW301579
	409073	109851_1	AA063458 AA063018 A1444822
5	409519	113722_1	AA075368 AA075369
	409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
	410008	116812_1	AA079552 BE142525 BE142527
	410615	1212203_1	AW772721 AW873372 H89212
	410672	1214882_1	AW794600 AW794730
10	410784	1221005_1	AW803201 BE079700 BE062940
	410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
	410888	1225955_1	AW861207 AW809508
	410901	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786
			AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960
15	410934	1227240_1	AW811114 AW811095 AW811087 AW811124 AW811054 AW811094 AW811157
	410945	1227561_1	AW811552 AW811470 AW811523 AW811482 AW811514 AW811456 AW811525
	410999	1228809_1	AW813004 AW812962 AW812961
	411004	1228975_1	AW813242 BE146089 AW813195 AW813173 AW813206 BE145953 BE146212 AW813196 AW854582 AW813241 BE061582
	411018	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
20	411139	1233781_1	AW819461 AW819478 AW819479 AW819559 AW819505
	411151	1234022_1	AW866497 AW819775 AW819868 AW866602 AW866561
	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
			AW848905 AW848214
	411514	1248638_1	AW850178 AW850233 AW850445 AW850446
25	411578	125013_1	AW238524 AA094059 R59022
	411745	1256160_1	AW867826 AW859896
	411880	1263110_1	AW872477 BE088101 T05990
	411905	1265181_1	BE265067 BE264978 AW875420
	412167	1280605_1	AW897230 AW897252 AW897244 AW897231 AW897263
30	412209	1283610_1	AW901456 AW901450 AW901441
	412248	1285000_1	BE176480 AW903298 AW903313
	412282	1287679_1	BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
	412303	1288130_1	AW936336 AW936339
	412566	1306469_1	AW962574 BE073261
35	412877	1333953_1	BE011168 BE006371 BE011172 BE011313 BE011166
	412879	1334272_1	BE092219 BE092361 BE006789
	413087	1348720_1	BE064655 BE153953
	413136	1350379_1	BE066941 BE066911 BE066979 BE066929 BE066925
	413252	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
40	413382	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
	413488	1373234_1	BE144017 BE185527 BE144023
	413499	1373910_1	BE144884 H97942
	413618	1380384_1	BE154078 BE154006 BE153891 BE153523 BE153983
	413638	1381238_1	H71252 BE154668 BE154642
45	413642	1381386_1	BE154837 BE154879 BE154850 BE154877 BE154835 BE154849 BE154902 BE154905 BE154867 BE154901 BE154904 BE154899
	413875	1396766_1	BE176776 H85072
	414109	1417307_1	BE250744 BE294770
	414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368
			BE011362 BE011215 BE011365 BE011363
50	414605	1465790_1	BE390440
	414935	1509157_1	C15671 C15333 C15833 D81433 C14657 C14811
	415236	1531080_1	R41400 H06659 Z38637 F02023 T16516
	415635	1540853_1	F13168 R21289 T77628
	415747	155189_1	AA381209 AA381245 AA167683
55	415980	1564218_1	R52414 R61681 H12009 T74429
	416288	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
	416337	1589299_1	H48713 H83057 H48694 H65247
	416441	159480_1	BE407197 AA182474 AA180369 BE275628 BE276131
	416548	1600181_1	H62953 N76608 N72413
60	416624	1604694_1	H69044 T47567 H75691 T50292
	416871	1626761_1	H98716 N90792 N24283
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	416972	163668_1	BE019670 AA191284 AA191255
	417561	168747_2	AW974345 BE145400 T97088 AA639076
	417648	1691070_1	R06552 T98985 R08656
65	417669	1692157_1	T99898 T92080 T91447 R07806 R07779
	417859	1703724_1	T26453 Z44226 R20425
	418378	174656_1	AW962081 AA218925 AA354237
	418636	177402_1	AW749855 AA225995 AW750208 AW750206
70	419546	185766_1	AA244199 AA244272 H57440
	419637	186639_1	W27493 AA248063 AA249685 AA429679
	419807	188252_1	R77402 AA262462 AA250988 R06794
	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	420621	195113_1	AA278808 BE082076 BE081812 BE081581
75	420637	195241_1	AW976153 AA278945 AA747691
	421065	198936_1	AA329711 AA287436 AA283148
	422063	210852_1	BE156476 BE156473 BE156474 BE156475 AA302839
	422156	212379_1	N34524 AA305071 AW954803 AA502335 A1433430 A1203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512
			A1334966 W32951 H62656 H53902 R88904 AW835732
80	422342	215498_1	AA309272 AA309312 AW961837
	422429	216469_1	AA310527 AW962295 Z44865 H06641
	422977	223410_1	AA631498 A1017191 AA491211 AA761823 AA714555 AA768099 AA808286 A1934069 AA570223 AA574389 AA582438 A1745346 AW964510
			AA319642 AW853758 H56414
	423121	225175_1	AW864848 AA322213 AA322209 AW961624

	423377	22769_1	AL049377 AL079930 AL047223 AW885968 AA385235
	423532	229362_1	BE090503 BE090490 BE090483 BE090501 BE090500 BE090365 BE090505 BE090509 BE090499 BE090502 BE090504 BE090497 AA327285
	423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA649496
5	423841	232507_1	AW753967 AA370795 AA331630 AW962550
	423867	232732_1	AA331886 AW962659 AW962655 T89841
	424872	244505_1	AA347923 AA347928 AW961769
	425201	247933_1	AA352111 AW962247 AA429695
	425497	252499_1	AA524596 AA358494 AA513507
10	425570	253248_1	AA359558 AA359819 AW963122
	426226	262918_1	AA769045 AA372590 AW963633
	426497	268121_1	AA379913 AA379981 AW963523
	426603	269825_1	AA382291 AA994657
	427551	280163_1	T96203 AA405343 T96121
	428048	286394_1	AA705745 AA420850 AA420433
15	428679	294049_1	AA431765 AA432015
	430212	314437_1	AA469153 AI718503 AA469225
	430818	324239_1	AI311928 AA936030 T51931 AA609816 AA487195 AA664207
	430844	324570_1	T94960 AA487679 T95013
20	430933	325757_1	AW863635 BE179901 BE179402 AW863789 AA489179 BE010747 BE010748
	431071	327550_1	AA491379 H86020 AW969148
	431169	328799_1	AW971240 AA493843 AA493723
	431322	331543_1	AW970622 AA503009 AA502998 AA502805 T92188
	431595	335512_1	AA508196 BE142920 AI280311 AI205616 D61709
25	431688	336609_1	AA513906 AA847734 AI357044
	432111	341618_1	AW972777 AA526795 AA526305
	432189	342819_1	AA527941 AI810608 AI620190 AA635266
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
	432779	354024_1	AW979241 AA565006 AA847102
30	432803	354267_1	AA565398 AW894072 H97930
	432869	355475_1	AW974094 AA569074 AA602574
	433347	36388_1	AF023130 AF181250 AA984703 AA694303 AA351792
	433492	367934_1	AW605849 AW262898 N41060 AA594852
	433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
	433644	371919_1	AW342028 AA641080 AA603282
35	433687	373061_1	AA743991 AA604852 AW272737
	434138	380572_1	AA625804 AW418787 AW074833 AI675642 AI393368
	434374	384889_1	AA631439 AI086355 AI082577
	434613	389550_1	AI821826 AA640657 AA658836 AA650055 AI821079
40	434638	38990_1	H50758 AF147434 H50666
	434950	396061_1	AW974892 AA654375
	434995	397210_1	AW974995 AI821880 AI821932 AI791196 AA659617 AI821137 AA658925
	435079	399783_1	AA664192 H60250 T71388
	435463	406582_1	AA682507 AW851124
45	435634	409239_1	T82384 R05307 AA693714
	436532	421802_1	AA721522 AW975443 T93070
	437146	43371_1	AA730977 AI261584 AA334473 Z43283 AW875861 AW938044 BE150701 AW936262 AA306862 BE565575 BE567380 AA728920 AA167612
	438005	447553_1	AI239729 AI251752 AA485791 BE568425 AW962958
	438458	457837_1	BE151746 BE336853 D63271 T94955 AA774994
50	438909	46684_1	AW975186 AA807807 D29548
	438993	467651_1	AF085839 R69137 AW188788 R69254
	440320	491930_1	AA828995 AA834879 AI926361
	440674	49997_1	AA879294 N67538 AI474541
	443613	575391_1	BE561546 Z25124 AI307139 Z28800
55	443657	576685_1	AI079356 W23287
	444314	600667_1	R14973 R14967 AI081006
	444610	612257_1	AI140497 AW749625 AW749626 AW749644
	444910	624951_1	AI174783 R83569 R12271
	446096	661959_1	AI201849 BE069007 AW946544
60	446901	697809_1	AI276454 AI633717 AI275116
	447197	711623_1	AI347274 AW844024
	448404	761515_1	R36075 AI366546 R36167
	449540	80945_2	BE089973 AI498612 AW805032
65	450024	82296_1	AA001713 H63836
	450458	83586_1	AA005129 AA679084 AA694399
	450522	837264_1	AA009926 BE149301
	451024	85565_1	AI698839 AI909260 AI909259
	451487	87131_1	AA442176 AA259181
70	452453	918300_1	AA018072 N46370 R84847
	452542	921410_1	AI902519 AI902518 AI902516
	453823	982526_1	AW812256 AW812257 AI906423 AI906422
	453901	986414_1	AL137967 BE064160 BE064186
	454190	1049996_1	BE065902 AW749032 AW003637
75	454193	1050256_1	AW177821 AW177896 AW177867
			BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091
			AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220
			AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129
			AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108
			AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156
			AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598 BE140957
80	454352	1129667_1	AW389668 AW389657 AW609198 AW389649
	454359	1130674_1	N71277 AW390764
	454389	115682_1	AW752571 AW847602 AA077979
	454403	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093



5	454455	1206965_1	AW752710 BE180336 BE180186
	454566	1224432_1	AW807605 AW807690 AW807839 AW807752 AW807673 AW807667 AW807955 AW807760 AW807615 AW807898 AW807849 AW807821
			AW807832 AW807842 AW807827 AW807822 AW807829 AW807830 AW807825 AW807603 AW807612 AW807908 AW807595 AW807617
			AW807678 AW807687 AW807918 AW807921 AW807596 AW807602 AW807688 AW807609 AW807684 AW807770 AW807593 AW807754
			AW807679 AW807957 AW807683 AW807763 AW807902 AW807840 AW807819 AW807836 AW807769 AW807685 AW807847 AW807674
			AW807686 AW807670 AW807917 AW807677 AW807680 AW807900 AW807669 AW807952 AW807907 AW807846 AW807756
			AW807835 AW807608 AW807753 AW807601 AW807956
	454574	1225636_1	AW809109 AW809112 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132
10	454600	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786
			AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960
	454678	1228915_1	AW813089 W28102
	454693	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
	454714	1230493_1	AW815098 BE154843 BE154831
15	454766	1234022_1	AW866497 AW819775 AW819868 AW866602 AW866561
	454784	1234630_1	AW820626 AW820621 AW820608
	454790	1234752_1	AW820852 AW820773 AW821088
	454836	1236509_1	AW833711 AW833620 AW833699
	454962	1246760_1	AW847645 AW847791 AW854083 AW853945
20	455047	1250536_1	AW852530 AW852527 AW852526
	455092	1252971_1	BE152428 AW855572 AW855607
	455100	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	455107	1253874_1	BE154113 AW856797 AW856847 AW861128 AW856817
	455114	1254106_1	AW857121 AW857123 AW861238
25	455170	1256906_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
	455201	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
	455226	1262534_1	AW902103 AW869012 AW869139
	455252	1266222_1	AW876627 AW876630 AW876631 AW876625
	455286	1273576_1	BE144384 AW887474 AW887403 BE144386
30	455310	1278158_1	AW893961 AW893998 AW894034 AW894019
	455431	1289854_1	AW938484 BE001245 BE001190
	455488	129372_1	AA102322
	455511	1321229_1	BE144762 AW979091
35	455512	1321443_1	AW983608 AW983628 AW983610 AW983688 AW983601 AW983645 AW983607 AW983640 AW983625 AW983612 AW983642 AW983687
			AW983602 AW983624 AW983634 AW983637 AW983632 AW983617 AW983635 AW983630 AW983636 AW983639 AW983616 AW983689
			AW983641 AW983621 AW983603 AW983609 AW983623 AW983644 AW983618 AW983615 AW983611 AW983604 AW983686 AW983622
			AW983619 AW983633 AW983589 AW983605 AW983626 AW983643 AW983631 AW983627 AW983613 AW983614 AW983685 AW983593
			AW983590 AW983594 AW983620 AW983638 AW983592 AW983588
	455571	1331885_1	BE003714 BE003721 BE003720 BE003716
40	455631	1347545_1	BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072
	455678	1349716_1	BE066007 BE066017 BE066074
	455685	1350393_1	BE066976 BE066928 BE066927
	455807	1370914_1	BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
	455821	1372714_1	BE143341 BE143344 BE143378 BE143358
	455866	1377119_1	BE149024 BE149056 BE152826 BE149025 BE149057 BE152819 BE149030 BE149062 BE149023 BE149055
45	455992	1398552_1	BE179015 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997
	455995	1398903_1	BE179408 BE179798 BE179980
	456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368
			BE011362 BE011215 BE011365 BE011363
50	458804	75803_1	AL157625 N72696 BE622492
	458861	798085_1	AI630223 AI630470
	459160	920051_1	AI904723 AI904725 AI904729 AI904722 AI904758 AI904736
	459201	925883_1	AW391177 W45021
	459267	966605_1	AJ003631 AJ003650 AJ003651

TABLE 29C

60	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
65	Pkey	Ref	Strand	Nt_position
	400451	8113550	Minus	82189-82320
	400462	9929659	Minus	197610-197785
70	400608	9887666	Minus	96756-97558
	400639	9887597	Plus	23150-23580
	400641	8117693	Plus	4786-4992
	400756	8119084	Minus	38734-38857
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
	400880	9931121	Plus	29235-29336,36363-36580
75	400889	9958234	Minus	169782-170036
	400983	8081198	Plus	107903-108832
	401045	8117619	Plus	90044-90184,91111-91345
	401049	7232177	Plus	149157-150692
	401078	3687273	Plus	105052-105171
80	401094	9965511	Plus	137130-137302,139283-139506
	401103	8568122	Minus	98330-98449
	401157	9438289	Minus	114133-114247,114567-114645
	401189	9690246	Minus	90815-90929

	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
	401213	9858408	Plus	98243-98380,98489-98619
	401254	9796309	Plus	152209-152383
5	401323	9212516	Plus	213509-214450
	401335	9884881	Plus	15736-16352
	401497	7381770	Plus	92607-92813
	401517	7677912	Plus	29278-29770
	401526	7770561	Plus	91570-93177
10	401575	7229804	Minus	76253-76364
	401694	3540172	Minus	64056-64168
	401793	7263888	Minus	102945-103083
	401862	7770606	Minus	55839-55993,59145-59293
	401878	8099802	Minus	162268-162474,163089-163195
15	401986	4406829	Minus	31137-31293
	402046	8072415	Plus	166394-166556,168167-168395
	402048	8072512	Plus	43936-44078
	402102	8117771	Minus	174566-174740
20	402103	7249203	Plus	14453-15414
	402230	9966312	Minus	29782-29932
	402318	7582559	Minus	12843-13403
	402490	9797648	Plus	149982-150929
	402745	9212200	Minus	76516-76690
	402800	6010175	Plus	43921-44049,46181-46273
25	402812	6010110	Plus	25026-25091,25844-25920
	402820	6456853	Minus	82274-82443
	402855	9662953	Minus	59763-59909
	403133	7331427	Plus	38314-38634
	403271	7230852	Plus	134283-134485
30	403277	8072597	Minus	27494-27642
	403310	8139936	Minus	183883-184026
	403329	8516120	Plus	96450-96598
	403356	8569930	Plus	92839-93036
	403378	9438244	Minus	44264-44443
35	403388	9438331	Plus	112733-113001,114599-114735
	403467	9929556	Minus	73431-73602
	403515	7656757	Minus	173358-179553
	403525	7960440	Plus	152431-153243
	403534	8076917	Minus	46652-47332
40	403568	8101145	Minus	85509-85658
	403574	8101156	Plus	5542-6176
	403637	8671936	Minus	142647-142771,145531-145762
	403677	7331517	Minus	55008-55083,62860-63051
	403691	7387384	Minus	88280-88463
45	403760	7712202	Minus	45910-46260,47563-47824
	403776	7770611	Minus	1414-1513,1624-1756
	403895	7381715	Minus	3502-4002,4070-4308
	403937	7711761	Minus	12609-12773
	404043	9558573	Plus	29042-29135,46597-46699
50	404097	7770701	Plus	55512-55781
	404200	6010176	Minus	7066-7210
	404249	8655533	Plus	64270-64633
	404274	9885189	Plus	104127-104318
	404285	2326514	Plus	32282-32416
55	404288	2769644	Plus	3512-3691
	404356	7630858	Minus	126433-126623
	404443	7579073	Minus	87198-87441
	404476	8080699	Plus	101841-102043
	404488	8113286	Minus	64835-64994
60	404513	8151941	Minus	112837-113339
	404548	8570305	Minus	83896-84162
	404555	7243881	Minus	63963-64157
	404561	9795980	Minus	69039-70100
	404588	6456726	Minus	40059-40210
65	404593	9944086	Minus	74922-75788
	404599	8705107	Plus	110443-110733
	404860	8979555	Plus	65852-66081
	404916	7341826	Plus	91057-91188
	404957	7407927	Plus	147512-148011
70	405041	7547195	Plus	121230-121714
	405059	7656683	Plus	349-822
	405090	8072525	Minus	38552-39202
	405257	7329310	Plus	73121-73273
	405336	6094635	Plus	33267-33563
75	405472	8439781	Plus	106297-106447,108462-108596
	405494	8050952	Minus	70284-70518
	405547	1054740	Plus	124361-124520,124914-125050
	405621	5523811	Plus	59362-59607
	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
80	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405759	3288022	Minus	18283-18399
	405829	7109593	Minus	15628-16127
	405848	7651809	Minus	28135-28244

405966	8247788	Minus	51762-51978
405970	8247789	Minus	45795-46295
406018	6758904	Minus	37795-38168
406091	9123919	Minus	197370-197935
406092	9123919	Plus	251370-251797,252168-252882
406149	7144791	Minus	44464-45164
406195	7289992	Minus	36293-36827
406333	9213235	Plus	64689-64798
406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
406506	7711374	Minus	6843-8077
406554	7711566	Plus	106956-107121
406603	8272659	Minus	39506-39694

TABLE 30A: ABOUT 1840 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO HYPERSENSITIVITY PNEUMONITIS (HP)

Table 30A lists about 1840 genes that are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with hypersensitivity pneumonitis (HP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 Gene Chip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" hypersensitivity pneumonitis sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90<sup>th</sup> percentile amongst idiopathic pulmonary fibrosis samples. The "average" hypersensitivity pneumonitis level was set to the 90<sup>th</sup> percentile amongst hypersensitivity pneumonitis samples.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of IPF (idiopathic pulmonary fibrosis) to HP (hypersensitivity pneumonitis)

Pkey	ExAccn	Unigene ID	Unigene Title	R1
450478	AW451709	Hs.271200	ESTs	20.2
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
406654				11.8
440209	H05049	Hs.22269	neurexin 3	10.8
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	10.4
439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	10.2
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	9.5
416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.3
420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	9.2
403574				9.1
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
419519	AI198719	Hs.176376	ESTs	8.2
435256	AF193766	Hs.13872	cytokine-like protein C17	8.1
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	8.1
429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	8.0
405443				7.8
428766	AA477989	Hs.98800	ESTs	7.7
441802	AA968636	Hs.127877	ESTs	7.6
453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)	7.5
447410	AI470235	Hs.172698	EST	7.2
442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
405494				6.9
442377	AA993807	Hs.167367	ESTs	6.9
409928	AL137163	Hs.57549	hypothetical protein dJ473B4	6.8
420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	6.8
415236	R41400		gb:yf94b12.s1 Soares infant brain 1NIB H	6.8
451562	H04150	Hs.107708	ESTs	6.8
403310				6.7
445189	AI936450	Hs.147482	ESTs	6.7
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.7
439780	AL109688		gb:Homo sapiens mRNA full length insert	6.6
402076				6.6
415025	AW207091	Hs.72307	ESTs	6.5
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	6.5
438557	AW364104	Hs.143509	hypothetical protein FLJ21924	6.5
428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	6.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	6.4
409545	BE296182	Hs.19002	hypothetical protein MGC4675	6.4
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.4
411966	AA099113	Hs.118609	ESTs	6.4
440274	R24595	Hs.7122	scrapie responsive protein 1	6.3
442879	AF032922	Hs.8813	synixin binding protein 3	6.3
419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
420185	AL044056	Hs.158047	ESTs	6.3
415672	N53097	Hs.193579	ESTs	6.2
455488	AA102322		gb:z190f03.r1 Stratagene colon (937204)	6.2
420026	AI831190	Hs.166676	ESTs	6.1
446868	AV660737	Hs.135100	ESTs	6.1
431622	AW979271	Hs.293184	ESTs	6.1
407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	6.1
421300	AW297398	Hs.96617	ESTs	6.0
416045	H15990	Hs.31403	ESTs	6.0

5	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	6.0
	424693	BE169810	Hs.47557	ESTs	6.0
	436397	AA715013	Hs.169835	ESTs	6.0
	440504	AI948966	Hs.130017	ESTs, Weakly similar to JN0908 H+-transp	6.0
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	6.0
10	403625				6.0
	418986	AI123555	Hs.81796	ESTs	5.9
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.9
	400292	AA250737	Hs.72472	ESTs	5.9
	442849	R10099	Hs.269805	ESTs	5.9
15	440887	AI799488	Hs.135905	ESTs	5.8
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	431374	BE258532	Hs.251871	CTP synthase	5.7
	444963	AI916973	Hs.213603	ESTs	5.7
20	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	5.6
	444992	R37658	Hs.21375	ESTs	5.6
	416575	W02414	Hs.38383	ESTs	5.5
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
	451830	H18433	Hs.21542	KIAA1035 protein	5.5
25	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	5.5
	404043				5.5
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	5.5
	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	5.5
	434683	AW298724	Hs.202639	ESTs	5.5
30	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	5.5
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	5.5
	428895	AA437124	Hs.187247	ESTs	5.4
	450018	AA421642	Hs.24309	hypothetical protein FLJ11106	5.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
35	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.4
	454039	AW079064	Hs.245540	ESTs	5.3
	403637				5.3
	414725	AA769791	Hs.125300	ring finger protein 21, interferon-respo	5.3
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG	5.3
40	403329				5.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	5.3
	459664				5.3
	401497				5.3
	410797	AW857191		gb:RC2-CT0304-080100-011-b12 CT0304 Homo	5.2
45	411402	BE297855	Hs.69855	NRAS-related gene	5.2
	448844	AI581519	Hs.177164	ESTs	5.2
	435202	AI971313	Hs.170204	KIAA0551 protein	5.1
	439418	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	5.1
	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	5.1
50	434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	5.1
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.0
	437636	AA764781	Hs.291844	ESTs	5.0
55	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
	455464	AW983901		gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.0
	418771	AA807881	Hs.25329	ESTs	5.0
	434820	AI821863		gb:ms90f05.x5 NCL_CGAP_Pr3 Homo sapiens	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
60	454482	BE147919		gb:RC3-HT0230-160200-016-a08 HT0230 Homo	4.9
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	4.9
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	4.9
	423607	AA328329	Hs.6591	ESTs	4.9
	407415	AF073328		gb:Homo sapiens tetracycline transporter-	4.9
65	401878				4.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	4.9
	451325	AA021283	Hs.59788	ESTs	4.9
	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	4.9
	406333				4.9
70	409105	AW467539	Hs.255877	ESTs	4.8
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	4.8
	421482	AL135462	Hs.104715	inversin	4.8
	442757	AI739528	Hs.28345	ESTs	4.8
	459717				4.8
75	436637	AI783629	Hs.26766	ESTs	4.8
	412222	AA528283	Hs.292737	ESTs	4.8
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
80	441640	AI733345	Hs.144104	ESTs	4.8
	422977	AA631498		gb:np83h04.s1 NCL_CGAP_Thy1 Homo sapiens	4.8
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	4.8
	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.8
	411965	BE467339	Hs.280115	ESTs	4.7
	403341				4.7
	411726	AW858612		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	4.7
	443271	BE568568	Hs.195704	ESTs	4.7

	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	426097	BE327369	Hs.112238	ESTs	4.7
	439199	R40373	Hs.26299	ESTs	4.7
5	440728	AW086077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	4.6
	434381	AA631834		gb:np77h05.s1 NCI_CGAP_Pr2 Homo sapiens	4.6
	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	431242	AA987742	Hs.251278	KIAA1201 protein	4.6
10	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	442360	AI374621	Hs.29055	ESTs	4.6
	452171	AI863302	Hs.211930	EST	4.6
	440801	AA906366	Hs.190535	ESTs	4.5
	411738	AW859353		gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
15	431447	AA505138	Hs.291341	ESTs	4.5
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
	401365				4.5
	408281	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	4.5
	411657	AW855583		gb:CM4-CT0278-221099-027-f07 CT0278 Homo	4.5
20	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	4.5
	428528	AI004034	Hs.98638	ESTs	4.5
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.5
	417252	AA195014	Hs.85971	ESTs	4.5
	417135	AA422067	Hs.50547	ESTs	4.5
	403089				4.4
25	420691	AA829433	Hs.275343	ESTs	4.4
	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	4.4
30	454438	AA224053	Hs.172405	cell division cycle 27	4.4
	435434	AA680387	Hs.187850	ESTs	4.4
	420828	AA280778	Hs.186878	ESTs	4.3
	435586	AI279137	Hs.151498	ESTs	4.3
	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
35	416170	H42454	Hs.220645	ESTs	4.3
	408691	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	4.3
	428912	AW103117	Hs.98949	ESTs, Weakly similar to MEA6 [H.sapiens]	4.3
	455511	BE144762		gb:CMO-HT0180-041099-065-b04 HT0180 Homo	4.3
	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	4.3
40	401189				4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	422654	AA314316	Hs.163725	ESTs	4.3
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
45	417919	AI928203	Hs.86379	ESTs	4.3
	405784				4.3
	431853	AA521034	Hs.70834	ESTs	4.3
	409629	AW449589	Hs.279724	ESTs	4.2
	403281				4.2
50	427173	BE255017	Hs.97540	ESTs	4.2
	433717	AF063536		gb:AF063536 Homo sapiens library (Yu Y)	4.2
	406777	T23625	Hs.150580	putative translation initiation factor	4.2
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	4.2
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.2
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	4.2
	449762	N93057	Hs.54888	ESTs	4.2
	421106	AA877124	Hs.172844	ESTs	4.2
	439382	BE247684	Hs.103070	ESTs	4.1
	404957				4.1
60	436332	AL049679	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	4.1
	446393	AW014174	Hs.301956	zinc finger protein	4.1
	452728	AI915676	Hs.239708	ESTs	4.1
	456386	W28481		gb:47e1 Human retina cDNA randomly prime	4.1
	406288	AW068311	Hs.311054	Homo sapiens mRNA full length insert cDN	4.1
65	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	403344				4.1
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.1
70	401596	AA172106	Hs.110950	Rag C protein	4.1
	418693	AI750878	Hs.87409	thrombospondin 1	4.1
	414299	AA142989	Hs.71730	ESTs	4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	458552	AW136139	Hs.245856	ESTs	4.0
75	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	441201	AW118822	Hs.128757	ESTs	4.0
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	4.0
	440472	AA886169	Hs.169071	ESTs	4.0
80	418379	AA218940	Hs.137516	fidgetin-like 1	4.0
	435878	R08330	Hs.20152	ESTs	4.0
	437263	AA747822		gb:nx97a04.s1 NCI_CGAP_GCB1 Homo sapiens	4.0
	444087	AV647899	Hs.282375	ESTs	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0

	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010566, mRNA,	4.0
	405521				4.0
	411597	AW852925		gb:PM0-CT0248-131099-001-f10 CT0248 Homo	4.0
5	415655	W05433	Hs.49890	ESTs	4.0
	404822				4.0
	441107	AA917075	Hs.190520	ESTs	4.0
	404834				4.0
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	4.0
10	428102	AA968441	Hs.126866	ESTs	4.0
	436511	AA721252	Hs.291502	ESTs	4.0
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoi	4.0
	453098	Z25935	Hs.86379	ESTs	3.9
	410811	AW805687	Hs.300648	ESTs	3.9
15	425048	H05468	Hs.164502	ESTs	3.9
	431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	452768	AW069459	Hs.61539	ESTs	3.9
20	455241	AW876249		gb:PM4-PT0019-131299-006-B05 PT0019 Homo	3.9
	409070	AA063003	Hs.224560	ESTs	3.9
	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.9
	419091	T85332	Hs.178294	ESTs	3.9
	422591	L07648	Hs.118630	MAX-interacting protein 1	3.9
	403188				3.9
25	418857	D10216	Hs.89394	POU domain, class 1, transcription facto	3.9
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	3.9
	436149	AI754308	Hs.159452	ESTs	3.9
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
30	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.9
	451221	AI949701	Hs.210589	ESTs	3.9
	455475	AW948126		gb:RC0-MT0013-280300-031-a12 MT0013 Homo	3.9
35	433197	AB040889	Hs.281022	KIAA1456 protein	3.9
	429881	T80112	Hs.192245	ESTs	3.9
	415598	AI433165	Hs.9856	ESTs	3.9
	431220	N52937	Hs.102679	ESTs	3.9
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
40	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
	404443				3.9
	407340	AA810168	Hs.284289	vittiligo-associated protein VIT-1	3.9
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviri	3.9
	412400	AW948066		gb:RC0-MT0012-290300-031-h10 MT0012 Homo	3.9
45	427167	AI239607	Hs.99196	hypothetical protein MGC11324	3.9
	438090	AA777534	Hs.191992	ESTs	3.8
	407938	AA905097	Hs.85050	phospholamban	3.8
	440454	AI733037	Hs.129990	ESTs	3.8
	417706	T90797	Hs.268623	ESTs	3.8
50	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	407762	AW235638	Hs.29475	ESTs	3.8
	420727	H75701	Hs.99886	complement component 4-binding protein,	3.8
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	3.8
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	3.8
55	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens	3.8
	459429	AA278779	Hs.335696	EST	3.8
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	437458	AL390131	Hs.128751	Homo sapiens cDNA FLJ12235 fis, clone MA	3.8
	451073	AI758905	Hs.206063	ESTs	3.8
60	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypothe	3.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.8
	444414	AW293214	Hs.8752	transmembrane protein 4	3.8
	402615				3.7
	410585	AW770523	Hs.337501	ESTs	3.7
65	425168	R96366		gb:yq37d04.s1 Soares fetal liver spleen	3.7
	449729	R72032	Hs.29235	ESTs	3.7
	459359	N99545		gb:za40a05.r1 Soares fetal liver spleen	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	439001	AF075068		gb:Homo sapiens full length insert cDNA	3.7
70	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen	3.7
	404193				3.7
	416379	N38857	Hs.203933	ESTs	3.7
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	3.7
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	3.7
75	412589	R28660	Hs.24305	ESTs	3.7
	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	3.7
	453375	AI990114	Hs.240091	ESTs	3.7
80	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-hergulin	3.7
	451882	AI821324	Hs.100445	ESTs	3.7
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp588E1624 (f	3.7
	405001	U58196	Hs.296281	interleukin enhancer binding factor 1	3.7
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	3.7

	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.7
	432781	NM_014133	Hs.278940	PRO0618 protein	3.7
	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.7
5	406964	M21305		gb:Human alpha satellite and satellite 3	3.7
	430682	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.7
	449804	AI535663	Hs.39379	ESTs	3.7
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.7
10	430503	AA533574	Hs.152274	ESTs	3.7
	443305	AI050693	Hs.133318	ESTs	3.7
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.7
	452280	AI911410	Hs.167224	ESTs	3.6
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	406992	S82472		gb:beta-pol=DNA polymerase beta (exon a	3.6
15	441416	AI990139	Hs.148609	ESTs	3.6
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
	413998	AW103807	Hs.243933	ESTs	3.6
	440385	AA884283	Hs.192136	ESTs	3.6
	431673	AW971302	Hs.293233	ESTs	3.6
20	401887				3.6
	404793				3.6
	422054	AA322506		gb:EST25146 Cerebellum II Homo sapiens c	3.6
	432030	AI908400	Hs.143789	ESTs	3.6
	449645	AI961092	Hs.196155	ESTs	3.6
25	404476				3.6
	449336	AL119995	Hs.15260	ESTs, Highly similar to AC007228 2 BC372	3.6
	401200				3.6
	403937				3.6
30	437918	AI761449	Hs.121629	ESTs	3.6
	443394	AI055865	Hs.133485	ESTs	3.6
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	3.6
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	436269	AA707472	Hs.190760	ESTs	3.6
35	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	3.6
	416394	H64111		gb:yr57f03.r1 Soares fetal liver spleen	3.6
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	439326	W07140	Hs.54721	ESTs	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
40	435766	R11673	Hs.186498	ESTs	3.6
	448067	R68568	Hs.183373	src homology 3 domain-containing protein	3.6
	441605	AA984647	Hs.128801	ESTs	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
45	418405	AI868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.5
	450350	T97817	Hs.174880	ESTs	3.5
	451704	AI755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	459037	AW439497	Hs.290656	EST	3.5
	419247	S65791	Hs.89764	fragile X mental retardation 1	3.5
50	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	426724	AA383623	Hs.293616	ESTs	3.5
	434273	AA913143	Hs.26303	ESTs	3.5
	438042	AW296971	Hs.255593	ESTs	3.5
	410500	R09442		gb:yi26c09.r1 Soares fetal liver spleen	3.5
55	416154	Z46122		gb:HSC0VB031 normalized infant brain cDN	3.5
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.5
	454447	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	3.5
	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
	444338	AI937026	Hs.146642	ESTs	3.5
60	427687	AW003867	Hs.1570	histamine receptor H1	3.5
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	3.5
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.5
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	3.5
	403515				3.5
65	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	439953	AA918129	Hs.124638	ESTs	3.5
	457620	AA602711	Hs.336753	EST	3.5
	442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypotheti	3.5
	453931	AL121278	Hs.25144	ESTs	3.5
70	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	3.5
	413468	BE504766		gb:h240g01.x1 NCL_CGAP_GC6 Homo sapiens	3.5
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.5
	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypot	3.5
75	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.5
	410908	AA121686	Hs.10592	ESTs	3.5
	440364	AA910460	Hs.128626	ESTs	3.5
	406190				3.5
80	430762	AI343652	Hs.105667	ESTs	3.5
	451182	D52562	Hs.296317	KIAA1789 protein	3.4
	432437	W07088	Hs.293685	ESTs	3.4
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
	405970				3.4
	407676	AW064111	Hs.279823	ESTs	3.4

	413141	BE166323		gb:QV4-HT0492-270100-086-e12 HT0492 Homo	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
5	459371	R20991		gb:yg06h01.r1 Soares infant brain 1NIB H	3.4
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	3.4
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.4
	420430	AI703192		gb:wd92h04.x1 NCI_CGAP_Lu24 Homo sapiens	3.4
10	443921	AI091310	Hs.134848	ESTs	3.4
	444453	AW379394	Hs.145126	ESTs	3.4
	443475	AI066470	Hs.134482	ESTs	3.4
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.4
	453263	R91778	Hs.99369	ESTs	3.4
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	3.4
15	456303	AA224872	Hs.115088	ESTs	3.4
	431474	AL133990	Hs.190642	ESTs	3.4
	439702	AW085525	Hs.134182	ESTs	3.4
	458797	AW001835	Hs.13323	hypothetical protein FLJ22059	3.4
	430140	AW296771	Hs.221999	ESTs	3.4
20	423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	3.4
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.4
	446672	T05514		gb:EST03403 Fetal brain, Stralagene (cat	3.4
	431548	AI834273	Hs.9711	novel protein	3.4
	416182	NM_004354	Hs.79069	cyclin G2	3.4
25	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
	417663	R07483	Hs.180461	ESTs	3.3
	405455				3.3
	426235	AI631964	Hs.34447	ESTs	3.3
	439567	AI056618	Hs.134314	ESTs	3.3
30	444848	AW451176	Hs.195954	ESTs	3.3
	451426	AW205003	Hs.208063	ESTs	3.3
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	3.3
	401626				3.3
	405780				3.3
35	417991	AA731452	Hs.190008	ESTs	3.3
	443212	AW269515	Hs.102500	hypothetical protein FLJ20481	3.3
	403356				3.3
	404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	3.3
40	413581	BE150618		gb:RC3-HT0272-110100-013-c06 HT0272 Homo	3.3
	426701	AI968103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.3
	445510	AA946676	Hs.282824	ESTs	3.3
	418663	AK001100	Hs.41690	desmocollin 3	3.3
	447617	AI400762	Hs.176675	ESTs	3.3
	448150	AI472167	Hs.302739	ESTs	3.3
45	410140	AL134435	Hs.22269	neurexin 3	3.3
	443283	BE568610		gb:601342622F1 NIH_MGC_53 Homo sapiens c	3.3
	454777	AW820027		gb:QV0-ST0294-240300-173-g04 ST0294 Homo	3.3
	410767	AJ001873	Hs.66185	Homo Sapiens mRNA, partial cDNA sequence	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
50	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	438456	AA913381	Hs.190513	ESTs	3.3
	411186	AW821257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.3
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	3.3
	433567	AF073299	Hs.103132	solute carrier family 9 (sodium/hydrogen	3.3
55	433805	AA706910	Hs.112742	ESTs	3.3
	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.3
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	456555	AW592167	Hs.293299	ESTs	3.3
	419189	T95862	Hs.112318	6.2 kd protein	3.3
60	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	3.3
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	3.3
	413200	AA127395	Hs.222414	ESTs	3.3
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.3
	416737	AF154335	Hs.79691	LIM domain protein	3.3
65	428356	AL046991	Hs.10338	ESTs	3.3
	429216	AI369472	Hs.65407	ESTs	3.3
	432488	AA551010	Hs.216640	ESTs	3.3
	433386	AW360833		gb:PM1-CT0243-201099-004-d08 CT0243 Homo	3.3
	400889				3.3
70	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	446190	AI279299	Hs.256564	ESTs	3.3
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	3.3
	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kd	3.3
75	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
	434294	AJ271379	Hs.76194	ribosomal protein S5	3.3
	452372	AI885742	Hs.228474	ESTs	3.3
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	3.2
80	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	3.2
	430548	AW450575	Hs.163203	ESTs, Weakly similar to B34087 hypotheti	3.2
	427119	AW880562	Hs.114574	ESTs	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
	437845	AA769578	Hs.90488	ESTs	3.2



5	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	414394	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.2
	417175	R44558	Hs.94002	ESTs	3.2
	456536	AW135986	Hs.257859	ESTs	3.2
	401132				3.2
10	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	450947	AI745400	Hs.204662	ESTs	3.2
	456605	AI827786	Hs.259044	ESTs	3.2
	452879	AW905328	Hs.180842	ribosomal protein L13	3.2
15	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	3.2
	429479	AA453488	Hs.99333	ESTs	3.2
	448090	AI608821	Hs.270289	ESTs	3.2
	401324				3.2
	404731				3.2
20	419936	AI792788		gb:ol91d05.y5 NCL CGAP_Kid5 Homo sapiens	3.2
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	3.2
	433990	AA889328	Hs.112950	ESTs	3.2
	415239	R42608	Hs.139270	ESTs	3.2
	418878	W20090	Hs.6616	ESTs	3.2
25	438079	R09664	Hs.191223	ESTs	3.2
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	457460	AI143312	Hs.129206	casein kinase 1, gamma 3	3.2
	454145	AA046872	Hs.62798		3.2
	446577	AB040933	Hs.15420	KIAA1500 protein	3.2
30	430664	AW969834	Hs.303303	ESTs	3.2
	404588				3.2
	407834	AW084991	Hs.26100	ESTs	3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	440790	AW593050	Hs.128580	ESTs	3.2
35	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	3.2
	421916	R34441	Hs.101007	Homo sapiens cDNA: FLJ23546 fis, clone L	3.2
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
	444771	AB023201	Hs.11912	KIAA0984 protein	3.2
40	445233	AV653034	Hs.297559	ESTs	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.2
45	403623				3.2
	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3.2
	444050	AW138295	Hs.135024	ESTs	3.2
	421036	AA810560	Hs.303577	ESTs	3.2
	401459				3.1
50	404404				3.1
	450438	AI696071	Hs.253800	ESTs	3.1
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	3.1
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypothe	3.1
	441274	AW593781	Hs.131357	ESTs	3.1
55	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	400816				3.1
	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
	431906	AW328038	Hs.37486	ESTs	3.1
60	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	450271	AI693900	Hs.200920	ESTs	3.1
	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	3.1
	415273	Z39840	Hs.22229	ESTs	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
65	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.1
	446364	AB006624	Hs.14912	KIAA0286 protein	3.1
	436638	AI271945	Hs.134984	ESTs	3.1
	418079	R40058	Hs.6911	ESTs	3.1
	448466	AI522109	Hs.171066	ESTs	3.1
70	448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
	415046	R40018	Hs.56400	ESTs	3.1
	448134	AI470790	Hs.34494	ESTs	3.1
	456027	BE327387	Hs.13913	KIAA1577 protein	3.1
	458023	AW978161	Hs.268555	5'-3' exoribonuclease 2	3.1
75	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.1
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.1
	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	449138	AW294215	Hs.195631	ESTs	3.1
	455756	BE079307		gb:RC1-BT0623-120200-011-g09 BT0623 Homo	3.1
80	428170	H05530	Hs.12565	ESTs	3.1
	429878	AA460188	Hs.127263	ESTs	3.1
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	3.1
	438369	T77886	Hs.83428	nuclear factor of kappa light polypeptid	3.1
	415840	R15955	Hs.21758	ESTs	3.1
	444955	AW002844	Hs.148641	ESTs	3.1
	436020	AA778177	Hs.121724	ESTs	3.1
	453051	AW196690	Hs.224269	ESTs	3.1

	425178	H16097	Hs.161027	ESTs	3.1
	402145				3.1
	410685	AA497117	Hs.129600	ESTs, Moderately similar to ALU1_HUMAN A	3.1
5	449238	AA428229	Hs.331561	muscle-specific RING-finger protein 3	3.1
	456737	BE247203	Hs.124831	CGI-67 protein	3.1
	438214	H06076	Hs.26320	TRABID protein	3.1
	436250	AY004867	Hs.85844	neurotrophic tyrosine kinase, receptor,	3.1
	411622	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.0
10	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
	449357	AI076363	Hs.288806	Homo sapiens cDNA FLJ11778 fis, clone HE	3.0
	418950	T78517	Hs.13941	ESTs	3.0
	431508	NM_012481	Hs.182979	ribosomal protein L12	3.0
	405090				3.0
15	445409	AI949081	Hs.147862	ESTs	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.0
	408235	AA053381	Hs.75969	proline-rich protein with nuclear target	3.0
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	3.0
20	452073	AA625150	Hs.82098	ESTs	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	427244	AA402400	Hs.178045	ESTs	3.0
	448405	AW207634	Hs.170849	ESTs	3.0
	433767	AA609245		gb:af13a11.s1 Soares_testis_NHT Homo sap	3.0
25	421376	AA287948	Hs.134110	ESTs	3.0
	441519	AA972740	Hs.127092	ESTs	3.0
	404367				3.0
	453502	AL039786	Hs.21273	transcription factor NYD-sp10	3.0
	421948	L42583	Hs.334309	keratin 6A	3.0
30	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
	400608				3.0
	404042				3.0
	405229				3.0
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0
35	415452	F09134	Hs.12839	ESTs	3.0
	430371	D87466	Hs.240112	KIAA0276 protein	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	429014	AI800518	Hs.118158	ESTs	3.0
40	405605				3.0
	400227				3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439693	AI741816	Hs.125897	ESTs	3.0
	427533	R36022	Hs.179566	hypothetical protein FLJ22624	3.0
45	418355	L42563	Hs.1165	ATPase, H+/K+ transporting, nongastric,	3.0
	433536	AI732163	Hs.188909	ESTs, Weakly similar to alternatively sp	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	449623	C00719	Hs.120440	EST	3.0
	445568	H00918	Hs.268744	KIAA1796 protein	3.0
50	440448	AA885428	Hs.125646	ESTs	3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	444148	AW003204	Hs.151167	ESTs	3.0
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	3.0
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	3.0
55	440925	AW511090	Hs.130419	ESTs	3.0
	428398	AI249368	Hs.98558	ESTs	3.0
	415913	H70302		gb:yr95f07.r1 Soares fetal liver spleen	3.0
	418145	AF121260	Hs.83577	cysteine and glycine-rich protein 3 (car	3.0
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	3.0
60	400335	Y13187	Hs.248067	Homo sapiens dmd gene, intron 11	3.0
	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	3.0
	436938	AW139680	Hs.161393	ESTs	3.0
	437980	R50393	Hs.278436	KIAA1474 protein	3.0
	455955	BE162394		gb:PM2-HT0451-170100-004-a08 HT0451 Homo	3.0
65	414899	AW975433	Hs.36288	ESTs	2.9
	403786				2.9
	430187	AI799909	Hs.158989	ESTs	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.9
70	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.9
	457041	AA399018	Hs.250835	ESTs	2.9
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.9
	422336	AI761322	Hs.115285	dihydrolipoamide S-acetyltransferase (E2	2.9
	451664	AA889081	Hs.153952	5' nucleotidase (CD73)	2.9
75	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.9
	455249	AW876538		gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.9
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.9
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (fr	2.9
	405302				2.9
80	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119	AA322201	Hs.131976	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	2.9

	425793	AA363946	Hs.20969	ESTs	2.9
	401462				2.9
	458817	AI522129	Hs.173119	ESTs	2.9
5	422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.9
	419875	AA853410	Hs.93557	proenkephalin	2.9
	423047	NM_005323	Hs.123064	H1 histone family, member T (testis-spec	2.9
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.9
	401368				2.9
10	418531	R96760	Hs.183758	ESTs	2.9
	447290	AI476732	Hs.263912	ESTs	2.9
	441143	AI027604	Hs.159650	ESTs	2.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	2.9
	405783				2.9
15	444459	AI680624	Hs.148676	ESTs	2.9
	402112	R58624	Hs.2186	eukaryotic translation elongation factor	2.9
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.9
	444827	R09764	Hs.20416	ESTs	2.9
	451195	U10492	Hs.438	mesenchyme homeo box 1	2.9
20	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
	431595	AA508196		gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens	2.9
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.9
	456699	BE068121		gb:CM1-BT0368-061299-060-a02 BT0368 Homo	2.9
25	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Brn52 Homo sapien	2.9
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
	423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
30	443185	NM_006134	Hs.284142	chromosome 21 open reading frame 4	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	2.9
	437183	AI928184	Hs.122011	ESTs	2.9
	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
35	442726	AW136066	Hs.19145	ESTs	2.9
	456189	H91010	Hs.44940	ESTs	2.9
	441115	R69910	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	2.9
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.9
	415628	F13080		gb:HSC3ID041 normalized infant brain cDN	2.9
40	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	443246	T75157	Hs.337603	ESTs, Weakly similar to T08680 hypotheti	2.9
	450877	AI799608	Hs.29178	ESTs	2.9
	439063	AF085922	Hs.113968	ESTs	2.9
	401526				2.9
45	408751	N91553	Hs.258343	ESTs	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	444125	AI124882	Hs.118121	ESTs	2.9
	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.9
50	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.9
	452589	BE159915	Hs.61406	ESTs, Weakly similar to 2004399A chromos	2.8
	403011				2.8
	436154	AA764950	Hs.119898	ESTs	2.8
	408221	AA912183	Hs.47447	ESTs	2.8
55	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.8
	415399	T26994	Hs.177198	ESTs	2.8
	441817	AW969706	Hs.293332	ESTs	2.8
	443556	AA256769	Hs.94949	methylmalonyl-CoA epimerase	2.8
	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo	2.8
60	439703	AF086538	Hs.196245	ESTs	2.8
	411024	BE062590		gb:QV1-BT0260-281099-023-f05 BT0260 Homo	2.8
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.8
	434715	BE005346	Hs.116410	ESTs	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
65	439235	N45513	Hs.46608	ESTs	2.8
	453736	AL118674	Hs.34871	zinc finger homeobox 1B	2.8
	404967				2.8
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	412887	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.8
70	426942	AA393551	Hs.97450	ESTs	2.8
	403513				2.8
	419077	AA233885	Hs.164526	ESTs	2.8
	421823	N40850	Hs.28625	ESTs	2.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	2.8
75	451007	H38108	Hs.32759	ESTs	2.8
	407803	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	2.8
	409642	AW450809	Hs.257347	ESTs	2.8
	439492	AF086310	Hs.103159	ESTs	2.8
	420814	AA721156	Hs.190440	ESTs	2.8
80	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	2.8
	428350	AW873520	Hs.112017	GE36 gene	2.8
	405456				2.8
	442459	AI264628	Hs.125428	ESTs	2.8
	415763	Z42285	Hs.5181	proliferation-associated 2G4, 38kD	2.8

	428532	AF157326	Hs.164786	TBP-interacting protein	2.8
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	449539	W80363	Hs.58446	ESTs	2.8
5	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.8
	408749	H65489	Hs.250659	ESTs	2.8
	404652				2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	424960	BE245380	Hs.153952	5' nucleotidase (CD73)	2.8
	402131				2.8
10	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	444217	AV648751	Hs.282395	ESTs	2.8
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	2.8
15	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	2.8
	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
	433513	AI566356	Hs.171437	ESTs	2.8
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
	451496	AW503407		gb:UI-HF-BNO-akw-d-11-0-UI.r1 NIH_MGC_50	2.8
20	420273	AI652864	Hs.197257	ESTs	2.8
	451949	U03884	Hs.463	potassium inwardly-rectifying channel, s	2.8
	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	425012	T77666	Hs.92414	Homo sapiens cDNA: FLJ22030 fis, clone H	2.8
25	441609	AA946764	Hs.133460	ESTs	2.8
	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
	451206	H86228	Hs.271780	ESTs, Weakly similar to I38022 hypotheti	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
30	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	2.8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	459450	AA426429	Hs.98463	EST	2.8
	424188	AW954552	Hs.142634	zinc finger protein	2.7
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	2.7
35	427443	AA402713	Hs.97872	ESTs	2.7
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.7
	413091	BE065063		gb:RC1-BT0313-110500-017-e02 BT0313 Homo	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
40	445611	AW418497	Hs.145583	ESTs	2.7
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.7
	408243	Y00787	Hs.624	interleukin 8	2.7
	407308	H67394	Hs.331325	ESTs, Weakly similar to I38022 hypotheti	2.7
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.7
45	404587	M99587	Hs.104134	homeo box (H6 family) 1	2.7
	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.7
	416431	AW384459	Hs.172004	titin	2.7
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
50	427134	AA398409	Hs.173561	EST	2.7
	428137	AA421792	Hs.170999	ESTs	2.7
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	441218	BE327561	Hs.202345	ESTs	2.7
	440911	AA909536	Hs.143562	ESTs	2.7
55	411131	AW819212		gb:CM1-ST0283-071299-061-c07 ST0283 Homo	2.7
	438602	AI167149	Hs.123374	ESTs, Weakly similar to mariner transpos	2.7
	441191	AI693930	Hs.148816	ESTs	2.7
	403776				2.7
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
60	427839	AA608823	Hs.98244	ESTs	2.7
	429905	AL080128	Hs.225998	DKFZP434C153 protein	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	450777	AA255646	Hs.60478	ESTs, Moderately similar to S47073 finge	2.7
	458043	AW979009	Hs.326108	ESTs	2.7
	405523				2.7
65	434849	AW292765	Hs.8053	ESTs	2.7
	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti	2.7
	438055	AA776655	Hs.270942	ESTs	2.7
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	2.7
70	405738				2.7
	417806	AI867277	Hs.183733	ESTs	2.7
	430698	AA492071		gb:ne97b04.s1 NCL_CGAP_Kid1 Homo sapiens	2.7
	441969	AI733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	446092	N33522	Hs.145894	ESTs	2.7
75	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.7
	444931	AV652066	Hs.75113	general transcription factor IIIA	2.7
	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.7
80	453264	AA034137	Hs.271955	ESTs	2.7
	438370	AA843242	Hs.48523	ESTs	2.7
	406092				2.7
	454874	AW836407	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.7
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7

	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU8_HUMAN A	2.7
	441884	AW172630	Hs.144884	ESTs	2.7
	416211	R14625		gb:yg45c03.r1 Soares infant brain 1N1B H	2.7
5	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	2.7
	453696	AI989482	Hs.146286	kinesin family member 13A	2.7
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.7
	425876	AW005887	Hs.234058	ESTs	2.7
10	450458	AA009926		gb:zi07e05.r1 Soares_fetal_liver_spleen_	2.7
	406603				2.7
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	410871	D78367	Hs.66739	keratin 12 (Meesmann corneal dystrophy)	2.7
	412706	R97106	Hs.167546	ESTs	2.7
15	422897	AA679784	Hs.4290	ESTs	2.7
	436329	AI798750	Hs.163960	Homo sapiens heat shock transcription fa	2.7
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	2.7
20	419296	AA236115	Hs.120785	ESTs	2.7
	454747	AW818535		gb:RC1-ST0278-140300-016-f05 ST0278 Homo	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	411409	AW844803		gb:RC3-CN0056-170300-015-f08 CN0056 Homo	2.7
	426662	AA879474	Hs.122710	ESTs	2.7
	400268				2.7
25	438782	AA828380	Hs.126733	ESTs	2.7
	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	2.7
	412486	AF210650	Hs.150858	NAG19 protein	2.7
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	2.7
30	457900	AW976692	Hs.291665	ESTs	2.7
	417376	AA253314	Hs.154103	LIM protein (similar to rat protein kina	2.7
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
	435608	AW183971	Hs.250896	ESTs	2.7
	413627	BE182082	Hs.246973	ESTs	2.7
35	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
	441396	AW293677	Hs.186890	ESTs	2.6
	452046	AB018345	Hs.27657	KIAA0802 protein	2.6
	454936	AW846082		gb:MR3-CT0176-081099-002-d01 CT0176 Homo	2.6
40	454434	AA083558	Hs.261286	ESTs	2.6
	436888	AI942357	Hs.187870	ESTs	2.6
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	416690	H84078	Hs.108551	ESTs	2.6
45	436471	AA719813	Hs.117662	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.6
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hig	2.6
	455544	AW993880		gb:RC3-BN0034-240400-017-d09 BN0034 Homo	2.6
50	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	2.6
	429864	AA460039	Hs.286	ribosomal protein L4	2.6
	456273	AF154846	Hs.1148	zinc finger protein	2.6
	402603				2.6
55	411162	AW819944		gb:QV0-ST0294-240300-172-e03 ST0294 Homo	2.6
	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
60	438295	AI394151	Hs.37932	ESTs	2.6
	450181	H05254	Hs.201198	ESTs	2.6
	433764	AW753676	Hs.39982	ESTs	2.6
	433229	AB040925	Hs.91625	KIAA1492 protein	2.6
	443718	AI083580	Hs.221373	ESTs	2.6
65	418246	AI472179	Hs.121276	ESTs, Weakly similar to R5HU7A ribosomal	2.6
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	2.6
	400365	Y10259	Hs.274501	H.sapiens ACTH receptor mRNA 3'UTR	2.6
	419318	AW969742	Hs.291005	ESTs	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	404414				2.6
70	446444	AI743737	Hs.24370	ESTs	2.6
	411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.6
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	2.6
	418310	AA814100	Hs.86693	ESTs	2.6
75	454481	AW794878	Hs.314230	ESTs, Highly similar to clock [H.sapiens	2.6
	441216	BE299830	Hs.192908	ESTs	2.6
	438257	AW474419	Hs.224794	ESTs	2.6
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	419505	AA243660	Hs.143061	ESTs	2.6
80	417596	R07343	Hs.226823	ESTs, Moderately similar to I54374 gene	2.6
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	454867	AW835924		gb:PM1-LT0018-250200-002-e09 LT0018 Homo	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6

5	457630	AI680803	Hs.112627	ESTs	2.6
	424210	T71397	Hs.222707	KIAA1718 protein	2.6
	447748	AI422023	Hs.161338	ESTs	2.6
	411970	AA099142	Hs.13804	hypothetical protein dJ462023.2	2.6
	441233	AA972965	Hs.135568	ESTs	2.6
10	400706				2.6
	436033	H75391	Hs.255748	ESTs	2.6
	440836	AW370882	Hs.222080	ESTs	2.6
	431086	AI829692	Hs.211561	ESTs	2.6
	455110	BE154505		gb:PM0-HT0343-281299-003-e06 HT0343 Homo	2.6
15	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.6
	413088	BE064962		gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.6
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	2.6
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.6
20	442690	AI014727	Hs.160047	ESTs, Weakly similar to B28096 line-1 pr	2.6
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	2.6
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.6
	403271				2.6
	429761	AI276780	Hs.135173	ESTs	2.6
25	437085	AA743935	Hs.202329	ESTs	2.6
	450822	AW771860	Hs.205130	ESTs	2.6
	457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	2.6
	416585	X54162	Hs.79386	leiomodrin 1 (smooth muscle)	2.6
	430357	AW976789	Hs.165607	ESTs	2.6
30	417249	N58198	Hs.182898	ESTs	2.6
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	2.6
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheri	2.6
	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	446302	AI285848	Hs.149757	ESTs	2.6
35	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.6
	428944	AA780181	Hs.41182	Homo sapiens DC47 mRNA, complete cds	2.6
	419647	AA348947	Hs.91816	hypothetical protein	2.6
	455500	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	2.6
	419435	AI200540	Hs.14877	ESTs, Weakly similar to (define not ava	2.6
40	452450	AW854891	Hs.194720	ATP-binding cassette, sub-family G (WHIT	2.6
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	2.6
	436421	AI678031	Hs.122813	ESTs, Weakly similar to ZN22_HUMAN ZINC	2.6
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.6
	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	2.6
45	426698	AA394104	Hs.97489	ESTs	2.6
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.6
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.5
	447624	AI640326	Hs.62713	ESTs	2.5
	411736	AW859089		gb:MR1-CT0350-150200-002-d02 CT0350 Homo	2.5
50	416334	H53139	Hs.36271	ESTs	2.5
	446818	AI342668	Hs.279765	ESTs	2.5
	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	442278	AI733477	Hs.166313	ESTs	2.5
	453393	AW956392	Hs.110376	ESTs	2.5
55	420854	AW296927		gb:UL-H-BW0-ajc-c-07-0-ULs1 NCI_CGAP_Su	2.5
	408729	AA195764	Hs.72639	ESTs	2.5
	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	2.5
	411660	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
60	409156	N76186	Hs.173518	M-phase phosphoprotein homolog	2.5
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.5
	430291	AV660345	Hs.238126	CGI-49 protein	2.5
	401785				2.5
	402369				2.5
65	439079	AF085937	Hs.38348	ESTs	2.5
	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	2.5
	411463	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	2.5
	413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo	2.5
	404988				2.5
70	409446	AI561173	Hs.67688	ESTs	2.5
	412613	AA653507	Hs.285711	hypothetical protein FLJ13089	2.5
	417909	R35614		gb:ygg6e08.r1 Soares infant brain 1NIB H	2.5
	454743	AW818456	Hs.79347	KIAA0211 gene product	2.5
	406364				2.5
75	404108				2.5
	411934	AW876538		gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.5
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	2.5
	443526	AW792804	Hs.134002	ESTs	2.5
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.5
80	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	2.5
	458771	AW295151	Hs.163612	ESTs	2.5
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	2.5
	426589	AW954460		gb:EST366530 MAGE resequences, MAGC Homo	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	2.5
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	2.5
	434784	AA649051	Hs.164007	ESTs	2.5

	429322	D86984	Hs.199243	KIAA0231 protein	2.5
	446252	AI283125	Hs.150009	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
5	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
	449410	AA001356	Hs.18159	ESTs	2.5
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	2.5
	458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Ce	2.5
10	416944	N22809		gb:yw41e07.s1 Weizmann Olfactory Epithel	2.5
	423010	W25436	Hs.90725	ESTs, Moderately similar to I38022 hypot	2.5
	412505	AA974491	Hs.21734	ESTs	2.5
	446399	AI298405	Hs.150080	ESTs	2.5
	412139	BE044976		gb:hn25b10.x1 NCI_CGAP_Thy7 Homo sapiens	2.5
	403691				2.5
15	424025	AI701852	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	2.5
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.5
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.5
	457770	BE065030	Hs.124179	ESTs	2.5
20	427731	AA411750	Hs.20943	ESTs	2.5
	426920	AA393351	Hs.132121	ESTs	2.5
	427794	AA709186	Hs.282963	ESTs	2.5
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
25	414550	BE379808		gb:601159567T1 NIH_MGC_53 Homo sapiens c	2.5
	436391	AJ227892	Hs.146274	ESTs	2.5
	401989				2.5
	423346	AI267677	Hs.127416	synaptojanin 1	2.5
	444905	AW135863	Hs.209228	ESTs	2.5
30	424539	L02911	Hs.150402	activin A receptor, type I	2.5
	400861				2.5
	458426	AI084514	Hs.249587	ESTs	2.5
	429520	AA160142	Hs.205058	hypothetical protein FLJ20075	2.5
	403568				2.5
35	430692	X80240		gb:H.sapiens endogenous retrovirus HERV-	2.5
	451078	AI927694	Hs.204470	ESTs	2.5
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.5
	427888	AA417088	Hs.137598	ESTs	2.5
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens c	2.5
40	422840	U44059	Hs.121481	thyrotrophic embryonic factor	2.5
	404708				2.5
	405008				2.5
	453772	BE281431	Hs.16323	Homo sapiens, Similar to G antigen 8, cl	2.5
45	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	449311	AI657014		gb:tt49a12.x1 NCI_CGAP_GC6 Homo sapiens	2.5
	454277	AW2395069	Hs.31743	ESTs, Weakly similar to Z157_HUMAN ZINC	2.5
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
50	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	2.4
	407851	NM_014496	Hs.40434	ribosomal protein S6 kinase, 90kD, polyp	2.4
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.4
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-lin	2.4
	406468				2.4
55	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.4
	408617	R61736	Hs.124128	ESTs	2.4
	409627	AW997628	Hs.313637	ESTs	2.4
	416665	H72974		gb:yu28a10.s1 Soares fetal liver spleen	2.4
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.4
60	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	2.4
	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	2.4
	429654	AI435046	Hs.164318	ESTs	2.4
	432253	AW090822	Hs.274174	transcription elongation factor (SIII) e	2.4
	439786	AV652707	Hs.33756	Homo sapiens mRNA full length insert cDN	2.4
65	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
	453052	R63050	Hs.223813	ESTs	2.4
	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypotheti	2.4
	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: hamy2)	2.4
	452843	AI796769	Hs.208320	ESTs	2.4
70	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	2.4
	449695	AA164569	Hs.34550	ESTs	2.4
	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.4
	400641				2.4
75	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.4
	432808	NM_015985	Hs.278973	angiopoietin-3	2.4
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411561	H81164	Hs.285017	hypothetical protein FLJ21799	2.4
	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypotheti	2.4
80	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
	435663	AI023707	Hs.134273	ESTs	2.4
	455879	BE153275		gb:PM0-HT0335-180400-008-e11 HT0335 Homo	2.4
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.4

	409041	AB033025	Hs.50081	KIAA1199 protein	2.4
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.4
5	448889	BE140902		gb:IL1-HT0028-240699-001-C11 HT0028 Homo	2.4
	439481	AF086294	Hs.125844	ESTs	2.4
	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	2.4
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	2.4
	409298	AA070211		gb:zm68c04.s1 Stratagene neuroepithelium	2.4
10	411322	AW887330	Hs.172405	cell division cycle 27	2.4
	447640	AI417187		gb:lg75g11.x1 Soares_NhHMPu_S1 Homo sapi	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
	458763	AI693417	Hs.293309	ESTs	2.4
	404638				2.4
15	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.4
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	2.4
	408238	W95901		gb:ze43d11.r1 Soares retina N2b4HR Homo	2.4
	436747	AW977192	Hs.291343	ESTs	2.4
	437048	AA743240	Hs.91582	ESTs	2.4
20	413143	BE067232		gb:PM3-BT0347-170200-001-b05 BT0347 Homo	2.4
	404561				2.4
	444009	AI380792	Hs.135104	ESTs	2.4
	400250				2.4
25	403891				2.4
	417002	T79613	Hs.14613	ESTs	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	441227	AW295407	Hs.128893	ESTs	2.4
	445038	AI635444	Hs.143917	dJ467N11.1 protein	2.4
30	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	459344	AW499533	Hs.257976	ESTs	2.4
	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	2.4
	457652	AF116656	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.4
35	450068	AW207212	Hs.280925	ESTs	2.4
	444750	AW242684	Hs.243623	ESTs	2.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	407264	L34727		gb:Homo sapiens T-cell receptor beta (TC	2.4
	443169	AI038687	Hs.133338	ESTs	2.4
40	426536	AI949749	Hs.44441	ESTs	2.4
	449752	AI668626	Hs.61773	Homo sapiens cDNA FLJ11648 fis, clone HE	2.4
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF I [	2.4
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
45	430484	D82880	Hs.241548	RAS p21 protein activator 2	2.4
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.4
	447375	AI376660	Hs.257822	ESTs	2.4
	444230	H95537	Hs.146067	ESTs	2.4
	439911	AA854024	Hs.189110	ESTs	2.4
50	421296	NM_002666	Hs.103253	perilipin	2.4
	449385	AI650471	Hs.270370	ESTs	2.4
	430044	AA464510	Hs.152812	ESTs	2.4
	427131	AA448460	Hs.112017	GE36 gene	2.4
	409103	AF251237	Hs.112208	XAGE-1 protein	2.4
55	421354	AA766485	Hs.269664	ESTs	2.4
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	2.4
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein	2.4
	441358	AW173212	Hs.129041	ESTs	2.4
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	2.4
60	414290	AI568801	Hs.71721	ESTs	2.4
	427342	AL110150	Hs.176680	Homo sapiens mRNA; cDNA DKFZp586D0724 (f	2.4
	459459	AA460445		gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_	2.4
	434638	H50758		gb:yp86e06.r1 Soares fetal liver spleen	2.4
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.4
65	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
	431169	AW971240		gb:EST383329 MAGe resequences, MAGL Homo	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	458734	AI554946	Hs.158794	ESTs	2.4
	449529	AI990559	Hs.232033	ESTs	2.4
70	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	2.4
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.4
	418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	2.4
	430957	AI937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.4
	418188	AW139413	Hs.151880	ESTs	2.4
75	424103	NM_001918	Hs.139410	dihydrolipoamide branched chain transacy	2.4
	454324	AW608930	Hs.52184	hypothetical protein FLJ20618	2.4
	437369	AA765230	Hs.121742	ESTs	2.4
	453211	W84829		gb:zh53f04.r1 Soares_fetal_liver_spleen_	2.4
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.4
80	400462				2.4
	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
	424195	U50536	Hs.142907	Human BRCA2 region, mRNA sequence CG011	2.4
	434163	AW974720	Hs.25206	group XII secreted phospholipase A2	2.4



	435985	AA703154	Hs.191934	ESTs	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	2.4
	458661	AI299789	Hs.166999	ESTs, Moderately similar to I38344 titin	2.4
	459023	AW968226	Hs.60798	ESTs	2.4
5	406005				2.4
	456561	AI868634	Hs.246358	ESTs, Weakly similar to T32250 hypotheti	2.4
	452161	R43077	Hs.221747	ESTs	2.4
	436590	AI393115	Hs.127655	ESTs	2.4
10	430151	AW968203		gb:EST380398 MAGE resequences, MAGJ Homo	2.4
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	433479	AW511459	Hs.249972	ESTs	2.4
	441676	BE564206	Hs.49889	ESTs	2.4
	407965	W21483	Hs.41707	heat shock 27kD protein 3	2.4
15	450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
	452958	AA883929	Hs.40527	ESTs	2.4
	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	2.4
	405347				2.4
	440577	AA889945	Hs.326381	EST	2.4
20	455780	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo	2.4
	457024	AA397546	Hs.119151	ESTs	2.4
	404249				2.4
	437511	AI807500	Hs.125247	ESTs	2.4
	421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	2.4
25	425146	AW954627		gb:EST366697 MAGE resequences, MAGC Homo	2.4
	428277	AA425220	Hs.179203	ESTs	2.4
	444870	AI200621	Hs.148504	ESTs	2.4
	402090				2.4
	458507	AI185703	Hs.206957	ESTs	2.4
30	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	2.4
	446534	AI307356	Hs.175225	ESTs	2.4
	453111	AB014598	Hs.31720	hephaestin	2.4
	405230				2.4
	405935				2.4
35	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
	420724	AA279694	Hs.191540	ESTs	2.4
	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.3
40	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRNA	2.3
	440621	AW296024	Hs.150434	ESTs	2.3
	423417	AP000365	Hs.128342	potassium large conductance calcium-acti	2.3
	424131	AA335714	Hs.199665	ESTs	2.3
	450737	AW007152	Hs.203330	ESTs	2.3
45	453687	T56674	Hs.283108	hemoglobin, gamma G	2.3
	442704	AI015463	Hs.130987	ESTs	2.3
	457756	AA126136	Hs.38125	interferon-induced protein 75, 52kD	2.3
	412732	AW993300		gb:RC2-BN0033-180200-015-g06 BN0033 Homo	2.3
	418998	F13215	Hs.287849	ESTs, Weakly similar to T22074 hypotheti	2.3
50	419751	AW195581	Hs.93121	KIAA0761 protein	2.3
	429485	AW197086	Hs.99338	ESTs	2.3
	433377	AI752713	Hs.43845	ESTs	2.3
	434896	AW022054	Hs.136591	ESTs	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
55	444711	AI188739	Hs.148488	ESTs	2.3
	445621	AI733818	Hs.145549	ESTs	2.3
	449182	AW292381	Hs.224150	ESTs	2.3
	430987	Y08564	Hs.248190	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.3
	404068				2.3
60	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.3
	438315	R56795	Hs.82419	ESTs	2.3
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	2.3
	447998	AI768289	Hs.304389	ESTs	2.3
	410150	AW382942	Hs.6774	ESTs	2.3
65	432792	AA448114	Hs.278950	protocadherin beta 1	2.3
	443363	AI792629	Hs.133293	ESTs	2.3
	440729	AA904739	Hs.128204	ESTs	2.3
	411045	AW854691	Hs.115325	RAB7, member RAS oncogene family-like 1	2.3
	459207	AW138410	Hs.45051	ESTs	2.3
70	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.3
	458684	BE281115	Hs.98855	hypothetical protein FLJ20909	2.3
	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.3
	401899				2.3
	432116	AA902953	Hs.308538	ESTs	2.3
75	404196				2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	413308	W28131		gb:4217 Human retina cDNA randomly prime	2.3
	430264	AA470519		gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens	2.3
	443482	AW188093	Hs.250385	ESTs	2.3
80	453305	R39224	Hs.267997	EHM2 gene	2.3
	451963	AI825440	Hs.224952	ESTs	2.3
	453043	AW136440	Hs.224277	ESTs	2.3
	435559	AF209198	Hs.42636	zinc finger protein 277	2.3
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	2.3

	434120	AI436050	Hs.143937	ESTs	2.3
	429768	AA805719	Hs.192154	ESTs	2.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.3
5	455841	BE145836		gb:MR0-HT0208-101299-202-b08 HT0208 Homo	2.3
	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	2.3
	430706	NM_003540	Hs.247816	H4 histone family, member C	2.3
	428268	AA424957	Hs.294132	ESTs	2.3
10	458833	AW236702	Hs.171431	ESTs, Weakly similar to A46010 X-linked	2.3
	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	2.3
	444109	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.3
	428411	AW291464	Hs.10338	ESTs	2.3
	433098	AW190593	Hs.151143	ESTs	2.3
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	2.3
15	453178	AA496086	Hs.61648	ESTs	2.3
	404569				2.3
	413841	M34276	Hs.75576	plasminogen	2.3
	424068	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	2.3
	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	2.3
20	442710	AI015631	Hs.23210	ESTs	2.3
	444206	AW301017	Hs.146492	ESTs	2.3
	451264	AI768235		gb:wg82g08.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.3
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3
	429080	AA446228	Hs.99057	ESTs	2.3
25	404166				2.3
	416327	R99822	Hs.36172	ESTs	2.3
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.3
	438504	AW665281	Hs.224625	ESTs	2.3
	435325	AI038388	Hs.119309	ESTs	2.3
30	421253	AI188102	Hs.31028	ESTs	2.3
	427046	BE246180	Hs.121385	ESTs	2.3
	432711	AA563785	Hs.152465	ESTs, Weakly similar to I38022 hypotheti	2.3
	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3
35	448458	AW614367	Hs.171054	ESTs	2.3
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	2.3
	417768	R24732	Hs.175139	ESTs	2.3
	427374	AI150033	Hs.143686	ESTs	2.3
40	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.3
	423600	AI633559	Hs.310359	ESTs	2.3
	413006	W03857	Hs.34298	ESTs	2.3
	434698	BE044674		gb:hm46f02.x1 NCI_CGAP_RDF1 Homo sapiens	2.3
	407639	AW205369	Hs.312830	ESTs	2.3
45	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo	2.3
	448117	H49129	Hs.172982	ESTs	2.3
	443931	H23213	Hs.22657	ESTs	2.3
	450795	AW173371	Hs.60435	ESTs	2.3
	418632	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.3
	419441	AW023731	Hs.274368	MSTP032 protein	2.3
50	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	2.3
	418291	BE300369	Hs.289038	hypothetical protein MGC4126	2.3
	455964	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.3
	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
55	449272	AW137656	Hs.197645	ESTs	2.3
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	2.3
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.3
	444715	AV650947	Hs.282464	ESTs	2.3
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	2.3
60	444140	AV648089	Hs.282383	ESTs	2.3
	423949	AI014546	Hs.130912	ESTs	2.3
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	445711	T79611	Hs.193691	ESTs	2.3
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	2.3
65	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.3
	429180	AA806287	Hs.58893	ESTs	2.3
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	2.3
	425523	AB007948	Hs.158244	KIAA0479 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
70	419337	AW291112	Hs.209978	ESTs	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypotheti	2.3
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
	436294	AA708310		gb:zg07b07.s1 Soares_pineal_gland_N3HPG	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
75	433939	AL133887	Hs.254122	hypothetical protein	2.3
	450048	AI693269	Hs.202273	ESTs	2.3
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	2.3
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	2.3
	405920				2.3
80	405747				2.3
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.3
	420457	AA482280	Hs.191656	ESTs	2.3
	407726	AA435679	Hs.88594	ESTs	2.3
	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.3

	409517	X90780	Hs.120036	troponin I, cardiac	2.3
	435352	AI056599	Hs.120893	ESTs	2.3
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
5	444098	AV647969	Hs.109694	KIAA1451 protein	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.3
	449015	AL038958	Hs.22868	protein tyrosine phosphatase, non-recept	2.3
	411377	AW841462		gb:RC6-CN0014-080300-012-B09 CN0014 Homo	2.3
10	429276	AF056085	Hs.198612	G protein-coupled receptor 51	2.3
	411816	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.3
	455280	AW886156		gb:RCS-OT0078-150300-021-E08 OT0078 Homo	2.3
	407809	AW082279	Hs.244106	ESTs	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kd (con	2.3
15	445117	AI208754	Hs.147369	ESTs	2.3
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.2
	420230	AL034344	Hs.284186	forkhead box C1	2.2
	411517	AW850267		gb:IL3-CT0219-161199-031-A09 CT0219 Homo	2.2
	403678				2.2
20	457003	S78234	Hs.172405	cell division cycle 27	2.2
	404531	Z25884	Hs.121483	chloride channel 1, skeletal muscle (Th	2.2
	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	2.2
	409427	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo	2.2
25	434745	AW974445	Hs.185155	ESTs, Weakly similar to T12482 hypotheti	2.2
	400696				2.2
	407259	L02256		gb:Human Fab fragment binding syncytial	2.2
	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
30	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	458303	AI264628	Hs.125428	ESTs	2.2
	405692				2.2
	403572				2.2
35	415380	F07953	Hs.16085	putative G-protein coupled receptor	2.2
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.2
	417859	T26453		gb:AB214F6R Infant brain, LLNL array of	2.2
	456472	AK001714	Hs.95744	hypothetical protein similar to ankyrin	2.2
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.2
40	428231	U17989	Hs.183105	nuclear autoantigen	2.2
	454086	AW885909	Hs.6975	PRO1073 protein	2.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.2
	416348	H65887	Hs.272163	ESTs	2.2
	403780				2.2
45	414262	AW975616	Hs.291469	ESTs	2.2
	419423	D26488	Hs.90315	KIAA0007 protein	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
50	416588	H66558		gb:yu16e04.r1 Soares fetal liver spleen	2.2
	425368	AB014595	Hs.155976	cullin 4B	2.2
	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.2
	441638	AW293202	Hs.133451	ESTs	2.2
	446845	AI343645	Hs.156108	ESTs	2.2
55	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	2.2
	436574	AW293527	Hs.126465	ESTs	2.2
	424584	H10692	Hs.13310	ESTs	2.2
	456347	U00803	Hs.89426	fyn-related kinase	2.2
	446901	AI347274		gb:tc05d02.x1 NCL_CGAP_Co16 Homo sapiens	2.2
60	459364	W69284		gb:zd46c03.r1 Soares_fetal_heart_NbHH19W	2.2
	430686	NM_001942	Hs.2633	desmoglein 1	2.2
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	2.2
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.2
	403525				2.2
65	453343	AA905353	Hs.121622	ESTs	2.2
	421574	AJ000152	Hs.105924	defensin, beta 2	2.2
	449327	AI638743	Hs.224672	ESTs	2.2
	454769	AW819848		gb:QV0-ST0294-070300-151-b04 ST0294 Homo	2.2
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	2.2
70	401614				2.2
	404767				2.2
	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	436193	AA706059	Hs.255286	ESTs	2.2
75	439626	N22415	Hs.189080	ESTs	2.2
	456481	AA258033	Hs.108110	DKFZP547E2110 protein	2.2
	441453	AW176106	Hs.285459	ESTs	2.2
	424946	M64572	Hs.153932	protein tyrosine phosphatase, non-recept	2.2
	437332	AA814943		gb:oc07d06.s1 NCL_CGAP_GCB1 Homo sapiens	2.2
80	454419	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	2.2
	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	2.2
	450579	AW136774	Hs.48614	ESTs	2.2
	400664				2.2
	447613	AL041057	Hs.33363	DKFZP434N093 protein	2.2

	402689	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	2.2
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.2
	432797	AA565264	Hs.136443	ESTs	2.2
	405608				2.2
5	426365	AA376667	Hs.10283	RNA binding motif protein 8B	2.2
	405634				2.2
	423646	H02364		gb:yj35d06.r1 Soares placenta Nb2HP Homo	2.2
	434690	AI867679	Hs.148410	ESTs	2.2
10	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
15	433781	AA609379	Hs.192083	ESTs	2.2
	450587	AI828854	Hs.258538	striatin, calmodulin-binding protein	2.2
	434077	AF116659	Hs.321151	Homo sapiens PRO1412 mRNA, complete cds	2.2
	448756	AI739241	Hs.171480	ESTs	2.2
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.2
20	454471	AW902125		gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.2
	419107	AW085152	Hs.292987	ESTs	2.2
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.2
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	2.2
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	2.2
25	456056	AA463550	Hs.337532	ESTs, Weakly similar to A47582 B-cell gr	2.2
	409998	M78345	Hs.98265	KIAA1877 protein	2.2
	422352	AA766296	Hs.99200	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Claspin	2.2
	433919	AA746311		gb:oa56d12.r1 NCI_CGAP_GCB1 Homo sapiens	2.2
30	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	2.2
	431632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fis, clone HE	2.2
	454716	AW850684		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.2
	413752	BE161807		gb:MR3-HT0446-300300-203-h01 HT0446 Homo	2.2
	458037	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	2.2
	434239	AF119910	Hs.283047	hypothetical protein PRO2964	2.2
35	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	2.2
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.2
	400697				2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
40	447039	AV661798	Hs.282915	ESTs	2.2
	404593				2.2
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.2
	421976	AL138443	Hs.23450	mitochondrial ribosomal protein S25	2.2
	401673				2.2
45	425001	U55184	Hs.154145	hypothetical protein FLJ11585	2.2
	447816	NM_007233	Hs.274329	TP53 target gene 1	2.2
	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	2.2
	419118	AA234223	Hs.139204	ESTs	2.2
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.2
50	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
	454749	AW818649		gb:RC1-ST0278-040400-018-e02 ST0278 Homo	2.2
	456933	AA363946	Hs.20969	ESTs	2.2
	402942				2.2
	437064	AI023264		gb:ov64h08.s1 Soares_testis_NHT Homo sap	2.2
55	458623	AI305223	Hs.148056	ESTs	2.2
	415257	F03016	Hs.27513	ESTs	2.2
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	2.2
	442783	AI017586	Hs.131181	ESTs	2.2
	444313	AI140494	Hs.197955	KIAA0704 protein	2.2
60	453444	AL036531		gb:DKFZp564l1162_r1 564 (synonym: hfr2)	2.2
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
	430013	AA463833	Hs.151275	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.2
	437138	AI935622	Hs.271245	ESTs	2.2
	406298				2.2
65	409723	AW885757	Hs.257862	ESTs	2.2
	414481	AW451956	Hs.8383	bromodomain adjacent to zinc finger doma	2.2
	433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
70	445061	AI253094	Hs.145227	ESTs	2.2
	442617	AW340093	Hs.130538	ESTs	2.2
	438298	H23542	Hs.181788	ESTs	2.2
	454916	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	2.2
	428017	AA424983	Hs.98312	ESTs	2.2
75	451149	AL047586	Hs.10283	RNA binding motif protein 8B	2.2
	418076	R61388	Hs.6724	ESTs	2.2
	403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	2.2
	441811	AI073548	Hs.164597	ESTs	2.2
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	2.2
80	447453	AW608645	Hs.18800	hypothetical protein FLJ20281	2.2
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.2
	415424	Z44766		gb:HSC28G081 normalized infant brain cDN	2.2
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	2.2
	421216	AV649282	Hs.102654	vesicle-associated membrane protein 4	2.2

	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.2
	448700	BE614182	Hs.123075	ESTs	2.2
	457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RDF1 Homo sapiens	2.2
5	437927	AI039789	Hs.25982	hypothetical protein FLJ21031	2.2
	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
	436640	AA724411	Hs.156065	ESTs	2.2
10	438290	AA843719	Hs.122341	ESTs	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	455735	BE161124		gb:PM0-HT0425-141299-001-A06 HT0425 Homo	2.2
	458455	AV648310	Hs.213488	ESTs	2.2
	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S	2.2
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	2.2
15	424063	NM_002019	Hs.138671	fms-related tyrosine kinase 1 (vascular	2.2
	441874	AA970389	Hs.128055	ESTs	2.2
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.2
	433629	R13140	Hs.13359	ESTs	2.2
20	415266	AA164199	Hs.270152	ESTs	2.2
	440633	AI140686	Hs.263320	ESTs	2.2
	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.2
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.2
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.2
25	401240				2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
	436992	AA741074	Hs.120750	ESTs	2.2
30	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.1
	400040				2.1
	458762	AW802754		gb:IL2-UM0076-030400-061-H01 UM0076 Homo	2.1
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	2.1
35	419953	BE267154	Hs.125752	ESTs	2.1
	410648	AW792909		gb:CM0-UM0001-010300-258-c05 UM0001 Homo	2.1
	423717	AA330036	Hs.152003	ESTs	2.1
	436683	AW991278	Hs.57787	ESTs	2.1
	445225	AI216555	Hs.202398	ESTs	2.1
40	410991	AW812790		gb:RC3-ST0186-141299-014-g08 ST0186 Homo	2.1
	412639	AW961284	Hs.296235	ESTs	2.1
	447777	AI424223		gb:te95a05.x1 NCI_CGAP_Pr28 Homo sapiens	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
	404526	AI912555	Hs.157195	peptide YY, 2 (seminalplasmin)	2.1
45	452492	BE063096		gb:CM4-BT0266-091199-039-a02 BT0266 Homo	2.1
	417154	AI674701	Hs.21388	ESTs	2.1
	428152	AA422030		gb:zv26h05.r1 Soares_NhHMPu_S1 Homo sapi	2.1
	442312	AI820617	Hs.129216	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	456513	AA279143	Hs.88561	ESTs	2.1
50	430712	AW044647	Hs.196284	ESTs	2.1
	441445	AI221959	Hs.187937	ESTs	2.1
	420288	AW071225	Hs.245556	ESTs	2.1
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo	2.1
	447033	AI357412	Hs.157601	ESTs	2.1
55	436853	BE328074	Hs.148661	ESTs	2.1
	455189	AW864176		gb:PM0-SN0014-260400-002-b08 SN0014 Homo	2.1
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	2.1
	458356	AI024855	Hs.131575	ESTs	2.1
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.1
60	424480	AA341442	Hs.205299	ESTs	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.1
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
65	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
	417725	R25257	Hs.21503	ESTs	2.1
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	2.1
	439474	AI824060	Hs.211501	ESTs	2.1
70	446895	AA166655	Hs.282803	ESTs	2.1
	448582	AI538880	Hs.94812	ESTs	2.1
	452783	AA028167	Hs.61486	ESTs	2.1
	442430	R89164	Hs.48320	double ring-finger protein, Dorfin	2.1
	428908	AW303529	Hs.144955	ESTs	2.1
75	427335	AA448542	Hs.251677	G antigen 7B	2.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.1
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	2.1
	416951	AA190926	Hs.190785	ESTs, Moderately similar to S65657 alpha	2.1
	439950	AW937417	Hs.293561	ESTs	2.1
80	458227	Z40670	Hs.181340	ESTs	2.1
	447179	AW015633	Hs.157299	ESTs	2.1
	454950	AW847460		gb:RC3-CT0208-270999-021-e04 CT0208 Homo	2.1
	404453				2.1
	420844	AA595522		gb:nh22c09.s1 NCI_CGAP_Pr1 Homo sapiens	2.1

	426456	AA580748	Hs.130658	ESTs	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	430879	BE149423	Hs.10554	hypothetical protein FLJ12761	2.1
5	444584	AI168422		gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.1
	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.1
	453853	AL040600	Hs.188083	ESTs	2.1
	414083	AL121282	Hs.257786	ESTs	2.1
	401645				2.1
10	436577	W84774	Hs.17643	ESTs	2.1
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.1
	409168	N94037	Hs.312938	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	410276	AI554545	Hs.68301	ESTs	2.1
	443372	AI792557	Hs.133107	ESTs	2.1
15	422093	AF151852	Hs.111449	CGI-94 protein	2.1
	402333				2.1
	409374	R87083	Hs.19081	ESTs	2.1
	412011	NM_000406	Hs.73064	gonadotropin-releasing hormone receptor	2.1
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
20	416085	H18072	Hs.92576	ESTs	2.1
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.1
	452374	AL037405	Hs.339639	ESTs	2.1
	450061	AI797034	Hs.201115	ESTs	2.1
25	450180	AW449644	Hs.257182	ESTs	2.1
	405120				2.1
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.1
	458890	AW865523		gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.1
	435600	AL047034	Hs.119747	ESTs	2.1
30	440964	AI733106	Hs.130218	ESTs	2.1
	417455	AW007066	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	2.1
	436461	AW511956	Hs.293261	ESTs	2.1
	436777	AA731199	Hs.293130	ESTs	2.1
	427521	AW973352	Hs.290585	ESTs	2.1
35	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.1
	413231	D87461	Hs.75244	BCL2-like 2	2.1
	423969	AI830571	Hs.331633	hypothetical protein DKFZp566N034	2.1
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	2.1
	443777	AV646510	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	2.1
40	416148	H22453	Hs.169187	ESTs	2.1
	402528				2.1
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	446209	AI375025	Hs.153368	ESTs	2.1
45	453362	H14988	Hs.107375	ESTs	2.1
	417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.1
	401089				2.1
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.1
	410966	AW812088		gb:RC4-ST0173-191099-032-a07 ST0173 Homo	2.1
50	447124	AW976438	Hs.17428	RBP1-like protein	2.1
	449939	T86420	Hs.272139	ESTs	2.1
	411693	AW857271		gb:CM0-CT0307-210100-158-g09 CT0307 Homo	2.1
	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.1
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	2.1
55	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	2.1
	404694				2.1
	406668	T62745	Hs.184411	albumin	2.1
	441092	T99289	Hs.126556	EST	2.1
	454643	BE006345		gb:RC2-BN0127-240300-011-d05 BN0127 Homo	2.1
60	426646	AA382787	Hs.122713	ESTs	2.1
	431605	AW972407		gb:EST384498 MAGE resequences, MAGL Homo	2.1
	414452	AA454038	Hs.29032	ESTs	2.1
	401991				2.1
	457176	AA436837		gb:zv57g07.s1 Soares_testis_NHT Homo sap	2.1
65	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	428208	AA442327	Hs.104854	ESTs	2.1
	445049	AV652718		gb:AV652718 GLC Homo sapiens cDNA clone	2.1
	419116	AF292402	Hs.283093	neuromedin U receptor 2	2.1
	427894	AL135709	Hs.28921	zinc finger protein	2.1
70	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	2.1
	424323	AA338791	Hs.177788	ESTs	2.1
	404582				2.1
	418631	AA225921	Hs.115105	ESTs	2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
75	452539	AW105321	Hs.49367	ESTs	2.1
	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
	440310	AA878939	Hs.125406	ESTs	2.1
	433297	AV658581	Hs.282633	ESTs	2.1
	410900	AW810169		gb:MR4-ST0124-040500-007-h07 ST0124 Homo	2.1
80	419386	AA236867	Hs.143868	ESTs, Weakly similar to I38022 hypotheti	2.1
	402451				2.1
	447842	AW160804	Hs.247302	twisted gastrulation	2.1
	453880	AI803166	Hs.28462	ESTs, Weakly similar to I38022 hypotheti	2.1
	425189	H16622		gb:ym26c07.r1 Soares infant brain 1NIB H	2.1

	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.1
	400612				2.1
	402318				2.1
5	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	2.1
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	412029	AW886238		gb:RC5-OT0078-280300-022-F01 OT0078 Homo	2.1
	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
10	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	444498	AI151413	Hs.26330	ESTs	2.1
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	2.1
	425324	M89470	Hs.155644	paired box gene 2	2.1
	430719	AA488988	Hs.293796	ESTs	2.1
	432577	BE208545	Hs.317590	hypothetical protein FLJ14640	2.1
15	407593	AW044083	Hs.237008	ESTs	2.1
	401098				2.1
	440299	AI871778	Hs.250112	ESTs	2.1
	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	2.1
	428627	BE002993	Hs.187660	putative Rab5 GDP/GTP exchange factor ho	2.1
20	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	2.1
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	2.1
	439831	AW136488	Hs.25545	ESTs	2.1
	451829	AW964081	Hs.247377	ESTs	2.1
	404595				2.1
25	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
	456083	U46922	Hs.77252	fragile histidine triad gene	2.1
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	2.1
	406413				2.1
	439483	T69980	Hs.58323	Homo sapiens cDNA FLJ11613 fis, clone HE	2.1
30	446242	N66336	Hs.7360	ESTs	2.1
	449625	NM_014253	Hs.23796	odx (odd Oz/ten-m, Drosophila) homolog 1	2.1
	457938	AI373638	Hs.133900	ESTs	2.1
	413101	BE065215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo	2.1
	408350	AW183350	Hs.250127	ESTs	2.1
35	419812	NM_000562	Hs.93210	complement component 8, alpha polypeptid	2.1
	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A recepto	2.1
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	2.1
	409955	U60665	Hs.57692	chromosome 6 open reading frame 10	2.1
	435579	AI332373	Hs.156924	ESTs	2.1
40	436088	AA704687	Hs.191294	ESTs	2.1
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.1
	416100	H18700	Hs.268799	ESTs	2.1
	403218	AL134878	Hs.119500	ribosomal protein, large P2	2.1
	409747	H60964	Hs.331250	ESTs	2.1
45	428764	W21550		gb:zb52f12.r1 Soares_fetal_Jung_NbHL19W	2.1
	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.1
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.1
	428299	AL038004	Hs.29419	ESTs	2.1
	406817	AI936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
50	411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
	412446	AI768015	Hs.92127	ESTs	2.1
	414012	AW452334	Hs.128148	ESTs	2.1
	421966	AA904519	Hs.130710	ESTs	2.1
	430566	AA481282	Hs.190149	ESTs	2.1
55	456606	AA292862	Hs.275369	ESTs	2.1
	451604	T65365	Hs.172851	arginase, type II	2.0
	440926	AW196772	Hs.131323	ESTs	2.0
	420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 fis, clone PL	2.0
	459082	BE551721	Hs.282149	ESTs	2.0
60	413241	BE073771	Hs.302414	Homo sapiens clone FLB8945 PRO2411 mRNA,	2.0
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	2.0
	447552	AI394125	Hs.160413	ESTs	2.0
	420905	AA521307	Hs.186651	ESTs	2.0
	428052	AA420477	Hs.26993	ESTs	2.0
65	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.0
	432527	AW975028	Hs.102754	ESTs	2.0
	430202	T85775		gb:yd60g02.r1 Soares fetal liver spleen	2.0
	446610	AV659433	Hs.282984	ESTs, Weakly similar to I38022 hypotheti	2.0
	427961	AW293165	Hs.143134	ESTs	2.0
70	455290	U75810		gb:HSU75810 Human Homo sapiens cDNA clon	2.0
	445564	AB028957	Hs.12896	KIAA1034 protein	2.0
	412811	H06382	Hs.21400	ESTs	2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
75	429418	AI381028	Hs.118769	ESTs	2.0
	431511	NM_012386	Hs.258581	Homo sapiens p95 paxillin-kinase linker	2.0
	445829	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	453123	AI953718	Hs.221849	ESTs	2.0
80	455401	AW936369		gb:QV4-DT0021-301299-071-d07 DT0021 Homo	2.0
	406666	V00495	Hs.184411	albumin	2.0
	445688	AI248205	Hs.153244	ESTs	2.0
	446131	NM_000929	Hs.290	phospholipase A2, group V	2.0
	440388	AI693520	Hs.223000	ESTs	2.0

	457128	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.0
	404416				2.0
	444187	AW138466	Hs.151274	ESTs	2.0
5	431552	AI815863	Hs.259873	axonal transport of synaptic vesicles	2.0
	455814	BE141689		gb:CM1-HT0092-220999-016-b09 HT0092 Homo	2.0
	454759	AW819455		gb:RC5-ST0293-021299-031-A04 ST0293 Homo	2.0
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.0
	404420				2.0
10	408112	AW451982	Hs.248613	ESTs	2.0
	432702	AW973953	Hs.293744	ESTs	2.0
	448587	AI539652	Hs.28338	KIAA1546 protein	2.0
	446854	BE268103	Hs.208914	hypothetical protein MGC10999	2.0
	410569	AA766825	Hs.205675	ESTs	2.0
15	432596	AJ224741	Hs.278461	matrilin 3	2.0
	402341				2.0
	452919	AW962167		gb:EST374240 MAGE resequences, MAGG Homo	2.0
	433632	AA649921	Hs.112553	ESTs	2.0
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.0
20	451927	AL355687	Hs.27261	Homo sapiens mRNA full length insert cDN	2.0
	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.0
	450895	N66727	Hs.10957	ESTs	2.0
	408459	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypothe	2.0
	400842				2.0
25	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.0
	400859				2.0
	405829				2.0
	411863	BE075244	Hs.12420	ESTs	2.0
	415258	AW752247	Hs.293853	ESTs	2.0
30	416093	R60685	Hs.268698	ESTs, Moderately similar to ALUC_HUMAN I	2.0
	420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypothe	2.0
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
35	457039	H29990	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.0
	454578	AW809178		gb:MR4-ST0118-261099-012-c07 ST0118 Homo	2.0
	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0
	415173	AW501735	Hs.253015	ESTs	2.0
	449011	AI655376	Hs.192693	ESTs	2.0
40	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.0
	416057	AI927382	Hs.29857	ESTs	2.0
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.0
	408531	AW207553	Hs.253639	ESTs	2.0
45	434663	AA641972	Hs.130058	ESTs	2.0
	428085	AA421081	Hs.12388	ESTs	2.0
	425006	R38685	Hs.332622	ESTs	2.0
	446139	H77395	Hs.39749	ESTs	2.0
	400049				2.0
50	428333	AW972668	Hs.293044	ESTs	2.0
	429458	BE161832	Hs.292689	ESTs	2.0
	425087	R62424	Hs.126059	ESTs	2.0
	457122	AI026157	Hs.33728	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	400310	X63966	Hs.135631	H.sapiens synthetic gene for platelet-de	2.0
55	451805	AI968300	Hs.208220	ESTs	2.0
	401986				2.0
	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0
	417756	Z43056		gb:HSC12B021 normalized infant brain cDN	2.0
	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.0
60	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
	429110	L29301	Hs.2353	opioid receptor, mu 1	2.0
	433755	AW085934	Hs.120868	ESTs	2.0
	434118	AF116715	Hs.256256	Homo sapiens PRO2829 mRNA, complete cds	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
65	443748	AW206447		gb:UI-H-B11-afg-g-02-0-UI.s1 NCI_CGAP_Su	2.0
	445205	D83776	Hs.12413	KIAA0191 protein	2.0
	458175	AW296024	Hs.150434	ESTs	2.0
	446419	AW576760	Hs.160726	Homo sapiens cDNA FLJ11680 fis, clone HE	2.0
	441627	AA947552	Hs.58086	ESTs	2.0
70	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.0
	455614	AI693369	Hs.202274	ESTs	2.0
	449899	AI610700	Hs.103280	ESTs	2.0
	420111	AA255652		gb:zs21h11.1 NCI_CGAP_GCB1 Homo sapiens	2.0
	437354	AA749215	Hs.291886	ESTs	2.0
75	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.0
	419691	W03298	Hs.193521	ESTs	2.0
	439724	AF086565	Hs.60351	EST	2.0
	413362	BE088812		gb:CM2-BT0693-230300-129-d08 BT0693 Homo	2.0
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	2.0
80	434361	AF129755	Hs.117772	ESTs	2.0
	442479	AF069484		gb:AF069484 Homo sapiens astrocytoma lib	2.0
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	2.0
	459323	AW062490		gb:MR0-CT0065-100899-001-d01 CT0065 Homo	2.0
	449438	AA927317	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon	2.0



	400285				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
5	417383	W02642	Hs.136102	KIAA0853 protein	2.0
	447153	AA805202	Hs.315562	ESTs	2.0
	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	2.0
	455696	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo	2.0
	456510	AK001652	Hs.99423	ATP-dependent RNA helicase	2.0
10	449815	AI671000	Hs.199739	ESTs	2.0
	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.0
	400238				2.0
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.0
	445073	AW291389	Hs.13056	hypothetical protein FLJ13920	2.0
15	455221	AW867751		gb:MR0-SN0038-290300-001-a03 SN0038 Homo	2.0
	413174	AA723564	Hs.191343	ESTs	2.0
	435810	BE349853	Hs.2785	keratin 17	2.0
	418687	R61650	Hs.22581	ESTs	2.0
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.0
20	431750	AA514986	Hs.283705	ESTs	2.0
	453242	T98327	Hs.18343	ESTs	2.0
	437074	AI286235	Hs.128905	hypothetical protein FLJ13204	2.0
	459411	N52920		gb:yv34h09.s1 Soares fetal liver spleen	2.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.0
25	409929	R38772	Hs.172619	myelin transcription factor 1-like	2.0
	406378				2.0
	459208	BE261314	Hs.149039	ESTs, Weakly similar to I38022 hypotheti	2.0
	445260	AI218133	Hs.147617	ESTs	2.0
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.0
30	445020	AI205655	Hs.147221	ESTs	2.0
	402048				2.0
	412695	AW984439		gb:PM3-HN0011-220300-002-c05 HN0011 Homo	2.0
	416408	R94725	Hs.35354	ESTs	2.0
	423347	AI660412	Hs.234557	ESTs	2.0
35	427836	AA416642	Hs.116176	ESTs	2.0
	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
	436902	AW247145	Hs.192729	ESTs	2.0
	440122	AI733011	Hs.127678	ESTs	2.0
	442901	AI023654	Hs.114191	ESTs	2.0
40	444097	AW517412	Hs.150757	ESTs	2.0
	447278	AI934935	Hs.158669	ESTs	2.0
	451361	AA053854		gb:zf52f02.r1 Soares retina N2b4HR Homo	2.0
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.0
	454423	AW603985		gb:RC4-CN0048-140100-011-a04 CN0048 Homo	2.0
45	458801	N98648	Hs.276860	ESTs, Weakly similar to C Chain C, Human	2.0

TABLE 30B

50	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
55	Pkey	CAT number	Accession	
	407593	1003161_1	AW044083 AW044094 AW370634	
	407594	1003220_1	AW057584 AW057585 AW044153 R34370	
	407639	1006924_1	AW205369 AW058599 AW207608	
	407676	1008294_1	AW064111 AW064450 AW064429	
60	407721	10108_1	Y12735 NM_003582 AW238970 R38268 R41411 R41419 T16717 AA002193 H62028 AI359545 AW105201 AW087158 AA699728 AI095264	
			AA002065 H62029 AI289101 AA884804 AA904950 AA609672 AI139874 H77896	
	407726	101126_1	AA435679 AA470655 H22526 AA044031 AA876426 W63767 AI421140 AI418990 H42329 H88910 AL041066 H88909 W94610 AW352277 W94648	
			W94167 AW952568 AI419653 AA335501 AA393641 AA044353 H41626 H22525 R58582 AW297645 C75230 AW368034 AW468904 AI272755	
	407762	101439_1	AW235638 AA346882 AW866803 AA361281 AW963163 AA044373 AA136755	
65	407764	1014849_1	BE008347 BE008320 BE083307 BE083311 AW075968	
	407788	10163_1	BE514982 BE614814 AW393078 AW238480 AA055637 N27644 AA641158 M87068 AA161019 AA161003 AA587315 AA716746 AA593632	
			AI354870 AW183492 Y07755 NM_005978 AW872948 AI608987 H64656 AF086003 AA643149 AI819402 H64555 AA858398 AA594885 AI436747	
			BE122811 AA587026 AW857106 AI950679 AA596012 AA654004 AW238238 AI971395 AA459074 AA458884 AI608591 BE181995 BE181970	
			AW195797 C00271 BE182043	
70	407803	1017498_1	AW081681 N36967 N36959	
	407809	1017982_1	AW082279 AW082688	
	407811	10180_1	AW190902 AI802788 AI041650 AI037867 AF110137 NM_013372 H99469 N35377 AW151676 AI678451 AW078795 AW087935 AI884505	
			AW044602 AB032372 AF045800 AI621183 AI750578 AA376403 AI910477 AA373348 AA373673 AI752124 AL359060 W48619 AA373298 AA373975	
75			AW604409 AW604404 AW368603 AA545734 AW361415 AA373557 AW956164 AW853798 AI750595 AL359059 AA344024 N31127 AW580737	
			N27040 AA071138 AI753050 AA599801 W48852 AA669811 AA112124 AI940705 W52686 AA084001 C01826 AI940729 AA373544 AW957491	
			AW383224 AW383164 AW383192 AW383125 AW383194 AW842507 AI940795 H80042 AW631119 W47324 W42884 AI750594 AI754387 AI753734	
			AA372833 AW069006 AI750577 AW473621 AI888605 AA600082 AI041803 W51909 W25447 AI521673 AI087351 AA670070 W47325 AA071381	
			W42791 AI090390 AI085102 AI302125 AA788723 AW069430 AW069485 AI754608 AA373014 BE140150 BE140166 BE140102 BE140143	
80			BE140157 BE140117 BE140098 AW005943 BE140108 BE140176 BE140171 BE140144 BE140175 BE140160 BE140152 BE140099 BE140177	
			BE140167 BE140145 BE140109 BE140163 BE140172 BE140161 BE140179 BE140147 BE140107 BE140146 BE140155 BE140173 BE140148	
			BE140174 BE140158 BE140149 BE140116 BE140156 BE140105 BE140103 BE140164 AW138508 BE140153 AW806557 BE140121 BE140162	
			C01953 AW806500 BE140124 AA329219 AW955642 AW069165 AI968107 N21113 AI754594 AW069264 AI754660 BE551937 AA543066 AA703927	
			AW130486 AI814434 AI924946 AA789056 AW173667 AW069841 AI022286 AI753523 AI753558 AI753482 AW068940 AI753002 AA669866	

			AI753593 AI753469 AI753506 AW008360 AI753255 AI949111 AI752123 W19275 AI679005 AI888455 AI677772 AI589279 AI968546 AW069588 AI754028 N20040 AI754354 AI752878 AA836970 AW631283 AI440410 AW016646 AI801326 AI610424 AI521669 AI446171 AI453455 AI753087 AA670062 AA599863 AI753621 AI802571 AI537325 AA669978 AI921732 AI811571 AI309543 H80043 AI623845 AI623852 AI075634 AI919521 AA729459 C01795 AA577421 AA688620 AA600003 AA653400 AI445339 AW468974 AW130343 AA600104 AW970482 AW806615 BE140122 AW084991 R54179 N64486 NM_014496 AF184965 H82896 H82897 BE075316 AW090150 AW589417 H47391 D61911 BE173252 AA905097 AI734242 BE044545 N86431 AA344041 C03245 AW963097 AI567324 AA045934 AW079233 R58274 AI744425 AI167427 R58176 R58598 AI969945 AI921684 AW013864 AI204559 AA909648 N84115 AA897468 AI668637 BE221753 AI355307 AI139542 N80934 W21483 U15590 NM_006308 N56314 AA126678 AA426507 Y17782 W24740 W05062 W21042 AA649552 AA093507 AA092088 AA476830 N88299 AA429090 AA095643 AI224915 AA443775 AI204315 AI333690 AA586584 AI275037 AI193915 AA659647 T82641 AA136048 T82643 T82647 F36041 N74099 AI572217 T82650 T82642 T82640 R47360 R47361 R47357 N74672 R47356 R47355 N93086 R47354 R47353 R47342 R47362 R47358 N93441 N56384 N93566 T82622 T82618 AI094748 AW241797 AI759976 T10509 AI814441 AI421977 AI423762 N73686 T11392 AA046406 L11690 NM_001723 M69225 H99965 AI750335 BE000199 M63618 N31521 AA112876 AW265395 AA088909 N21507 X58677 U04850 AW864903 AI830854 AW361101 AW379356 AA301170 T29232 AW965998 H26216 H44230 H44784 AA808916 AA514765 H44575 AA705179 AA586735 AW589403 H25843 AA654993 AI783826 BE087370 AW451982 AW157117 AW161544 W02488 AW167479 AW361027 AW833243 AA912183 AA541622 AI673341 AI266109 AI335896 AI421010 AA053327 AI982962 AI372854 AI674348 AA531087 AI801016 AI372855 AI817816 N52151 D62928 AI401633 AI378549 AI378800 AI37972 D62536 AW972977 AA135826 BE222491 D62195 BE326453 AA225293 AA236461 R85586 AA625141 AA058641 AI135825 AA234644 H50784 R71863 AA053381 W95901 AA053387 AA121501 Y00787 M28130 D14283 BE439795 BE439924 AA362187 BE439515 M17017 C05929 AA381897 AA346136 AA381472 C06304 AA381670 AA381679 AA381965 T11274 AA381318 AA381601 AA381700 AA381952 AW950718 AA381992 D82198 AA381914 AV653399 AA362140 AA381592 AA381967 AA381454 M26383 AA362188 AA382057 AA381781 AA362246 AA381669 AA381395 AA381845 AA381848 AA381603 W40425 AW663238 AA381702 AA381355 AA381356 AA381653 AA362127 AA374516 AA381426 AA381767 AA362270 AA381459 AA362358 AA362160 AA304441 T27482 D83848 AA381877 AA381623 D83851 AA362133 AA381999 AA372837 AA362192 AA362196 AA381806 D82132 AA362107 AA363589 AA296403 T11316 D82218 AA381456 W56111 AA381435 W40163 T11379 W40283 D82615 AA382121 W40401 AA381699 T68485 D82618 W52968 W39356 T27467 D83813 Z11686 T10915 AW367405 AW604306 AA363550 AA363514 BE004230 AA381218 W40279 AA363545 AW377023 AA363453 AA363559 AA381833 AW850620 AA381813 AA381710 AA381584 AA381577 AA381715 AW376990 T11334 AA305271 AA363554 W52491 AW631242 AA363599 D82254 AA363540 AA363596 AW951160 BE122704 AA380965 AW850702 AW630501 AA381229 AA381228 AA381576 AA381795 AA381816 AI274317 AA360958 AA381517 AA381618 AA381891 AI310352 T11037 BE122702 AA834388 W38334 C01358 AW059870 AA371394 AW075978 AI922031 AA381189 AW468452 AI375262 AI870149 C06055 AA381309 AA381625 AA381252 AI620395 AW467642 AJ227913 AW780131 AI742278 AI564251 C75559 AW272612 AI634748 AW339521 AI079248 C75557 AI569162 C75493 AW591509 AW769268 C75524 AI469809 AI579895 C75486 AI697109 AI475413 AI355474 AI282685 AI087873 AI469815 C06100 AA568576 AW014817 C05914 AW272671 C75615 AW337841 AI380580 AW467270 AA847352 W46290 AW780211 AW440851 W45324 C06017 C75643 AI346866 W45040 C05698 C05704 AA381931 AA381177 AA382015 AI476632 AA381274 C05758 C75413 W45362 AW951601 C05910 C75382 W60423 AA095727 C75410 AW188453 AW341742 W60450 AW613454 AI469266 AI473944 BE042737 AW273112 AW467973 C05693 AW272835 W45409 C05668 AI431254 T29157 AI953422 AW510601 W45271 C75538 BE138893 AW662358 AA102526 AI457250 AW615017 AW662707 AW051250 AW470168 AI952442 AA362337 AW015490 AA362269 BE122713 C06363 C06353 AW779405 T68419 AA381217 AA362139 T11140 T11198 AA363591 AA362138 AA362357 AA362344 D56519 AA362132 AA361981 AA362159 AA362110 D83856 D82102 D83842 AW959358 AI373550 AA362225 BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091 AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220 AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129 AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108 AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156 AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598 BE140957 H91230 AW182672 AW514652 AW612492 AW182695 AW183350 C03487 C05115 AF070571 H70949 AW149569 AI804276 AA936447 AA987912 N35082 N35065 N43822 N43804 H69776 T80170 H09701 R35799 R19028 AW196589 AW207553 BE221925 BE551043 R61736 AW242757 R53961 T33418 Z45363 AW250525 BE265117 AA195764 AA167076 AW937980 AA166917 AA056984 AI206035 AW023639 AA195520 AA329676 AA678589 AI784331 H65489 AW876581 AW876552 AW268587 N91553 AW268820 AW566003 W19061 BE397160 AW274839 BE296227 AF008551 Z43879 AA313688 AW409753 AA298501 AW957623 BE299015 BE093498 AA431134 N64029 AI038260 AW732512 AI917458 AA628301 AA291514 BE092461 H63889 AI126792 BE092286 H72166 H57643 AI884785 R96793 AW516673 W78726 H78488 BE011847 AI638439 AA834453 AW014897 AI004050 AA804577 AI207188 AW365050 AI689761 AA432153 AA767736 AI738674 R19158 BE503915 AA629662 BE465533 AA602467 AI859635 N58083 AI828708 AI859629 AI148444 R97724 AI652950 BE243218 AI318096 AA704673 AI318080 BE465518 AA745859 AI026750 AW409660 AI266728 AA748628 H58486 AA486497 AI750284 H79032 H54313 H78390 H63492 AW272138 AA488685 R07581 AA736853 AW594462 AI500164 AA832386 Z39943 AA598643 W80533 AA243133 AF011468 NM_003600 AA373999 H54104 AW136695 BE547389 H70678 AB033025 AL359061 AL045836 AI751521 AI752804 AI752650 AA853580 AI752290 AA853460 AI752769 AA852309 AA853785 AA853219 AW068503 AI752069 AL049389 AW068368 BE439518 W52813 BE141833 AI940574 AI750606 AL109718 AA242845 AA315795 AA307741 AW954603 AI752070 AA350794 AI752649 AA307755 AW951677 AA298896 BE439692 AA852453 AW068826 AW853984 AA418236 AA639417 AW290917 AI750592 AI752768 AL045837 AI926513 AW262903 BE439819 AI459360 AW339074 AW295181 AW029483 AI750945 AI750659 AI752525 AI147688 BE440122 AI751522 AI473816 AI752291 AI694639 AI925816 AA599476 AA242752 AW021892 AI750598 AW469299 AW769363 AA853579 AI784082 AA852454 AI925501 AA976657 AW150473 AW166734 AI129586 AA455078 BE536256 AA834910 AI264121 AA715165 AI675186 AA878884 AI937502 H41127 AI613527 AA136856 AI858126 AA062762 AI351420 AW195729 AI493903 W78038 BE143223 AA136950 AA193470 AA082447 AW796079 AW996023 BE065712 AA063003 AI880645 AI880644 AA063458 AA063018 AI444822 AF251237 AA412359 T19106 AW975988 AA948244 AI954712 AA620697 AA758618 AI631681 AA648117 BE620755 BE620196 AW386187 AA747475 AI205793 AA730288 AW467539 AW468376 AW467312 AW337844 AW337833 AW467317 AW467401 AW468247 AW440988 AW440830 AW467337
--	--	--	---

	409156	110362_1	N76186 R69723 AW444682 BE220376 W49490 AA961099 BE218202 N53704 W73451 AI823360 AW675687 N64773 AA064629 AA064753 AA527475 AW473807 AA199658 AI090198 AI374757 AI769715 AI026060 AI801785 W49491 R72390 R63399 AI742199 AI190947 R69629 AI287331 AI769707 AI219372 D20803 AI187711 AI472100 W73390 N94037 N94055 AA064789 AW835560 T84873 AW818390 AW818237 AW858911 AW858977 BE072544 W26498 AA070211 AA070030 AA070114 AA070198 AA070217 AA070106 AA070265 AA070334 AA070101 AA070302 AA070278 AA070231 R87083 R01811 T81648 AW383308 AW389668 AW389657 AW609198 AW389649 D49372 Z75668 Z92709 NM_002986 U46572 U46573 AA125790 AW294260 AA127067 AI080514 U34780 AI867933 AA910483 AI446061 AI913625 AI913629 AI537716 AI357416 W69211 AW805343 C21564 AF278761 AA461577 AA460289 AI561173 AA600224 AA074612 AW382145 AL045940 X90780 C03339 C03114 W07136 C02994 C03103 C04896 C05070 W17389 C04180 C05502 W19390 C04558 C04543 AA311399 C05351 C04551 C04456 X54163 NM_000363 C02730 C05613 C05482 R57607 BE140258 M64247 C04434 AI265781 AI950215 AI634065 AI760600 AI367238 AI864649 C03467 AA992938 C05063 C03065 AI185229 AI003859 AI193201 AI355654 AA935234 AW207185 C03193 N91524 C04315 AI657074 C05024 C04608 C03333 AI193911 AW003240 AW003043 AI650950 AA092543 T12017 N90905 N90947 AI652255 AI969724 T12391 T29798 T12073 AA158797 N93687 AI369979 BE296182 AW629821 AW997628 AW449319 BE068930 AW449589 BE219028 BE503053 W74001 AA316156 U04313 NM_002639 T27595 AA294992 AW951580 AW814845 BE122694 W72351 AI989728 AW362665 AW379980 AI656538 AI633911 AI656426 BE122695 W93572 BE152369 AI589723 AI435384 AW274531 AW173600 AW151556 AI559971 AA583423 AA583421 AI042520 AI041742 AI863998 AI924540 AI168755 AF086216 C00555 W93726 AI081348 AW609782 W30956 AA284290 AA662428 AI276525 AI242306 W02802 AI913973 AI913861 AW450809 H06661 AW860936 D86640 NM_003149 AA451622 AA558394 H14661 BE262331 AI741761 AW137199 W49541 AI288524 BE220310 AI800206 AI471117 AA450217 AI370524 W49772 AW885757 AW885748 AW885693 AW885549 AW572414 AW470595 H60964 H57755 AW473583 AI137163 AA101422 AW367010 Z83826 BE167397 AA813575 AI280253 AI277959 R28517 R28131 AA375127 R76478 W21429 T62693 AI433432 AI401346 T62844 BE552077 AI277896 AW338135 AI435513 AA873621 AA528626 AI961880 AW338124 AA127501 AI918990 AA876737 AI365181 N92911 AI077290 C00153 AI580500 R38772 AW510843 H16714 U60665 AL034394 AA897135 AL035445 AW665839 AI935027 AA936514 AA629287 M78345 T07132 AW566007 R83578 T36151 H08587 Z45984 R61252 AW966442 BE180035 AA428482 AB024518 W79345 AA449389 AL080211 AA249114 W05152 AA345239 W79445 AI146674 D60585 AA046754 W07067 AA315195 AW954874 T69187 AI150705 N78517 R35444 R33255 R33248 N78928 D61726 AI636918 AI675380 D62188 AI935469 AI375549 D79309 AI610794 AI281303 T69129 AI587330 AA046641 AA479893 AI085845 AI474465 AW028856 H12424 D60584 AI016160 AI766477 N92986 AA582759 R67773 AL134435 N99191 AA081918 D81425 D60802 D81310 D52972 D52986 Z45092 H00118 AW382942 AA249770 AA249043 AL133837 N85732 AA249732 AA081961 R19529 R13631 Z43675 H11407 AA376302 T25307 AI468210 R54453 AW291931 AA814911 AA828285 AA731670 AA553734 H17613 AW780162 AW780176 AW182524 AI743107 AI635064 T32609 AW192433 AI307672 AA994018 AA082285 AI671334 AI862698 AW583237 BE219648 AI985157 AI610704 BE328117 Z38374 AI083538 AA099352 T35606 BE088282 F08855 AI554545 AA083514 AI633826 AI765624 AW169852 AI656026 AI363822 AI739159 AA040433 AL047873 AA037778 AI205645 AF022913 Y07596 R18975 AA366192 AI904896 W05406 AW130797 W38804 AW628276 AL035409 N70544 AI123406 AA330449 AW950460 AI926246 R4860 AA746741 AW612942 AI539700 N69061 AA481761 AI559559 N93182 AI245742 AA814787 AA464862 AA084050 AA084064 AA084174 AI287518 AI243745 AW196535 AW102813 AA834941 H24627 AL050199 W21139 N53879 H84695 AA424083 AI872323 AI475291 W69379 AI919258 AA557197 AI581597 N66899 AW604533 W69378 R16586 AA559860 AA559908 R34107 AW750133 AW750120 R21663 BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671 R09442 AW846115 AW846108 AW751967 AW846083 AW846087 AW846090 AW905138 AW753008 R13818 Z43519 AA373210 H91768 BE172318 AA371497 AA085843 AI307247 AI824005 AW261982 AI625754 N27830 AI679467 AI078259 AW594323 AI335252 AA122264 AA994930 AA111902 N21680 AI498311 AA633551 AA455980 AI625756 AA938642 AA766825 AA811180 AA085906 AI762946 AW977820 AW770523 BE503941 BE219626 AW770778 BE551458 BE550838 BE549582 BE328860 BE550143 AW792909 AW876101 AW792964 AW876100 AW876099 AW792910 AA497117 AA497039 AA996105 AI042190 AI910528 AA088543 AI733733 AA732081 AI269879 AJ001873 R58869 AJ001874 AW301235 AA496916 Z41363 AW857191 AW857192 AW804060 AW805687 H88503 H88502 AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280 AW807283 D78367 NM_000223 AF137286 AB007119 C00499 AW809201 AW809176 AW809258 AW809266 AW809236 AW809213 AW809243 AW809187 AW809235 AW809142 AW809186 AW809152 AW809146 AW809144 AW809141 AW809145 AW809170 AW809248 AW809149 AW861207 AW809508 AW810169 AW809654 AW809839 AW810090 AW809703 AW809891 AW810564 AW809733 AW810616 AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960 AA121686 AI276195 AW117710 AI401471 AW972533 AW237287 AW304874 AI720005 AA441903 AA442009 AI884441 AA505929 AA112361 AI695051 BE175525 BE466445 T06998 T59728 Z25022 AA861746 BE073181 T63311 AA992785 Z44588 BE544748 AW805672 N31268 W93499 AA090503 AW811114 AW811095 AW811087 AW811124 AW811054 AW811094 AW811157 AW812088 AW812105 AW812082 AW812790 AW813072 AW813062 AW813004 AW812962 AW812961 AW813428 AW813444 AW813367 AW813368 AW813429 AW813424 BE062590 AW813565 BE147101 AA857218 AI304833 R68303 R42247 R44174 R74002 R44219 R49558 AA090979 Z38312 F01959
--	--------	----------	--



5	411565	1249756_1	AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628
	411597	1250843_1	AW852925 AW852922
	411622	125205_1	AI807894 AW340512 R94399 AW082409
	411657	1252980_1	AW855583 AW855628 AW855653 AW855611 AW855631 AW855629
	411660	1253078_1	AW855718 AW855740 AW855748
10	411693	1254206_1	AW857271 AW857308 AW857296 AW857258
	411726	1255048_1	AW858612 AW861964 AW858600 AW861945 AW858445 AW861901 AW858546 AW861921 AW858395 AW861968 AW858394 AW858401
			AW858404 AW858399
15	411736	1255573_1	AW859089 AW862098 AW859088 R97592 N28912
	411738	1255755_1	AW859353 AW859365 AW859362 AW859356 AW859351 AW859354 AW859355 AW859361 AW859348 AW859364 AW859372 AW859352
			AW859349 AW859367 AW859360 AW859374 AW859350
20	411745	1256160_1	AW867826 AW859896
	411770	12572_1	NM_014278 AB023421 BE168265 BE092854 AA431598 AA431172 AA432192 AA402062 AI655325 AI626866 AA398923 AA975783 AA451968
			AI917699 W00516 AW966019 AA364471 AW804981 AA421206 AA405106 AW338926 AI337285 AI271953 AA625996 AA151812 AA405659
25	411772	1257386_1	AA478479 AI478380 AI863753 AI077291 AI280476 AA149534 AA932462 AI915816
	411816	1259632_1	BE170301 AW861539 AW904851 BE154336 BE154090 BE154275
	411863	126201_1	AW864609 AW864592 AW864594
30			BE075244 AA190379 F13175 AW674857 T76947 R57804 AA345136 AW963229 AA721138 AI688819 AA095982 AA463295 AA428673 AA169109
			AW003758 AW057536 AI186079 AI478215 AI913806 AW075976 AW119020 AI968588 AI768030 AA927649 Z40571 AA190788
			AW872477 BE088101 T05990
35	411893	1263110_1	R82845 AW873969
	411934	1264302_1	AW876538 AW876567 AW876619 AW876629 AW876537 AW876566 AW876547 AW876576 AW876535 AW876564
	411940	1266140_1	AW876686 AW876717 AW877215 AW876691 AW876722 AW877218 AW876694 AW876725
40	411965	1266262_1	BE467339 BE217847 AW879135
	411966	1267729_1	AA099113 AI090211 AW665171 AI887642
	411970	126794_1	AA099142 AA099240
45	411987	126821_1	AA375975 AW954415 AW954409 AA497124 AA551693 BE001643 AW771919 AI344328 AI924091 AA497046 H19580 AI082176 H42450 AA737000
			AA975029 W31663 AW204912 AI804483 AW935085 AI521818 AI352532 AA227921 W15587 AA099293 AW468884 W35363 AA456286 D20889
			W04722
50	412011	12713_1	NM_000406 L03380 S77472 L07949 S60587 Z99995 U19602
	412029	1272597_1	AW886238 AW886229 AW886244 AW887891 AW886289 AW886146
	412074	12758_1	S74683 NM_004314
55	412105	1277509_1	H07971 F05875 AW893090
	412139	1279175_1	BE044976 AW895327 AW895462
	412147	1279411_1	AW895984 AW895982 AW895983 AW895918 AW895772 AW895843 AW895847 AW895653 AW895652 AW895648 AW896054 M85583
60	412222	128403_1	AA528283 AW971270 AI801420 AA398112 AA101106 AA394152 AW971279
	412228	12842_1	AW503785 AW503590 NM_001877 M26004 AW502871 AW504784 M26021 Y00649 AW505211 AW499938 AA648953 AW503883 AA465705
			AA262317 AW968570 AW505438 AW505320 S62696 AW408330 AA459563 AW512602 AA262382 AW361297 AW401642 T29776 AW951599
65			AW503293 AI765035 AI635781 AI819443 AI627832 AI432980 AW303499 BE466519 AW080149 AW977511 AI015545 AA482292 AA521362
			AA521363 AI439900 AA767159 AA804757 AA829329 AI953525 AA443336 AA807223 AI468848 AI373520 AW515814 AI433669 AI934444
			AA974992 AI758133 AI953576 AI468894 AI695225 AW770076 AI559791 AI880641 AW866194 AI253682 AW317053 Y00649
70	412236	1284501_1	AW902583 AW902585 AW902695 AW902568 AW902580 AW902692 AW902684 AW902595 AW902573 AW902681
	412323	1288770_1	AW937143 AW937150 AW937141 AW937151 AW937132 AW937160 AW937191 AW937174 AW937195 AW937173 AW937159 AW937139
			AW937171 AW937142 AW937145 AW937165 AW937163 AW937164 AW937137 AW937179 AW937156 AW937140 AW937135 AW937170
75	412329	1288943_1	AW937445 AW937457 AW937364 AW937374 AW937395
	412400	1292900_1	AW948066 AW948106 AW948020 AW948047 AW948011 AW948033 AW948034 AW948041 AW948028 AW948048 AW948046 AW948056
			AW948025 AW948053 AW948043 AW948032 AW948037 AW948050 AW948060 AW948059 AW948051 AW948027 AW948038 AW948052
80			AW948036 AW948031 AW948030 AW948035 AW948039 AW948026 AW948044 AW948049 AW948042 AW948054 AW948055 AW948013
			AW948058 AW948045 AW948057 AW948029 AW948003 AW948016 AW948123 AW948008 AW948001 AW948022 AW948014 AW948023
			AW948004 AW948000 AW948018
85	412446	129614_1	AI768015 AL120184 AI769949 AI633838 AA102645 AA617929 AI669212 F09778 F04816 F02721 BE184363 AA151245 Z41449 AA987907
			AW890837 AW898604 AA934514 AI632924 AA151244 Z45815
	412486	12_1	AF210650 AI305158 AI918630 AI887719
90	412494	1300_1	AL133900 NM_001656 L04510 AW993847 F11746 T65453 T08981 AI121038 H78121 N94301 AI021991 N72762 AI287306 AW592270 AA489014
			AI077521 T65376 AA706974 AA642485 N69692 AA693768 AA913755 R60064 AA689423 H78122 N59815 AA814447 AA913261 F09406 AW304804
			BE178123 AW043693 AI679418 AI679608 AI001923 H92443 AI679928 H19413 N58948 AI973246 D55063 AA527126 AI744410 AI808080
95			AW193091 T08980 R60128
	412505	130132_1	AA974491 AI206314 AW022585 AW291873 AW204274 AW014186 R15834 AI056304 W80448 AW080599 AA678677 AI343530 AI675512 AI370947
			AI123123 AA744915 N62839 AA112318 W78137 AA577026 N75543 AW237510 AW242698 AI078049 BE536805 AA429809 AA705732 AI559392
100			AI935601 AA587653 AW043778 AI457895 AW978291 R92989 H88620 H22144 H88619 AA806925 AA434019 AW021712 AA446146 W79476
			W05336 N77746 H07864 R51778 AW193285 AA460545 W02297 H22181 AI222051 N72976 N20524 AA351581 R35103 W79044 R49490
	412566	1306469_1	AW962574 BE073261
105	412589	130937_1	R28660 AI683378 AI249381 AI018052 AI742043 AW191911 AI587398 AI264257 AW008123 AA113387 AI624266 AW072688 AA574127 AI961922
			AI289578 AW970835 AI687304 D79818 D62948
	412613	131306_1	AA653507 AI209166 AI469529 H05663 R67271 R16037 AA280024 R52899 AI688328 AI690591 BE463813 N62171 AA806288 AW592389
110			AA927153 AI336807 AA767138 AI090000 AI090001 AA114171 N62802 AW303301 AA194072 AA149585 AI128102 AW057592 AA134534
			AA815131 AA737546 AA458847 AI538210 AA978182 AA740637 AA151800 AA193681 AI417149 AA190568 AW444980 AW965997 AW819899
			AA280093 N93916 H05662 AI653910 N48344 N30139 N35259 N25776 AW176403 N35258 AI656458 BE467469 AA312984 BE503040 AA988512
115			N31408 R52898 R16341 AA234870 N40400 AA134533 R13914 N44257 AA379725
	412639	131675_1	AW961284 AI962899 AI740649 N49746 C01777 D62520 AI431795 D62457 AI742960 AA327801 AI123532 AI635323 N48187 AA115107 AI167508
			AI082125 N52675
120	412695	1322022_1	AW984439 AW984371 AW984349 AW984443 AW984356 AW984433 AW984451 AW984444 AW984367 AW984449
	412706	1322406_1	R97106 R92747 AW991241
	412732	1323951_1	AW993300 N23107 R22345
125	412768	1326095_1	AW996044 R54798 H12046
	412798	1328107_1	AW998657 Z42273 R20217
	412811	132943_1	H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148
130			AA598689 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202
			R17734
	412887	1334741_1	BE007420 BE007419 BE007421 BE007422
135	413006	1343534_1	W03857 BE046646 R89470
	413087	1348720_1	BE064655 BE153953

5	413088	1348732_1	BE064962 BE064979 BE064853 BE064857 BE064856 BE064977 BE064960 BE064860 BE064815 BE064957 BE064804 BE064816 BE064850 BE064806 BE064796 BE064818 BE064975 BE064819 BE064810 BE064668 BE065059 BE065063 BE064727 BE064736 BE064976 BE065215 BE155544 BE155541 BE155540 BE155542 BE155543 BE166323 BE067045 BE067232 BE067221 BE067228 BE177730 AA723564 N33229 AA127258 AW579163 AA127395 N68223 AA363498 D62246 D87461 AL157542 BE184393 NM_004050 U59747 AA429751 AW204767 AW131571 R60850 H19373 T97644 AA456480 R13646 AA007327 AW452223 AA351094 AW954619 AW954626 AW954628 T80465 AI694772 AA411378 AW905655 AV645465 AW905605 W23853 AA406309 AA156593 R83489 H92364 AA476672 W00451 W02937 R70836 AI796974 W25268 AA813734 W07063 AA098908 AA092352 C75306 AA625058 AA524030 AA148504 AA193421 AA187643 AW901736 AW972233 AW080354 AA007328 W39084 AI913405 R60851 AA553972 AI279367 R70783 AI310328 AI086373 AI679347 AI335949 AI167654 AI122655 H18933 AI025024 AA741032 AA035238 AI972640 AA954705 AI093767 N72171 AA557539 AA741293 AA621499 AI274864 AI242314 AI972692 R38496 H95621 AI970809 AA351093 AA454588 AW055376 AI214584 AI681508 AI222600 AA099828 N78923 N94633 AA931492 AA918712 AI810698 AA194030 AA938747 AA854581 AW571442 AW026947 AA834389 T97645 D62606 T16699 BE073771 BE073783 BE073773 BE073767 BE073764 BE073719 BE074910 BE074913 BE074911 BE074903 BE074892 BE074935 W28131 BE081198 BE088812 BE088819 BE088823 BE088754 BE088753 BE088757 BE504766 AA129728 AA129747 BE502207 AI657193 BE145899 BE145848 BE145849 BE145853 BE145927 BE145925 AA319146 NM_003469 M25756 AL120036 AI570611 AI912721 BE549650 AI971452 R58883 T08333 T08149 AW950837 T09414 AW498993 AW293628 F07298 AA319366 BE312495 AA384796 H54915 AA319530 AI697961 AI357661 AW005233 H54916 AI813750 AW899932 AI986411 H40604 AI079115 AI692409 AI004935 AI865871 AI589482 AA975308 AI079373 AI291758 AI278032 AI146562 BE219052 AA988981 AI472913 T28854 AA128988 T23971 R41603 T24044 H27864 AW455808 AA350446 H52828 R18638 BE150618 BE150616 BE150626 AI133452 AF118092 AV646997 AA344298 AV648471 AV653839 AV649557 AA344215 AV652159 AV653760 AV659239 AV659188 AV653911 AV653431 AV660891 AV657526 AV653737 AV645785 AV659170 AV659334 AV653798 AV655244 AV651743 AA344639 AV659220 AV656889 AI207493 AV657434 AI133243 AV646671 NM_000509 AV662079 AI207651 AI132918 AV661755 AA343699 AA345917 AA343490 AA344610 AA343434 X51473 AA343808 AA344285 AI174692 AH33515 T67625 T58788 T73352 AA344354 AA360361 T69352 T94626 AA344529 AV656138 T50845 T74670 AA332162 AA345589 AV646330 AA343225 R28773 T67608 AF113681 AA127901 AV653213 AA312911 AV661947 T86050 AV661818 AV661899 AV661905 R28960 R28837 AV649290 T66810 AA312743 AA345150 AA344513 T64763 AI064984 T51155 T40196 AA344031 AA345795 AI065032 T53919 AI065018 AV650157 AA344728 AV662173 AV650840 AV658467 AA344294 AV662232 AI207724 AV662312 AA345561 AV654559 AV652797 W92647 AA344388 R09360 R06530 AA345478 Z20522 T50870 W77961 AV654163 H49804 T69653 W66580 T68149 AA337510 AV653519 AV656147 AI989422 AI984220 R01859 AI954841 AI201573 AV656799 AA328409 AV647604 AV646927 AV660491 AA344654 AW339929 AI110791 AF074698 AA345475 AA313496 AA779747 W72217 T40133 AV651093 AV651109 AV651041 T83205 AW269523 AI064748 AA344540 T68003 AI568934 AI189826 AV659219 AI911879 AV654713 AW665993 T64315 AI187086 BE250740 AA936960 T67507 AI174843 AI092886 AV646035 T64666 T64115 T62908 AI313492 T73291 AI917303 T74611 AI186901 T55856 W79416 R00044 AI266531 AA906009 AW074348 AW805833 AI825233 AA968875 AV655180 AI580756 T73437 T64651 AW950039 T27841 T53800 AI283155 AI989903 T87137 T69024 C20909 D12274 R85625 AA344998 AA312959 AA313165 AA331360 T70574 T94279 AA313014 W78014 T55851 T74885 AA345347 AV661196 W78129 AA382681 T68193 T50716 W68581 W94563 AI140948 N79517 AA345466 AA345467 T46873 T69258 AA313185 T52365 AV662293 T69277 AA343530 T58721 T69397 T69582 AA312904 T50690 AA313124 T67493 AA313373 AA331364 AA343475 H89500 T50709 T41064 T58776 T72273 T74553 AA345122 AA360373 AA345423 T40932 AA345221 T24021 AA313498 T23996 AA313189 H77838 AA345257 AA345507 T41037 T72141 AA360365 AA313286 T73555 T90758 T72290 R09244 AA344638 H75468 AW014527 T61761 T58742 T58809 H62832 T41027 R06531 R01860 T61213 BE155373 BE155412 BE153516 BE153752 BE155131 BE153613 BE182082 BE182099 BE182108 BE182097 BE182102 BE182114 BE182100 BE182112 T84969 T81533 AA130913 AW968260 AA258851 AW023999 T95054 T81358 T91219 T95151 BE154837 BE154879 BE154850 BE154877 BE154835 BE154849 BE154902 BE154905 BE154867 BE154901 BE154904 BE154899 BE155042 BE155040 BE154987 BE155012 AA131315 AA987985 AI350169 AI608814 AA328505 AI674807 BE161807 BE161584 BE161700 BE161748 BE162391 AA314337 AI805587 AA402097 AA293631 AA658356 BE566333 AI557276 AV651311 NM_001011 Z25749 AI525506 R97869 BE546683 AA155861 AA532947 AA329269 H63470 AA187471 AV660956 AV650019 AA380909 AW327895 BE313243 N93984 AA354585 W19057 AA428966 T55686 AW958123 AA315872 AA081305 AA083776 AW961442 AA352331 H00860 AA206205 W21515 AA149180 H13044 AA372080 AV658875 AV658874 AA337727 BE276865 AA247683 AA209449 AA393619 AA147378 AW404839 W19374 AW247081 AA311228 BE615971 AA308572 W01826 AA310230 AA412606 AA420575 AA362646 H70797 AA525988 AA311440 BE564044 AW967302 AA302565 AA531021 AA312653 D52864 AA312582 AV654672 AA308096 AA308509 AA308491 AA305867 AA306813 W75940 AV653876 AA365315 AW408185 AA308217 AA122395 AA314083 AA315981 AA311782 AA310647 W46668 N31114 AA180871 AA187276 N72805 AA312418 AA304985 AA167580 AA307881 AA310961 AW674912 AA310126 H82669 AA132497 AA809088 AA155963 AA640361 BE618580 AA229152 AW404970 AA306621 AA308276 N98583 AV660766 AA654587 AA206190 AA312305 AA580740 AI568153 AI718253 AI860477 AI872388 AA873460 AA405147 AA315435 AI129479 AI888709 AW583033 AW089596 AW264185 AI653503 AA858344 BE619226 AA187721 AA306691 AW439857 BE616042 AI889905 AI862869 AA309960 AA307823 AI148769 BE619772 AA582168 AI963414 AW168760 AW167856 BE619400 BE378974 BE619933 AW958117 W49703 AI951380 AA306263 AA583192 AA356605 AA897095 AA149141 T53975 AI744255 AA845352 BE312890 AW961435 AW583101 W24684 BE619333 T96513 AI491903 BE272296 AA315556 BE539380 BE619999 AW084687 BE465646 BE262138 AA999923 BE260616 BE276306 D55310 AI186578 AI707735 AW404371 BE274614 AW512395 AA650425 AI439470 AA513739 AW404673 AW404664 M77233 AI970731 AI880754 AI418821 AW273410 AA069936 AW058084 AA719351 AW404422 AW405314 AI523106 AA393107 BE408961 BE252375 AA578681 BE513748 AI749494 N36979 N43025 D11774 AW391958 R34130 BE394953 AI865715 AI018059 N46292 AA908866 AA907443 AW081633 AA622318 AW438511 BE262297 AA565643 AI018057 AI440067 AI719291 AA135054 BE222834 AW262240 AA081120 AA442581 N86460 AA583569 AI061357 W72482 AA148278 AI186761 AA512934 AW615804 AA595332 AI831069 AA778136 AA657641 AI433175 AA339868 AI735084 BE183158 AI566940 AW304785 AI401846 AA506149 AA102508 AA736531 AI027939 AW000716 AA861339 AI027937 AA575877 AA639090 AW129111 AI421179 AA506553 AA936780 AA972869 AA563975 AA582448 AI802748 AI471162 AA586422 N86248 AA528142 AA551225 AI566307 AI206730 AA513485 AA363629 AA436824 AW575828 AA180774 AI001103 AA932070 AA613667 AI337566 AA582127 AW2327319 AA610833 AI333738 AI708124 AI349480 AI240444 AI225152 AA570790 AI539813 W80674 AI33517 AI181299 AA315527 AI719857 BE087137 AW474616 AI510739 AA614724 AW337476 AW951820 AA149181 AA149142 AA523097 AA428873 AI708760 AI978984 AA946913 AA844685 AI440225 AA306527 BE349026 AI659593 AA845752 AW327366 AA311945 AA595594 AI027199 AI499554 AI262336 AA398535 AI333388 AW575598 AI472745 AI476623 AI150520 AW897766 AI864033 AW584030 AA148411 BE348977 AA420550 AW768575 T27844 AI349314 AI371037 AI675707 AW102842 AI203978 AI719821 AW768495 AW021575 AI686981 R36541 AI346551 AW888705 R25390 AA209335 AI342426 AA056446 AA582981 AA890201 AW026850 AA857587 N91141 AW768541 T55235 AA401942 AA080860 AI291273 AI312669 AA412271 AA890649 AA846264 BE019907 BE090895 T56904 H70798 AI500573 AW327642 F17734 AA157192 AA152417 AW327670 AA985481 H71524 AW439687 AA968516 AW327857 AA405330 AI342315 H01239 AA878156 AA148279 H71525 N52399 AI991878 AA878100 N93956 H56020 AA132515 W49704 H63414 AI717990 AI814318 AA912383 AA922317
---	--------	-----------	---



5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

R97819 AI860255 AI335093 AI187843 AW270357 AA187646 AI190237 AI991126 W07024 BE539453 AI819841 H75424 AA102446 AW026974  
AI923973 AW001389 AA337759 N70772 AW022155 AA336624 AI219252 N89590 AA664546 AW339690 AA651993 AA608735 H65064 AA857788  
T81916 AA860215 AI031685 AA133689 AA186954 R16825 N27213 AA857155 N69981 AA318664 AI735334 H82411 AI460293 AA205819  
AW803086 AI922965 N33363 AA580622 AA664756 AA651961 AI201624 AI066494 AA834187 AA187722 AA652066 W80675 AW051553 AW263699  
R34131 AA340971 AA364263 AI824574 AI356913 AI439263 AA205822 AI540881 AA640625 AI206794 AI198883 AA167581 AA970474 AA299068  
AA157088 N90120 AI371330 AA090914 AI889887 AI274617 AA730747 AI745000 AW265227 AI358313 AA122396 AA501489 AA918963 AA953637  
AI434343 AI707767 AA603889 W04799 T55604 AA614231 AA071264 AA083777 AI880809 AI185259 AA747112 AA908459 AA134970 AI192649  
BE046107 AI358698 AA310968 AW517574 AA984892 W46578 AW105597 AA224970 AA747937 T96514 AI472689 AA283670 AI186789 F35482  
AW873463 AW361039 AA583072 AI872660 AA040277 AA224895 N85343 AA484723 AA937597 AI304419 AA228409 AA501488 AA664896  
AA664966 AA482963 AA736806 AA528814 AA927560 AA328094 N83225 AA582536 AA938377 AA916871 AA507716 AA101182 AI720885  
AA876858 AA483322 AA362647 N75592 N23917 AI193949 N74054 AI352629 D51754 AI570783 AA470923 AW975162 AA328256 AA659768  
AI919411 W40458 F00799 AA147346 AA728856 AA528675 AI676101 AA523785 T52866 AA533842 AW516442 AA554875 AA886066 AW518472  
AA971169 AA908345 AI561318 AA482746 AA482735 AA482882 AA188350 AA629989 AA482917 AW263351 T52867 D52318 AI696386 AA689276  
AI719128 AI719124 AA541702 X85626 AA640165 AA228408 AI832575 AI143550 AI281727 N73099 AA733095 AI749387 X85625 AA640766  
AA652170 AA652139 AW606146 AA649563 T25406 AA327330 AA080984 X74803 AA746016 AW957997 AI005578 BE547070 AA886825  
AA927742 AI927866 AA528573 AA665260 AW270340 AI698507 AA501524 AA483113 AA506345 N91789 AI933429 AW904843 BE092709  
BE093487 BE093472 BE092712 F22641 N80062 AW455220 BE079292  
M62246 AI133913 AA448292 AW193851 AI380851 AI457761 C01505 H20670 AA132089 AL041398  
M34276 T73184 NM\_000301 X05199 M74220 T70980 T62125 T61282 T61696 AV650284 AV658097 T68673 T53896 R17073 T73378 AA700207  
T71704 R17074 T60976 T70455 T60602 T40071 T86499 T78795 AV654588 T40195 H72598 T68959 T02922 H54245 H94827 R28928 R91117  
T89505 T82089 T77573 R08226 AA343990 H49223 T77537 H63293 T89681 T78412 T95646 R08908 T81776 R08171 T84137 T81942 AI061613  
BE348267 T62069 AW104579 AW271976 T74268 T74274 AA722885 AI351543 T69403 T67697 AW950594 T61611 AA931947 R98489 T91387  
BE326889 AA995929 H72599 AI631756 T68303 H73743 AI768449 T28527 R94209 T73090 AI640315 N55181 AV657296 AA953491 N38794  
N68493 T69454 H37824 H73209 R91118 H65506 H57610 N33950 AI985353 T53187 R94743 H49409 T68593 AI758373 H90875 T68886 H61585  
T89378 R96483 H73406 AA862393 T73102 T73313 AW044457 T64233 H94974 T60447 T64119 T61200 AW827293 T53188 M86876 AV646001  
AV647453 AV646861 AA382677 H79780 H73620 M86873 W03318 AI377474 H73407 T69246 AI633979 AI279395  
BE173561 R35315  
Z43567 H24159 AA134240  
AW103807 AI669017 AA134420  
AW452334 AI360642 AI703446 AI208419 AW172666 AI864132 AW241354 AI659456 AA971832 AA134566  
AI121282 AA135311 AW964241 AA136392 AI474666 AA386019 AW469017  
AA812434 AI831542 AA766261 AI769894 N63376 AA214392 AA135833 AW605017 AI135965 AW450072 H04812 AA446459 AW439151  
AA426273 AI061423 AA598549 Z40087 AI753216 AA743075 AA854268 AA458920 AA843893 AI566516 AI864957 AI566634 AW971760 AA211796  
AA430089  
BE549372 AA135959  
AI308876 AW292946 Z39141 AI338622 AI277014 R59726 AA599661 AI190051 AI367593 AI283131 AI815184 F02205 AI278525 AI377442  
AA136216 AW088869 F02286 AI168803 AI435938 AI139951 AW021021 AW022730  
AA425085 AA136904 H12660 Z33546 AW978185 AL049138 N84118 N84179 AI827678 AW104044 AI627540 AW975128 N98679 AI827775  
AI635146 AI093542 AI096829 AA662351 AA665049 AW453066 AW044461 AA779594 AA574238 AI139745 AI379627 AI263398 AI140450  
AA551570 AI277705 AW513186 AW058384 AI601124 AA136875 H12610 AI127657 AI619554 AA805917 AA904081 AA406377 AA927284 AI005577  
AI192415 D58115 AI418757 AI537607 AW024905 AW591483 D57809 AI285981 D57394 D57567 AA649811 AW027762 AA889085 AA927293  
D56768 R26144 N86658 D19655 D57922 AI651567 N49107 AI866400 AA258593 D57813 AA831062 D56689 D56680 D56608 AA555231 AI382401  
D56711 D57801 D58062 AA233612 AI471347 AI471166 AA625308 AW835580 AI264317 AI333656 N66156 AI972387 AI468556 D45626  
AW975616 AA137098 AA720795  
AW970254 AA040232 U68398 NM\_001828 AW514554 L01664 R09331 AW970335 AI243705 AC005393 AI066757 AW274543 AA984998 AA534845  
AA452521 AA454104 AA039869 AW292557  
AI568801 AI637568 AI139775 AW138143 AW206893 AA909633 AI183677 AA142913 AI890950 AI659181 AI970878 AA985394 AI217372 AI215398  
AI377927 AI801758 AI469896 T05812  
AA142989 AW974726 AA649871 AA730301 AA150979 AW779103  
BE512968  
BE549143 BE390613 BE277344  
AI904738 AL043702 AI929363 AI904746 AU076758 BE003097 X52104 AW161549 AW161518 AL035985 BE297948 BE241643 BE245077  
BE163299 AF015812 BE439910 AL038502 NM\_004396 X15729 AI929113 AW163816 AI879248 AV645537 AI815966 AA016122 AA305524  
AL047520 AA338086 AA374359 AA336336 AA220219 D56025 AA375816 AA318625 AV657572 AV657570 AA333401 AA331853 BE541660  
AA344143 BE410184 AA381617 AA317028 BE268866 AW630947 BE390294 AA375651 BE256393 BE388908 BE251807 AW239458 AA351226  
AV648645 AA386094 BE279907 AI249379 BE265226 BE294083 AW150193 AA355992 AI750633 AA325108 AA335390 AA3300843 AA306195  
AW955242 BE619384 AI460003 AA331574 BE535284 BE563619 AW238939 BE312057 BE613719 AI929288 D55853 AA084703 BE548399  
AA356860 AA371223 H27564 AA082571 AA356699 AA223423 AL040607 AJ010931 AA375522 AA216205 BE536415 AW204726 AA985164  
AA445964 AI908319 AA358844 AA558037 D82242 AA263173 AW366625 R55452 AI904763 AI431475 AW704159 AA191193 AW275947 D56090  
AW411115 H27646 AW073742 AW401853 AI247756 AW946599 AW946598 AV653933 AA370389 BE327780 AW339236 AA383627 AW169407  
AA595868 BE172280 AA173460 AW946690 AA337335 AA082091 AA301156 AV654088 AA361125 W75994 AW239034 AA336409 AI973245  
AA383735 AI000218 AI678609 AA321184 AW390358 AW390434 W57781 BE299179 AA070542 AA974702 AA333349 AW965348 AA090876  
N86851 N36666 AI311098 AV656543 F11307 W74108 BE613865 AW361181 T83771 N26938 AW607574 T83567 AA360446 R51147 AA425613  
BE614471 AA334976 AA332061 D56476 AA089780 N32715 C06223 AI185704 AW873392 T18511 W16692 AA373151 AA091358 W68816  
AA112668 H30474 AA383460 BE019903 AA343935 AA343741 AA779490 AA055883 AA302453 W37671 AA334180 BE566906 W02536 AA311463  
AA716173 AA824358 AW994059 BE614604 R57123 AW900324 AA314327 AI590970 BE185145 BE001196 BE161224 BE185519 AI209200  
AI207322 AA344708 BE176468 AI201155 AI984571 AI084607 AI200878 BE542694 AI565613 AI928842 H49167 AI683831 AI889435 AI719657  
AI609405 AI419080 N81173 AI572873 AI624137 AI564475 AW805795 AL043703 AI982652 AI984884 AW149053 AI002970 AI721255 BE176536  
AA218888 BE006756 AI625663 AW601668 BE006758 AI561164 AA322195 AW385333 AW516012 AI979104 AI635691 W44365 AW169138  
AW026791 AI760714 AA995696 AA368956 AW024589 AI074936 AW376345 AA304400 AI924705 AW516019 AI890496 AW157775 AI591361  
AW190100 AW169314 AW368631 AL038503 AW368644 AW368630 AW190890 BE350284 AW166884 AW151506 AW247137 BE138882  
AW512697 AW169365 AI394504 AI570796 AI564981 AW469331 AA383638 AW152502 AI983575 AW338907 BE049594 AW903760 AI826105  
AW190030 AI913034 AI814998 AI859667 AI954037 AA101136 AW005020 AW152117 AW173541 AW919290 AA878298 AI951429 AI936001  
D58265 AW471377 D57839 AW029563 AW276247 BE043979 AW513446 AI983668 AI596991 AW075973 AI963451 AW515019 AW057726  
AA740382 AA902684 AA302274 AW390220 AW150174 AI263721 AI623875 BE043963 AA522478 AI750634 W68530 AI885606 AI799680 AI570125  
AW262919 BE221265 AA380235 BE220942 AW575503 AW129590 AA595743 AI755065 AI241673 AI922595 AI677800 AW078780 AW440453  
AW190198 AW073397 AI654030 AI887292 AW087903 AI961579 AI498951 AW069244 AI565012 AA532847 AW189321 AI687428 AI984580  
AI735604 AW073715 AW074269 AW664545 AI963610 AA442268 AA737132 F08135 AA614399 AI873654 AI688611 AA470125 AA425396  
AA595156 AI719944 AA933580 AI476326 AW675539 AW510368 N32259 AA599732 AA725677 AA831646 AA587804 AI476549 AW517305  
AW337472 AI288073 AW591886 AA771999 AI624658 AW339561 AI281756 AI568001 AA430017 AA563718 BE045037 AA001454 AA640676  
AI206497 AI536759 AW591611 AA5517138 AA772014 AI445891 AI628031 AI434396 AA453211 AA723958 AA598539 AA633548 AW513576  
AI187217 AI755188 AW513563 AI590149 AA568281 BE464698 AI954423 AA570721 AA872438 AA580281 AI858357 AW193939 AW090026  
AW768237 AI089269 AW339628 AI537193 AI289793 AA937348 AI214153 AA682282 AA043843 AI286318 AW303943 AA483702 AA987202

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

414400	1442_1
414452	144729_1
414481	145206_1
414494	145380_1
414523	14568_1
414546	1460704_1
414550	1460990_1
414591	146481_1
414725	148115_1
414831	14960_1
414884	150257_1
414899	150433_1
414955	1509869_1
415025	151592_1
415046	1517244_1
415076	15199_1
415131	1523680_1
415173	152713_1
415236	1531080_1
415239	1531201_1
415257	1531869_1
415258	153186_1
415266	153226_1
415273	1532427_1
415318	1533859_1
415319	153389_1
415380	1535430_1
415399	1535970_1
415424	1536402_1
415452	1537085_1
415533	1539520_1
415598	154030_1
415628	1540769_1
415655	1541447_1
415672	1543861_1
415716	154888_1
415747	155189_1

AA504171 AI087134 AA878555 AW972028 AI185958 AI538569 AI566986 AW662656 AW272635 AI811679 AI682697 AI805650 AI809230  
 AW068724 AI926231 AI537724 AW627658 AA927102 AI687388 AI879630 AA189092 AA070465 AI860071 AI225209 AI144383 AI002799 AA365442  
 AW768290 AA496992 N55306 AA614689 AI374777 AI095866 AW505409 AA928948 AW244104 T48386 AI364751 AI371977 W45718 AI961868  
 AA016032 N59850 AW057880 AA015785 AA693473 AA330302 H99074 W37531 AW157122 D56557 AI264705 AW473814 AI952359 AI567043  
 AA778082 AI953555 AI174956 AI129309 AW193296 AI356946 AA731093 AA451670 AI299814 AW019938 AI299812 AA219598 AI858125 AI582968  
 N33355 AI174581 N24687 D58056 AA164344 AI200183 AI358131 AW028439 AI538217 N23007 AA996300 N79497 AI640900 AA581623 AI619959  
 AA112669 AI699732 AW992571 AA504170 AI523962 AA709166 AI474021 T57372 AW089065 N22275 AA019163 AA112695 AA977719 AI932545  
 AI049881 AI583428 D57499 AW474287 AI865799 AI952658 AW242085 AA776562 AI460259 AI362581 D56516 AI440154 AW768962 R49074  
 AI991666 AW511509 AW664722 AI992113 AW894385 AA487033 AI858911 AW021385 AW193142 F22174 AI932519 AA470918 H18448 AA350757  
 T49828 BE541130 AI815085 AI003106 AI431239 BE440236 AI084725 AV661023 D57834 AV661032 AI865420 AI473833 AW074495 AA962567  
 AA350378 AI367216 AI886697 AA173404 AI753652 AI470726 AA586517 AI248262 AI520723 AA629191 AA507265 AA620897 AW972608 F08967  
 AW189663 D29182 AI174379 AA665534 AA133151 AA868150 AA350789 AW470575 AI471923 AI568079 AA223473 AI886327 AA650331  
 AA782678 AA055818 AI870088 AW515051 AW411116 AI696761 AI866369 N58407 AW440827 T82276 AW519186 AI802207 AI933784 AA580633  
 AI926272 AI932869 H75639 R51037 R97493 AA653946 AW873473 AW591842 AI566636 AI630603 H53870 AI934121 AI619977 D57344 D58180  
 AW389404 AA743949 AA911469 AI275778 AW868653 AA369751 AA592996 AI866105 N74334 AI889525 AI932708 AI869373 AA508623 AA877030  
 AW472763 AA581351 D57608 AA363397 BE348921 AA295523 AA080969 C06315 AA701037 AW300937  
 X06948 NM\_002001 L14075 J03605 AW612525 AI676114 AI685796 AI676097 AI765235 J03605  
 AA454038 F07163 AA248755 BE000930 AA147565 AW956227 AA453620 AA441959 H03791 AW386521 AW386517 R69785 AW386600  
 AW386433 AW601734 AW386493 W56171 R81898 AA293463 BE551036 BE222431 AW969646 H89191 AI902723 AI636266 H02891 R69786  
 AI479177 AI002977 AW195442 AA501355 N20552 AI090073 AA156437 AI758191 AI088523 H89090 AA401763 AI431934 AW271839 AI001196  
 AW470322 N64157 D62872 AA417899  
 AW451956 AI123814 AW020913 AA759356 AI827831 AW082019 AW263097 AA678440 AI564845 AI991451 Z38284 T19431  
 AA768491 AA76251 AA809748 AI186268 AA621244 AI379029 BE550341 AA651915 AI216376 AI215585 AI471780 AA772159 AW181980  
 AI151169 AA759270 AI675769 AI018776 AA757335 AA148511 AI138378 AA504167 AI420617 AW261930 AW872797 N51769 AW614403 AI860533  
 AW573108 N64830 AI693732 AI436159 BE501089 AI436163 AA971485 AI269364 AI935358 AI222050 AW303978 AW573247 AI871154 T16758  
 AI765893 AW969016 AA744720 BE094085 AA743769 AI476407 AA156619 AI768535 R81435 D45332 N75682 N51177 AW207406 AA425184  
 R20997 AA504168 Z43298  
 AU076633 AA343348 M68516 AA337389 S69366 J02639 BE387640 U35464 AW051592 AA336837 S58545 AL042078 AL080185 W86431 H63588  
 AA337834 AA337741 AV647684 AA337274 AA319283 T19297 AW583861 AL046056 AI132932 AV654311 AA337036 H57410 W87887 AA701671  
 R92069 N77072 AL042079 AW190847 H61028 R87086 H64931 AI686889 W58665 AA649953 AA876209 AW338903 AI912422 AI114432 R10481  
 AW951306 T29357 AW393838 AW583493 AI223428 AA576058 N59025 AA604743 AA564914 AA858026 AA922777 AA934730 AI565898 AA613884  
 AW016086 AA999925 AI584097 AA576176 AI623737 AA004247 N66729 AA576841 H63619 H47369 AI040614 AA918753 H63571 T58868  
 AA699440 W58666 AA906781 AA906782 AA687579 R84409 AA005324 AI569319 H64932 AI806531 AI245508 AA703634 H63546 R89333 W87814  
 H65690 H58683 AI351804 AI696609 AI241083 AW194217 R10382 H82423 AA569950 AI470884 R97526 AI701190 AA922910 R86958 AL043448  
 H57362 AL043447 AA837688 AA706828 AA642674 AA689492 H47459 H82683 AI493551 T59927 T98665 H61029 AI698395 AA334681 T98721  
 BE379492 BE391967  
 BE379808  
 AI888490 AA662564 AW028504 W45712 AA233892 AI201627 AI921193 AA149800 AA534817 AI473541 AA729422 AI758369 AW970373  
 AA149845 AW970294 AA552180 AW079308 AI400436 AA234027 R81036 AA424364 AA530943  
 AA769791 AA628389 AA227117 AI628362 AI873518 AI701653 AI650276 AI672377 AI651327 AW271565 AW771249 AW052076 AI338826  
 AW873562 BE503226 AI654206 AW612116 AI470776 AI207150 AI650258 AI207149 AA718936 BE501740 AW772451 AA588100 AW271269  
 AW974257 AI650537 AW235852 AL043894 AA625445 AI984770 H50872 BE222316 BE220093 AA151628 H61051 AA609539 AA609112 H86984  
 H61613 H86985  
 M31158 NM\_002736 AA339672 AA374640 AA744536 D51568 D51558 AA595812 D45457 AI885772 AI806649 AA551058 AA089521 AI582332  
 AW467649 AA663483 AA887427 D54509 AA640912 AA731762 AI224607 AA569921 AI708184 AA991328 AA180007 H39950 AA824579 AI630179  
 AW028423 AI424780 T96338 D57984 M78041 H28459 D55926 F03112 AI473509 D54627 AA483463 BE067779 BE067773 R77765 AI720453  
 AI792179 AI733577 AI081026 AI915939 D51418 AA828306 AA158104 D51544 AA158105 C18185 AC004492 AA375679 T93506 AA450175  
 AI341761 AA083538 AL119760 AA181500 F06849 BE220099 T29208 AW960200 D52899 D52688 D52958 AI025657 H26901 W31099 R77857  
 R54418 N21008 N71554 H77755 AA694279 AA157529 AI935439 AA677075 H63121 H65853 R93632 AA772826 R93631 N99562 H63207 H56570  
 H77754 H65852 AW452609 AI370456 AA625326 AA158182 N30982 AA767175 H56571  
 AW975433 AA767931 AI685399 AI458084 N73742 AI916090 H73264 AA157814 AA720538 H48817  
 C15506 D80541 D80506  
 AW207091 AA873302 AW470722 AI282097 AA159355 AI521782  
 R40018 T03563 F09202 Z40191 D51031 F04159 D51371  
 NM\_000857 X66533 AW407576 AA018579 H86506 F06464 AA457178 AA845996 AW378353 AW378354 AW378355 T06391 R16193 AW796136  
 AI050064 AW950677 T28656 W93727 R70090 AL133938 W73204 AW952694 AW583758 AA280531 AA419206 W73155 AW664687 W93728  
 AI805317 T06392 AW173355 AI923361 AA878642 BE501357 AW976017 N40472 AI341123 AW592638 AA569389 AI189698 AI569599 AA018580  
 R16192 W69902 AI242641 AI537121 AI830730 AW271616 AA648501 AA458785 AA747631 AA291938 AA747509 R70042 AI472922 AA932013  
 AA419138 AW079067 AI537448 BE046337 AI870690 AI087886 AA971490 F02745 AI982637 AI784630 AW118143 H86484 W69901 BE326853  
 N48510  
 D61119 D81508 D81734  
 AW501735 BE244012 AA368583 BE294810 AW192700 AA160864  
 R41400 H06659 Z38637 F02023 T16516  
 R42608 R51822 H24349 R15887 T23742 T23745 F03535 F03513 F02173 T16744 F03515  
 F03016 N39101 N34820  
 AW752247 AA167125 AA161495  
 AA164199 AI334641 AA255520  
 Z39840 F08829 R42823 F03720  
 T06544 Z44549 F05465 R61128  
 AA659823 AA837251 AI868843 AA164413 D60698 D60700 AI087872 AW027258 AW189300 AI698680 N20929 AI274461 D62009 AA682908  
 BE379643  
 F07953 F07260 R52015 H29397 H13350  
 T26994 T26995 Z45228 F07865  
 Z44766 F08356 R11847  
 F09134 F09627 T65445  
 T74009 H14386 T65172 F11763 F12598 T65493  
 AI433165 AA847805 AA165270 AI699580 AI767750 AI619882 AI468845 D60542 N40981 H30262 AW118751 AI250810 AI651312 AW978867  
 H03885 T55132 H30324  
 F13080 R34751 T75411  
 W05433 Z25322 F29200 N70563 F37502 F27903 F30994 F31752 F19683 F32651 F18577 F17375 F20867 Z28857 F17543 F17411 F15601  
 N53097 Z30225 F21685  
 N59294 AA167269 AI168404 R77813 AW367347 AW963530 R78181 AA380160 AW172716 AA487388 Z30218 AI267588 BE143412 N77065  
 AA381209 AA381245 AA167683



5	415763	1554077_1	Z42285 R15162 H00117 R15327
	415811	155705_1	AA450191 AA425009 AI630917 R58148 AA448713 AI089470 D80942 D81183 AI077471 AW939319 AA300988 AW954276 AW959425 N94857 AA169612 AW386244 AW974607 D80480 AI266549 AA649005 D60876 AW193345 D52426 D59960 AI445748 AI583996 AA448623 AA450125 AA255509 AW193749 D60740 D60588 AA971081 AW513848 BE328723 AA888175 AA995923 AA182655 AW009242 AI304474 AI273237 F08953 AA662493 AA652449 AA255537 AI187873 T16506 F09771 AI144133 AA886533
10	415817	15573_1	U88967 AI867704 AI961037 NM_002851 M93426 AW892755 AW149516 M85576 D56415 X54135 H17826 F05242 H17827 R58813 AA351386 AW379107 F05995 AW950896 AW950900 R59633 T28809 BE551526 AA424757 AW054767 D54903 D52462 AI970301 AI633894 AI394544 AI638428 AI435360 AI356883 AW593917 AI808073 AW590108 AW086482 AA976036 AI017625 AI625010 AA425781 AI365365 AI359121 AI096518 AW594199 AI359879 AI076051 R59575 H18465 N50894 AI470985 AI359225 R36986 AW103731 R49348 AA814553 F02235 F01496 AI090956
	415840	1558630_1	R15955 H05329 Z43429
15	415871	1559982_1	R55995 T08053 H06790 R24959
	415913	1561293_1	H70302 H29797 H08896
20	415929	156192_1	AA724373 AA171718 AI241720 AI025398 AA617765 AI636080 AW271980 AI802103 AW194465 AI868460 N67510 W23467
	416009	1566379_1	Z43062 R13213 H14422
25	416035	1567254_1	H42314 H43080 H45217 H15384
	416045	1567804_1	H15990 H23067 H16091
30	416057	156821_1	AI927382 AW958524 BE551575 AW104433 BE217738 R37191 H99930 AI735430 AW090802 AW236478 R79245 AI920856 AA678611 AA176267 AA173191 AA176243 AI198475 AI696030 AA890110 AA380591 BE501166
	416085	1569726_1	H18072 R62333 R26700
35	416093	1570130_1	R60685 R37691 H18526
	416100	1570291_1	H18700 H40484 H23822 H18799 H50011
40	416143	15726_2	AI955650 AI655812 AI635765 AI625806 BE465887 BE465871 BE178730 AW576847 AW576835 AW950812 BE048520 AI969523 BE178670 N25559 AW104307 AI676188 AA915986 AI151392 AI986150 AA745605 AI278924 AI278546 AI280994 AA281234 AA809678 AW204668 AA922311 F02735 T05478 AI915622 T08599 AW342041 AA732436 AW628399 F04402 BE619664
	416148	1573418_1	H22453 H46657 H22488 H46419
45	416154	1573965_1	Z46122 H23303 R56554 H23055 T80310 R13090 Z45524
	416170	1574639_1	H42454 H23819 H41658 H41689 H23839
50	416182	15756_1	NM_004354 U47414 AA281861 BE000891 T26977 Z46163 BE000937 AA370680 AL119433 F11807 T65607 T65616 T65464 F11821 AA384022 AA429991 AA489752 AA195611 AA173621 AA461025 H19079 AA371455 AW389537 H21595 R68318 R81279 W38816 AA523034 AI271688 AA281779 AA761867 AI658967 BE176223 R81174 D52648 AA868246 AW134535 AL080193 BE068215 AI362007 AA443790 AI862544 R68280 AA056115 AI492402 AW073547 AA838795 AA974468 AI401470 BE464550 N92533 AA584309 AI628472 AI985769 AI806035 C01336 AA502959 AW076029 AA843918 AI571464 AW190700 AI670797 AA489647 AW297911 AW148640 AI222811 AI942279 AI471521 AA706555 T65541 D53692 AA610186 D53233 BE439781 R42447 C14042 AI627751 AI660379 BE467047 AI862838 AI860076 AA505381 T65387 AA460693 H18981 AI885543 F09470 AI277097 AI633074 T26976 AI005541 AA618031 F05043 AI708991 F09455 AI357853 R18384
	416192	1576_1	NM_005036 S74349 Y07619 N83771 Z79997 AL078611 BE019481 BE019407 Y16186 L02932 AI761514
55	416208	157875_1	AW291168 AW341127 AI914027 BE350547 AW770317 AI860806 AI458749 AI298421 AA423914 AA988491 AA693397 AI952353 AA770658 AW058645 N79004 AA845540 H89882 AI701028 AA176438 H89881
	416211	1578993_1	R14625 R17952 H29120 R14650
60	416225	157972_1	AA577730 AA601199 AA176586
	416248	158112_1	H99169 BE501076 AW590471 AA176769
65	416294	15867_1	D86980 AA100863 Z44504 F11614 AW501276 F11740 AA102381 AI951899 AA476869 R66865 AA091214 AW999689 AA081620 AI016654 AI697677 AW015853 AI220705 AI167957 BE501709 AI912273 BE220140 AI804850 AI703107 AI887154 AI419880 AA879129 AA864602 AI969931 AA977051 AI243403 AA767639 AA921946 AA905866 AI633925 AI692307 AA084508 R67955 AI148775 Z40406 H17830 F09269 F09400 AI910366 F04025 AA917724 AA626581 R36567 R54271 R23513 AI420103 BE005661 R13436 Z44466 R52356 R59055 T31981 N79108 AW235608 AI861998 AW237723 AA651865
	416327	1588956_1	R99822 H48253 R99821 H48344 R02195
70	416334	1589198_1	H53139 H48570 H64332
	416348	1589887_1	H65887 R10388 H49492
75	416379	1591772_1	N38857 R96257 H52386 H51712
	416394	1592742_1	H64111 H52945 T83815 T95222
80	416408	1593272_1	R94725 H70496 H53606
	416421	15937_1	AA134006 U46347 NM_001968 M15353 AA314629 AA044918 AI751010 AA193254 AW401933 BE565143 AI002807 AA092651 D56296 AA204823 AA376271 AA361356 AW403060 AA313327 R57488 R10570 AI950481 AI671180 AI797351 AA583646 F11703 AA369700 AW951369 AW385837 N88206 AW291269 H04445 AA977486 AL040855 AW792812 AA398782 AA165013 AA421111 AW860341 AW993206 AW268640 AI559631 AA587077 AA936197 AW862417 AA928352 AA923536 BE088665 AI264473 AI498661 BE169482 R96644 AA707932 AA983646 AI123347 AI278425 AI950080 H82794 AW815240 AW019946 AA522892 BE550426 AI650532 AW298233 AI380556 AI698033 AW074034 AI493081 AI093961 AW296539 AI751011 AI654727 AA847807 AA194246 T28200 AW001759 AW571426 AA916189 AI306623 AW103257 AW469883 AI797113 AI571021 AA744601 AA219430 AI917202 AA508206 T89747 H01943 AA610526 AA845529 F09361 AI075701 AA159904 AA766354 AI280792 D20745 AI832246 C04246 N22333 AA080948 AI702304 AI742789 AI741355 AW856681 AA632160 N79869 AW855824 AA507270 AI093385 AA854764 AA258534 AI720716 AW362936 AA206089 T15602 AI688059 AA804754 AW204222 AA044919 AA039894 AA648270 AA648249 AA736593 AA809905 AA233796 BE569095 BE568401 N85355 AA333510 T89843
85	416431	159418_1	AW384459 Z24880 N56268 AA180288
	416509	1597896_1	N57713 H60016 R97202
90	416548	1600181_1	H62953 N76608 N72413
	416575	1602095_1	W02414 N76798 H65590 W01477
95	416585	16026_1	X54162 NM_012134 BE254187 BE501513 F26865 AW840949 AA936258 AL043187 BE140732 AA442043 AA131279 AA131510 AI377085 AI719370 AI288379 F13289 AA441933 AI468264 T77389 AL048378 AI804776 AA524026 AI376095 AA377153 AA034393 AA478654 AW950519 T28381 AA335749 AA335961 AA335725 AA335341 AI659811 R23823 R78321 R78196 AI620200 AW190368 AI905922 AW029302 AI048153 AA194981 AA195112 AI678993 AA482339 AI678985 AL048154 BE551530 AI423213 AA031585 AW388110 AA857709 AW190627 AW338494 AI281332 AA482242 AI246287 AI089330 AI588987 AA709021 AI537069 AA031494 AA558527 AA507270 AI093385 AA854764 AA258534 AI720716 AI281739 AI435920 AI810269 AI932279 AI309903 N27347 AA258325 F17755 AI535894 AI199293
	416588	1602827_1	H66558 R91743 T78777
100	416653	160683_1	AA768553 AA521367 AI740696 AW207697 AA182680 AA864609 AW469360 AA745615 AI223345 AW611500 N63420 AI953373 H70731 AA883275 Z21229 X85609 R57894
	416665	1607797_1	H72974 W28967
105	416677	1608621_1	T83470 T84283 H74054
	416690	1609095_1	H84078 H84972 H86134 H75594
110	416737	16128_1	AF154335 BE297492 AF153882 NM_003687 X93510 AI879108 BE261586 R48104 AA436793 AA284637 AA243781 AA099269 AA031877 AI421682 AI609529 R21435 AA227820 W68763 AI884787 AI123597 AA235420 AI417602 AA243766 AI579949 AI493890 AA130144 AI337842 AI090200 AI979127 AA975138 AI379100 AA232653 AA400018 AI400022 AI934728 AI401501 AI191372 AI367836 AI752362 AI143428 W68617 AI400340 W47651 W47650 AI953400 AI093499 W42424 AW630499 AI189181 AA604429 AA227994 AI079305 AW183509 AI418740 AI290260 AI572290 AA401183 AI290505 AW050515 AA031694 BE043409 BE043434 AI345082 AI334917 AI344787 AI308041 AI246809 AW969482 AI307421 AI275357 AI381814 AI344912 AI223739 AI250974 AI223698 AI223642 AI223597 AI250407 AI249638 AI252695 AI246986 AI223757 AI224180 AI249285

5

416747 161386\_1

10

416805 16200\_1

15

416944 1632816\_1  
416951 163406\_1  
416972 163668\_1  
417002 163955\_1  
417079 16478\_1

20

417135 165229\_1  
417154 165360\_1  
417175 1654894\_1  
417177 16554\_1

30

417181 1655\_1  
417229 165977\_1  
417249 1660991\_1  
417252 166103\_1  
417320 166704\_1  
417376 167184\_1

40

417383 1672847\_1  
417404 16758\_1

45

417428 1679519\_1  
417430 167953\_1  
417455 168222\_2

55

417508 168471\_1  
417563 168749\_1  
417596 1688394\_1  
417663 1691897\_1  
417706 1694172\_1  
417712 169469\_1  
417725 1695580\_1  
417756 1697154\_1  
417768 1697604\_1  
417801 16994\_2

65

417806 169990\_1

70

417859 1703724\_1  
417909 1707657\_1  
417918 170855\_1  
417919 170889\_1  
417991 171348\_1  
418007 17145\_1

75

80

418076 1719859\_1

AW302860 AI251089 AI224800 AI252911 AI249422 AI250966 AI270849 AI249277 AI246962 AI309490 AI250122 AI249312 AI246856 AI250984  
BE041242 AI053715 BE043115 BE041892 BE041795 AA503375 H27484 AA128537 AA045672 AI610767 H26372 AA045673 AW590987 AI564965  
C00296 AI254547 AI246821 AI271203 AI312996 BE043354 BE049056 AI250428 AI254397 AI344262 AI252892 AI337781 AI252530 AI306325  
BE139295 AI252987 AI581259 AI436487 AI431573 AW271061 AI253000 AI246928 AI307921 BE043293 BE043285 BE043129 BE041876 BE041793  
BE041801  
AW876523 AA223779 AW969586 AA337022 AA337678 AW960756 AA187068 AW892479 T85455 AA449038 D31263 R63328 AW903750  
AW003442 BE463863 AI796149 BE049580 AA639761 AA403121 H97603 AI935499 AW291136 AI917885 AW516258 AI376672 AW516237  
AI471679 AI374745 AI637533 AI478450 AA970251 AA569809 AI636326 AW976037 AA570163 AA693452 AW298815 AI687470 BE242979  
AA678727 AA805870 AI619618 AI219757 AI802582 AA449754 AA747471 AA748105 AI418802 AA918164 AW338393 R63329  
F13271 U79242 T78193 T77298 H06832 T27142 AF052171 H06360 R56730 Z43732 AA332709 R41950 BE467680 H17316 R56884 H05702  
D60132 D80715 AI887800 F04277 R38853 D60786 Z39799 F02476 AI701759 T15551 Z39793 AW297388 Z39706 F10870 R37861 R38183 R45014  
F01759 R41752 H06833  
N22809 N22821 N22808  
AA190926 AA731652 AW505199  
BE019670 AA191284 AA191255  
T79613 AI479578 BE463488 AI936360 AA191612 H46176  
U65590 X52015 X64532 R34906 X53296 AA381142 AW951593 M63099 BE184286 W78043 AW262191 AA768860 R50241 R46871 AW083357  
AW379511 AA631286 AA704518 AA808207 AW265330 AA327613 AW949966 AI096561 AW366784 R46774 BE148883 W95638 AI270076  
AW352217 R50708 AI825682 AA497140 AA497131 AI453052 AI652467 AI825830 AI814526 AI829895 BE184485 AI638681 BE046001 AI637877  
AI656642 AW376305 AW376303 AW272661 AW794717 AW590057 AA883879 AW023126 AA497064 AA497054 BE181431 AI023908 BE182384  
BE504639 AI637734 BE504650 AA835355 BE006261 AA523931 AW238275 AI739184 AA766057 AA195304 AI298452 AW263886 T72877  
AI273425 AW613807 AI343927 T29769 AI983971 AI090904 AI243012 AW013866 AA877799 AI648618 AW004808 BE182358 AI250162 AA834958  
AA422067 AW614120 AI341461 AI822098 AI338541 AW297273 AI338546 N74690 AI457756  
AI674701 R20670 AI005236 AI819351 AI806563 AI658548 AI089177 AW468985 AI804973 AA194070 AW662504 AI992153 AW662347 AI683062  
R44558 N71087 N50903  
NM\_004458 AF030555 AL036290 Y12777 H92505 BE086194 AA243094 AA243113 AW402273 AW084968 AA337384 AW614408 AI431845  
AV645940 AV645406 N41995 AW385520 N87302 AI767234 AW838022 Z28855 T30794 AW952170 AI124853 N30273 C01890 R28548 AA069611  
N56454 Z25225 AI950028 BE004640 AA313009 AA169527 AA449659 AA251884 AA258995 Z43734 AW578274 BE177625 AA094592 BE620455  
R26216 AA484810 AI632904 H82144 N42718 N33823 AW393121 AW393101 H13717 BE620684 H01277 R28456 AA648617 H12572 AW967690  
AW967694 AI631863 AA173190 R62511 N32505 BE466636 AI572823 N24946 AI359286 AI305180 AW440578 AI619785 AI540829 AI263521  
AI610538 AA633818 AA258172 AI269401 R26217 AA148674 AW131010 AI802974 AA564168 AA232192 H82050 AI691029 AW974390 AA831304  
AW006907 AA169358 AA251792 AA921702 AW083407 R28686 AI476545 AI282399 Z39796 C01690 AA761149 H01184 AW089807 AW131902  
H13670 H69470 H69875 AW390449 AW390452 H12573 C04775 C03284  
L10123 NM\_005129  
AA975096 AW001045 AA194882  
N58198 R99317 T78869  
AA195014 AI342271 AA256543 AA195120 AA256586  
AA195667 R22272 R22250  
AA253314 AA708845 AA927795 AA253484 AA649529 AA649555 AI452745 AA443846 AI352240 AI991816 F00241 F00161 Z19383 F00106 F33877  
AA196325 AA196322 F00752 F29125 Z25079 C03535 AA248635  
W02642 W03157 R94802 N76243  
NM\_007350 Z50194 AF239986 AA316916 U92983 T09403 AW651728 BE262241 AA313553 AA376262 AW861888 AV647322 AA380178 N40634  
AA332511 AF220656 AW751416 AW992472 AW993603 AW992480 AW992523 AW856678 AW275975 AW992558 AA576961 AW793420  
AW994787 AI079417 AI955093 AI923078 AI650566 BE004770 D79238 N27861 AW673189 AI868760 AI828327 AI423373 AA641278 AW382798  
AW993828 AA088194 N73008 N35619 AA258396 AI589460 AI824968 AW151392 AA857168 AI203273 N21585 D12298 H92531 Z21892 AW408804  
D56582 AI352031 AA113084 AW615278 AW993746 AA307019 AW578852 AL121002 AI795908 AW071648 AI693672 AI359865 AI926866 AI813785  
AI679493 AI079737 AA806210 AI913138 AI675042 AI371462 AW837426 AA995175 R66601 AA856996 AL120038 BE182773 AA374767 AW954373  
AV653394 AA253384 AW057588 AW239306 AV653046 AA242962 AW291143 H25689 BE092061 H26271 AI040259 AA253410 AW005975 C02236  
AA626217 AL120842 Z20550 AI273382 AI640428 AI948802 AV650612 BE221065 R87579 AA020770 BE615603 AL120624 AA088367  
N87579 T93706  
AA984546 AW827432 AW872732 AW969888 AA199662 AA610519  
AW007066 AI869968 AW273225 AI700037 AA443693 AI420588 BE328045 AA777593 AW291991 AI457222 N99910 AI033693 AW084920  
AA379692 AW958390 N99913 AI954483 AW194899 AA777584 AI049858 AI150737 AA527616 AI458637 N75501 AI214958 F10487 AI241596  
BE163512 N47294 R52186 AA203411  
AA203701 R66895  
R07343 T79587 T98764 R01068  
R07483 R08181 R93967  
T90797 T78340 R10097  
AA205569 AL038444 AL038443 AW374915  
R25257 R13966 R11696  
Z43056 R13398 T80474  
R24732 R13862 Z42922  
AA417383 AA446268 AA852682 NM\_004791 AF072752 AW068908 AA136657 AI750990 AA047109 AA150407 AA317245 AW967050 AA149419  
AI679980 AI889756 AI539422 AI189000 AW304902 AI984090 AI752854 AI123024 AI095919 AI954496 AA047265 AA723730 AA136596 AA150286  
AA149305 AI129506 N52541 N52533  
AI867277 AW517791 C15003 D81787 D81512 AA626423 C15677 BE258889 BE410715 BE295241 BE272750 BE258969 AW247026 BE292890  
BE391065 AA360962 AW403967 AA340908 AA333954 AW296646 AW0022671 AA767820 AI682294  
T26453 Z44226 R20425  
R35614 R24837 R52440  
AA209205 AW360859  
AI928203 N66315 AA745665 AI627525 AW264846 AA454543 Z19498 AA209248  
AA731452 AA210888 AA251362 AA807250  
M13509 X54925 NM\_002421 M16567 X05231 M15996 W39354 AA186634 AA852324 AA187507 AA081149 AA186524 AA187264 AA187361  
AA386155 AA186973 AA374217 U78045 AA081230 AA188049 AA186393 W56827 AA852602 AA157468 AA308204 AA186754 AA186808  
AA082516 AA304334 AW376428 BE439384 AW376420 AA156273 T18504 AA186521 W49496 AW084608 AA083575 AA372360 AW963590  
AA132297 W47445 AA186376 AA157628 AW003999 AI037890 AI858060 AI589010 AI743739 AI452673 AW304188 AW117854 BE439933  
AA157416 AW778966 AI038497 AA081006 AA100829 AA181048 C02231 T27821 W23960 AW954802 AI471432 AW801296 AW801289 AW801603  
AW801523 AW801292 AW801542 AW801601 AA181134 AI445147 AA191501 AA582862 N94407 AI147810 AA181880 W49497 W52714 AA188249  
AI932881 AI082493 AA503656 AA182682 AW801393 AA182830 AA181882 AA182826 AI613182 N94510 W47343 AI085755 AI076956 AI918426  
AA081208 AI282835 AA147528 AI081490 AI654536 AA181875 AA081282 AA186389 C06085 AA083542 AI800644 AA157642 AA101069 AA157752  
AA158121 AA143331 AA081283 AA852603 AA188296 AI932880 AW449628 AA187348 C02091 AA514656 AA082736 AA308786 AA143201  
M16567  
R61388 T16660 Z38827 R14252

	418079	1719989_1	R40058 R56243 T32997 T17149
	418105	172138_1	AW937488 AW937509 AW937514 AW937497 AW937528 AW937519 AW937518 AW937569 AW937520 AW937684 AW937572 AW937693
5			AW937625 AW937692 AW937683 AW937615 AW937619 AW937617 AW937610 AW937626 AW937601 AW937686 AW937687 AW937673
			AW937694 AW937681 AW937624 AW937675 AW937674 AW836848 AW836927 AW937567 AW937571 AW937603 AW798672 AW937688
			AW937620 AW204461 AI208118 Z39097 BE001182 BE001237 BE072181 AI653800 AI569611 AW138236 AW168268 AA405535 AW937516
			AW167818 AI799646 AA405524 AW937566 AW937648 AW937646 AW364837 AW937663 AW937682 AW937685 AW836839 AW937679
			AW836844 AW836847 AW836838 AW937526 AW937524 AW937515 AW937517 AW937523 AW937525 AW937522 AW937676 AW937521
10			AW937570 AW937678 AW937691 AW937543 AW937690 AW937606 AW937568 AW937599 AW937564 AW937565 AW937600 AW937622
			AW937574 AW937607 AW937563 AW937562 AW937621 AW937558 AW937612 AW937560 AW937613 AW937611 AW937689 AW937559
			AW937510 AW937605 BE150278 AW937511 AW937618 AW937513
	418122	1722487_1	R42778 R52079 R55261 Z41648
	418145	17241_1	AF121260 AA248575 U49837 AA096283 C05020 C03296 R58663 AA328566 W68761 AW960490 N88723 R57351 U20324 NM_003476 U72899
15			R57261 C04586 AA347358 AA328331 R58224 AA216109 N85521 AA089676 AA092769 AA247199 AA310931 AA095980 AA091736 AA382414
			C04383 AA216055 AA096345 N86254 N87427 R57457 U72898 AA195937 AA196406 AA728836 N84658 AA092239 W55978 AA179102 AA216111
			R58384 R58397 AI147018 W68615 R57306 AA195959 AI091769 N89376 AA936373 AI184982 AI621108 AA182871 AA659023 AW469576
			AI184063 AI334243 AI024704 F24625 AI220014 AW086432 F21665 AI018334 AI969927 W96469 F32090 N85589 F26127 F21893 AW4729159
			F37281 AI183696 W81425 F25024 AW183810 F28252 F17381 AA179103 AI203800 F17018 F17350 AA192614 AI184002 AW975276 AA805862
			N89358 W96569
20	418188	172801_1	AW139413 AI458997 AI279028 AA214175 AA214174 AI702703 AI693133 AA962518
	418246	173323_1	AI472179 AI868535 AI752087 AI140405 AW204510 AW243154 AA758060 AI420957 AA782594 AI342597 AI768940 AA405815 AA773925
			AA405816 AI147434 AA446829 AA215331 AA609252 AA283388
	418291	173565_1	BE300369 AA215600 AW006873 W32239 AA741125 AA627973 AA749030 AA748557 AA813972 H99202 AI138661 AI685305 AA768499 W02040
			AI796325 AA227998 AW137937 BE464171 AW976180
25	418301	173646_2	AW976201 AA749369 AA215690 R40111
	418310	173698_1	AA814100 AA825469 AA761909 AA828525 AA837287 AA279628 AI862674 AA805630 AW968684 AA731893 BE219360 AA279627 AA485001
			AI474528 AA215747 AI568384 AA480886 AI224077 AI281592 AA648414 AW016604 BE465508 AI520832 AA748011 AW512599 AI831169
			AA287128 AA741076 AW337508 AA227646 AI766596 AI702501 AI416965 AW571414 AW474852 AI434301 AI080700 AI864832 AA287489
			AI814085 AI568297 AI864701 AI682620 AA480944 AI749462 AI253701 AI817153 AA505050 AW946383 AA286702 AA287127
30	418343	174120_1	AA216372 AA226383 AI399945 AI382486 AI339045 AA226458 AA229528
	418355	1742_1	L42563 NM_001676 U02076 M16797 AA366996 X69824 AI015475
	418375	17462_1	NM_003081 D21267 AA326229 AA326483 AA323202 AA324035 AA776173 AA325397 AA323987 AA322600 AA322536 AA326107 AA321829
35			AA323247 AA017038 L19761 AA322062 AA324840 AA324489 AA322893 AA334413 T08455 AA663803 AL039051 AA321762 AA984695 AA351657
			AA323854 AA663884 R13962 AW950938 AA776081 AA663812 AA351165 AA351308 AA351274 AW905120 F05374 D45307 AA322916 AW371768
			AA081771 AI267238 AI267552 AW892883 AI253339 AI267648 F05466 AA332738 D56189 F11636 AA325060 AA322597 AA322983 AI929643
			AI929044 AA317252 AA322584 D55232 D55580 AA214637 AW498558 T08108 L19760 AA324712 F05633 F05634 AL119440 AL133870 AA322054
			AI372574 AL023913 F08717 AA322969 AA883658 AA093447 AA325162 AA214217 F08091 AA984285 AA322529 AA326582 AA324416 F05689
			T28056 AA325738 AI000358 AA348455 AI204963 AA663804 AA323214 AI267336 AA984430 AA679418 AI299556 BE348772 AW898911 AA063498
40			AW898545 W17215 W17204 AI567722 AA773023 AI928784 AW162097 AW901118 AA626193 AW905270 AA778540 AA324823 AW905383
			AA322050 AW905264 AI240247 AW905271 AW905279 AW905382 AW905276 AW905334 AW905331 AW162496 AI372575 AW905333 AW905329
			AA565393 AW900470 AW905275 AW905332 AI016301 AW905323 AA679187 AA017039 AI240240 AA169277 AI339345 AA701059 AW129098
			AA701124 AA774099 AW900427 AW780417 AI002881 AI341833 AA084617 AA663517 AA776106 AI075874 AI125157 AA912216 AI348283
			AI030043 AW020840 AW020911 AA214182 R40022 AW901182 AW105633 T28865 AI372573 AW900471 AA321761 AA321828 M78521 AA404383
			F02132 AW498559 F05002 F09290 T23470 N89719 AA350200 AA350800 F04329 T08864 AA084540 AA351273 M78930 F01894 AA350266
45			AA814482 F01624 F01725 AI267208 AI267492 AA166848 AA633870 AA633610 AW905273 AA404389
	418378	174656_1	AW962081 AA218925 AA354237
	418379	174665_1	AA218940 AA805691 AA806972 AI654654 AW512037 AW268660 AI352323 AI040150 AI080811 BE220801 BE220786 AW974606 AA447290
	418405	174911_1	AI868282 AI743222 AI091178 AA219258 AA362582 T68831 AA251559 AI376568 AW967665 AW967660 AA521264 D61977 D79349 AW959373
	418432	17537_1	M14156 X57025 AA135910 H49187 M27544 M27544 AI425054 X00173 M29644 X56773 X03420 AA542914 AI248089 AA913900 AA621551 X03421
50			AA993659 H49376 AA456717 AI033043 AA225088 AI865207 AA595528 AA225219 AA128355 AA578974 AI769767 AA883233 AA156944
			AA578948 BE044197 AA904407 AA041277 AA456321 X03422 AW204378 N79008 AW884914 AI904096 AI273559 W77782 AL048606 AW029547
			AW369593 AA018135 R93847 H39008 AI972496 AI432396 AI810531 AA464222 AI857901 R76989 AI400683 AW571744 AA642532 AW020738
			AW196961 T27669 AW945144 AW515411 AI914781 H88012 AI288568 N69062 AI040715 AI420267 D58343 AA041267 W02248 AA128498
			AW297586 W02080 AA216368 H89154 AW022660 R21202 AA229206 N67876 AA572844 AA574301 AA631921 AA574374 AW088430 AA229172
55			AA723451 AW517507 AI457887 H88928 AI499907 H03270 AA954497 AA506468 AA516521 AA571554 AI201410 AI678264 AA580109 AW102819
			AL045447 H03269 AI047056 R57957 R22816 AW880690
	418454	175699_1	AA315308 AA223392 BE538098 BE087173
	418531	1765298_1	R96760 T97555 T88774 W86501 R97688 W86483
	418631	177361_1	AA225921 AA226038 AI732142 AI732148 AI820955 AI820960 AA226077 AA226108
	418632	177373_1	AW118745 AI333767 AI468802 AA988845 AI914533 AA226020 AA225941 BE549459 R96897 T52618
60		17770_1	AK001100 BE005707 AW377891 AW377992 BE006319 R28481 AW379556 AW377915 AA495774 AI797281 AA227823 AW006721 AW662293
			AA495830 AI080165 AI144476 AA130221 AI274999 AA458629 AA227997 AI143128 AI474215 AI857602 AI375944 AA527263 R32665
	418687	178096_1	R61650 AI436195 AA227025 N31261 AW392069 H13402
	418693	17813_1	AI750878 AA853767 M14326 NM_003246 X14787 M25631 X04665 AA853089 AA773505 AA257124 AA235269 AA404574 AA461130 W16745
65			AI284148 AA236646 AI812030 AI250909 AI269249 BE465062 AI963323 AW028334 W30751 AI000621 AA291474 AA878172 AA460828 AA884863
			AI000849 AI379665 AI263550 AA593663 AA884172 AA878373 AI803562 AI042554 N94526 AW192233 AI085533 AA257020 N77812 AA852575
			AI092991 AA235270 AA236145 W52528 BE552472 AI928020 AI086779 BE089560 AW362285 AW362261 AW362367 BE089561 AI866968
			AI588960 AI435009 AI804154 AI492979 AI041974 AA527055 AI763324 AA243572 N26247 AA526978 AI750209 AA256369 R52032 AI278172
			AI306124 AI572353 AW614480 N35411 H26096 AA256479 AA464532 AA426510 AA243836 H24875 AW576784 N39897 AI753454 AA464630
70			AA256885 AI751155 AA852234 AA852974 AA256821 N48043 H40049 AW068763 AW067905 BE002241 AW994516 AI750449 AW753655 N42923
			N85003 AW389277 AW995299 AA852235 AA852979 AW581273 AW868821 AW868820 AL047248 BE002218 AW068451 AW992583 AW992583
			AW068086 AI752766 AW997017 AW752585 BE002552 AW847916 AW604150 AW604145 AA376395 N98278 BE168445 AW601027 BE168043
			AI750877 AA027234 AA703916 AA852402 AV653807 AA368984 M99425 AA149184 AI692802 AA081392 AA853378 AA374765 AI281724 AI003785
			AA600110 AA853090 AW994576 AI147763 AA149185 AL047409 AI750450 AW996793 AI768560 AA132207 AI765822 W93760 BE087365 W93493
75			AA027235 AW050808 AA308199 AW068710 AA373772 AA373735 AW954365 AA080998 AA147963 AA372834 BE158021 AA132064 AI597702
			AA371272 W47517 N98350 AA853826 BE003134 AA852274 C01864 AA852340 W24155 AV656963 AI750260 AL079948 AA043624 BE158037
			AA599373 AI750876 AA188473 BE151310 AW938210 AW938209 AA370310 AW938211 BE122739 AW938212 H62153 BE001303 H77645
			AA007557 AW242688 AI752623 AI093436 N99136 AI755232 AW069822 AI754150 W47518 AA343622 AI373733 AA135843 AA373994 N63907
			AI077756 AI828265 AI048098 AA164488 AW630665 AA043285 AI358576 AA344995 AI240286 AA056491 AI752508 AA343471 AW963038
			AA037609 H98155 AW008151 AA493195 AA225530 AA775913 AA599857 AI659579 AA852724 BE122738 AA344177 AA419134 AI202460
80			AA329919 AA316388 AW193072 AA056585 AW893058 R78085 AW844061 AW843880 AW068403 AW068611 AA345809 AA313173 AW068176
			D45506 AA226117 BE092720 N70154 AI950521 N32982 AW068363 AW068501 AI248597 AW615014 AI752767 AL048099 AA599930 AW068869
			AA599790 AI754476 AA007558 AI750259 AI752622 AW613349 AI572033 AI677990 AI139209 AW449199 AI002688 AI678555 AA852401 D29388

			AA852975 AW067935 AI753854 AA081394 AA225254 AA080999 H77646 AW769422 AW069887 T28616 AA852725 AI913010 R78033 AI269247 AI263852 AI755103 AL048309 AA853913 AA375073 AA037309 AA373962 AV656566 AA373293 AA327376 AA308864 AA095749 AA807881 AW975195 AI278781 AA972195 AA719291 AA757944 AI139653 AA629991 AI587372 AA227986 AI978727 AW263583 AI168721 AW043602 AI079906 AI581282 AI381218 AI124883 R73580 R72963 R39512 H92700 AI267571 AI267568 R39513 AW474547 AI830378 AW474497 AW474534 AI902632 T26672 AW044135 Z40760 AW518599 H88189 H88190 AW514672 AA229293 AW880766 W02102 W32308 AA229405 AI702552 D10216 NM_000306 X62429 X72215 L18781 AI743103 AI743104 AI911222 W20090 T51897 AA382074 AA382149 AI802247 AW072906 AW954464 BE087857 AW368936 T83256 N54013 T03063 BE540738 BE163916 AW166506 AI356082 AA229991 AA454896 AI918954 AA993769 N90430 N48287 T16496 AW468770 N24746 AW003348 AI217537 T90726 AA970052 T51851 AW070518 AI767457 AI290365 AI363018 AA917526 AI333900 N49015 AW137669 R56634 AI634062 AI949160 AI968162 AW593826 AI383052 W25206 AA639926 AI870040 AU076801 X83228 NM_004063 U07969 AW853021 AW854674 AW609540 AW753432 AW604493 AW391746 AW854701 AW854703 AW604484 AA308216 AW862312 AW753130 AA053188 AW859530 AW859603 AW859550 AW859567 AW859489 AA102326 AI733765 AW859487 AW879361 AW859497 AW351846 AI347909 AW351659 AW375303 AW375298 AW351613 AW578054 AA376878 AA088861 AI732453 AW887172 AI262603 AW375947 AI920859 AI566493 AI623483 AI922856 AA305406 AA056417 AA313526 AW950160 AA565642 AI732393 AA053102 AI688206 AI721059 AI601183 NM_000685 S77410 M93394 M91464 Z11162 AW373806 H66116 AA470024 AA442719 AW601630 R01615 AW601631 AW601632 BE069501 BE069503 H00331 R71303 AW373039 T28644 AW950657 AV646497 AV646596 AV652107 R29547 AV646533 AI968386 W93626 AI768584 H03529 BE501476 R30777 AI911517 AI911539 AA412302 R71251 AI373895 AI240900 AI016286 BE501493 H00293 R27618 AI378001 R01616 H03447 N54086 W93558 T78517 T83916 T72681 AI123555 AI888276 AW662679 AI143392 AI168774 AA233151 H89140 H88919 AW963331 AI799050 AI375941 AA233227 AA362889 AA296520 AL021940 M30640 NM_000450 M24736 M61894 AL047443 H39560 AI694691 AA916787 AI214796 AA939085 AI150616 AA412553 AA412545 AI051015 T27654 AA694430 F13215 Z44179 R59895 H10672 T75427 AW249493 AA776718 AW023438 H06840 AA233885 AW205603 Z39420 N32169 BE536468 T85332 T86843 T87127 AW085152 AA625642 AA234510 AI480091 AF292402 AF242874 N45474 AA234223 AI806059 AA236355 AW851980 AA234661 AA767955 T95862 T95868 T97012 AU076718 NM_002993 U81234 U83303 U83303 Y08770 AW515797 AI668847 AW191857 AI391519 C06110 AI889554 AI860457 AA330447 AA328371 AA329787 AA426498 AI761578 AI095823 AA235412 S65791 NM_002024 X69962 AW938458 BE074796 AL119734 AI218079 AW841733 AW191644 L19493 BE174695 AW451018 AA688051 AW444687 AW452162 AW136112 AA281812 AA151811 N46529 AW813032 AW582019 AV653905 AI743037 BE378090 AI949051 AW291012 AA746321 AI273322 AA922941 AA648969 AI381404 AI478824 N49132 AA757356 AI262950 N80297 AA773874 AI691113 AA134558 AI968115 AI640539 N90836 AW194547 AA631252 BE326826 AA134552 AW192790 AW243010 AI701970 AA775260 AI868007 AA805391 AA954623 AI580277 AI298749 AA993967 AA810444 AA991492 AI264330 AA878956 N48355 AA463496 AA815227 N48622 BE463946 AI358803 AA151709 AI913279 AA908750 AI302575 AI953545 AA830684 AA834570 N39121 AW023849 AW195688 AI766096 AA280303 AA134559 AI274459 AI761984 AW196139 AI985139 AA134553 AW001682 AI925048 AA993229 X14767 NM_000812 M59216 AW903030 R45230 T48783 R24969 X07876 NM_003391 T99653 W78848 AI200003 AI379153 H04408 W88685 AI797230 AW340415 AI249171 AI078280 AA703406 AW072799 AI123773 AA634564 AI221988 AI859017 AA676311 AW754042 W17194 T99055 AA601910 N78828 W80746 W93205 AA970688 AI202170 AW189711 AW084652 W93113 AI200512 AA868787 AI807269 AI128114 AI745267 AW574993 AI962915 AW594634 AA808265 AA828115 AA236031 AI350750 AI338007 AI742490 AA620733 AA828100 AI005125 AA778655 AA897706 AI860061 BE302139 AI078560 AA620703 AA620856 AI631061 AI079299 AI537746 AW181897 AI983637 AI804241 AW271765 AA766687 AI015774 D79789 AI236115 R62209 R83509 AW967529 W73890 AI435401 AI472207 AA542987 AI275046 AI458258 AA648778 AA814680 AA505797 AI040806 AW518419 AA748158 AA737513 AI369921 AA659134 R64590 AW969742 AA483577 AW087620 AA236288 AI830539 AW607911 BE167253 T16544 AI611279 AW291112 AI807627 AW025875 BE552020 AA236565 AA236590 AW967537 AW971535 AW966917 AA281926 H42871 AW999060 AA236867 AA237066 AA354236 AW957759 H08961 D26488 BE384100 AW839070 AK000836 D87716 BE408569 AA468890 AW367262 AW088023 T29045 AA156138 BE349630 AI961936 AW276385 AI457359 AW118220 AA580434 AA810557 W19428 AA044399 AW009935 AA156487 AA315159 AW949331 AW385246 R83248 AI472170 AL036780 AI651834 AA865370 D53186 C15566 D60354 D61035 C14847 C14848 AW593733 AA470934 D57375 AA507337 AA516497 AW242347 AL121450 AI200540 AW970247 AW970328 AA749081 AA534752 AW134505 AI222246 T81312 AA766655 AA764820 AA282886 AA767994 AI767158 AA242881 AA983324 AW262486 AW023731 BE122862 AI754737 AI537929 AI298045 AW052187 AI374879 AI807078 AI690573 AA423850 AI695414 AI016179 AW025386 AI814695 AI418188 AI363094 AW172992 AI089742 W81563 AI500261 AI143689 AI539096 AA804848 AI827047 N51469 N51483 Z25374 N32995 AA740648 AI453506 AA256901 AA256276 AI678717 AA252220 C21008 AW303553 AI422496 AA242935 H53367 AW391624 AW391628 BE150859 BE150889 BE150927 D56900 AW748800 AW391623 AW582448 AW371072 AW394222 BE150992 AW582422 AW380570 AW609712 AW379934 AW380565 AW380692 AW394209 BE151003 BE151002 AW379937 BE151246 AW380688 AW816182 AA256900 AW748804 AW394224 AW380676 AW394214 AW380555 BE150888 AA256816 AI332357 AA504149 AI370795 F30478 AA443426 AW971866 AA479743 AI719434 W81562 N53610 N53626 AA243660 AI401477 AI125425 AI826167 AI971347 AA429750 AA358550 AA243780 BE080508 AI198719 AI620570 AI695853 AA564802 AA456099 N48974 BE178425 N45692 N53291 AW363661 AA678242 AA455601 AA243868 X98330 NM_001035 Y08218 X91869 AA776632 AW894044 AJ002511 N87200 Z30126 Z32832 N85743 T94696 F05905 F12039 F05904 T65667 N44993 AA928013 C05113 AL043917 AA343083 F09683 F02154 F02153 AW665252 AL043826 R24839 H08482 H06993 R54549 R14512 F11637 F07641 C02710 AA426108 AW418731 AW452418 AW628936 AI218003 H05446 H08762 AA405868 R44543 T19747 AI806702 F09291 F03893 R44577 R54451 W27493 AA248063 AA249685 AA429679 AA348947 AK000017 R58875 AA398050 W19844 H59188 AI147953 AA335965 R19933 AA382339 AI142236 AA383413 N43928 AW583147 AA352538 AA366562 AI372034 AI363009 AW014233 AI125352 AI760948 AA399108 AA757015 AI208815 AI340945 AA447995 AI654053 AA834387 AI215051 AA911892 AI066511 AW593832 AI970156 AI122811 AA843397 AA927374 AA977640 AA662785 AW025509 N91114 AW131664 N34855 AI867695 AA709336 AA836402 AA779642 AW172826 AI766993 AL037389 AW137825 AW028137 BE327137 AI697752 AI873371 R44734 AI375557 AI741262 AW007760 BE620726 AI470725 N71858 AA448137 H59141 W03298 R91771 AW453073 AW511955 AA248998 N56663 N56651 AI741253 AW369728 AI913451 N30318 AI151200 N30327 H13842
--	--	--	---

5	419751	18775_1	AW195581 AW242846 AI990749 AI224972 AA281915 AI382101 AI423776 AA916497 AW594528 AI963879 AI651487 AA629203 AW411291 AA877273 AI093148 AW294106 R46693 AI333001 AI168676 AI375226 AA705562 AA704898 AI168181 AI766777 AA780095 AI633511 AA612980 AA424572 AI768428 AA233172 AI343490 AW591977 AI275107 AI446154 AA424669 AW805505 AI762004 AA476617 AI865895 AW070607 AW613755 AA229210 AA233248 AI631855 AA883493 U31973 NM_006204 U20212 X94354
	419758	18782_1	NM_000562 M16974 U08006 T69692 T71233 AA344521 AA343878 AW963056 T69068 T69060 T51706 T72935 AA343585 W87334 T68983 T68733
	419812	18827_1	T68989 W86807 AA699772 AI051231 T51917 T28622 H53865 N93779 AA853410 AI879200 AA853082 AI752346 N28824 J00123 NM_006211 V00510 AW885489 AA224793 AA244405 AW379079 AI675880 AA780348 AI962427 AI831688 AI962195 AI971209 AI652049 AA505670 AI918759 AA572862 AI799925 AW883685 AI671929 AI459701 AI879583 AI363200 AI867854 AW236911 AA244338 N23352 AA224770 AI611304 AI752347 H97965 AA853083 AW135612 AI969083 AI637848 AI792788 BE142230 AA252019 BE267154 AW672789 AA461368 AI970472
10	419875	18868_1	W55956 W56137 AI459292 AW383402 N44715 AL110152 AA363622 AW955557 AA042839 BE620067 AA512882.W31499 AA039829 AA030036 N75125 N75133 W20219 AA452000 W19462 AW195335 AA479261 AA846729 AA056071 W45008 BE501532 AI806599 AA706724 AA724378 AW003724 AI609525 AI028108 AA843409 AI949374 AW466980 AI129292 AA846827 N90579 W39235 AI478383 AA700507 AA772128 AW469889 AI031774 AA056023 AI802270 AA846163 AW197629 N52355 AI082553 AA044387 AI022608 AI079146 AA846140 AW591424 AI206246 AI056148 AA424153 W04599 AI031992 AI335584 AA479110 AI026963 AW235807 AA854249 AI168397 AI026964 AI023934 AA843263 AI022871 N35347 AA028004 AA723602 AI026070 W15275 AA772698 N52362 AA724104 W32433 AI478133 R54828 AA411010 D79420 D79933 AI382712 AA029907 N94993
	419936	189181_1	AI345455 AA411714 AI803259 AA427608 AI191278 BE047216 AI187954 AI066770 AW070873 AA628848 AW340621 AI085606 AI889238 W02728 AA506453 W30938 AA284147 AA406092 AI246234 AA770579 AA935693 AW770506 AI247960 AI168723 AA252592 AI168719 AI568285 N44948 AI885386 AI286203 AA291225 AA805724 AA737120 AI831190 AA252915 AA253227 AA625194
	419953	189344_1	AA255652 AA280911 AW967920 AA262684
15	419983	18964_1	AI572490 AW008646 AA398470 AA481278 AA835846 AA480879 AA424540 R72278 AI745338 R26733 AI655888 AI082409 W92777 AA496957 R62168 AW051062 AA255986 AI669890 R67074 H56702 AW968664 R62194 AA424608 AA256248 R26962 R66195 R72315 R62278 AA401875 AA481584 AW968488 W92878 H56520 D63178 AL044056 AI694501 AW057713 AI445728 AI567918 AI362734 AW137633 R24469 AI560113 AA973346 AA256199 N44348 AI886676 W44682 BE048764 AW271213 AA256290 AI420623 BE348449 AW903942 AI887849 AA312915 AA975919 AI034344 AF048693 AF078096 NM_001453 L12143 U13221 AI333220 AI935186 AI659865 AI817619 AI819982 AW451610 AW451944 AW263103 AA022618 AI804844 AI453830 AI763387 AW195359 AW997570 AA348051 AW961791 AA334694 AI261688 AA977661 BE551261 N75774 AI342983 AA022755 N22552 AA885880 N40575 H89575 N40582 AA495846 AW020540 AA232742 AW022802 W77980 AW770239 AI285890 N25875 AA424787 AW021261 AA424381 AW084229 W94714 W94629 W73917 AA424466 AA232201 AI023501 N25867 AW139831 AI216334 AW304880 AA776534 AA865139 AW975334 AA902429 AA551599 AA688135 AA886687 AI652864 BE502475 AW474352 AA694260 AA258021 AW971707 AW071225 AA258148 AA831425 AA768904 H81671 AA625530 AA258410 BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 AA814732 AA485077 AA746374 AW387318 AA261927 AA741470 AW387437 AW387471 AW387470 AW387353 AW387385 AW387473 AW387379 AW387488 AW387485 AW581823 AW387438 AW387433 AW387419 AW387418 AW387374 AW387430 AW387431 AW387451 AW387476 AW387456 AW387382 AW387371 AW387395 AW387415 AW387399 AW387372 AW387444 AW387466 AW387381 AW387383 AW387380 AA888386 AW387360 AW387432 AA876381 AI201846 AA748462 AA747918 AI869027 AA805606 AA262803 AI703192 AW901259 AA278523 AA262062 AA482280 AA459371 AA262310 AW968047 AA482185 AA459596 AA262365 AA521259 AI038565 AA446125 AA262487 AW967882 AW967892 U50525 AL048649 AA417201 AA417224 AL037399 AI635113 AW967913 AA262677 AA604910 AA278808 BE082076 BE081812 BE081581 AA279392 AW849112 AA397743 AW848282 AA829433 AI018600 AW978846 AA279413 AA279694 AA280805 AW082699 H75701 L11245 AV649361 AV649182 W25717 T40073 T40148 T40098 H48637 N57243 M29964 AV653408 BE545748 AA677687 AW470131 AW973305 AI190008 AA551907 AA677301 T67936 AA678194 AA682648 H63408 W90571 AA969142 AA680088 AW050851 H48824 H75630 AA009658 T40992 T41007 T40922 N29827 N58042 AW973306 H78142 C20987 H52688 T41009 T41035 Z20963 AI024214 AA411800 AA480646 AA698909 AA280027 AA402123 AA280096 AA721156 AA873726 AA280675 AA280778 AA856748 AW978923 AW978912 AA884886 AA281444 AI215955 AA595522 AA280981 BE464358 AW296927 AI684514 AI263168 AA281079 N31165 H83594 N27032 AA281276 W07491 N33975 N44778 AA521307 AW969226 AA281607 AA281644 AL049974 AI301495 AA995308 H00414 AI742253 AI310966 AI445704 AA447504 AA723718 AI159777 AW025579 AI004093 AA933984 D79261 R36888 R40575 AI983213 BE011658 BE011660 BE011653 AW962515 N28249 AA330120 AA401855 AW971358 AA524680 T23909 AW195367 AA983271 R14285 R12126 AA447503 H00413 N63125 AA933850 AF044197 NM_006419 AA406115 AW610301 AW868976 AW868965 AW946987 W80984 AI621076 AI620182 AI740786 AW445025 AA700829 AI950325 T54899 AI890483 AI767090 AI819524 AI612763 AW466999 AW515662 W81087 AW003921 BE503228 AI762886 AW440518 AI150743 T54986 AI433102 AI735608 AI203175 AW589686 AI282093 AI634142 AA410383 AI682498 AW516336 AW768461 AI360623 AW169338 AI214312 AA983434 AI699488 T40833 AI650870 AI040146 AI365297 AI702642 AI381379 AJ002211 AF029894 AA298459 T39765 T55152 T72080 AA348594 AW956845 AA282584 AA374723 AA810560 AA282918 AW977543 AI684808 AA827134 AI982955 AW590327 AW237028 AI652140 AI769763 AA282920 AW263539 AW977684 AA283129 AI039322 AI039469 N68441 AI375124 Z39368 AW993448 AA603554 H30637 AI187992 AA329711 AA287436 AA283148 AA283628 AA489689 AW968808 AA877124 H30741 AA283818 AA402902 AA610768 H30825 AA284220 AA405396 AV649282 AA774871 AL035296 AA374514 AA448191 AW971810 AW968757 AW269429 AI018129 AA495797 AA491221 AI381679 AA884073 N51629 AW511250 AI760481 AW243298 AW611630 AA954039 AA401519 D61763 H18005 AI188102 AW449611 AI985573 AA286711 H11105 H15798 AA453014 H29527 H19499 H18196 AI039072 AA621673 AI458638 AI693220 AI290784 AW770530 AI692591 AA503614 H11200 H19582 H18195 AI904919 NM_002666 AB005293 AL119059 AL080025 T70850 H45316 AI703322 AV657998 H45252 AI423231 AI014646 AI024802 AI208525 W95194 AW983661 AA320510 AA781073 T70586 AL119060 AI126205 W94688 AI183365 AI354709 AA515436 AI800214 AI656848 AA625576 F19558 AI187870 AA713632 AI076643 AW297398 AI377300 AA287041 AA910231 AA907716 AW512539 AI439704
	420026	189972_1	
25	420111	190755_1	
	420159	191051_1	
30	420185	191240_1	
	420195	191325_1	
	420230	19169_2	
35	420273	192198_1	
	420288	192314_1	
	420314	192557_1	
40	420352	192979_1	
	420407	193418_1	
45	420430	193538_1	
	420457	193762_1	
	420478	193920_1	
50	420481	19396_1	
	420493	194086_1	
	420621	195113_1	
55	420687	195620_1	
	420691	195640_1	
	420724	195891_1	
60	420727	19591_1	
	420756	196181_2	
	420814	196701_1	
65	420828	196794_1	
	420844	196986_1	
	420854	197072_1	
70	420879	197253_1	
	420905	197546_1	
	420908	19755_1	
75	421003	198430_1	
	421036	198729_1	
	421037	198731_1	
80	421065	198936_1	
	421083	199182_1	
	421106	199346_1	
	421253	200707_1	
	421296	20099_1	
	421300	201010_1	

5	421308	201075_1	AA687322 AA642329 AI080760 AI039479 AA832416 AA807302 AA854015 AA889829 AW771843 AI608865 AI819500 AW663364 AA905058 AA287115 AW974492 AI312843 AW302499 AA287443 AA419385 BE084078 AI478347 AA766485 AW977429 AA287667 AA287948 BE349120 AI078121 T61964 AL079622
	421338	201378_1	AL135462 AF084382 NM_014425 AF084367 AF039217 AL135316 AA401160 AA434147 AI808384 AI867937 AA580524 AA704068 AA706642
	421354	201579_1	AI421758 AA452316 AI245721 AI142391 AI147381 AA411470 AA400817 AI652253 AW590294 AI653316 AA890523 AI792224 AI016015
	421376	201839_1	AA292084 AI821578 AI732693 AA425787 AA424898 AI734099 AA292121
	421482	20290_1	Y11339 AK000113 AW674477 AW860233 AL120518 AL120519 AA233673 AW167654 AW517203 AA527075 BE501325 AI860695 AA878120 AI829215 AW340140 AI687053 AA824284 AI858970 AI983809 AA723802 AI910795 AW673220 AW195947 AW132045 AA494414 AI289782 AI688681 AI688692 AI680070 AW439152 AI368513 C00730 AJ000152 AF071216 NM_004942 Z71389 AF040153 BE181080 BE181076 AW169454 AI700226 AA297138 AA325582 AE298850 AW966436 AW020185 AW020518 AW022436 AW195586 AW170319 BE550836 AI765038 BE466934 AI913501 AI913482 AW015469 N00850 AI806324 AA298713 AI418451 AI807749 AI916381 AI693516 AI094298 BE551185 AI217467 AI803632 BE501927 AI078538 AW573187 N30198 AI138673 AW196898 AI140950 AA626065 AW236420 AI377111 D61823 D79385 AI240122 AA463689 R65677 D62019 C01197 D62572 R65676 R34441 AA300168 AW957006
10	421574	20403_1	L42583 NM_005554 L42601 BE183076 AI541221 BE140567 L42610 V01516 J00269 AW275792 AW383052 AW380143 AI541102 BE612846
	421755	206472_1	AI541344 AW238368 BE613405 BE615705 BE615530 BE615301 AW379823 AW794706 AA194806 AA194992 AW384024 AW384000 AA641239 AI246504 AI540333 AW238681 AA640939 AI540863 AI608860 AW862564 AW366725 AW368983 AW366870 AA596020 AW794721 AW794511 AI591181 BE182523 AW794644 AW794620 AI935234 AI608903 AI608623 AW797060 AW084935 BE182517 BE182319 AI890082 AW238346 AW797012 BE182522 AW794838 AI608794 AW304289 AA147193 AA595995 AW381128 AW366720 AA583718 AI828416 BE122864 AW368343 AA431080 AW082039 AW380976 AA587144 AA443636 AW872937 AW794448 AW378382 AW085761 AW794718 AW263895 AA583587 AA583991 AA583994 AA586886 AA586880 AW368365 AI814460 AA586991 AI282829 AW378406 AA586721 AI609242 AA431973 AA232959 AI831095 AW263854 AW378391 AW378415 AW378381 AA036990 AW238395 AI285446 BE208219 BE049526 AA583605 AA583918 AW366711 AI285580 AW082642 AI285712 AA582875 AW591216 AW368719 AW378408 BE122835 AA582976 BE350422 AA418328 AI541454 AI565930 AA583700 AA150575 AW238427 AI287474 AA912658 AA584223 AW238528 C17918 AW136169 AA159847 AI923797 AI609009 BE182479 AI915198 AW378114 AA147179 AA584239 AA150532 AW168862 AW085999 AW082480 AA659742 AW079703 AI872793 AA583981 AI824571 BE182316 BE182507 AA233331 AI824572 AI540586 D29492 BE182931 AA036948 BE551821 D29401 AW378365 C00141 D29181 D29567 AW103359 W95238 AI991663 AA587298 BE184608 AA099833 W95121 W95150 D29584 AI934111 D29456 D29533 AW265380 D29290 AW238463 AA121041 D29204 AA595925 D29441 AW081840 AA587018 D29323 AA582891 BE182433 BE182437 BE158295 BE182434 AA904519 AA301105 AA927867 AI026743 AW662787 AA926677 AA883570 AA904797 AA910052 AA812900 AA962351 AW340761 AL138443 BE543896 BE176029 AA346914 AA301300 AA322506 AA302771 AW959785 AF151852 NM_016037 AA362915 AA314256 AF067802 AA317206 AA327697 AV659749 T95453 AA279602 AA352617 D61557 AW380448 BE150572 AW380621 BE617144 AA283599 AW380615 R36819 AA441867 AA143375 BE150496 AW380625 AA092914 AA056934 AA282707 AI589633 AW027187 AI192946 AI435094 AI453732 AA604235 AA564222 D62764 AI090679 AA622593 AI033674 AI740684 AA865759 AI582838 AA040452 AI497924 AA441805 AI678266 AI219466 AI760761 AA040453 AI093005 AI016871 AA700575 AW804199 AI539809 AI240969 AI219468 T89284 T47705 AI453735 AA991787 AI123012 AA860466 N35449 AA748149 D19697 W69417 D29220 AI475673 AA279763 F17344 AA045539 T95352 AA909357 AW518806 AA143326 AW953600 AW380624 AF027208 NM_006017 AW999490 AW995306 W27006 BE000017 AW995305 AI052686 R36499 R32598 AW794374 AA620583 AW389222 AW994698 AA555310 AW028039 BE501788 AI860475 AI638154 AA577606 AI635532 AI952842 AI921537 AI811470 AI273443 AI362100 AA777838 R40057 AI332611 AI308936 AI825560 AW243596 AI380254 AI537752 AI469575 AW614306 AA622198 AI766048 AI962172 AI916863 AI638218 AI652966 D25789 AL043892 AW197532 AA305579 AW407510 AA431698 AL035563 AI623164 AI971434 AA609978 AA609959 AW003303 AI968799 AI269486 AA902281 AA813548 AA974140 AA833611 AI200873 AI806942 AI283593 AI962376 AI025344 AA908942 AA910166 AA431491 BE044325 AW952722 D60947 AF182291 AJ238097 NM_012322 R35468 W80883 BE567078 N84167 W95301 AA453273 AI860953 AI864478 AI208804 AA576040 AA576863 AF743617 AW024498 AI432336 AW268723 BE076669 AI872222 AW131501 AI798857 AI276769 AA492331 AI139461 BE076674 W94785 AW269882 AW024824 AI800809 AA805818 AI208806 AI016898 AI279397 AI424749 AI335782 AA659244 AA027086 AW119133 AA918454 AW188760 AI198149 AI669940 AA723921 AA541384 AW873609 AI337840 AA954080 AA961257 AI080437 AA662797 D19669 AW059685 AI208697 AI330078 AA835397 AI873049 AI678449 W80756 AI523338 AA746877 R34272 AI074912 AF077756 AI280303 T07152 AA248432 AA223837 AA455394 U85990 H25610 H25564 H88461 BE183485 AA456033 AI942278 AI042024 AW123962 H88391 AF077757 AA906427 AI371066 AI332867 AA662061 AA652143 AA649779 BE073130 T31793 AW965487 Z44923 AA461126 Z45595 W05402 AW803834 AA448775 AI680807 M78897 W21100 AA779684 AI990126 AI393307 Z99357 AI375921 AI972840 AA663405 AA308885 AW952286 AW304325 N70540 AA974270 AW136476 H40712 AI126358 AA460824 AA745745 AA448679 AI141365 AW203996 AI140937 AA836514 AA909052 N93713 Z41283 F03886 AI889479 AI761322 Y00978 BE513176 AA082311 AA772815 AA336525 AW498537 AA334879 X13822 AL040276 T29022 N99373 H10159 R19436 AI419467 AA315214 AW950165 N77305 AI335753 W46504 AA906600 AI343654 W46396 AA639499 AW235135 F00720 AI700076 X85590 AW236592 R02205 AA234145 N28789 C03439 AA281656 AA091346 N42953 AA228079 AA455345 AA457421 AA400884 AA281787 M77924 AW970520 AW237732 AA831974 AI376777 AA776989 AA830439 R44685 N23208 AW136894 R02093 AW023062 AI382333 AI569123 AA176281 AL133725 AA309272 AA309312 AW961837 AA766296 AA810118 AA449449 AW977392 AW204852 AW137391 AW134659 AA309368 AU076442 BE148646 NM_000494 M91669 AW379328 U76604 AA418509 AI184334 AA418412 AE680357 AW366480 M63730 AW381501 AI366395 BE615848 AA366091 H87535 AW377762 AA366989 T29336 AA602441 AF136185 BE155683 AA036676 AW374450 W79203 AW579800 C00407 AW606580 AA044571 AA128560 AA033913 N58654 AA568429 AW083397 AA044893 AW384269 AW384280 AW384268 AI373457 AA641352 AA034033 AA128561 AI688441 AI572644 AI373447 H87536 AI637697 AI962306 AA718952 AL041597 AA658228 BE299342 BE304418 BE094076 AA312406 L07648 NM_005962 U32515 D63940 AW138956 BE219807 BE219953 AA179689 AW950924 BE467412 AA976717 AA350689 AW950109 AW205694 AA676607 F07426 AA348542 BE169490 W38808 AW276960 AA114957 T81614 W25067 C04536 H49869 AW896121 AW896127 H66956 AV659619 AW607603 N45031 H51820 H86688 AA342309 AA349245 W32663 BE003894 AA086035 AA313550 AW665174 AA009641 AW241712 N92841 N93226 AI288871 AI139671 AI367648 H51252 N59130 AI612982 AI342867 AI298979 BE218033 H96976 AA136083 AA934552 N33269 N35022 AI224554 H66957 AI571968 AW572122 AI350136 N68536 R37256 AA427603 AA713780 AA115514 H25706 AA524144 AA481653 AA664992 AA988959 AA176635 AI868464 N47454 H66690 AA705886 AI811501 T28858 N74211 R86840 AI373426 AW090202 AA528346 AW518017 AI431635 AI702591 AA885488 AA404377 AI928606 AA741337 AA450066 AI983525 AI376050 F03656 AA757255 AI580855 W32477 AW304753 AI222856 AI973243 AW008458 F02259 AI272357 AI382764 AI382906 AW514226 H25707 T63780 AI087032 AI208051 AW393856 AA640393 AA452708 W01212 BE326532 BE219755 AI807287 BE551377 M85527 R12328 AA314316 AW961209 AW937826 AI142572 AA453333 AW022925 AW022855 C02077 AA483625 W95374 AA315767 AW020679 BE439820 AW973162 AA464846 AA934610 AA536135 W95483 AA496995 AA659920 Z40593 AA598635 D12163 AI625153 AI909935 AA316552
15	421823	207922_1	
20	421916	209042_1	
	421948	2094_50	
25			
30			
35	421966	209677_1	
	421976	209827_1	
40	422054	210795_1	
	422093	21126_1	
45	422163	21247_1	
50	422182	212782_1	
	422183	21279_1	
55	422306	214_1	
60	422321	215208_1	
65	422342	215498_1	
	422352	215575_1	
70	422511	21727_1	
75	422563	217937_1	
	422591	21822_1	
80			
	422654	219392_2	
	422728	220438_1	
	422757	220997_1	



5	422840	22195_1	U44059 NM_003216 U06935 AL035659 AL120537 BE295612 AW836791 AW836776 AW500333 AI014348 BE145955 BE146408
	422897	222788_1	AA679784 Z45173 T10285 T31222 R13042 H12961 R52470 Z45583 T31140 R35946 R53264 R56435 R18993 AW964447 AA318910 T83131
	422899	22279_1	D16471 M85821 M85310
	422977	223410_1	AA631498 AI017191 AA491211 AA761823 AA714555 AA768099 AA808286 AI934069 AA570223 AA574389 AA582438 AI745346 AW964510
10	423010	223862_1	AA319642 AW853758 H56414 W25436 AA486084 AI279018 AA320267 AA828484 AW746199 AI914022 AW887874 AW886272 AW887876 AW886274 AI927954 D45711 AW891131 AW891132
	423017	22395_1	AW178761 NM_006919 S66896 U19556 U19568 AW178766 AW178768 AW178769 AW178767 AW352105 AW352104 AW382741 AA292860 AW366750 AW366692 AA861180 AW366635 AW083861 AI625274 AW802938 AW192466 BE181420 AW383152 AW182777 AW383117 AA398883 AW797283 C06452 AW196155 U19557 U19576 X89015 BE156502 BE156503 AI081890 AW366645 AI686575 AI613307 AW368118 AW051189 AW872674 AW178773 AW178752 AW178772 AW382726 AW796088 AW381318 AW178758
	423025	224038_1	AA831267 R41803 R43649 AA724937 AI023641 R49442 AI096632 AI089202 AW183843 AA523733 AI952670 AI076860 AI042051 AA983353 N24716 AA760964 BE464917 AW964549 AI904962 AI376267 AI033136 AA702514 AL120100 AA320551 AI535679 AI536095 R39319 AW449679 AI379476 R05425
	423035	224126_1	AW967472 AW978919 AI024789 AI538450 AW135089 AI831980 AA648898 AI700833 AA021491 AA836550 AA743661 NM_002595 X66360
15	423045	22422_1	AL049132 AL119276 BE180005 BE180006 R84856 BE542240 T29233 AI949640 NM_005323 M97755 M60094 R96158 AI432318 AW469161 AI452422 AA321245 AW952196 F09493 AA322201 AA323585 AI039344
	423047	22424_1	AW864848 AA322213 AA322209 AW961624
	423065	224484_2	AW897586 Z45221 D53705 D53135 D81470 D81085 AA361574 R12983 R13892 H13376 H20860 AA376208 N28317 AW996765 H91926 BE222833 AA322288 AA326532 AI393791 R71693 H16892
	423119	225168_1	AL049227 D80985 D80603 AI302346 AW470790 AA962550 AI299767 AA938345 C00860 AA195536 AA503000 AA194937 AA856612 AW960473 AW272270 AI760628 AA328233 AI823839 AA769629 AA829221 T69990
20	423121	225175_1	W27595 Z44415 AL120374 H17680 AW299700 BE300188 AW628698 AA325319 AA322769 AI827735 AI027741 AW468728 AI539767 T99474 AA774545 AA809692 H89490 AI096982 AA826272 AI004507 AA918185 AA630039 AI809309 R13498
	423130	225245_1	AI039379 AA324664 AA323622 AW022834 AI267677 AW471227 AI537253 H54934 AW964682 AA323703 H61362 T33182 F13224 Z44564 H05544 T75467 F12150 AA371406 T66346 R26316 BE220282 BE218124 AA095491 AI267340 H12808 R90842 AB020717 AI741382 H05085 AI094578 AI472019 AI579992 R26105 AW152516 AI079363 AA773075 H12764 AW014803 AI253254 T66294 T33181 R39238 F10825 AA593321 F09787 R34588 Z40447 AA664639 D20358 AA491513
	423347	227272_1	AI660412 AW027339 AA324683
	423417	22806_1	AP000365 NM_014406 AA969090 AW014427 AI221641 AA974111 AA367824
35	423454	228361_1	AL110456 AA360875 AA448597 BE075866
	423492	22881_1	AF020761 NM_004777 AW384407 AW996252 AI816048 AW363595 AW996604 AI924924 Z25195 AI816068 AW856207 AI813597 AW513111 H12682 AI800875 AA148102 AI860082 AI341493 AA215839 N84173 AI246338 AI189220 AW296505 AI474628 AW050567 AW363598 AF035960 BE140575 BE140571 BE140573 AI834226 AW752782 BE150628 AW139216 AW752916 AW752909 AW752920 AW752939 BE150800 BE165571 AA352974 AK001408 BE153544 AW815161 AA359048 AW815132 BE150792 AW401732 AA326055 AW753328 BE166933 AW853850 AW367599 H93164 AW083098 AA987538 AW883373 AA775444 AW083065 AI659400 AI911260 AA922769 AI867754 AW275928 AW275942 AW103169 AW271295 AW237818 AI831905 BE002214 AI436689
	423532	229362_1	BE090503 BE090490 BE090483 BE090501 BE090500 BE090365 BE090505 BE090509 BE090499 BE090502 BE090504 BE090497 AA327285
	423554	2295_1	M90516 NM_002056 BE001731 AA382565 AA223635 AL134915 AA085567 AA657488 AA868696 AA330466 AA868697 AA027889 AI014916 AA314909 R51715 AI761822 BE551543 AI962254 BE502374 AA304506 AW589985 AI990211 AI968871 AI963910 H03156 AW665977 AA877271 AW995311 BE566421 C17964 AI921899 AI832941 AI948614 AI971346 AI452662 AI656487 AA219684 AA218627 AW008287 BE327759 BE218160 AW997016 AI002024 AW269487 AI863522 AW262929 AW610101 AI754406 AI393819 AI817682 AI262418 AI222777 AA526727 AI635799 AI199256 AI348034 AI192238 AI277083 AA062587 AI272789 AI304649 AA970642 AI637824 BE618120 AW451029 R61744 AW008004 H03963 BE175953 N92520 AA098918 T28395 AI698369 R51628 AW896529 AW604887 AA027828 AA663174 AI304614 AI269790 AW581986 AA621711 AA063060 C18863 AW962374 R23311 AI803648 AW338280 AI436772 AI696921 AI354737 AW473587 R23236 AA968951 AI969390 AI383075 AA722452 AA327799
40	423575	229728_1	AI633559 AI768171 AW007174 R61893 N22132 AA836779 AA328238 AW952414 AA328329 AW952420 AI590238 R45358 F10954 T16463 AI253133 AL137279 AA908976 AI126295 H02364 AA329065 AW958111 AW961436
	423600	230016_1	BE003054 BE003273 BE440047 L23808 NM_002426 AW996471 AW996697 AW998735 BE005069 BE005207 BE003108 BE003109 AW993099
	423607	230073_1	BE003025 BE003177 U78045 BE003323 AW992178 AW996437 AW996369 N41372 N41366 AW361840 R63637 AI635789 AW999703 AW014205
	423637	23052_1	N30844 AW471033 AW197615 AW470356 AI299124 N30838 AI707582 AW515256 AW170498 AA639771 BE466774 AW172994 AI343504 AW779050 AI523465 AI352562 AW515388 AI348185 AI368844 BE440051 R92994
55	423646	230597_1	AA330036 AW962511 AI700659 BE090840 AI028739 AA639800 AI289771 AA593730
	423673	2308_1	AL044191 H08391 AW861014 AA458675 N48846 R26037 W48596 AW170065 AA330061 AI459066 BE222229 AW961550 AA431105 AW861214 W856995 AW861250 AI816806 AI949835 AI760797 AW236715 AA724392 AW466924 AI421673 AI275614 AI334398 AI769710 AW418862 AI376732 AI127680 AW079670 BE045322 AI632908 BE502784 H43249 AI559661 W48597 N46341 AI278021 AW275150 AA972203 R26835 AI521564 AW135526 AI818309 AW612776 AA432292 AI688332 AI891154 AI915906 AI282118 AW339013 AI955500 R22417 AI371493 AI371495 R22466 R30903
	423717	231331_1	AW891294 AA775966 AI911138 AA905367 AI041551 AW087720 AI015013 AF069512 NM_004858 AF107099
	423720	231349_1	U07701 NM_006310 AW408104 AW160904 AA682926 AJ132583 AW161660 BE267830 BE397119 BE513530 BE267755 AW512435 BE018888 BE251921 BE253168 BE255877 BE256005 BE255386 BE245328 AI904679 AW996579 AW246924 BE207210 BE207218 AA086030 BE275861 T79910 Z46195 AW250513 AA278470 BE408743 W88933 AA306767 AW845107 AA191370 AA356510 N87603 AA053733 AW055008 AW148960 AW672944 AA079607 AW166905 AA076585 AA448981 T35932 T35931 AW241819 AW249850 AA503249 AW963761 W89190 AW615663 AI869693 Z45846 AW075412 AL134687 BE208326 AA026655 AW170785 AW474894 AA043325 AW250785 N26972 AA311941 AA705351 AA962342 AI500627 AI191221 AI129440 AA969976 AA043326 AI686440 AA760940 AI934766 AW515849 AA076586 AI358780 AA654057 AI219289 AW276194 AA053549 AI911617 R39082 AA234379 N42938 AW305272 N42944 R81278 R81001 H02390 AV661605 AA811730 AA811175 AA953827 AI300613 AI350198 AI300615 AA527546 AA281550 W63744 BE467460 AA634383 AA775234 T59688 AI371747 AA716290 BE156288 AA430444 AA479773 AA335436 AA235023 R24894 W92574 D53060 D55858 AA379057 AA043567 AW958347 AA379160 AA495731 AA972560 AI907616 H42433 AW173229 W78070 AA864462 AW068750 AA236597 F35993 AA085988 AA043238 AA583041 AA680041 AW190703 D25741 AW262710 AI417739 H41106 AI500415 H99098 AA194661 AI016872 AW572592 AW183101 AI018254 AA628984 H98949 AA884277 AA887191 AI721203 AI290813 AI086732 AI362992 BE183523 AI377963 R43275 H01206 H88732 N29793 AI469313 N29798 AI093936 AI979157 AI923340 AW662871 AI001942 AA477344 AA551216 D52240 C15614 AI922960 AI139445 AI242109 AA480335 AA281551 W92575 R32450 AI342805 AI273075 H02286 R80799 AA243024 AI218271 D60291 AA719692 AI026850 AI910502 H92317 AA781991 AA235018 AI362571 F04707 AA379056 AI351223 AA913019 AA883761 AA700786 H88733 BE258771 BE278478 AI492841 AA216452 AW518195 AI874115 AW014674 BE269835 AW753967 AA370795 AA331630 AW962550 AA331886 AW962659 AW962655 T89841 AA331906 AA332484
60	423728	23143_1	
	423740	23155_1	
70			
75			
80			

5	423949	233591_1	AI014546 AI190544 AW469634 AI682199
	423969	233798_1	AI830571 AI089583 AI089581 AA333151 BE263812
	424012	23421_1	AW368377 AW379300 AW379322 AW378045 AW378036 W76490 W95575 AA253503 AA456398 AA025569 W72411 AI971226 AI332920 AI130787
10			AI566859 AI377044 AI379687 AI278271 AI127157 AI122593 AI092947 AA868893 W95468 AW043902 AW292021 R87785 AA455929 AA253400
			AA604168 H00545 AA733135 AA025687 AA283461 AF091627 AW382125 AW382186 AW605859 AW368378 AW382679 AW382589
			AW382639 AW382671 AF075433 AF075431 AW368381 AW368384 AW368375 AW379296 AW377887 AW377871 AW378022 AW377931
15			AW377844 AW378016 AW377883 AW377973 AW377860 AW378007 AW378033 R37897 AW377968 H00544 AA331477 AA331426 AW965256
			AW377796 AW377791 AW377946 AW378008 R37821
			AI701852 AA846872 W44584 AW135733 AW135718 H69957 AA976589 BE467582 BE222059
20	424025	234463_1	AB014594 AI653069
	424029	23449_1	NM_002019 X51602 AF063657 AW604538 AA369229 AL042601 AI761753 AA360979 AI091473 T52674 AA203425 AI470381 AI470382 AW058556
	424063	23493_1	AL046476 AL045872 AI002162 BE180461 AA449559 H78852 R86020 AI741860 T66911 AI672269 BE041482 AA406097 AA626337 T29349
25			AA257133 BE174463 AA058828 AW195451 AI763166 AI697503 AI417186 AI860768 AA449301 D51090 AI378355 D51411 R179985 H80097
			AI570188 AA516129 AA256945 AI564429 AA548253 AA772444 AA678204 T66910 N47214 W63700 R63663 T52673 R80086 AA193326
			U050531 AI207676 AI207668 N94861 L44472 N63540 BE178583 AW804123 AI799089
30	424073	23502_1	U03493 NM_005497 AI003367 AI096357 AA027950 AA027964
	424103	23506_1	NM_001918 X66785 M27093 J03208 AA853011 BE281449 AI744652 AI004719 R23046 AL041514 AA386388 T28500 AI806161 N87059 N87974
			AW079831 AW950581 BE175701 BE175668 AA344133 AW965095 R89083 R27465 AI971464
35	424131	235765_1	AA335714 BE466492 AI673329
	424152	23602_1	AL133591 AI908341 AA324370 BE314794 AA723715
	424188	23643_6	AW954552 AF020591 NM_014480 AA325598 BE391569 BE391872 BE264459 AL044289 AF026090 AW993914 AW993908 BE004153 AW084763
40			AW606240 T60903
			U50536 BE219335 AA988098 AI820583 AI670902 BE220021 AI268141 AA825434 AI732885 AI214643 AW878259
			T71397 AW500085 AA336908 AW966205
45	424210	236716_1	NM_003181 AJ001699 AI651456 AI337100 AI797600 AA994493 AI341816 AI524025 AW135369 AI611325 AW197374 AW515803 AI634133
	424235	23708_1	AI792207 AI733499 AW593536 AI001036
			AI631874 BE088604 AI375818 AI131114 AA954443 AI926203 AI951154 AW511993 AA885685 AI360436 AW070185 AI868761 AI274650
50			AW006529 AI659834 AI809140 AA338482 AI078154 AI652269 AI654436 AI686208 AI969975 AI978594 AW960906 AW206122 AI375324 AI799885
			AW241483 AI867194 AW206455 AI025419 AW241426 AI970045 AW087722 D60799 BE301281
			AW975531 AA641889 AI356701 AA338634
55	424308	238014_1	AA338791 AW952780
	424323	238121_1	AK001563 AW888435 AA383371 AV649490 T05389 AA815045 AW590416 AW006474 AW515696 AI671277 AI240723 AI085578 AW512438
	424419	23916_1	AA341442 AI823432 AI740544 AI743336 AA716087
60	424480	239880_1	L02911 R15958 NM_001105 Z22534 AA215852 BE294447 F07050 AA361093 R20505 R21293 BE260991 R20290 H18725 H10813 AA378163
	424539	24061_1	AA378197 BE072725 AA318569 W95660 N89083 T29135 AA298554 AW960274 H75731 H56328 H90808 D56707 AA024668 AI151258 AA136910
			N55119 W67515 AA627196 AI745187 AI797231 AW299624 AI652453 AI631189 AI652431 BE218469 AW237556 AI263425 AI587200 AW118702
65			AI493854 AI139747 AI087081 AI333515 H96907 AA136882 AW264442 AI743929 AI127396 AI934448 BE503067 AI520721 D57752 D58183
			BE243165 AI656271 H93089 R45324 BE221970 H75380 AW242833 AI867206 BE242045 AW166059 D56938 D58664 AA968955 H96913
			AW029054 AI161095 H90756 AI002350 R45384 N66988 F03328 W95661 D56654 N62309 AI623705 Z19442 W68128 AA025278
70	424560	24083_1	AI158727 U79274 T77653 AA452083 AI654842 AA328680 AW958081 AW961390 AW383233 X85574 BE080942 AW383235 AW383228 AW383207
			X85559 AA158728 AI804139 AI798930 AI825255 AA764751 AW196225 AA523887 AI804921 AA973030 R87558 AA287898 AW301996 AI054329
			AW589591 AW271155 AA071543 AI250935 AI288620 AI682447 AI374616 AA081906 AA451900 AI360434 AI092774 AA869127 AA648904
75			AA649004 AA878507 AA319762 AW151470 AW383218
			AW102723 AI468168 H23049 H19241 AI393827 AW117228 H22136 T90233 AW882130 AI675218 AA343245 AW956540
			H10692 R56746 R19095 H94940 AA343627 AW952938 Z42462 T77969
80	424584	241150_1	BE169810 N79901 AI375752 AA345356 AW956680 AA449136 N52855 N62993 AI827433 AI565303 R13780 R23679
	424693	242571_1	AA164366 BE551634 H84384 AA308735 AI752723 AL137759 AI752724 AA999941 AI336913 AW844324 BE245161 AW103820 AW517916
	424698	24264_2	AI797587 AA278959 AA824527 AA927790 AV653167 AW997574 AA382919 AA604704 AI738989 AI374914 AI261206 BE245105 AV646600
85			BE391897 BE391960 AA278485 AI207757
			AF230877 AW819598 AL080153 AA621969 AI366813 AA169400
			AI057094 AW629859 AI891096 AI870691 AA347378 AA876626 AW976988
90	424736	24310_1	AK001432 BE301947 BE171786 AI935292 BE159917 AA416633 AI302849 AW384790 BE045290 AA740370 AI244113 AW795111 AI245059
	424827	244074_1	AA347746 AI821000 T52841 AI925835 AA779437 AI682960 AI469706 AA737692 T52999 AA737689 T52842 T52873 T52998
	424834	24414_1	AA347923 AA347928 AW961769
95	424856	244361_1	AI379461 AI382993 U69127 BE535251 AW062608 AW369616 AW993511 BE169541 N32437 AW403461 AA258489 AA479586 AA292357 C19093
	424872	244505_1	AI417611 BE175449 AA477425 W07367 BE379962 AA093120 R32789 AI084944 AW866116 AI336245 AI761380 AI423423 N81076 H22025
	424882	24462_1	AI367536 AA258570 AA865581 AA772622 AI371499 AI565200 AA659137 AA879034 AI423953
100			M64572 NM_002829 S39392 W88578 AW835496 AW835410 AW845396 AW290915 H68967 AW294865 H40245 BE296046 AA180246 AW8055738
			F07320 T28461 AW950566 F00194 H27932 H28395 AI857765 AI040327 AI074453 W39625 AA804869 AI963765 AA888128 AI264339 AI001902
			AI243621 AI025939 AW571708 AA633158 F00833 AW451127 AA745804 AW591211 AA682684 AW169564 AA931375 AA878622 AA829343
105			AI200280 F31945 AI091104 AA178958 AW301070 W15441 AW450830 F36113 F03573 AI972139 F29738 F37092 H40246 H68936 AA312719
			BE245380 NM_002526 X55740 AA375089 AA337142 F06822 R60402 AA333950 H82585 AA309908 AA384469 F11913 R52584 T78117 T65189
			W45644 H28752 AA331558 AW965258 AL047515 W45664 W44658 AA090423 N40242 N42863 H98118 BE005594 AW072424 N44688 AI588886
110			AA621900 AI984862 R23041 W74576 AI570057 AW662470 W74760 AI634738 AI579947 AA621189 AA911886 AI184750 H98119 AI472021
			AI276702 AW069621 AI755260 AI073668 AI955512 N34456 AI913119 H00389 AW025343 AI912978 AI953566 H28776 T65120 AI566437 AI630949
			N35316 AW614793 R60343 R37850 AI468669 BE088656 W44659 H00328 AA373392 F09560 F01662 F03087 AW383380 AW194605 BE547456
115			U55184 C16033 N46366 AA478853 AW162080 AW450573 AA235429 AL120649 AI082827 BE504287 AW156895 N37055 AI452450 AI827985
			AA973921 AI078763 AA479952 AW263536 AA234773 N30706 L10665 NM_002071 H49600 H41799 H49592 H43011 H41837 H49694 H49683
			H42188 AI277641 H42191 AW960075 D54398 D52975 AI024119 H17636 C00861 R20102 AW138751 AW237500 AI743654 AA642492 AW044105
120			AA876365 BE242003 AI693444 BE218931 AI693433 AA492549 AI687074 AI241026 N20828 H77392 AI582745 AI362752 AI989343 BE169365
			R52708 AA946636 W40411 H77393 AA488909 AI864923 BE169804 AA487362 AW841219 H05313 AI382931 AI623550 R39198 AI625086
			AA728766 AA206921 T15418 F10584 D53449 AL047642 T28449 AA418957 H43008 AW389735 AW389737 AI242468 AA418749 AL134374
125			AA827103
			R38685 AA349659 F10576 R49229
			T77666 AL120974 AW953137 AA349723 W27543
130			H05468 R60139 AI671855 R42911 AW295135 AW295046 AI916957 R53431 BE219414 AI694401 D54194 D54238 T08354 AA897682 AA350118
			AW297137 D81130 C15689 D81152
			NM_013989 Z44085 AF093774 U53506 AC007372 AA508214 AA502876 AL119287 AI681940 AI702973 BE551156 BE466333 AI681219 AA864322
135			AI239761 Z40113 AA018134 AA128286 F07762 AA157029 AI701403 BE178035 AF123661 AW503060 H94524 R21707 T78847 AF007144
			AI126107 AA150404 AA018182 H94437 H09861 Z42476 AI888658 AW903454 BE168315 AW136957 AW205190 AI056876 AI038059 AI032938
			BE045510 AA777254 AW367980 AW367990 AA443225 N44267 AA984252 AA625356 AA384182 AW956767 T99415 T67097 T67093 R62242
140			BE439562 BE180804 AW271438 AI973006 AI743884 AI962292 AI341352 BE466580 AW029226 AW770495 BE549547 AI458655 AI681552 T99521
			AI801101 AI248279 AI697311 R46598 AI248910 AI032418 AI222943 R62138 H44780 AI269118 T67096 AI468645 AI865780 AI866905 H44779



	425075	2464_1	AA506324 AA244003 NM_001099 M97589 X53605 T29524 M24902 X52174 M34840 U07097 AA244034 AA370422 AA371462 AI557152 AA371312 AA559165 AA370116 AA370907 AA370806 AA559352 AA642055 AA508355 AA492280 AA659719 AA527805 AA533057 AA369877 AA224876 AA228288 AI611683 AI417485 AA370186 AA602957 AA564484 AA527737 AA502979 AA507777 AA687674 AI821627 AA420721 AA568138 AA226366 AA613900 AA225411 AI547266 AA550913 AA573645 AA603487 AA603374 AA579543 AA603504 AA531198 AA504027 AA654378 AA524778 AA654286 AA532701 AA304845 AA654793 AA541709 AA536037 AA492388 AA658213 AA613916 AA532485 AA507735 AA658552 AA661553 AI826518 AA503930 AA659546 AW974889 AA653856 AA635363 AA492232 AA595853 AI097515 AI810547 AW970997 AA533398 AA579285 AA614165 AA574271 AA224879 AA602106 AI680583 AA513560 AA635456 AA641194 AA574278 AI359820 AA216360 AA507606 AA533172 AA640672 AA525029 AA225232 AA531057 AA507770 AA524780 AA640508 AA226453 AA228672 AA503139 AA650355 AA622824 AW137215 AA480545 AA569791 AA573630 AA507710 AA661901 AA640749 AA665287 AA569735 AA225383 AA603907 AA225146 AA225386 AA640832 AI928272 AA639911 AI826687 AA640364 AA514799 AA531382 AA657931 AI670092 AA614077 AA225527 AA654031 AA643799 AA978215 AA603863 AA548498 W57824 AA468243 AA603506 AA225469 AA657510 AA469463 AA507690 AA468274 AA572717 AA492165 AA630918 AA602090 AA224845 AA809521 AA579441 AA468201 AA513568 AA230147 AA650340 AA468315 AI621137 AA467755 AA492279 AA467793 AI732062 AA493280 AI685444 AA226678 AA565429 AA574197 AA658851 AA225793 AA533879 AA226541 AA531364 AA226206 AA658390 AA229980 AA527610 AA226698 AI401663 AA502080 AA508392 AA564283 AA468972 AA225786 AA635299 AA229727 AA226365 AA507972 AA507213 AA559173 AA526555 AI810857 AI826536 AI926993 AI971003 AI597835 AA532598 AA225414 AA502179 AA653047 AA658361 AA467937 AA527905 AA228275 AA225135 AA230012 AA507232 AA573601 AA579479 AA492263 AA468504 AA494247 AA652678 AA492335 AA658231 AA569773 AA508004 AA658008 AA613784 W57562 AA469306 AI685773 AA531127 R62424 AW051270 R45542 AI129156 F11022 T65132 AA889113 AA350521 AW162959 AW954627 AW954629 AA351258 R25935 R96366 AL133929 AA351636 H78818 AA477084 Z28957 H80194 H16097 AA351812 AI571332 H67036 H68118 H16622 R17322 AA351959 AL049280 AW152633 AA741089 AA760684 AA812041 AA328087 AW962377 AA252268 AA603497 AI804718 AI768661 AI478789 BE350516 AW236212 AA252353 AA805516 AA806034 AI494462 AA642399 AW761615 AA721744 NM_005824 U32907 AA096222 AA334484 AA247900 AA340865 R57279 R57541 AA374860 H09504 AW368452 H17686 N87278 AA788586 AI468405 AA423870 AA373664 AW149645 BE048016 W76244 AI826284 T40283 AI922105 AI090581 W73007 H17071 AA617709 AI016297 AI051739 AI016427 AI203567 AA723242 AA398411 AA878804 W23747 AW238956 M89470 NM_000278 AI732763 AA581078 AA834107 AI917268 AA425234 AA355635 AA355933 AW962813 AI341498 AI362967 BE090965 BE091125 R15684 AA513812 AB014595 BE549052 AL079783 AW842238 AW842237 AW504517 AA190949 AW007522 AI201705 BE003303 AA227425 X85560 AI815440 AW163047 AW161255 BE001511 U58091 AA307915 AI656644 AW304206 AI949013 AI889832 AI889824 AI970255 AI989484 AI656656 AA581535 AA780712 AI650819 AA112914 AA321976 AA046163 AI825510 AW138099 AI674478 AI657117 Z20333 C01429 AL045646 AV659245 AV659250 AV659519 AV659468 AV659445 AV659562 AV659492 BE549776 AW614070 AI203129 AA045927 AA670272 BE327288 AA600959 AA999824 AA446740 AA372696 AA249425 AA359319 AI039046 AA737448 AA385008 AA350418 AA370874 N44736 W67131 AV654097 N25440 AA432055 AA393189 AA348376 AA301781 AA258986 AI687684 AW305321 AW157078 AA329487 AI816381 AI039047 AA071278 BE221452 AI887295 AW157684 AI963347 W67132 AI889906 AW474599 AW072843 N33028 AW194005 N62127 N33201 AA258165 AW440427 N42088 AA814821 AA047890 AI635036 AA398649 AA649177 AI620856 AI024832 AW241219 AA149125 AA365985 AA149196 AA149195 AA149124 AA902483 AA989057 AI818523 AI927107 AA731012 AI473774 AA370873 AA191762 BE536385 AA350417 AA224552 AI377464 AI436078 AA557547 AI367206 N67210 AL049689 Z99715 Z99715 AI338459 AI803573 AI378673 AA558949 AL023753 AI339502 AI339503 AB007948 H14670 AA084242 T80564 AW965592 T08726 AA976626 AA984639 AI337424 AA588602 AW005050 AA326118 AW962207 AW615661 AW893632 AA431837 AF086038 H91584 H90656 BE327219 AA431435 AW022042 AA828735 AA084243 AW148531 AW071638 AW394117 AI656857 H14580 AI989612 AI631636 T17111 AI968812 R38865 AL119450 AA323669 AW899190 AA984667 AL044819 AA359119 AW963014 D79884 U65652 NM_006382 AW062475 AK000590 BE144244 AI377522 AJ006276 AF080394 NM_004621 AJ271066 AI658667 AK001960 AA633029 AI381238 AW303658 AF086426 W79110 W79774 M73531 M62958 NM_000322 U07149 AL049843 AW449228 AA730457 AA730355 AA318111 W28118 T27927 AA424414 AI289049 AI632717 H95891 C20745 AF115402 AW298576 AI268429 AW612206 AI912678 AA055327 T64537 AI912165 AI279543 AI274977 AW118829 AA417641 AA723422 AI298602 AI150696 AW014929 AI279525 AI284295 AI097525 AA932396 AI266066 AA055924 AA419547 F13287 AF052091 T77387 AW867681 AI827051 R05478 F10886 U44080 NM_002763 BE047570 BE047575 BE088152 H82136 AW978755 BE044288 AI680748 H82137 AI911215 AA832394 AA363946 AA628263 AA628262 AA364002 AI522307 AW005887 AA907101 AI630642 AI630724 N24869 AI475011 D79942 AI784323 AW263388 AA365280 AA365938 AW959986 NM_007159 AF100750 R57162 T18599 AA253131 AI744040 AA406512 AA406472 N21213 N95371 AA912933 AW294944 R27061 AI685054 N27488 AI350565 AF038007 NM_005603 AW449488 AW993526 AW578168 AW993697 BE392855 AF032442 BE143053 AW661893 AA594617 AA877251 AI393019 AI902868 AW629758 AW878490 BE327369 AI004422 AW665078 AW070313 AA369807 AA370501 AW962784 AA370727 AW131888 BE326579 AI457906 AW612080 AW206822 AI199327 AI700770 T15911 AW183067 AA372349 T06587 AA367019 AW583873 M27602 NM_002770 AA363791 AA366588 AA366273 AA367072 AA366377 AW962451 AF009664 AW583921 AA366904 AW583654 AA363829 AW583886 AA363667 C06412 AW583876 AW583293 AA367124 AA367299 AW582950 AA363713 AA366637 AA366063 AA367435 AA367170 BE019915 AA312880 W52559 T11260 AA367300 W74014 W40168 T11271 W56209 AA287071 AW583940 AA366636 AA366280 AA367192 AW583081 AW582903 AW582911 AW583674 AW582960 AW583205 AW583828 AA367195 AW583109 AW583826 AW583902 AW583809 AW582987 AW583611 AW583710 AW583923 AA366235 AW583438 AW316709 AW583935 AW583431 AW583464 AA367131 AA366066 W39288 AW583373 AW583253 AW583227 AA921373 BE045846 AA366605 AA921377 AA921374 AA921371 AA363666 AA921365 AA367045 AW583506 AA921385 AA835570 BE047045 W40281 AW583211 W63611 AW951190 AA363653 W45364 W52733 AA844925 AA921380 AA835562 AA844955 AA835323 AA844935 M22612 NM_002769 T10955 AA295542 AA835325 AA835336 AA363710 AA366863 AA367380 AA366578 AW583699 AA366965 AA367402 AA366864 AW583899 AW583702 AW583632 AW582965 AW583129 AW583169 AA366660 AA363817 AW583806 AW582910 AW583562 AW583766 AA295487 AW583929 AA845158 AW583743 AA366843 AA363815 AA845119 AA835297 AA366564 AA835310 AA845153 AA835292 AA921345 AA845097 AA294877 AA366165 AA845132 AA844855 T18493 AA844947 AA835311 AW583878 AW582893 AW583592 AA845169 AA366759 AW583729 AA844840 AA844825 AA294968 AA295316 AA844741 AW582929 AA295330 AA835235 AA295785 AA366948 AA835227 AA295107 AA295676 AA366686 AA366113 AA835231 AA367122 AA367035 AA844748 AA844888 AA844836 AA367243 AA845095 W40511 AA366325 AA366734 AA367269 AA366527 AA844934 AA366993 AA366846 AA835283 AA844742 AA835390 AA845151 W73107 AW583667 AA366372 AW583605 AA835270 AA835128 AA284528 W52636 AA844807 AA835143 AA367396 W56847 W52956 AA835135 AA294872 AA835251 AA844793 AA844962 AA844862 AA835103 AA835132 AA844906 AA844868 AA835243 AA845090 AA844858 AW583952 AA835090 AW583381 AA844869 AA835280 AA835249 AA835209 AA844827 AA844784 AA844978 AA845029 AA835193 AA835125 AA844923 AA366097 AA835284 AA394198 AA295433 AA366927 AA974854 AA845041 AA835164 AA844988 AA835114
--	--------	--------	--

5		AA366314 AA835172 AA844823 AA367109 AA845005 AA835118 AA845009 AA367078 AA835147 AA844994 AA844996 AA844991 AA835166 AA844738 W52402 AA366718 AW583239 AA835395 AA844920 AW006358 W60521 AA835159 AA295721 AA835088 AA835169 W60195 AA844959 AI570916 AA835303 AA844928 BE049602 W45297 BE045874 AA835301 AA835386 AA295618 AW583258 AW584010 AA366877 C05819 AA293076 AA385995 AA293488 AW583362 AA845054 AA921355 AA845038 C05708 AW583114 AA845130 AA844813 AI820022 AA835204 AA844937 AA844777 D82123 AA835136 AW583524 AA845076 T29250 AW582925 AW583762 AW583580 AW583646 C05916 AA835161 AW583429 AA877248 AW583951 BE045881 BE045905 BE045887 AW583094 AW583480 AA921339 AA921389 AA921379 AA366036 AA921349 AA921401 AA366106 BE047029 C75283 BE045786 AA921381 BE045792 AA844936 AA844933 AW583272 AA845135 C05981 AW583385 AA844932 AW189864 AA845184 AA845138 AA844892 AA845177 AA844954 AA835321 C06039 AA844942 AA835265 AA835263 AA845165 AA835404 AA845115 AA835398 AA845157 AA835149 AA845111 AA845096 AA845068 AA835223 AA845122 AA845100 AW583249 AA845072 AW583775 AA835220 AA835392 BE045858 AA845053 AA844837 AA835216 AA845101 AW583442 AA844824 AA844822 AW583338 AA845086 AA835255 AA835151 AA844983 AA835188 AA844958 W45381 AA835203 AA845037 AA845032 AA844881 AA835112 AA845066 AA835189 AA844964 AA835154 AA835117 T10937 AA835201 AA844905 AA835108 AA835200 AA844921 AA845047 AA835084 AA845043 AA844780 T11034 AA835156 AA365929 AA835332 AA835168 AA835134 AW874329 AA367304 AA835210 W40390 AA835086 AA845092 BE045859 W31860 W52637 C75312 AW583097 W52122 AA835160 AA835182 AA363654 AA363655 AA921343 AA835122 AA844811 W59986 AA835180 AA835322 AA844798 AA844804 AA835288 AA835568 AA835163 W60335 AA369685 AW873932 AA845007 W60434 AA844875 AA835144 AA844909 AA366074 AW964251 AA294912 AA845098 AA835146 AA835402 W45369 AA835195 AA835399 C75360 AA845075 C05968 AA844761 C05745 AA835110 AW873949 AA363814 T29257 C75531 AW873798 AA367049 AW874444 C06438 C75599 AW583418 AW873928 AW873859 AW874347 AW583466 AW874434 AW873947 AW873871 AW874450 AA845087 AA835261 AA844943 AW873856 AA363652 AA366472 AA844915 AA835101 C75501 AA835407 AA844812 AW873857 AW873894 AW873913 AW873925 AW873800 AW874440 AW873933 AA363612 AW873922 C75423 T81095 AW873839 AA835254 AA845028 T11241 AA845179 AW873855 AA835206 T11080 AA844786 AW583978 AA844916 AA835253 AA844802 T11060 AA835240 AA835290 AW873786 T11285 C05874 T11327 AA835102 AA835158 C75374 AA844917 AA844941 AA835165
10		AI631964 AA534522 AW299321 AI051585 AW173307 AI972360 AA829542 AI401808 AA972107 AI082039 AA468840 AI376243 R91498 AI097049 AI672993 AI244391 AI346218 AA554218 AI190534 AA652243 W51962 W48817 AI310055 AW613645 AW613629 AW819086 AA372900 AW963647 AK001104 AW854974 AA987455 AA179323 AI024477 AA377155 AW963992 AW963994 R60843 R34737 AA127262 AI082249 AW772509 AI917738 AI765311 AI569854 AI744759 AI079350 AW469770 T80049 AW015424 AL133095 AA127263 AI094178 AI860770 AI886517 AI886702 W90805 AW994945 AA644603 H96715 W90749 R49610 AA983768 AA677746 AA904877 R38813 AW444725
15		AW242243 AW248399 X75535 NM_002857 Y09048 BE242615 AB018541 AA337880 AW751574 AW751625 AW375025 AW375032 AL040144 AW375035 AW375030 AW375042 R13532 AW375034 AW248280 AW674997 AA352592 AA346944 AA001116 AW375022 AW375026 AW375037 AW375040 AW375021 AW375020 AW375024 AW751626 AW375023 AW374974 AA912723 AI910515 AA135069 AA380174 AW732488 BE179715 R93633 AL079766 BE001073 BE001074 AA355408 AA045972 W02563 AA100823 R73716 AI914243 BE179971 R34184 BE151814 BE149447 BE151826 R28991 W24416 AA639888 AA011267 AI479901 AW510942 AW245060 AW628674 AA218649 AA100759 W56458 AI160103 R20653 AA633593 AW149802 AA134906 AI760805 AW592736 AA484863 W56355 AI870819 AI022759 AI361132 AW130780 AI190183 AI589085 AA976276 AA758828 AA045838 F29271 W19841 AI273045 AI700772 AW182221 AI200142 AW580396 AI139887 W00340 AW135091 AW118811 AI139885 AI381546 AW080250 F27983 F25148 N73597 AI191313 AW674418 F35539 AA767806 AA011348 AA679601 AI057395 N95284 AA761914 N46575 AA808395 AI185227 AI131399 AA813677 AA977836 AA410801 AA291891 AA713798 AA292947 AI364144 R34305 BE242328 AI200412 T28723 AA713794 AA927703 AA293637 AA292954 AA661861 AI247669 AW842548 W78829 H70176 AW207382 AW205160 W78915 AA001346 W94992 N99446 AW205247 AA001117 AA152063 W44405 AA906747 AI129977 BE7623 AW207257 AA936477 AA230754 AW338609 N40527 AA620993 N54933 AI334003 AA707581 AA001977 AA789213 AA136162 BE350870 AI432421 AI079335 W44541 W94265 AI144419 AA149970 AI350742 AA169621 AI151126 AI127924 W93377 N71574 AA699907 AA136093 N72091 BE535802 AA663182 AI300910 AI802444 AI285068 AI264386 AI208555 AA830732 AI092354 AI090538 AI277494 AI208688 AI333525 AI823323 R93634 AI522090 AI566033 W80728 AI686091 AI188300 AW375031 BE548382 AA936559 AI634539
20		H15302 R20857 Z44841 T34574 AW380909 AL110252 AA333910 AA316370 H92417 BE075192 N48838 N48854 N46225 N46261 N46350 W93708 Z44965 W93776 N46262 N46226 H15696 N76156 BE552062 R42037 AI339369 AI640234 BE552078 AI654708 R60383 AW190038 AI631500AA631870 H92634 AW137562 N46332 Z40623 AI954697 AW022912 N46815 BE349303 AA993206 AA855008 R60325 AA993190 AW016619 R43375 AI474423 N40957 AI555223 Z40710 AI952019 R22671
25	426235	263113_1
	426237	26313_1
	426261	26350_1
30		AA376667 AW956336 T82365 AW840423 M62126
35		AV655843 N71738 AA307059 F07897 H12173 W19969 AA211619 AA357440 AA313638 AW951700 BE258542 R57598 NM_000126 J04058 BE385597 AA100779 F00046 W78946 BE208282 AV657205 AW603706 F01049 H48604 W39100 W33008 W19485 AW404656 N53901 AI940453 AA091670 AA626774 AI679128 R21171 AI870537 AA732234 AW337922 W01635 AI192719 AW514430 AW337167 AI918127 T58002 AI129937 W76231 AA677290 AA534875 AA614072 W52522 AA211564 AA284605 AI817260 AA907237 AI927619 AI138708 AI138709 W47093 AI245875 BE301390 AA872403 R62195 AI679702 AA902546 AA844408 AA915960 AA917408 AA854901 AI003111 AA703572 AA835744 BE502117 AI148359 AA628846 AA508748 AI291555 AA694151 AI141494 AI311649 AA936709 AI193194 AA134106 AA745922 N70736 AI336177 N25315 AI282104 W72994 BE549146 AI360025 W47131 AI282788 AI056779 C18052 W35395 W15262 AA705725 AA508699 AA682383 AA995280 H48797 AW193194 AI950546 N89438 AW780091 AA765045 R22789 F00520 AI364921 AA777409 N51606 T29313 AW951265 AW589605 BE535447 AA058542 W85863 AA557337 AA773020 T46838 AA974298 AA677957 AI525280 AV658235 AA321586 W25372 R19580 T57919 AI373807 AW511722 AA100780 BE566039
40		AA580748 AA379040 AI005488
45	426269	26359_1
	426365	265764_1
	426447	26729_1
50		AA379913 AA379981 AW963523
	426536	268856_1
	426589	269685_1
	426603	269825_1
	426646	270259_1
	426662	270415_1
	426682	2705_1
55		AV660038 BE569193 AI916245 AI307269 AI765716 AI831562 BE379923 AI480360 BE293867 AW970306 AI635995 AW051715 AI767470 AW082933 AI761074 AW151709 AW300312 AI936384 AI634349 AI925914 AW469219 AI948948 AA085987 AI253019 AA586566 AI566081 AI282087 AI244891 AI580503 AW473818 AI953220 AW589228 AI949842 Z19987 AI439491 AA126225 BE463427 T29671 T70999 AI768418 AI934932 AI767228 AI803745 AI948942 BE464422 AI334971 AW300303 AI309209 AI479279 AI760341 AA534685 AI927039 T61064 AI478649 AI795931 AI244386 AI924727 AW300622 T61370 AA932983 AW271724 BE464060 AI796108 AI984823 AW235682 AI913741 T69624 BE464186 BE464379 AI767337 AI985133 AI628755 BE221997 AI590308 AI287371 AI700816 AI632797 AI493104 AW028986 AI913618 AI985249 AI244717 AI768541 AW614437 AI364965 AI262996 BE463503 AI650792 T61166 T69701 BE293771 AW951426 S55985 AF056188 AV652040 AV646537 AV646429 BE305055 BE293701 BE249897 BE249993 U89508 AW848583 AW848987 AW848498 AW578365 AW578364 AF030310 U89507 AA394104 AA398133 AW958766 AI024944 AA725855 BE551679 AI638423 AA992611
60		AI968103 BE045996 AI808851 AA383370 AI016809
	426698	270753_4
	426701	270786_1
	426724	271003_1
	426803	27215_1
65		AA383623 AW292978 AW291044 BE545693 AI816007 AA903140 W68447 N91863 AW467509 W23925 BE350989 W23914
	426917	27349_1
70		AA362568 AW339596 AF008915 AI078143 T65001 AA478512 AI91075 AI694123 AA730225 BE348582 AA507635 AA573246 AA478513 AA693846 AA628572 AW297422 AA262153 AA621415 H91310 AA641101 AI636082 AW001051 AA772947 F05127 H29381 F05844 Z42583 W47260 AI690224 AA344272 AW952960 AA334033 AA333986 H29292 AA640754 AA446058 AA609950 AA609062 N45010 AI887934 AI862428 AI635805 AI291247 AI375721 N41000 AI399790 AW440792 W47387 AA725529 AA730465 AI872801 Z38177 C02379 AI864789 BE568810 AA337006
75		AA913814 AA776812 BE246828 AA158341 AI815669 AB033105 AW732458 AI751022 AW296869 AI887822 AI681148 BE466501 D60085 AW291629 AA385200 BE179775 F12694 AA449872 T74711 N87473 AA090524 R56590 AA384909 AA309057 R66201 AL050190 AA044719 AA324124 AI751023 AA897613 AW275221 AW275245 AA912428 N98306 T89975 T92205 R48856 AW967978 AA262807 AA947477 AI904465
80		

5

426920 273511\_1  
426942 273690\_1  
426985 274097\_1  
427027 27453\_1

10

15

427046 274652\_1  
427050 274718\_1  
427088 274994\_1  
427099 27506\_1

20

427119 275184\_1  
427131 275252\_1  
427134 275289\_1  
427167 275656\_1

25

427173 275681\_1  
427244 276501\_1  
427335 27737\_1

30

427342 27748\_1  
427374 277836\_1  
427443 278861\_1  
427469 279155\_1  
427521 279897\_1

35

427533 27996\_1

40

427535 2799\_1

45

427687 281995\_1  
427731 282695\_1  
427794 283352\_1  
427836 283841\_1  
427839 283856\_1  
427888 284237\_1  
427894 284255\_1  
427961 284969\_1  
427962 284976\_1  
428002 285602\_1  
428004 285631\_1

50

55

428017 285783\_1  
428042 286292\_1  
428052 286428\_1  
428062 286582\_1  
428085 286824\_1

60

428102 287058\_2  
428137 287455\_1  
428152 287660\_1  
428170 287873\_1  
428192 288021\_1  
428201 288120\_1  
428208 288156\_1  
428231 28832\_1

70

428268 288865\_1  
428277 289113\_1  
428299 289473\_1

75

428333 289916\_1  
428336 28992\_1

80

R54751 AA578324 AI022469 AW192959 BE077500 AW384969 R67079 AW373616 AI879972 AI744516 BE217927 AA631111 AI491993 BE504395  
AI796679 BE207852 AI590655 H95752 AW015016 AI391746 H19627 AI146355 AW384972 R56591 AI375200 AA877518 N66235 H18891  
AA158342 AI800746 H46708 H20977 D60084 AI306690 AI799371 AA862713 AI424153 H19644 AA449827 AA989523 H06409 AA670043 AL047964  
AA173449 AW078615 AW129247 AI368492 AW517911 F10303 AA890599 AA887891 R54940 AW338884 D60315 AA262729 AW518818 H56540  
R48857 AA173315 N55424 R43488  
AA393351 AI149963 AI041262 AA398685  
AA393551 AA400795 AA812825  
BE394849 AA393984 AW135409 AA398022 AI041252 AI971262 AW090197 AA927047  
AI924294 AF217510 AI912740 Z38896 AF161405 AI815973 AK000891 Z42295 W52707 T32795 D56169 AA167526 AA187778 AW406483  
BE001138 BE047647 AA463589 AA167536 BE537171 AW268373 AW237391 AI653184 AW301135 AI628730 AW299610 AW271455 AI015533  
AA182787 AI418986 AA806889 AW299620 AI459392 AW206032 AI394086 AW615301 AA962104 AI675468 AI696192 AI675246 AI863705  
AI654880 AA678306 AI758145 AI375457 Z42743 AA625410 H82592 H04176 AA035317 N50273 AA043669 BE218084 AI816056 BE220413  
BE465619 AW342105 AW469785 AA043798 AW118078 AA983939 H04177 AI301830 AW662864 N49223 AA993060 AI038412 AA4788674  
AA897377 T32794 T23569 AI565359 AA887703 AI804432 AW449283 D62756 Z38526 H18187  
BE246180 BE244095 AI688816  
AA397789 AI969332 BE466646 AI825226 AW236471 AA399536  
AA398085 AA954546 AA634531  
AB032953 AW269265 AL137500 BE142323 AW875427 AW875419 AW178509 AW178510 AW875579 AW875580 R95485 AA446367 Z45705  
AA334973 AW139310 C04250 C03609 C05620 C05198 AI492934 T07457 AI859144 AW069752 H19880 AW615139 BE184375 D29453 AW419319  
M78386 AI692521 N71920  
AW880562 N93524 AA928778 AA398288 AA657797 T86243 N46929 AA657405 AA401804 W21329 AW474123  
AA448460 BE501072 BE501065 AA398369 AA868975  
AA398409 AI473896 AA403060  
AI239607 AI765384 AA398819 AA476677 AA449292 AI369488 AI028202 AI052530 AA449236 BE349224 AA843870 AA514936 AA863345  
AA887296 AI339959 AA923696 AA887321 AA873214 AI868408  
BE255017 AI073669 AA398846 AI183963 AA435891 AW206823 AA401482 AI499651  
AA402400 AA399995 AA401410 AA412033  
AA448542 NM\_001474 U19145 NM\_001476 U19147 NM\_001472 U19143 AF058988 U19146 NM\_001475 AF055473 NM\_012196 NM\_001477  
AF055474 AA447559 AW510753 AA913206 AA760996 AA738037 AF055475 AI187350 AI381509 AA868226 AW016546 AW102587 X93834  
AA738394 AI968311 U19144 NM\_001473  
AL110150 N48853 N46343 N46349 N48848  
AI150033 AA401494  
AA402713 AI821640 AI821639 AA402719  
AA403084 AI223084 AA411815  
AW973352 AI264125 AI798842 AW243450 AW016853 AI627517 AI651829 BE551767 AA558414 AI339359 N79575 AA406213 AI961162 AW117516  
AI206165 AI206248 AA548736 AI431857 AA768578 AW470154 AI539081 AI341422 AA736837 AA480892  
R36022 AF035310 U79246 T77495 AI743849 AW512351 AA007252 Z40475 AA970178 AA258689 AW043622 AA523453 AI566661 R02226  
AA694030 AI242310 AA213647 N48672 R39538 R49104 R38380 R16162 AA258547 AI940035 AI940038 AA489007 AA634354 D20392 AA494547  
AA534938 AA515483 AW972169 AA598726 AI081996 AI698868 R01190 AI934961 R15422  
R29543 H54668 T87356 NM\_002704 M54995 W02354 R64229 H94245 W93309 R92891 W67392 AW752219 T80607 R64130 AW449305 H56950  
T97260 T78867 R94831 AA884049 W92812 AI800574 AA952921 AI581312 W67149 H93019 N72706 AI128304 H82783 R62614 T97371 R62664  
AI183906  
AW003867 AA613545 AI926322 AA410933 AW085500 AW452821 AW044630 AI203543 AI742102 AA582697  
AA411750 R20483 Z44336 F11384 F05532 R11898 H16024  
AA709186 R44257 R43746 AI557431 AI797627 BE550594 AA412471 N75500 AA431825 AW295288  
AA416642 AA993387 AI028360 AA626846 AI126202 AI004481  
AA608823 AA759070 AI184735 AA416662 AA421127  
AA417088 AI139899 AI149861 AA454032 AA453615 AA954533 BE046928  
AL135709  
AW293165 AW207243 AI130807 AI589287 AI049743 R41294 AA418039 Z41811  
AA946582 AA418047 AA418218 AA446780  
AA418703 AA418711 BE071915 BE071920 BE071912  
AA449563 AW003675 AI635120 AI663907 AI367057 AI014626 AI971137 AI494447 AI609297 AI281376 AI373054 AI251932 AI742954 AI740967  
AI801501 AW300541 N74050 AA418734 AI373041 AA745033 AI566948 AW300457 AA449306 AW778854 AW304276 N47894 AI093285 AA915893  
AW016881 AW628125 AW025177 AA781262 N45129 AA992189 N47969 AI991544 AI720284 AI804958 AW273690 AI468602  
AA424983 AA418895 AI800304 AW264269 AA460211 AW028491 AA418896 AI917673 AW874501  
AA419529 H97089 H96977  
AA420477 Z38326 F01558 AA420476  
AA420683 AI990874 AI631711 AI095506 AI658624 AA689489 AA456082 AI223791 AI273705 AI796127 AI082100 AI093661 AA420823 AA455585  
AA421081 N99403 AA460513 AW771586 AA781188 BE326945 AA860910 H08088 AA781845 AI027285 N73782 AI627805 AI208471 R41444  
AA889700 R38703 F03385 AI830535 AI474644 AA459870 AI023552  
AA968441 AA904603 AA812449 AI688708  
AA421792 AW510957 AI494059 AI146683  
AA422030 AA625195 AA625411  
H05530 F09743 F08956 Z38234 AA423893 BE501880 T72537  
AA424051 AW104616  
AA424158 BE220054 AI761331 AA451734  
AA442327 AI188208 AI123441 AA770175 AA909271 AI027637 AI150580 AW631178 AI150190 AF012356  
U17989 AA358216 BE006441 R41548 AA836616 AW134626 AW248733 AA808621 AI470372 AA418821 AW001731 H47460 H47370 AA308075  
AW960386 AA663103 AA287463 AA069721 AI015766 AI081274 AI685493 AA418918 AW243088 AW104574 AW070834 AA572712 AA358215 5125  
AI696581 AA579156 BE167392 BE082928 BE080590 AW503404 AW859520 AA069680 AA484215  
AA424957 AW979182 AI742773 AI858807 AA834743 AA873670 AA424958 H40147  
AA425220 AI015260 AI628081 AI628091  
AL038004 H88576 AL038006 AA600152 AA872191 H16238 AA425604 BE466068 AI637829 H88531 AW977930 AI129178 R74354 AI654876  
R74452 6237 D31489  
AW972668 AW138062 AA426120 AA526531 AA725013 AI243610  
AA503115 AA639312 AA551737 AI820972 AA225025 AI820915 AA225308 AA508636 AA225322 AA244074 AI298524 AA225213 AA530974  
AA533053 M34376 AA759159 AA530882 AA574208 AA657541 AA507968 AA225206 AA535744 AA603362 AA244091 AA603877 AA177023  
AA524914 AA574209 AA508348 AA574212 AA229223 AA503909 AA504066 AA493332 AA653754 AA493445 AA508144 AA502154 AA532472  
AA502981 AA507217 AA469209 AA508096 AA650283 AA469373 AA508078 AA653855 AA226101 AA531498 AA658873 AA578900 AA469154  
AA654920 AA630927 AA507769 AA552827 AA530906 AA502180 AA527825 AA654197 AA524675 AA657531 AA635394 AA572857 AA659592  
U78976 AA507789 AW971043 AA420632 AA226680 AA470548 AA492327 AA658414 AA420826 AA469201 AA507215 AA578799 AA532710  
AI380796 AA507281 AA568108 AA579008 AA229964 AA244052 AA508128 S67815 AA504051 AA229756 AI014614 AA507685 AA493268

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

AA506197 AA226227 AA533961 AA492334 AA225409 AA650220 AA420633 AA216404 AA569556 AA494243 AA492312 AA662125 AA603879  
AA502978 AA492295 AA177153 AA528273 AA532578 AA654869 AA492389 AA578701 AI806839 AA657479 AA244289 AA640929 AA532712  
AA225880 AA507664 AA503609 AA557804 AA507659 AA654847 AA557784 AA492411 AA507545 AA568415 AA526491 AA687632 AA595627  
M15885 AA507510 AA579351 AA588270 AA492445 AA516492 AA635332 AA579004 AA492329 AA371241 AA502973 AA640342 AA643813  
AA506330 AA506731 AA492382 AA532960 AA659778 AA541611 AA551842 AJ133356 AI299122 AA369995 T29527 AA507983 AA370902  
AA642080 AA371211 AA225143 AI936199 AA507093 AA652184 AA513240 AA225228 AA507128 AI936190 AA492168 AA650261 AI420347  
AA662090 AA650177 AI659278 AA469131 AA657686 AA531381 AI658598 AA551698 AA507669 AA507679 AA662301 AA176984 AA652201  
AA531361 AI674197 AA469293 AA531341 AI814096 AA541768 AA244178 AA507759 AA532912 AA603827 AA661727 AA574273 AI380716  
AA652486 AA603437 AA642520 AA636004 AA530954 AA469226 AA640904 AA657938 AI826292 AA530942 AA541576 AA244017 AA809523  
AA687536 AA531208 AA502071 AA635542 AI829244 AA507995 AA397457 AA570614 AA588630 AA809593 AA225974 AA177029 AA5053429  
AA226556 AA593049 AA420631 AA494246 AI865520 AA650255 AI674405 AA492163 AA492451 AA715325 AA535497 AA506319 AI424343  
AA226240 AA225152 AA507778 AA558634 AA603351 AA226459 AA502191 AA516500 AI420846 AA533162 AA225963 AA506475 AA592985  
AA507996 AA503682 AA662784 AA527728 AA558248 AA470501 AA587824 AA492204 AA640298 AA507633 AA508360 AA639995 AA514915  
AA230005 AA225109 AA507785 AA565164 AA494242 AA502078 AA229482 AI668890 AA635549 AA507230 AA506914 AA526493 AA593065  
AA507287 AA226010 AA226623 AA551727 AA548220 AA492255 AA503677 AA503349 AA492438 AA508013 AA225879 AA522599 AA503688  
AA650213 AA492311 AA502074 AA514804 AA594830 AA503926 AI970015 AA507373 AA657800 AA551825 AA224959 AA657658 AA654956  
AA635909 AA508112 AA552829 AI804931 AI659409 AA533031 AA503340 AA533211 AA507652 AA532567 AA507305 AA550791 AW951397  
AI668283 AI783781 AA535922 AA492207 AA554999 AA654952 AA226384 AA525091 AA654614 AA420697 AA244480 AA530391 AA530939  
AA244432 AA507369 AA635264 AA503689 AA502200 AA657393 AA580026 AA228949 AA244452 AA654876 AA657456 AA654521 AA659224  
AA226632 AA506804 AA229222 AA551463 AA503666 AA507615 AI380700 AI391507 AI818002 AA534135 AA548400 AA588853 AA594923  
AA564966 AA541642 AI972507 AI669303 AI420876 AI972995 AI658868 AA570183 AA533045 AA657506 AA654201 AA807843 AA508900  
AW973122  
AW873520 AA426345 AI982792 AI223334 AI352566 AW590382 AW510979 AA435875  
AL046991 AI080419 AA429307 T54829 T58175 AA426458  
AI249368 AI742316 AA428062 AA442089 AI864189 BE349478 AI803475 AI584049 BE552085 AI088609 AI264197 AI886144 AI129474 AI307145  
BE181300 AW058403 AI696838 AW748598 AA442196 AI216428  
AW291464 AW014826 AI581001 AI129720 H15097 AI936319 AA428239 AI624119 AI696190 T58065 AI273557 AW105084 AA977710 AI803738  
AA905144 AI375633 AI216363  
AW363590 AW449208 AW577643 D45555 AI924632 AW167610 AW167650 BE073612 AW384404 AW381927 AW384405 BE073529 AW996310  
BE073528 BE061388 BE061400 BE061395 BE061393 AW176329 AW176325 BE061398 AW176323 BE061399 BE061381 BE061376  
BE061386 BE061382 BE061377 BE061385 BE061383 AI909965 BE061394 BE061402 AI909964 BE061396 AW176327  
AI902398 AI936329 AI563922 AW418963 AI816876 R92171 BE463420 BE504887 AI767806 AI476219 AI628562 AW139845 BE220214 AI631026  
AW299996 AW301647 AI580507 AI675080 AI216455 AI824917 AA926706  
AI004034 AI222128 AA4429885  
AF157326 AI034263 AA846643 BE019018 AW503583 AB020636 AW505012 AW500057 AW503098 AW367000 BE142887 AW847702  
AW847704 AW604144 AW604159 AW604156 AW604148 BE142870 AW503445 AW500130 AA504941 AW993157 AA948067 AW499499 AW501244  
AA774790 AA179457 BE281406 AW847896 BE540668 AW847823 AW847822 AW847691 AW847872 AW847822 AW847822 AW847822 AW847822  
AK001791 BE081567 AW751564 BE538744 AA135935 W53038 AA505786 T68025 AW401643 AW577480 BE539649 N47219 AA127605 BE619491  
AW367689 AW367659 BE148064 AW851296 AW390271 AW801921 AK000976 AL133560 BE548753 R22838 H19003 AW080261 AI683350  
AI690844 AA490747 AI638817 AI963937 AW003342 AA070388 BE550518 AI299947 AI355003 BE537306 AW264359 AA923370 AW513655  
AW385429 AW385428 AW385423 AA092197 AI827494 AW589828 AW593387 AW117969 AI570870 AW020724 AI188999 AI907362 W92140  
AI372056 AI184771 AI803505 N47220 AA812088 AI339216 AI675857 AA836773 AI493577 AI990217 AA761758 AA057121 AA070501 AW003152  
AW590316 AA825894 AI907376 AA613786 AW439957 BE502430 AA687281 AW137950 AI825181 AI687479 AI638673 AW605375 AA514379  
D29124 AA491234 AW235429 W92280 AI696234 AI128318 AA834905 R51841 R49406 AW967460 AI907419 AI907415 AA452989 AA441844  
AA234482 AI376628 AI784498 AI318095 H19300 AI285846 H16182 AI049879 AW305346 AA339535 AA353422 T12498 AW952806 AA765341  
BE091131 AW204964 AI246166 AI985298 AA837147 AW675511 AW058094 R46045 AI633773 AI632566 N48777 AW272158 AA472263 H14904  
AA744806 AW709152 AI740927 H01766 R63424 AA179314 AA236485 AA708948 AA761434 AI862736 AI470182 BE170684 AA976015 AW058602  
AA830942 AA441789 AA806410 AA766567 AI696090 AI636141 H01020 AA101076 AA483384 R63373 AW450175 AI990817 BE551173 AA482750  
T67874 BE391639 BE540593 AW672834 T85725 R31617  
BE002993 AW501988 NM\_014504 AJ250042 BE002622 AW403300 AK001702 Z46131 AI678330 W44319 AA970430 AI016058 AA448353  
AW612450 AI917356 AI690197 AW029161 AW867923 H86510 AI370782 R55242 AW183458 BE548663 AA361375 AA485806 AA427680 AA419577  
AW392574 AW392579 N45664 N42532 AA400961 AI734030 H18719 AA300689 T85495 AW801575 F11331 R17285 AA059488 AA040566  
AI742550 AA077990 N29884 W95774 AA703087 AI821642 AA769015 T85285 AI418440 W45691 AI288358 AI820077 AW572466 AI078450  
AW663070 T79773 AA448209 AI023026 N48907 AI538401 AW085098 AA461356 AA670378 AA468867 AI014815 AW242379 AA993231 AW970839  
R55243 AA678490 C00809 AA452608 Z20696 AI672378 AI742790 AW468433 AI017465 AA400892 AI017520 AW196783 AI161194 H18636  
BE181035 AI471735 AA427535 AA045498 AA580194 AA461180 AA760896 AI218525 W95732 AA574148 AI017612 AI061350 N62605 T03907  
AI420730 F08991 AI300254 AI933906 AI188515 H77349 AA001163 AA019463 AA017731 AA018536 N78374 N49066  
AF052728 AI760876 AI885207 R07383 BE551346 AI630201 AA203512 AA427666 AI494574 AI051655 BE218498 AA812211 R55358 AA994176  
AI597635 AI365412 AI813479 AI659760 AA625744 H17088 AA151410 AI220422 AI806794 R07336 AA386088 AI928596 AA151411 AW138328  
AI560480 AA427490 AA340285  
AI372822 AL110238 AW957403 AA371247 AW149757 AI372823 AA443853 AA737194 AA191100 AA088297 AW023187 AI334033 BE086903  
D62684 AA911105 W84787 AI814960 AI47029 C00522 AI699395 AA701517 N84403 AW612846 AI050780 BE087653 AI383715 AW085184  
AW193486 AW087618 H19251 AA349191 R82818 AA598711 AA426063 AA928080 AA910710 AI470319 AI582687 AI581662 AA370801 H18482  
N22730  
BE268717 AA432045 BE295472  
W21550 AA434169 H24366 R59619 AA609711 N95202 AW081118 AI093821 N36797 AI675167 AI885657 N26628 AI436122 N20490 AI937638  
R39205 F01462 AI370207 AW865669  
AA477989 AI821633 AA434242 AA477550  
W28418 BE241648 AA127801 AW820534 AF076531 NM\_005472 AW194853 AA515221 AA132718 AI221445 W26126  
AA578229 AA436432 AA481375 AA481363  
NM\_000346 Z46629 S74506 AI348085 AW381053 AA090808 AA334252 N85428 AI382146 AW379683 C15879 AW897800 BE003539 AW360802  
AW360836 AA657762 AA333065 AA884178 AW888412 AI934455 AW005563 AA527295 AI299871 AA576678 AI870355 AA913619 AI380233  
AI681309 AA331097 AW087477 AA912521 W24710 AA778589 AW994011 AI453423 H90100 AA469143 AW075227 AW994272 AA420456  
AI985948 AA400739 AA469215 W95308 BE348559 H90010 AA322324 AW003292 AA400464 W94793 AW020030 W07405 AI467955 AI380934  
AA385905 BE004865 AI076205 AA975310 BE089397 AI498936 BE004863 AI670844 AI700913 Z33575 AA778708 W46414 AA628091 AI676052  
AW080366 AI970798 AI744134 AW374875 AW130000 AW303312 T24741 AW005638 AI379929 AW183687 AW276611 AW151188 AA535677  
AW072243 AI364948 N80276 AI538944 AW235096 AW193094 AI810275 AI281304 AI270170 AA884334 AI968800 AI572187 AI014655 AI934198  
AW629195 AA983635 AA375477 AW951463 AA770266 H89609 H88219 AA622877 H88220 H89373 N92393  
AA437124 AA437101 AA640696  
AW303529 AA437243 AI806912 AI218642 AA442308  
AW103117 AA437267 AA442344  
AA780181 AA442074 AI200043 AI339855 AW901823 AW901821 AW901830

5	428976	29792_1	AL037824 AL037822 AL037802 NM_004675 U96750 R35089 H09686 BE168318 AW296231 W76278 AA627313 AL138214 W72033 AI681554 AI380093 AI422262 BE468055 AI095129 AI148762 AI423639 BE549545 AI692753 AI215023 T17198 AL037823 AA878446
	429014	298367_1	AI800518 N72229 AI474268 AA443214
	429063	298229_1	AW363845 AW364447 AW368600 AW385513 AW372878 AW385503 AW835728 AW385511 AW363846 AW835575 AW835574 AW819737 AW819745 AW819733 AW835570 AW835666 BE160360 BE160278 AW835569 AW835747 BE160268 BE160350 AI820838 AI216577 AI820837 AI215924 AW364436 AW051605 AA444394 AW027812 AI745274 AW628512 AI352138 AA564378 BE047228 AA639775 AI792675 AI792674 AI468185 AA780090 AI371193 AI910398 AA446228 AA446229 AI822019 AA917621 L29301 NM_000914 L25119 AL132774 AA806287 AI566837 W86772 AA447568 AI057384 AA778241 AW978260 AI369472 AA448161 AW770245 T17370 Z41436 H73347 AI700251 AF056085 AF069755 AF095784 NM_005458 AJ012188 AF099033 AF074483 H14151 AI214087 T07621 AW897153 AW897155 AA324303 Z43654 AI968032 AI341249 AB015334 AI937563 AI500214 AI000006 Z39716 AA323988 AW960960 D81914 AA325383 AL134169 AW953321 AA351058 T75187 AA062586 R14988 AI074442 AA453101 BE219144 AW896767 AA775405 AI417329 R45679 AA063059 AA707764 AA011645 AA452928 AA351057 F10549 AL037762 R38632 AW960962 AL137977 D86984 AA247631 AA226442 AA907782 AA904282 AA393777 AA397614 AA435733 AI826537 R15065 AI720465 AI627768 AW023821 AW272914 AW469553 Z38792 F10748 T32564 T32942 Z42622 F13145 F08294 AW953104 R23437 AW390469 AW854036 AA249094 AW150568 AW022123 R41498 AI056064 AI475900 N79669 AI381028 AI381651 AA993515 AA452560 AW021769 BE161832 AA453224 AA485772 AA453488 AA453489 AW117434 AW197086 AA453623 AA766126 AA454041 X99133 X83006 W38398 AA401137 AA298242 AA366738 AA308126 AW583781 AA298668 AW845024 BE140204 AW845005 U47734 AA837575 NM_005564 AA329732 AA421943 BE171567 S75256 AI750047 AI762213 AA100735 AW612993 AI474120 AW062884 AI940001 AW062852 AW062899 BE182639 AW778875 AA528093 AW517424 AI939989 AA076188 BE182636 AA169569 AA167439 AI283967 AA167783 AA076140 AI749649 AA166792 AI708618 AA400973 AA514773 AA514789 AA164458 AA167440 AA074845 AA421944 AA514874 AA079557 AA102361 AA587027 AA642930 AA878029 AA164459 AW176400 AW475086 AA857522 AA148193 AA838234 AA593897 AI284506 AW193324 AA148194 AW583341 AI669077 AW264913 AA074902 AI680515 AA169874 AA169614 AA079651 AW591737 AW190644 AA076565 AA662747 AA075896 AA535642 N27757 AI306666 AA074727 N79823 AA524360 AI826800 AA173827 BE140374 BE004062 AW265060 BE184103 AI199258 AA857853 AA299459 AA837890 AI626104 AA503624 BE183618 BE183717 AA573267 AI833071 AW270590 AA506601 BE004010 AA837854 AI675895 AI810491 AI184883 AW664712 AA076046 AA515574 AW352267 AI797418 AA172395 AI749194 AI559933 AA502597 AA321220 AI866124 AI695633 AA494293 AW085635 AA165649 AA165663 AL031228 Z97184 AA382427 AI216166 AA160142 AK000082 AI744018 AA160143 AI935627 AI628742 AW771832 AW611969 AI745188 AA576763 AK000332 AA329421 AA329639 AW500761 AW389977 AF106046 AA434057 AI702707 AA987337 AW977541 AI218973 BE243703 AA812443 AI741316 AW591662 AI372956 AA434121 AI950226 AI638015 AF002246 NM_006614 T05949 AI474737 M86085 AW896359 AL119288 AA297308 T05243 AI157515 N93899 F05271 N76705 AI816885 N64008 AI591072 AI002813 R13014 Z43820 T04846 AW965681 T33886 H05873 H15266 Z38291 BE501503 Z43404 AW902172 BE069654 M78328 T07470 D55804 C14146 AI693381 AI971581 AI267614 AI632478 AI341141 AI828871 BE349191 AI360581 AA502521 AI075746 R40400 H15267 H05766 BE501732 AI917014 AA486412 AA916966 H06401 AI377651 AW129544 AA455600 AW581198 AA456098 AW579258 AI435046 AI580178 AA456010 NM_006306 S78271 D80000 AW271698 W22762 AI795837 AI795827 AW070763 BE328717 AI888409 AA113894 AI906408 AI907174 AI907202 AW852133 AW501330 AW500375 D17084 AA017617 AW249432 AA523516 AW102745 AA132903 BE394209 AA329880 AA353740 H10247 AW837033 BE080728 BE080717 BE612545 AA090634 AW503020 AW503626 R60116 F12536 R18750 AA309116 T74145 T55015 AA314169 T80889 H99540 H64047 AA055274 AA055028 AA334824 AA227772 AA227771 R98283 H81515 R07816 AW803219 AW803219 AA335888 AA335364 AA369747 R27262 T70312 AW022321 BE620138 AW501208 AW501370 AA905503 AA781457 AA584520 AI688644 AW023370 AW071831 AI034435 AW250036 N51820 AA829840 AW076005 AI561204 AI669003 AI440428 AI923572 AA598887 H90062 AA228103 AI433133 AI753164 AA227772 AW439747 R60054 AA017560 AA649135 R43070 F10156 AA744798 BE348941 AW515134 AW169949 AA836056 AI475387 AW166712 H63998 H10198 AI243977 AA640530 AL041743 AA588031 AI784330 D79869 AW960083 AW080425 AA608926 AW131691 R94625 R98046 AI002924 C00362 D17256 BE260374 AI276780 AI633509 AA458660 AI091006 AA805719 AA458836 AA4994908 AB023021 NM_006581 AJ238701 AA460039 Z45438 R18353 AA460188 AI640484 AA938882 AI221939 T80112 AI142229 AA460281 AA461569 AL134197 AW207881 AI003191 AA460466 T15845 Z39335 H97961 N20667 T03823 T15737 T15879 AW088206 BE351035 AA987933 D55944 D52262 D53558 D58663 AA829782 T32237 D54955 D55851 D63330 T06956 D52638 D55817 R49678 R52614 AL080128 AA725806 AA862836 NM_001115 Z35309 M83533 R61009 R19100 BE501141 BE177617 BE048304 AI866507 AI674049 AI016175 R60892 AA463193 R44767 AA463833 AW023166 AL079385 C02726 C04766 C04178 AL079386 AL079388 AI479277 AW467107 AI168764 D61990 D62617 AA464510 AA631257 AI740516 AI739132 AW972467 AI741376 AW068935 AI467852 AI752240 AI123717 AI754551 AW205510 AW044211 AW028889 AW198033 AI538632 AA513096 AW296771 AW971783 AA927070 AA465722 AW968203 AI732757 AA470353 AA468025 AA468479 AI734151 AI799909 AA468795 AA469401 AI380732 AI492231 AI421064 AW969270 AA469402 T85775 AW968345 AA468998 AB025904 NM_012113 H83666 H84836 AA401879 AA322820 H59688 N28007 R87427 R85022 H82563 AI800075 AW904436 AA418208 H97489 AI686505 N35685 H99095 AW023374 R07706 H60753 N67776 AA418073 AI168759 AW027850 AA012999 H59689 AA620395 AA700811 N36146 H60754 AA688368 H83667 AA339201 AI015805 AI582759 AA205528 R07653 N26551 N69337 AA640177 NM_002514 X96584 X78351 AA852490 H15316 AA605073 AA298840 AW966606 AA604355 R16276 AI207782 AA081850 R25930 R25912 H29804 AA852491 Z20214 Z20281 AA630741 AA074792 AW770888 D62224 AI925863 AW020075 H29805 AI301479 H88805 AW874265 D79225 AI433548 AA687861 AI446675 D79330 AW591335 AI424056 AA910443 N22234 AI055954 R41819 AA470519 BE303010 BE302954 BE384120 AV660345 BE261715 AF151807 NM_016002 AA310308 AW956324 AA214475 AA515478 AA449327 AV651790 AV651086 R09589 AA203390 H17224 AI909657 R32666 W47513 AA336306 AA074610 H12975 H09852 AA005018 H77802 AV659085 AA365043 AW959884 AW953951 AA007460 AA573144 AW129961 AI983151 AI978717 N92125 BE550937 BE326528 H68722 BE221501 H00583 AW513164 AI023529 BE155290 BE153740 BE155333 AI023528 AA005019 BE154028 AI281472 AI307122 AI138990 AI097101 AA429301 BE155320 AA843528 AI126957 AW748966 AA074611 AA724365 W74039 AI151489 W47514 AA621024 H00584 AI963099 AI023888 AI052664 AI369723 AI470114 AI093686 AA634442 AI131387 AI289000 AI288995 AW296547 AA758859 H75637 AI080292 AA663901 AA873611 AA609107 AA470883 AA937147 AA463447 AA612948 AA682658 AI014968 AI092232 AW009774 T99925 R28482 AA443488 AJ243243 AI076595 AI050921 AA862640 AA426125 AI246182 AA508211 AW445069 W19308 AA865885 AA889290 AI636974 AI247759 AI266464 AI798308 W72360 BE008036 W90696 H09766 AW264053 N63685 AA524719 AI742730 AW467054 AA425024 F29136 H17118 AA429478 T03696 AA843783 AA635518 AI263801 D52605 AW008958

			AA214378 AI949439 AA527842 R74175 AI208556 AW292289 H66723 T15857 F08852 AI214371 AW242017 AA777199 AI424270 AW204790 H05615 AA665847 BE466323 AI800859 N58769 AA677609 AI126501 C16157 C16165 AI247803 AW515488 R00275 AA677714 AI381746 AI094495 H75708 N77454 R74259 R02421 AA449585
5	430345	31627_1	AK000282 AA182952 Z24940 AA034118 Z28660 AW294137 AA034148 AI024012 AA333516 Z46021 AW957839 AW957914 AW957841 AW957917 AA313796 T30258 F12225 R14557 R12078 T66354 R14725 F07667 Z44964 F06557 AW364722 AI206023 AI652407 Z19306 AA463547 AW576947 AI142290 AW021072 Z19307 AA411744 D53906 AA447920 AA082694 AA458681 AA256197 AA192363 AA009820 AA101926 AA135779 AW975893 AA568142 AI949933 AI672317 AW090253 AI949924 AW242795 AI346981 AI814146 AI917296 AW007100 AW190720 AI796105 AA866023 AW003796 AI638594 AI367727 AW590477 AW300033 AI631666 AI683535 AI812007 AI990112 AI346605 AI625132 AI619434 AI333211 AI961275 AW205078 AA975051 AI990673 AI219765 T66301 R42503 AA009710 AI627502 AW073263 AI288494 AI308214 AW512150 Z19292 AI374953 AA181091 AA448857 AI262452 AI221508 AW590848 R49300 AA578970 AA411745 AA099176 AI653218 AI918779 AW023519 F09853 Z40709 AI446595 AI264433 AA781785 AW194887 AW270932 AA909801 AA458682 AA923768 Z28455 D58132 AI625873 T06286 F02827 AW512678 F03922 AA182624 BE613096
10	430357	316558_2	AW976789 AW451973 AI766808 AI376202 AA760752 H88069 AA781175 AW173607 AW872975 AA992090 AI654796 AA946869 AW515075 AW664845 AA479666
15	430371	31695_1	D87466 AW188126 AA973155 AA779297 AI553970 AL045312 R66419 H08158 R01915 T75488 R52813 AA010394 Z41823 F03794 AA887912 AW151544 AI150128 AW131406 H83852 AI500467 AA194584 AI139399 AI087327 AI004128 AI801388 AI910805 AA774580 BE041711 AI000146 AW014661 AA058677 R57531 AA406422 AL047872 AI798347 W00547 AI034095 BE177920 BE177928 N53883 AW794524 AW797298 AI493310 AA213561 AA632203 AA719762 AA057862 W23512 AW195432 BE549625 AW057509 AI654059 AW276124 AI419011 AI190813 AI142036 AW014354 AI352435 AA410430 AI985089 AW195385 AI375767 AI628263 H37939 AI032291 AA056986 AI123538 AI123550 AA854727 AA934908 AI377133 AI363350 AW189466 AA854732 AA782079 AW263041 AI142347 AI926293 H83853 H83832 AA976158 AI357510 AI434436 AI678390 AI147338 AA977648 AI669139 AI433882 AA213653 AA058795 AA194501 H83831
20	430388	31725_1	AA356923 D59253 NM_007362 X84157 AA094779 AA249121 D80082 AA307272 AW405730 AA613033 AA226546 AI619551 AW352081 N86805 AL048652 AA361455 AA303494 AI955092 AU077124 AI619498 AA385894 BE167222 AF039390 NM_005118
25	430403	31757_1	D82880 NM_006506 AF115573 D78155 BE086133 D78156 AF236711 AA297259
	430484	31874_1	AA533574 AA480264 AW969415 AA480254
	430503	319191_1	AW450575 AA481135 AA806760
	430548	319836_1	AA481282 AW971791 AA938165
	430566	319970_1	AW969834 AA528493 AA483165 AW969842
30	430664	321423_1	AW138724 AW204165 AI802637 AA877677 AI821801 AW004997 AI821052
	430680	321744_1	AW971949 AA662553 AA483689
	430682	321777_1	NM_001942 AF097935 X56654 BE185305 T99003 W94221 W72927 AI208332 T98952 AW238521 W76205 AF088042 W72968 AA041427 AI127361 W32235 AI217100
	430686	3218_1	X80240 AI064750 AI133594
35	430692	32200_1	AA492071 AA484229 AW969850
	430698	322100_1	NM_003540 AL031777 M60749
	430706	32222_1	AW044647 AI670953 AI656180 AA484715 AI659205
	430712	322397_1	AA488988 AW968906 AW382542 AA488768 AW969793 AW969791 AI014480 AA910211 AA484868 AI808265 AI308233 AI658816 BE503558
	430719	322506_1	AA495812 AI634138 AW236923 BE504004 BE326350 AA954672 AI695249 W21487
40	430762	322981_1	AI343652 AI732823 AA485451
	430838	324502_1	N46664 AI372473 R60867 AI360125 T65312 AI869984 AI422816 AA602607 AI609820 AI418316 AI361572 AW088275 AI186236 N62854 AI418900 AI423640 AA903735 AI361259 T33437 F09883 AA877472 AI372471 T33369 AI031715 AA487577 AI356715 AA488701 F10609 Z38848 AI419139 T33368
45	430844	324570_1	T94960 AA487679 T95013
	430879	325129_1	BE149423 AA488453 AA864186
	430881	32516_1	NM_000809 U30461 AW204396
	430882	325188_1	BE174240 AA488528 AL042253
	430884	32520_1	AF053748 AF063586 NM_000514 L19063
50	430899	325436_2	BE018217 AI500123 AA488829 AI911560 AW085198 AW237499 AI281417 AI276690 AW451214 AA548082
	430957	326116_1	AI937072 AW444769 AI634779 AI984961 N94384 AA489642 AI831879 AI474926 AI767386 AW610264 AW194744 AA489746
	430982	326544_1	R17432 R55260 Z46038 AA490218 R52171
	430987	32659_1	Y08564 NM_003774 AW780136 AW835269 AA312506
	431071	327550_1	AA491379 H86020 AW969148
55	431086	327783_1	AI829692 AA491730 AA934125
	431169	328799_1	AW971240 AA493843 AA493723
	431211	32963_1	M86849 AA315280 NM_004004 AA315269 BE142653 AA461400 AW802042 BE152893 AW383155 AA490688 AW117930 AW384563 AW384544 AW384566 AW378307 AW378323 AW839085 AA257102 AW378317 AW276060 AW271245 AW378298 AW384497 AI598114 AW264544 AI018136 AW021810 AA961504 AW086214 AW771489 AW192483 AI290266 AW192488 AW384490 AW007451 AW890895 AA554460 AA613715 AW020066 AI783695 AI589498 AI917637 AW264471 AW384491 AI816732 AW368530 AW368521 AW368463 AA461087 AI341438 AI970613 AI040737 AI418400 AA947181 AA962716 AI280695 AW769275 AW023591 AI160977 AA055400 N71882 AA490466 AW243772 AW316636 AI076554 AW511702 N69323 H88912 AA257017 AI952506 H88913 AI912481 AA600714 BE465701 N64149 C00523 N64240 AA677120 AA496078 AW572915 BE500968 AW418725 AI638675 AI631708 AW024125 AW104268 AA934362 AA812885 AA911102 AA931770 AA758532 AA968716 AA608859 AA973942 BE041425 AI651682
60	431215	329720_1	N52937 AA725524 AI913219 AA496222 AA984383
	431220	329852_1	AA987742 AI690089 AI823732 BE044440 AW593335 AI457432 BE500943 AI800952 AI335264 AL045875 AW614213 AI377308 AA427719
65	431242	33032_6	AA609689 AW301169 AA609080 AA976385 AW513284 AA287056 AA558285 AA084839 AI913627 AI985093 BE464670 AI589730 AI261322 H92175 AI214453 AW205365 AW593181 AI479744 AI690644 AI498555
	431291	33105_1	N25521 AJ245586 N20488
	431292	33106_2	AA370141 AL035461
70	431374	33253_1	BE258532 X52142 NM_001905 BE247524 BE256229 H05341 H11807 R15838 AA373891 BE293678 BE305085 BE393959 BE394113 AA190722 AL041570 BE265014 AW470245 BE388684 BE540103 N83259 AA805325 AA132649 AI905730 AA814761 AA614324 AW662931 H09614 AW206190 H05291 H11731 AI793330 R15837 T28502 BE293379 C04582 AA136515 Z21171 W49824 BE293848 W25271 AW950582 W45678 AA632297 AI989584 AV654716 AL041571 AI979043 BE293811 W44416 AI950210 AI655438 AW027521 AI659220 AA132742 W19164 AW014511 AI078679 AI174423 AI337084 AA135134 AI190299 BE042716 AA476603 AI652120 AA191481 AW611499 BE328358 AA788667 AA992545 AA055002 AA196899 AA653125 AA196826 BE249966 BE537348 BE250030 BE255331 BE313047 BE382916 AA366135 BE269073 AI703490 BE467663 BE219789 BE396388 BE269159
75	431418	33308_2	X68242 AA806977 AA902831
	431447	333342_1	AA505138 AA730263 AW969145 AW977187
	431474	333733_1	AL133990 AI128582 AI829770 AW972505 AA505700
80	431508	33416_1	NM_012481 AF129512 AI040940 AW071111 AI660183
	431511	33419_1	NM_012386 AF112366
	431532	334555_1	AI537817 AI537825 AA506831



5	431548	334680_1	AI834273 AJ243247 AW276747 AI138586 AI433913 AW410590 AI918642 R60873 H11940 AI439654 AA507009 AW972573 AI932865 N66981 AW029229 C20715 AI393401
	431552	33479_1	AI815863 AI878864 AA985367 NM_004321 X90840 AI363308 AI816019 AI879422 AF004425 AI570691 AI339237 AI933167 AI948449 AI360405 H92234 AI125165 AW897946 AA683104 M78705 U37194 AA775971 AF038173 AF052089 T77291 AI133766 AL119246 L79946 R11991 R12962 AA326327 AL119540 AI912372 AI240041 T15633 R40156 R39830 AI611831 AL120303 AW905726 AW905700 AA350361 AL118691 AI124534 T07754 R86661 AW452922
10	431595	335512_1	AA508196 BE142920 AI280311 AI205616 D61709
	431605	335582_1	AW972407 AA508398 AI792208
15	431613	33565_1	AA018515 AL161968 W00432 AA251993 AA018466 AI719229 AW967686 AI633671 H63609 R93395 AA045066 W00405 AI701675 AW385738 AA233714 AI581080 AA251737 BE546071 AW385734 AB002439 AA827529 R24470 AA459973 AA232800 N72127 R93439 AA151716 AW511644 AI262749 AI087944 AW024377 AW080566 AW188881 AI860901 AW519183 AI245625 AI760922 AI936546 AI765706 W20071 AI383536 N72165 AW979271 AW337799 AA766423 AA878433 AA508712
	431622	335774_1	AK000992 H83580 AI806278 AW300804 AI561302 AA846665 H82712 R41831
20	431632	33594_1	AW971302 AW452382 AA513555 AA524663
	431673	336392_1	AA514986 R42732 AA860469 AA776492 AW264515 AI399697 AI401765 AW263039 AA602608 AA573594 BE002619 AI971240 AI299719
25	431750	337357_1	AW104017
	431853	338484_1	AA521034 AW969180 R94874 AA781489 R97484 T96780
30	431906	338876_1	AW328038 H57686 AW328039 H67403 AI681235
	431912	338951_1	AI660552 AI688604 AI688540 AI380340 AW006764 AA594441 AI700219 AW004785 AI659950 AI759158 AI581803 AI832419 AA594533 AW296326 AW295479 AI695451 AI581787
35	431954	33943_1	AK001974 AA192266
	431980	339829_1	AA523696
40	432030	340616_1	AI908400 AW380792 AI908368 AI908404 BE467466 AI829032 BE219085 AI694059 AI273676 AI167466 AA524619 AA828567 AA828698 AI129629 AA828754 AA828797 AI468573 AA828777
	432116	341692_1	AA902953 AW972660 AA526421
45	432189	342819_1	AA527941 AI810608 AI620190 AA635266
	432223	34334_3	AA333283 AW007537 H70941 AI184812 N30698 W89071 AA700130 AW965342 AI333194 AI969801 AI765299 AW207825
50	432253	34376_1	AW090822 NM_016427 AB030834 AA861139
	432365	34550_1	AK001106 AA262920 BE081328 AA252781 AW403969
55	432374	34559_2	W68815 AW117862 AA642987 AW381579 AA730105 AI220853 AI474539 AW452308 AI745535 AW276480 C00410 AA627916 AI969511 AW662302 W68529 AW628474 AI611676 AA631033 AW381130 AI220849 D29313 AW381131
	432415	34659_3	T16971 AW964330 T08802 AW967226 F07786 Z45168 N30967 AW161341 N42363 N21561 N31708 N31709 AI122773 AW975899 AW162643 AW161798 AI808825 AI360866 AI804220 AI031947 AA843394 AI123189 AI472045 AA578830 AA729170 AI740490 R40236 H09495 AI741083 AI283334 AI224956 AI079635 AW194138 AW054706 AI744193 AA843979 F04060 R20726 T23457 F04044 AA723859 AA977643 AA283764 AI123609 AA609495 AW161086 R12814
60	432437	347090_1	W07088 N49359 AI620881 AW972920 AI670115 AA860498 N49257 AA541536 AW296679 N77921 AA555152 AI611254
	432488	348491_1	AA551010 AI935377 AA887383
65	432527	349165_1	AW975028 AA551969 AA644028 AA689303 AI220334 AI220090 AI925480 N66393
	432577	350239_1	BE208545 AW582213 AI879483 AA553761
70	432584	350424_1	AA928829 AW195875 AW363225 AI636959 AW363241 AW363239 AW363251 AI916034 AA554045 AI638649 AA994913 AW363235 AW363263
	432596	35075_1	AJ224741 AI820674 Y13341 T94707 AJ001047 AA460127 AL134335 AW959262 AW190549 AI983860 AI813908 AA461483 AA295621 AA759320 AW022018
75	432702	352967_1	AW973953 AA593373 AA559945 AI241877
	432711	353168_1	AA563785 AI378347 AI082130
80	432779	354024_1	AW979241 AA565006 AA847102
	432781	35402_1	NM_014133 AF090937 AI064829
85	432792	35412_1	AA448114 AF152488 NM_013340
	432797	354190_1	AA565264 AW274285 AI377989 N22605 AW351447 AI338361
90	432808	35433_1	NM_015985 AF074332 AF113708
	432839	354984_1	AA579465 AA568401 AW752043
95	433014	35742_1	NM_014711 AB007879 AI110758 AF074665 AC003108 AI909701 AW900180 AL043539 AA373285 AW957468 R09790 AI698739 AW979089 AA827980 AA828737 T18951 AW021147 AI681371 BE465001 AI765028 AA625653 AW512972 AW970095 AA987370 AI129176 H44182 AI926004 N48065 AA528667
	433098	358798_1	AW190593 AA576926 H26279 AW023845
100	433128	35945_1	AB021923 R22285 R22229 AA971058 R22919
	433132	35952_1	AB026264 BE465780 BE084102 AI401162 AA020853 BE379660 AA247144 BE502473 AW006857 AI142901 AA885535 C00308 AI611292 AW608092 AW608134 AW608083 AW608125 AW294759 AA179057 AW403438 AA455563 N51807 N94795 W37415 N36781 AA151626 AI968205 AW167014 AW591250 N63492 AI927709 N24854 N33453 AI379722 AI831117 N51719 T64930 AI921674 AI799231 N23957 R89597 AI244596 W37416 AI869023 AW513726 AI300283 AW500445 AA456060 AA099049 AA405474 AI381742 AA020830 N51669 AI683602 AF231338 AW594706 BE183704 BE465964 AI218390 AI738643 AW512763 AA576971 AW797301 AW797303 AW797358 AB040889 H11206 AV650927 AV650835 AI864178 BE326300 BE178331 R97970 AW594161 BE326226 AW514472 AW970833 AA579969 AB040925 F06391 F05980 R52809 H11799 N54098 H08526 R11686 N45731 AW084660 N79408 N79394 R51484 AW074849 N51830 AI873913 N93902 N62789 AW771124 N49008 R52810 H11727 AA936576 AW474884 N62508 N62494 R51380 Z39305 AI829289 F02223 R17666 BE618285 N47251 H89464 R34562
105	433266	361434_1	AI863224 AA580765 AW804110
	433297	36237_1	AV658581 AV658591 AV658626 AF009271
110	433347	36388_1	AF023130 AF181250 AA984703 AA694303 AA351792
	433377	364549_1	AI752713 AA860695 AI367849 AI358832 AA585475 AI160216 AI086261 AI681976 AI628569 N26713 W37418
115	433386	36478_2	AW360833 AW360828 AI471560
	433479	367580_1	AW511459 AW183824 AW973891 AA594438
120	433485	367731_1	AI493076 AW192174 H70554 AA594609 H65646 H53999
	433513	368567_1	AI566356 AI859031 AW301628 AA595752 AI755153 AI810711 AI620158 AI813782
125	433532	368950_1	AW975367 AA598607 AA742735
	433536	369004_1	AI732163 AI821728 AA665614 AA598678
130	433567	36987_1	AF073299 S83549
	433629	371685_1	R13140 AW366682 AI765437 AI335240 AW966647 AW241581 H28931 AW470817 AI310758 BE327017 AI915099 AW237679 AW264795 AW205091 R40621 AI493045 AI767972 R38885 R46147 R37962 N70822 Z41616 T36264 AA649921 AI821790 AA602992
135	433717	371701_1	AF063536 AI110662 AF090889 AW859744
	433717	37360_1	AW085934 AA609148 AA725844 AI187356 AA776771
140	433755	373923_1	AW753676 R11789 AW001886 AA609219 AW780420 AI860557 AI280331 AI334300 AI288870 AA669343 N29918 BE537790 AA934687 H79075 N42970 R63752
	433764	373989_1	

	433767	374014_1	AA609245 AA724581 AW241989 AI377274 T47300
	433781	374141_1	AA609379 AA885236 AW661704
	433805	374391_1	AA706910 AA825341 AW300364 AI698261 AA609651 AI088709 AI619704 AA825354 AI281035 R94745 AW118721 AI350378 AW373771
5	433919	377243_1	AW373619
	433939	37786_1	AA746311 AA927492 AA617995
			AL133887 D64159 AF112218 AI766633 AL039303 AL133888 BE620604 AW976259 AW262792 AW591383 AI365413 N36652 AA807027 AI472041
			BE620065
10	433990	378422_1	AA889328 AW628014 AW183783 AI220441 AA758090 AA621200 AI269496 AI696046 BE466894
	434001	3784_1	AW950905 AA324741 NM_000029 K02215 K02215 X15324 AA449554 AL133832 H54824 T10891 AA349956 M69110 AI751551 T66204 M24689
			AI061624 N80498 R59122 R59168 H63320 H62653 T67578 F05310 AI174256 R19563 H17197 F07780 F08756 F13204 F08439 H22747 F08397
			AV659557 AV659398 AA326597 F05521 R13521 T53953 AA325841 AA324805 AA324207 F11370 T58009 T75399 T77952 T51428 AA351781
			T73502 AA349887 H73089 AA351628 AV655546 R12304 AA334415 H61925 W03930 C05200 H66013 H57666 AA334006 R11239 N99853 H77469
			H58442 H69443 W32242 R94296 T74494 T77767 W01494 AA484909 AA484836 N94252 N80523 H65262 N98545 R97913 T84628 H70571 H70582
15			H60975 H64379 R99768 H95829 H48647 H57009 H63673 H93257 R89190 T97863 H59299 H65705 H81367 AA488105 W01597 N72496 N58641
			AA360325 AV653782 AW008537 N78173 AA300076 N78006 AW466933 N83812 AI937205 W03497 N99027 AA305209 N53493 AI174855 N73174
			AI801931 N91668 AI332826 AI953028 AI702817 BE348379 BE043090 AA595006 H93129 N45277 AA013213 AI560263 AI801920 W58705
			AI859522 N58416 AI190167 R20643 AW148630 AA885688 AI751552 AI095044 R93138 N99817 T90658 C20544 H66586 T91398 AW001495
			N66941 AI700299 R88286 T77768 N07017 H81311 AA991682 N65987 R50859 H23175 T50713 R42546 R19376 R41939 R39208 H09821 R49100
20			H23160 T54549 R97914 R37235 R94201 H95830 H58443 H73090 H63242 R59123 R44583 BE223055 R11187 AW136995 N59620 H94275 H54776
			H66143 H82651 H08790 H57162 R45438 N68084 H24028 R41183 N80173 H47595 AI356814 R44772 H77470 R29198 R89085 AA019428 F05040
			R59169 F10440 AA506105 H08746 T23450 F10806 R94760 H08578 AI265922 F04033 T57925 H72048 AW128903 T98911 AA917395 N63721
			AA628858 AI678833 H63950 AA576107 H17974 T16325 H65706 AA777041 T17343 F04774 F04658 F04660 H62569 R07030 H61721 H57942
			H58506 F04254 H66014 T66140 AW128887 H66592 T69463 AI359985 AA954240 H56916 H58036 H48483 N68651 AA662362 F01566 H66587
			H61548 H80154 N71350 N71400 AI074586 H66593 T91055 T52545 AA350842 AW148566 H59255 T73433 T53821 T28822 R43591 N57986
25			AA350277 N58109 AI669901 F01793 AW892259 AW118522 F09764 AW803620 AW803634 AW803499 AW803704 AW803691 AW803706
			AW803772 AW803501 AW803572 AW803633 AW803569 AW803573 AW803769 AW803766 AW803490 F09032 AW803623 AW803485 AW803712
			H62470 AA865244 N71251 T60921 AI568584 AI497964 AI143932 AA058839 N39212 BE218542 AA299950 T16891 F12837 H23174 H47677
			AA323521 F12125 AA326025 R87561 H08464 H09916 F08567 R14017 R35200 R36018 F08435 H66560 H57238 H82650 H72134 R19106 T50867
			H61495 H08577 R98990 R39140 AA988495 AI262199 T4118 T97757 AI337507 T70516 R14776 T83186 T54590 N55584 R14523 D11802 H23159
30			AI244020
	434077	37975_1	AF116659 AI114806
	434118	38029_1	AF116715 AI207476 AA953390 AI340058 AW419340
	434120	380357_1	AI436050 AA625558 AI208663
35	434163	380993_1	AW974720 AW189373 AI824959 AA933973 AI809801 AI809806 AA626261 AI810247 AA649828 AI950317 BE243641
	434222	38199_1	AF119886 AI174866
	434239	38223_1	AF119910 AI207600
	434273	382714_1	AA913143 R40752 AA961605 AA628511 AI377374 AI126888 AI350766 AI024804 AI401236 H87750
	434283	382833_1	AW235341 AI678484 AW196611 AI989889 AI521189 AI962500 BE504950 AW197205 AI699926 BE502640 BE503403 AW589663 AI655196
40	434294	383102_1	AI383646 W84815 BE552455 AI680206 AA628642 W84814
	434352	38444_1	AJ271379 R38420 R45334 AA971835 AA910404 AA628945 AI341642 BE018701 R20673 R12849
			AF129505 AA248485 W07478 N86813 AI355905 AA248067 AA389647 AA214147 AA214155 AA092554 AA211521 AA094015 AA247862 R58129
			AA249722 AA211443 AI355904 AI355903 AW170011 AI090520 F36800 AI190689 AI333485 AI355676 F26916 F31142 AI824667 AI355906
			AA214031 F16837 AI381720 N75838 AA247872 N55839 AA249531 N56276 AA249723 N84085
45	434361	38456_1	AF129755 C02325 AA282384 W79129 AF086438 AI806507 AA641044 N45290 W94027 AI817043 AI885487 AI813317 AI076274 AW953001
	434377	384921_1	AW137148 AA631504 AW593970 AA906342
	434381	385155_1	AA631834 AA633425 AA632455 AI792312 AI792311
	434627	389799_1	AI221894 H72290 AA641096 AW129158
	434638	38990_1	H50758 AF147434 H50666
50	434663	390429_1	AA641972 AI418535 AA903496
	434683	390738_1	AW298724 AA642419 AI693480 AW976226
	434690	390901_1	AI867679 AI087279 AW470213 AA642619
	434698	391427_1	BE044674 AA643497 AW827541 AA643491 BE044925 BE044737
	434699	391602_1	AA643687 AI091154 D20754
	434715	392095_1	BE005346 AW242890 AA644351
55	434745	392632_1	AW974445 AA830983 AA648355 AW204266
	434763	392847_1	AA648618 AW974389 H51771
	434784	393210_1	AA649051 AW977458 AW977465 AA767692 AW977462 AW977463
	434820	393886_1	AI821863 AI821865 AA658496 AI821118 AA650153 AA650132 AA650428
60	434849	394351_1	AW292765 AI860857 AI003941 Z38409 AI263121 W02067 AA651847 AA789099 AA830294 T33546 Z39455 AA884939 AW269426 H18495 H51128
	434896	395228_1	AW022054 AW135576 AW150707 AW051952 AA653141 AI821735
	435079	399783_1	AA664192 H60250 T71388
	435090	400027_1	BE217923 BE463875 AW024115 AW024111 AI631205 AI471776 BE501143 AI091082 AI282201 AA664593 AI625012 AI470957 AA831104
			BE090456 AW853895
65	435113	400524_1	AA665469 AI821725 AA678771
	435133	40102_1	AJ010482 AW868740 AW884416 AW880881 AW366574 Z25023 AA196387 AA100598 Z25283 AF177291 AI969816 AA559891 Z25061 AW841825
			Z28904 AW959514 AA192917 Z30103 BE179924 AA921922 AI276872 AI014904 F28861 AI769295 AI139506 AA192805 F27810 F28522 F31301
			AA662333 F35933 F34419 F23435 F19078 F25502 F28223 AW573178 F36429 AI972305 F25248 H16233 AI927622 AI932901 H03779 R58599
			AA026651
70	435191	4022_1	R15912 Z45805 R56366 H09688 H28906 Z42110 AF070577 H15499 Z45171 T80013 R19744 R12077 H41631 M62055 H28907 AI670949 H15441
	435202	402737_1	N59804 AW015150 AI655738 T17312 H42324 R37140 R15911 AI361490 R42494 AA912236 Z40896 F04673 AI217847 R56270 R45163 T03442
	435256	40352_1	F01647 N72748 H42333 H41621
			AI971313 AW855041 AW991934 BE005447 R59093 AA670383 N79509
			AF193766 AA448744 T82005 T83161 AI742654 AA460463 H61567 AA701618 H57113 AI127309 AI633508 AI571360 T90634 AA233071 AA448648
			AA897786 AI206655 AI589742
75	435325	404382_1	AI038388 AA677963 T86982
	435352	404634_1	AI056599 AA678238 AA704443 AA704720
	435413	405993_1	AI267476 AI565484 AI866193 AA680045 N47090
	435434	406256_1	AA680387 AI140534 AA704460 AA703562
	435451	40646_1	AF195420 AA702693 AI076124 N73156
80	435463	406582_1	AA682507 AW851124
	435559	40812_1	AF209198 AA251397 D81981 AA082116 BE536905 W81660 AI872970 H82577 W19613 AA102582 AW966886 AW967510 W81219 AI635559
			N27946 N24381 AI077944 AI763038 W61334 AI624272 AI972115 AI375987 AI378124 AI086015 AW028141 H99133 AW971529 AI198751 AI671325
			N90026 AI241170 AW207070 AI423885 AI865150 AA626093 AA554588 AI222670 AI927421 AI193218 AW305284 AA251239 AI638572 AA486306



5	435563	40823_1	AF210317 F00548 BE463553 AW300078 AI766064 BE464196 AW263084 AI671682 AI433678 AI312682 AA918717 AW614815 AI022719 AA918718 AA918939 AI671678 AI700871 AA059043 AI580406 AI302080 AI796223 AI300071 BE466457 AI671399 AI913595
	435579	408457_1	AI332373 AI333796 AA688232 AW975345 AW592953
	435586	408547_1	AI279137 AI290738 AA688341 N66427
	435600	408804_1	AL047034 AA689487 AI821857
	435608	409071_1	AW183971 AW341427 AA693524
10	435634	409239_1	T82384 R05307 AA693714
	435663	409442_1	AI023707 AA693940 AI075300
	435766	410653_1	R11673 AA699970 R00740
	435793	4108_1	AB037734 AI350748 Z38942 F01814 H13007 H05896 Z45594 H12106 H18730 AA249485 Z42339 R14983 R55164 AW957717 R54369 W60887 AA010504 AA099463 W60805 R49440 AW901726 R38025 AI367370 AI537878 BE503519 AW167870 H44902 AW130792 AI740821 T03753 AA010505 R54824 AA708629 AA443681 R45674 AI284856 R45286 F09255 AA729642 T16068 AI564764 T33869 AA099384 Z38565 H18644 AA447068 F11599 R35922 H06346 H06936 T78310 H06937 R56539 R20468
			BE349853 AA771928 AA700433
15	435810	411064_2	R08330 AA701418 W88583 W88497
	435878	411895_1	AA703154 W80635 R08362
	435985	413228_1	AA778177 AA777469 AA703516
	436020	413539_1	H75391 AW298387 AW854959 AA703650
	436033	413663_1	AA704687 R99220 R10653
20	436088	414403_1	AI754308 AW069285 T71338 AI378245 AA705384 AA973318 N74598
	436149	415010_1	AA764950 AW418719 AI420075 AW084601 AW977003 AA705446
	436154	415063_1	AK000883 AW799155 AW799153 AA300122
	436168	41524_1	AK000998 BE157076 BE157298
	436187	41550_1	AA706059 BE218269 AW294253
25	436193	415573_1	AK001074 AA354117
	436194	41557_1	AK001084 AA078092 AA829049
	436196	41562_1	AY004867 AI813270 AA349423
	436250	41647_1	AA707472 AI684396 AI283534
	436269	416768_1	AA708310 H52584 H52175
30	436294	417339_1	AW293496 AI188642 AA716002 AA708470 AA708756
	436298	417417_1	AI798750 AI221709 AA709226
	436329	417990_3	AI049679 AA577969 BE166265 AA315705 AA329923 AW962505
	436332	41800_1	AJ227892 AA338715 BE074475 BE074469 BE074474 AW006182 AW572953 AI831725 AI762923 AI341466 AW449335 BE551686 AI692895
	436391	41899_1	AI040410 AI276881 AI891008
35	436397	419098_1	AA715013 AW468194 AI476329 AA992943
	436421	419635_5	AI678031 AW173312 AA812698 AA729849 AI380375 W25689 AI344299
	436461	420667_1	AW511956 AA719488 BE071580 AW748028 AW896108
	436464	420676_1	AI016176 AI091255 AA719507 AI128614
	436471	420879_1	AA719813 H18655 H08201
40	436508	421577_1	AW604381 AI185428 AA985353
	436511	421589_1	AA721252 AA737475 AA730237 N66701 AW977061
	436572	423035_1	AA723274 BE503172 AI457238 BE467884 BE221090
	436574	423192_1	AW293527 H30261 AI628505 AW073905 AW087393 AI092824 AI208455 AW338087 AI935381 AI434683 AW007605 BE327828 AA913315
			AI749624 AI457483 AI348298 AI348270 H30323 AA723461
45	436577	42320_1	W84774 AJ009817 N29755 AA834395 AI249064 H54235 T95647
	436590	423462_1	AI393115 AA961280 AA723779
	436637	423940_1	AI783629 AI637609 AI655377 AW074703 AW449028 AA890668 R60313 AW243019 BE464436 AA973133 AI263065 AI582600 F03414 AW236442
			AA873868 Z38275 AA724332 W23675 W15388
			AI271945 AI271818 AW235681 AW051010
50	436638	423997_2	AA724411 AI286124 AW340053
	436640	424008_1	AI127483 AA725246 AA725281 AI676162 AI744107 AI745374 AA838337 AI675430
	436679	424709_1	AW991278 AA771917 AA725348 AW816293 AI744435 BE085750
	436683	424793_2	AW975902 AA729344 AI557342
	436720	425676_1	AW977192 AA730050 AA731416
55	436747	426172_1	AA731199 AW975817 AW241735
	436777	426966_1	AI684535 AI884856 AI499858 AA731767
	436820	427433_1	BE328074 AI700552 BE467938 BE218850 AI807702
	436853	42803_1	AI942357 AI253135 AA761673 AA736675 AA748004 AA814004 AW978076 AW978086
	436888	428768_1	AW247145 AA737014 AW592475 AA884380 AA883987 AA905207 AW976117 AW976124
60	436902	429024_1	AW139680 AI934979 AI480295 AI809768 AA738123 AI080339 AI423832
	436938	429795_1	AB018305 BE315203 AI569725 AL133797 AK001584 H09449 F08408 AW998309 R25793 AA449547 H38279 AI871669 M78530 R57626 AA244349
	436982	4306_1	AA244163 AI700043 AI632649 AI632660 AA622344 T23690 AI567994 AW044114 AI654454 BE047014 AW594714 Z41397 C15384 H61875 H24153
			N77073 AA127579 AA453668 R67153 AW390446 AW390451 W93800 AA358644 AW959169 AA034237 AI689608 AW197421 R91784 AW088291
			AW194393 BE049402 AA534904 AA428038 AW662968 R27202 H01251 H13082 N42254 N57202 R82261 AI972556 BE464017 BE348770
65			AA449113 AW152432 AI206902 N32810 W93989 AI799502 AW665638 AW571858 AI23145 AW514573 AW197663 AA053930 AW665686
			AI376613 AI479938 AI218225 AI656541 AI128371 AA127466 R59973 AA427924 AA776360 AI817703 AW088405 AI361508 AI859002 R27203
			H55900 AI824832 AW190558 AW470416 AI565066 AI858842 AI674914 BE463424 R91785 AI401062 AW103934 AW276699 AI809596 AW628378
			AW071546 AI189019 AI002857 AW206484 AA364666 H01166 N59385 AA773930 AW027775 N29781 AW953931 AA447735 AI285163 AI633932
			AI290045 AI360254 R82206 AI638501 AI690373 BE222634 AW027793 AW027950 AW182096 AW592205 H24046 AI811525 AI885290 AI744720
70			AI274485 AI800088 C04100 AA055339 AI800087 AI803875 AI360174 AW572585 AI081359 AA904821 AI874167 AA421739 N39444 AI219568
			AA257059 AW451191 AA502410 AI143661 AW276821 AW276891 AW515195 AA055340 D25758 AA327290
			AA741074 AW448312 AI827330 Z44512 AW779332 AI761428 AW295099 AI.134768 AI627818
	436992	430854_1	AA745625 AA743054 AA741154
	436998	430929_1	AA743240 AI458566 AW613503 T25344 T40899 AW976433 BE350724 AI954132 AA830804
75	437048	432140_1	AI023264 AA161185 X52350
	437064	43234_1	AI885608 AA743734 AI034154 AI075224 AI656815 AI887898 AW243126 AI950513 AI869093 AI273184 AA912285 AA912258 AW976672 AI335673
	437073	432564_1	AI080389 N79728
			AI286235 AI767243 AA761662 AI672630 BE047809
	437074	432577_1	AA743935 AW341613 AI700300
80	437085	432740_1	AI935622 AA745086 AW513654
	437138	433575_1	AI928184 BE048934 AA746057 AI206024 D57453 AI076908 AI089589 AI283431 W58768 AA778157
	437183	434235_1	AA747822 AA836580 AW976205
	437263	435353_1	AA814943 AA748879 AW976617
	437332	436150_1	

5	437354	436383_1	AA749215 AW977706 AA828269
	437369	436493_1	AA765230 AA749338 AA815142 AW977102
	437396	43676_1	BE140396 AW751035 N42527 AA295056 AW956904 R14484 AL359591 R70080 AW583879 AW583509 AW468806 D20186 AA825408 AW298825
10	437458	43734_1	AA883397 AA533987 AW964653 AA323067 D61834 AA334078 AA334509 AW965404 AA604382 AI290792 R70033 AI690103 AI660777 AI564165
	437511	437876_1	R40833 N29880 AA970033 AI660800 AW269065
	437636	439842_1	AL390131 H10243 H13026 AW884449 AI261735 AA765587 AI793003 AI261674 AI793181 AW008025 AI830423 AW026745 AL042088 AI692942
15	437642	43997_1	AI566063 W19458 AW024146 AI672313 BE505023 AA910482 BE552316 BE045456 AL042087
	437733	441579_1	AI807500 AI018652 AI675776 AI028672 AA868586 AI028284 AI221090 AA758562
	437783	442787_1	AA764781 AA825890 AA767119 AA767133
20	437845	443938_1	AL079309 AA281819
	437846	44394_1	AI792574 AI792570 BE138486 AW302291 AA766788 AI054393 AI054222 AW977428
	437913	445109_1	AI683150 AI287315 AA768264
25	437916	44515_2	AA769578 T40348 T41207 N93007
	437918	445197_1	AA773866 AA773398 BE350358 BE141332 BE141359 BE141393 BE141302 BE141304 BE141303 AW082220 BE141299 AW170024 AW872428
	437927	445481_1	BE141368 BE141390 BE141410 BE141419 BE141334 BE141209 BE141361 BE141373 BE141366 BE141376 AW265501 AW238399 BE141320
30	437980	446952_1	BE141301 U47646 BE141409
	438005	447553_1	AI140825 AI457644 AA771908
	438018	4477_1	BE566249 BE220229 BE566059 AW891489 AW891478 AW891477 AW891483 H02687 AW891474 AI306487 AA693989 AA860996 AA102571
35	438042	448602_1	AW572775 AI308192 AI334618 AI632845 AI913841 R36857 AI282042 AA313548 AI378960 AL046364 AA256840 AA256799 AI123953 AI167448
	438055	448913_1	AW957176 R16314 R59474 Z44227 T09476 AA227619 H98566 AW957823
	438079	449524_1	AI761449 AI041998 AA772004 AI828835 BE503340
40	438090	449648_1	AI039789 R53007 AI886071 AI091770 AA772319 N69923 R25368 N98914
	438165	451108_1	R50393 AI453463 AA774209 AI741882 AI151043 AI151039 W04928 M85879
	438188	451691_1	BE151746 BE336853 D63271 T94955 AA774994
45	438214	452349_1	AK001160 H05092 AW752992 F12992 H59405 AI207832 BE301806 AI612764 AW008237 D25954 AW057870 AI979095 F10587 AW087232
	438257	45327_1	H60061 AA738335 H51595
	438290	454094_1	AW296971 D61655 AA776286 L44452
50	438295	454167_1	AA776655 AW157227 AW131593
	438298	454177_1	R09664 R09551 AA777372
	438315	454723_1	AA777534 T89357 R83009 T88887
55	438361	456028_1	AA779344 AI052496 AI078472 AI033593
	438369	45614_2	AA779975 AA977711 AI239774
	438370	456174_1	H06076 R56200 AI287520 AI393984 AA780790
60	438456	45775_1	AW474419 L31942 AW292681 AI952897 AW072430 BE169336
	438504	458710_1	AA843719 AA782939 AA970830
	438557	459956_1	AI394151 AI924944 AI654001 AI879872 AA783022 H61142 AA902440 AI688735 AW166630 AA897136 AI377880 AW022201
65	438563	460086_1	H23542 AA783033 Z40720 F03262
	438602	461046_1	R56795 H08794 AA789222 N40438 N40477 AI078226 AI916316 BE504572 AI921527 AW073893 AI049802 F10745 F02419 F02402 AI078329
	438660	4624_1	AA805666 AI262530 AI281289 AI264548 R58399
70	439001	46771_1	T77886 T86845 AI365486 T53788 H00310 BE541756
	439037	46803_1	AA843242 AW188023 AI097383 AW150759 W70259 N62361 AW300432 AI290520 R69412 W70258 AA805834
	439063	46828_1	AA913381 AI698624 AA724832 D17234
75	439079	46842_1	AW665281 AA808871 AI951088 AI688631 AW820984 AW613195
	439107	468664_1	AW364104 AA810522 AI149869 AA905517
	439199	469726_1	AA810665 AI339625 AI095642 AI089393 AI686212 AW976919 AW243119
80	439235	47009_1	AI167149 AA811737 AA830443 AA865701 AW001834 AW977970 AI917630 AI671461
	439294	4707_1	U95740 W52220 T81920 T83826 R05641 T87556 T81229 R12856 AL118819 R96446 BE299456 AI372829 AI816392 AW157195 AA130289
	439492	47297_1	AA135799 AA164900 AW294821 AW410635 T99321 AI816276 T34819 H19250 AA774185 BE503588 AA083117 AI005469 AA027340 T15996
			AI312448 AI312197 C02151 AI589559 AI612103 AA019881 AA894568 AA770240 R38428 AI435842 H98210 BE466428 AA888588 AI936995
			AI214546 BE206053 AW902297 R08085 AI219844 BE467931 AI813994 AI198968 AI637808 AI802351 AI452706 T83662 H52123 R96447 H16697
			T33003 T78862 AW629539 AI804202 R42142 R41504 Z41102 AI300274 T30646 AA970855 T81921 AW296590 AA432023 AI423512 R05531
			F18392 R42920 F25527 R08035 F34433 T16797 AL118820 AA115521 AI377644 AA114950 AW894971 AA114923 AA431770 AI373441 AI222162
			AA134062 AI417110 AI219437 AA978205 AA115526 N74543 AI803155 AW051574 AI028740 D79266 AA135800 AA954386 R12182 H11948
			H16696 T16951 AA164351 R12714 W02938 AA321873 AA610440 AA421885 H52006 AI372828
			AA828380 AA825578 AA883636 AA913703 AW977745 T40920 AA983447 AW028851
			AA828995 AA834879 AI926361
			AF075068 R92636 R91382
			AF075084 H53157 H53054
			AF085922 R98284 R98047 H60425
			AF085937 H65281 H65280 H65719 H65720 AA292576 AA235664
			AL046134 AA830269 H15250 Z40884 AW978412
			R40373 AW872832 AI968979 AI291173 AA831470 H49446
			N45513 AF088011 N75893 N46429 N59158
			AW975328 AI420330 AA149511 AW748944 AA688092 AL117352 AW382608 BE004263 N44539 AA834784 AA149643 AA508346 AI127748
			AW408810 AI027647 AW059748 D19764 AW953111 AA349462 C15482 AW851386 AA370652 AA370198 AA385806 H24135 H08650 AA477530
			AA203627 T77949 AA203123 H56028 AA846715 AA328402 D82524 H08497 AA442115 AA453001 Z25120 D82526 D82474 T10772 AA325886
			W88637 T86104 T86401 AW377115 T74461 F13474 T08154 T86365 R18274 AW377116 H16440 AA465445 W90048 AA442204 AA442169 H60364
			AA218859 AW466993 AI814390 AW500165 N94739 AI338468 AA058603 R15577 AA776470 AA777649 AW028118 BE549724 AW118873 AI889182
			AI038086 AW058542 AW302201 AI261586 AI803064 T86302 AA442065 AW440623 AA969289 AA426118 AI129606 T84064 AI590199 H08774
			AA587997 AW504429 AA452862 AI242610 H08651 R42254 AI017372 AA479047 AI033228 AI241602 AA705970 AA745763 AW769960 AI335551
			AA133175 AA648167 AA465370 AW302548 R42953 C06435 N67780 W88555 AA463878 C75525 AA349461 AW081189 D20156 AI475416
			AJ227859 AW611503 H59092 F10246 F13771 AA370197 AI370219 AA703118 T16351 AI948928 AI216237 AW291869 AI394635 AI927363
			AI459067 BE244770 R18054 W90004 W03406
			W07140 AF086140 AI822063 N91527 AI822117
			BE247684 BE246891 AW016625 W46364 W46224 AF086187 AA284275 AA909563 AI075688
			AI282149 AW050766 AI431887 AF086235 W57731
			AI927629 W67460 AF086266 AA934119 W67461 AI376255 AI823382 AA131325
			AI824060 AA836320 AA906496
			AF086294 W70254 AI218651 W70255 AA885186
			T69980 W73223 AI343367 AL120439 W73838 AF086297 W86441 W73694 AA042918 W84335 W84396 W86509 AA701234 AI653722 AI683403
			AA042906 AA936438 AI381739 AI247805 BE045944 AI421349
			AF086310 W69933 AI375695 AW373265 AW608623 W69803 AA604952

5	439560	47377_1	BE565647 AA384580 AI985958 AW118400 AA131255 AI017605 BE546585 AA131345 AA318529 AA316901 AW014441 AI632144 AI765495 AI745595 AW473886 AI263026 AI377804 AW664079 AI806774 D20313 AA864830 AA993300 AI991497 AI092233 AI253607 AW237133 AI638158 AI223187 AA653544 AI972790 AW966478 BE175948 AI056618 AI076321 W79643 AF086388 AI418395 AI743471 AI744094 W74123 BE549611 AI796878 W79123 AF086432 W79920 AW873727 AI611298 N22415 AA838783 AW450533 W79377 AF088065 BE348731 AL119650 AA166648 AW016476 W81285 AA258105 AL119947 AA331387 AW965247 R53043 AA290926 AI741816 AI761457 AI453831 AA888796 AI051065 AI075210 AA843898 H87971 AW004862 AW085525 AL043807 AI435445 AA844005 AI079684 AF086538 W95969 AI631911 W95835 AA524504 AF086549 AA931946 AI052102 W94492 AF086565 AA010135 AA010136 AL109688 R23665 R26578 AV652707 AA693817 AV647943 N69453 N70232 N94146 R92830 AL359654 N76783 H73446 H74127 H40442 R97678 H82906 W01021 W03283 AA007527 T81163 N63789 T58818 AI769510 H73934 N63729 H40443 R93048 T95956 H63718 T95962 AV649374 H82907 R97679 T80868 AL360137 AA455730 AL138067 AW978717 AI741559 AI034231 AI679611 BE044415 AA824642 AI350608 AI683265 AA598951 AW136488 AA854689 AI299060 W37504 N38890 AI970972 AI936400 R48273 R88518 AA847584 AI940762 AI940747 AA854024 AA889110 AW937417 AW979195 AA856979 AW999881 AA918129 AI732900 AI272847 AI278764 AI285200 AI339550 AA857118 AI263965 AI793156 AI952997 AW402306 AK001345 AI693653 AA465467 AW974459 AA081718 AA648450 AA927610 AA764878 AI636548 AA465468 AA449153 AA989477 AA350600 R14621 Z42414 H12254 AA663805 AI625726 H48597 H08479 AW080101 AW080074 AA322400 H62103 W94460 H80467 AA295083 AA045999 AA322642 AW021802 AA040820 AA335467 AW952566 AI476789 AI744598 AI608724 AI271619 AI951091 AI884709 AI744653 AI978846 AI660134 AW800463 AA700728 BE220512 W94351 AA749238 AA970637 AW057695 AW571668 AA831554 AW043767 AA040157 AI810228 H48791 H81387 AA046104 AI813379 AI026643 AW102687 AI095327 AI015840 AI277634 AA835199 AA640450 T17078 H12255 AI338417 AA854569 AA836209 AI061248 BE242087 AI298338 AA838341 AA643527 AI061232 AI915382 BE243602 AI915493 AW999552 H61198 Z38620 AI868473 AI471191 AA868059 F02599 R49291 R46153 R13438 R21307 R40949 R45608 AA897461 AI376820 AI809991 AW661854 AI829714 AW572368 AA862176 AI733011 AA865542 AI791407 AA865818 AI732997 AA977633 AB002297 R21019 R24849 Z46003 R53332 R35190 AL118982 AA355887 Z43686 T78686 F11356 AA888981 AA412141 M78951 AA394289 R50850 R53937 AW303583 AI656559 AW589817 AI621051 AI933711 AI825042 R44552 R39312 R46134 AI302700 N51360 AI651758 T17357 AI161203 Z38651 AI961153 N50920 AW090632 AI423054 AI167950 AA976204 AI360906 M79104 R39087 F09016 Z39744 T80400 AL040356 AW893434 T05544 H05049 AI129949 D60235 AW517611 Z40823 C15241 D81133 H23869 D60505 AA872685 D79646 D62470 H23868 H23914 D61233 D60722 D61106 60930 R24595 NM_007281 AJ224677 Z45077 F05970 AA448520 AA128221 AA399071 AA418665 AA444139 AA401420 AI588970 AA393569 AI379612 AI658841 AI129258 AI685542 AI435359 AI005196 AI800686 AI953018 AI885864 AI018515 BE218367 AI375426 AI094019 AA447539 AA127018 AA620952 AI374902 R40285 AI005649 AW008672 D62671 AA400285 AI474174 D79860 D79837 D61885 AW136117 AI028787 AA759022 AI341750 AA443959 AA435498 AA460975 D62374 AA707516 R44400 D79883 AI129874 AI129876 AI274085 AI494379 AA782944 Z40803 T23467 F02215 AA910488 AI431623 AI473290 AA774444 D62484 D79233 D79872 D79372 AA418611 AA412171 AW582828 AI871778 BE045724 BE218008 BE328896 BE220092 BE463428 AW291567 AW445158 AW291349 AW182128 AW340989 BE466977 AA878939 AI733078 AI791571 AI933184 AA969205 AI937212 AI571347 AI554779 AA883627 AA910460 AI540234 AA883849 AA884283 AA905558 AW190026 AI693520 AA884289 AA974674 AA909944 AA994364 AI243754 AI911339 AI024071 AA884496 AW888581 AA885428 AW269903 AA969749 AI733037 AA885583 AI791527 BE503100 BE045608 H92571 AA885704 AI272165 AA886169 N58344 T74597 AI948966 AI733048 AA887457 AW418994 AI763059 AI131245 NM_006323 AA331660 N44578 AW371307 BE176956 BE176989 BE176992 AA186526 AL048468 AW852333 AW376339 Z43853 BE090810 AA288026 AA256423 AA194812 T18561 Z43797 H15282 AA255856 AA279589 R20079 T27087 Z42889 R36319 AV652550 AA234430 R85595 AA215680 R05490 AA227601 AA375965 AA860951 N28686 N31219 W96079 AW138352 AA318705 AW891762 N75153 AW175957 AA165272 AA194999 AL048469 N21283 BE467238 BE046998 AI971076 AW140072 AI655646 AW204730 AW149689 AI631865 AW593881 AA215681 AI669703 AI631673 AI432147 AI829789 AI521142 AI492434 AI674128 BE551662 AW614108 AI400478 AI081573 AI521685 BE502950 AW614587 AI651180 AW129475 AI193145 AI342508 AA182803 AI278064 AA182828 AI126161 BE502323 AI985255 AI341841 AI399915 R49251 W96080 AI797704 AW129480 H15283 N58817 AI225122 AI239883 AW770467 AA234343 AW192261 AA227901 AA991931 AW083386 AA165273 AI978564 AI282883 AI309945 AA256535 BE045834 AA552024 R41213 AA935846 Z39864 T27086 F03103 AA506888 AA508821 F02354 AA283940 AA971119 AI470509 T23687 AI969367 AI267407 AI267408 AA593122 AW970524 AA186490 R05597 R14552 R11785 AV657117 AV657137 BE279960 AW183106 AI417824 AA524489 AA877208 AI031680 W46305 AA738371 AI142429 AA037511 AW025976 AW027133 AA215471 R72282 AA460670 AA026291 AA164681 AI042007 AI290331 AI290351 AI366685 AI189645 AI333703 AA425386 AA633287 AA706737 AI221810 AI052430 AA652027 AA972920 AI282965 N29732 AI263145 AI187154 AI183295 AA946683 AA461169 AA435685 D60552 AI040554 AA651973 AA579689 AA150718 AI027047 AI183293 T24483 AA889945 AI034423 AI377295 AI733055 AA894776 AI791545 AW296024 AA897109 AI015000 AI140686 AI376524 AA897333 AI073991 AI494628 AA904701 AW086077 AA904727 AI609130 AW612173 AA904739 AW268617 AI223339 AW269923 AA906176 AA972307 AW593050 AA909915 AA906131 AA906366 AI910938 AA938956 AW370882 AA907048 AA910431 AI799488 D61945 AA909069 D79285 D79629 AA909536 AI147364 AI142372 AW511090 AI698754 AA909924 AW196772 AW340608 AA909939 AW444669 AI936616 AI208871 AI733106 AA910921 AI791603 T99289 AA916698
	439567	47389_2	
	439606	47435_3	
	439626	474565_1	
10	439634	47465_1	
	439693	475350_1	
	439702	475444_1	
	439703	47545_1	
15	439715	47556_1	
	439724	47571_1	
	439780	47673_1	
	439786	47682_1	
20	439818	47731_3	
	439831	477578_1	
	439871	478212_1	
	439911	480063_1	
25	439950	481368_1	
	439953	481468_1	
	440046	4839_1	
30	440048	484235_1	
	440122	486363_1	
	440129	486597_1	
	440184	4877_1	
35	440209	488434_1	
	440274	4906_1	
40	440299	491353_1	
	440310	491687_1	
	440356	492503_1	
	440364	492704_1	
45	440385	493106_1	
	440388	493112_1	
	440400	493296_1	
	440448	494143_1	
50	440454	494275_1	
	440460	494368_1	
	440472	494688_1	
	440504	495609_1	
55	440515	4959_1	
60	440527	49640_2	
	440577	497567_1	
	440615	498522_1	
	440621	498744_1	
70	440633	498929_1	
	440727	501406_1	
	440728	501427_1	
	440729	501435_1	
75	440790	502642_1	
	440801	502835_1	
	440836	503385_1	
	440887	504806_1	
80	440911	505196_1	
	440925	505525_1	
	440926	505537_1	
	440964	506316_1	
	441092	509342_1	

5	441107	509652_1	AA917075 BE550501 AI352666
	441115	509816_1	R69910 R70859 W37379 AW594566 AI797410 AI962344 AI655722 AL041380
	441143	510608_1	AI027604 AI377787 N95552 BE326812 AA918459
	441191	511796_1	AI693930 AA922245 AI209140 AI240647 AI240037
	441201	512170_1	AW118822 AI572563 AA922703 AI304670 AW027079 W32420 AI861802
10	441216	512508_1	BE299830 BE326294 AA923118 AI914145 AA935529 F19112
	441218	512531_1	BE327561 BE467043 AI914338 AA923146 AI702963
	441227	512660_1	AW295407 AA978280 AI356225 AI356223 AI934375 AW591616 AA923305 AW591522 AI818014 AI809608
	441233	512775_1	AA972965 AI685347 AA923446
	441247	513160_1	AW118681 AA926689 AA970358 N47565 N47576
15	441274	513708_1	AW593781 AI652488 BE550283
	441358	515468_1	AW173212 AA983948 AI080705 AA931334
	441396	516356_1	AW293677 AI694402 AW470554 AI912235 BE502721 AI457491 AA932388 AW341805
	441398	516366_1	AA932398 BE061185 BE061182 BE061183
	441416	516661_1	AI990139 BE463783 AI633376 AI950180 AI365307 AI202877 AA932762
20	441445	517339_1	AI221959 AW050689 AA934051
	441453	517467_1	AW176106 BE090052 AW900530 AA934424
	441519	518936_1	AA972740 AA936360 AI218569
	441605	521245_1	AA984647 AI733398 AA969514 AA946664 AI733260 AI791810 AI793284
	441609	521332_1	AA946764 AI733357 AI791693
25	441627	521970_1	AA947552 AI039639 AW129567 W70242
	441638	522131_1	AW293202 AW003993 AW593790 BE501226 AI968324 AI825626 AI637708 AA947748
	441640	522148_1	AI733345 AI733846 AI214791 AA947765 AI792668 AI791681
	441675	523040_1	AI914329 AI992361 BE502899 D25933 AI760161 BE219948 W35402 AA952962 AI476738 AI681485
	441676	52305_1	BE564206 AI445657 AI822078 W05423 AA342991 AI822134 AW195490 N70553 AA714919 N99767
30	441700	52349_1	AA233556 AA326421 AW962211 AW298715 BE564252 AA287248 AA504105 AW969009 AA831589 AW021233 AI926966 AA845327 AI638536
			AI807521 AI378892 AI393737 BE350596 AW076057 AI425017 AA029853 AW291206 AA496993 N40998 AI560716 AA976890 AI927916 AI251923
			T19728 AI076039 AA001568 AW772170 AA828483 AA748527 AA678626 AI276340 AA830226 AI424779 BE327768 AA806319
			AA968636 BE326305 AI703164
			AI073548 AA992962 AI809805 AA968945
35	441802	526422_1	AW969706 AA456258 AA491881 BE501639 D62113 AW969710 AI591236 AI379869 AW968997 AA040053 AI807206 AW663917 AA454645
	441811	526641_1	AA489238 BE241958 AA743491
	441817	52669_2	AA970389 AI024294 BE550476
	441874	527877_1	AW172630 AW510707 AA970664
	441884	528091_1	AI733386 AI733449 AA972780 AA988876 AI791748 AI791798
40	441969	529902_1	AW975183 AI365103 AI301787 AI699495 AA973583
	442006	530581_1	AW268583 AW664901 AA975481
	442078	532175_1	AA977235 AI733211 AI793144
	442137	533597_1	AI278777 AI820598 AA988103
	442264	537153_1	AI733477 BE550823 AI820652 AA995972 AA988595 AI791878 AI792046
45	442278	537543_1	AI820617 AA991149 AI792013
	442312	538387_1	BE379594 AI192455 AI039862 AI744012 AI761735 AW243181 AI743687 AI928223 AI423022 AI627855 AI636059 AI651571 AW802044 AI826995
	442353	53973_3	AI431733 AI539125 AA863056 AW270910 AI768930 AW008835 AW615183 AW591147 AI695294 AI672108 AA506358 AI308060 AA011556
			AA962437 AI935488 BE219625 AI004356 AW151394 AI218466 N66178 AI419784 AW242519 AW946907 D60374 AA989263 AI698799 AA470460
			AI824167
50	442360	539963_1	AI374621 AI949385 AW005031 R70012 R70057 AA993031
	442377	540653_1	AA993807 T77400 F13359 R21559
	442430	542268_1	R89164 H77767 AA995737
	442459	543175_1	AI264628 AF017648 AI872732
	442479	543556_1	AF069484 AF069485 AF069486
55	442617	547171_1	AW340093 AI733574 AI004175 AI792175
	442690	548911_1	AI014727 AI694063 AI434799 AW611629
	442704	549542_1	AI015463 AI239705 AI023561
	442710	549696_1	AI015631 AI971547 AW027492 AW450071 BE501147 AI637836 R42871 R37086 AI668981 AI949558 AI634411 AI656975
	442717	54984_1	R88362 AA352467 AA322363 N84512 N56275 T66643 R20865 F06960 Z43996 F11883 H08487 R14090 BE548683 W25130 T75336 F13074
60			BE093651 BE567745 BE567025 AI240085 AI819379 AA843681 AW973427 AI024131 N75689 N77138 AA521252 BE552422 AI609112 AA805736
			AA805768 N93288 N35117 R42045 H08766 AI383445 F09530 AA570560 F10668 T16757 AI205823 N59330 AI862990 T65572 AW118458 Z40051
			F03229 T16472 N66503 R39961
	442726	550048_2	AI136066 AW207524 AI016019 W93091 R01213
	442757	550839_1	AI739528 AW451488 R63510 AI338940 W72910 AI016891 AI147482 R62633 H87957 R78135
65	442772	551188_1	AW503680 AI017286
	442783	551467_1	AI017586 AI375709 AI805833
	442789	551579_1	AW904361 AI017707 AI733633 AI792353 AW889402 AW383190 AW383198 AW383220 AW383258 AW383135
	442849	552953_1	R10099 AI022302
	442879	5535_1	AF032922 NM_007269 D63506 AV661506 N87584 AI383990 AA166699 R61138 F07137 R13734 AA173515 AA344140 AW965096 T24862
70			AW630812 BE009339 AA207077 AI760059 BE003841 AI669581 C03115 AW517672 AI598267 AW769244 BE003851 BE464825 AW081457
	442901	554142_1	BE003849 BE003850 AI031901 AA873292 AW080551 AI560158 BE048958 AW074547 AI635695 AW001685 T48216 AW627572 AI985385
	442927	554754_1	AI598106 AA831878 AA598778 AI356988 AI888542 AA173425 AI695353 AA669965 AI933914 R20770 BE349623 Z40240 R61856 H21607
	443054	5582_3	AI023654 H65786 R00075 AI263386 H65785 R00386
			AI024347 AI191965 AI191954 AL119005
75			AI745185 AI080391 N36089 AA708798 AW081855 N24539 N25254 AI453014 AA757558 AW117329 AI224863 AW129441 AI911652 AI590105
	443162	5613_1	AA948114 AI346143 AI281049 AI381643 AI264814 AI521478
			T49951 AA025326 H04839 AA393303 R63101 W57657 W25628 AI961431 R71165 N39940 H01548 H01759 AA641624 AI634930 AA595296
			AW994770 AW994747 BE047247 W38159 AA858133 AI701944 AW386273 AA676625 R24676 R79410 AA922863 AI151319 H01013 AA024482
			W02674 H01456 AI150858 AW135972 AW631167 AI270332 H04750 T49622 AA004543 R63061 AI093066 AI247539 H01225 H03388 AW472933
80			AA382448 AI219287 N27194 AW389613 AA649738 AW994764 AW389614 R25176 AA897262 R71626 AA909471 R71240 AW811917 R76109
			AI202312 AI866010 R76162 AL117538 R79411 T58656 AW994674
	443169	561642_1	AI038687 AI056040 AI277376
	443185	5621_1	NM_006134 AF045606 W24960 AI277739 BE256559 BE259499 AW937970 W69668 AF086280 AW937958 BE221676 AI498344 N95717 W69669
			AI521497 AA700519 BE142872 W06899
	443212	56298_2	AW269515 AI189011 AI076872 AI866729 AI499523 D62701 D62523 R50930 AA450334 AW518379 AA621080 C01621
	443246	56370_2	T75157 D80121 N98792 AW079529 AW243564 AA917457 N66589 AI805853 AI698508 AI364248 AF281037 U54720 N98659 W56141 D81911
			F13480

5	443271	56450_1	BE568568 AI760908 AA934755 AI654187 AI984325 AW303997 AW085188 AI823317
	443283	56492_-1	BE568610
	443305	56552_1	AI050693 N75861 N22065
	443363	567586_1	AI792629 AI335223 AI792549 BE139219 AI252829 AI254595 AW302734 BE138428 AI053810 AI053473
	443367	567595_1	AW071349 AI792491 AI792441 AI275251 AI271041 AI289554 AI307043 AI340919 AI305954 AI492706 AI341041 AI313310 AI308281 AI733965
10	443372	567646_1	AI308430 AI305589 AI270815 AI305846 AI309341 AI275254 AI309794 AI306757 AI312359 AI340760 AI432284 AI306045 AI334694 AI492798
	443394	567996_1	AI308597 AI308410 AI349657 AI611456 AI349920 AI054382 AI053506 BE043384 BE043150 AI570494 AL046013
	443458	569736_1	AI792557 AI792476 AI348915 AW271932 AI335391 AI311278 AI254532 AI254565 AI377181 AI377169 BE139112 BE138474 AI378703 AI349125
	443475	570368_1	BE139422 AI144072 AI054039 AI053629 BE139209 AI345509
	443482	570596_1	AI055865 AI188819 AW999478 AW606195 AW382864 AW382862 AW382830 AW382806 AW606193 AW382764 BE153628 AW292813 R97578
15	443486	5707_1	R05385 AI061251
	443526	572763_1	AI066470 AI889955 AW770868 W46957 AI913228 C01207
	443555	57342_1	AW188093 AW188180 AI066737
			NM_003428 M27878 AA353240 X60156 AW389350 T28241 AW949471 BE154245 AW993912 AW797295 AA091326 AA648691 AW797309
			AL041644 AI652238 AW594530 AI972064 AI125934 AI373883 AA403146 AW771804 AA587259 AA401082 AW152027 AW952639 AA632889
20			AA572909 AA528434 T04918 T63002 AI625085 AI817337
			AW792804 AW792795 AW792796 AI075911
			N71710 AA259158 AA449636 AI817388 AI263621 AA648782 AI017500 AI453043 AI830660 D62609 AI631311 AA904879 AW612058 AW294250
			AI015722 AI453475 R39884 AW188277 AI264031 H07929 AI300234 AW516556 AI424714 AA172012 AA013250 AW439941 AW189712 AW028517
			AA172063
25	443556	57345_1	AA256769 AA345353 AW963237 AA210810 AV645652 AV645913 AV645970 W90355 AA449283 AI934339 BE048840 AI832091 AI627802
			AI634661 AI522317 AW451433 AI633181 AW029157 AW300163 AW772209 AI141749 AW300172 AI000130 AW237845 AI350320 AI802086
			BE219105 AI299838 AA935949 AW967952 AA704553 N54296 AI206526 AI201757 AI033764 W90356 AA037807 AW134960 H97986 AA830516
			AA535540 N20010 AA262693 AI927096 AA703604 AA009872 Z26980 AA210691 AA999675 AA999660 AA449228 BE439590
			AI807036 AI589217 AA884119 AA650257 AI125304 H03099 AI953750 AI339433 BE245994 AA907844 AW608751 AW608742 AW608749
30	443614	57545_1	AA738171 AW875727 AW937979 AW875884 AW608782 AW608744 AW373413 AW373402 AW875793 AW875808 AW875880 AW875789
			AW875883 AV645774 AW608798
			AV655386 T53934 H65614 N91293 H60133 H61872 AI057008 H60652 N91067 N54429 N68450 H89498 N73582 T53810 H55898 H60134 H64326
			T90818 H59838 H54060 T68461 AA342972 AI651926 AW241535 H65615 N63663 N74009 AV652052 AV651432 AV661013 AV661021 AV660949
			AV660972 AV645892 AV652930 AV655585
35	443657	576685_1	R14973 R14967 AI081006
	443682	577184_1	AI383061 AI921238 N51392 AI333936 AI458514 AW195151 AI277672 AI081587 AI351334
	443718	578436_1	AI083580 AW025217 AI949865 AI828836
	443748	579192_1	AW206447 AI248530 AI084433 AI400976 R16553
	443764	579650_1	F23283 AI084941 F35774
40	443773	57996_1	AV646452 AV646460 AV646805 AV646815 AV646479 AV652020
	443777	58009_1	AV646510 AV646816 AV646779 AV646466 AI698180 AI700981
	443921	584994_1	AI091310 AI435135 AI742662
	443931	585184_1	H23213 R44634 R44521 AI091520 Z38545
	444009	588627_1	AI380792 D20062 AI095370 AW073511 AI914042 AW190876 AI858380
45	444050	590366_1	AW138295 AI356654 AI097659
	444087	59164_1	AV647899 AV649427 AV649454
	444097	591988_1	AW517412 AI123734 AI373818
	444098	59198_1	AV647969 AV647970 AV647936 AV647971 AV649444
	444106	592164_1	AI123922 AI123933 AW603804
50	444109	592368_1	AI124553 AI124570 AI742533 AI820068 AW503547 AW903120 AW500995 AL134993 AW896969
	444125	592659_1	AI124882 N67984 R68189
	444140	59308_1	AV648089 AV648224 AV648066
	444148	593201_1	AW003204 AI125596 AW183056 AW468834
	444187	595096_1	AW138466 AI272647 D61994 BE551020 AI306142 AI127700 AW341329
55	444206	596553_1	AW301017 AW071152 AI698742 AI129324
	444217	59708_1	AV648751 AV648948 AV648755 AV648579 AV649100 AV648717
	444230	597450_1	H95537 AI252647 AI130943 H95525
	444313	600664_-1	AI140494
	444338	601755_1	AI937026 AI141771 R87302 BE048158
60	444414	605446_1	AW293214 AI147743 AW026298 AI939329 AI160101
	444453	607269_1	AW379394 AI149818 R57034
	444459	607543_1	AI680624 AW268824 AI203891 AI150108
	444493	608458_1	R59410 BE144663 AI151123 BE502907
	444498	608711_1	AI151413 H28792 R45290 AI472924 AW070437 Z38752 AW593412 AI651293
65	444517	609298_1	AI939339 AW051016 AI160276
	444575	611385_1	AI264847 R43910 AW614197 AI863821 AW467620 AI695292 AI672346 AI302090 N81071 AI611641 AW166600 AI168293 AI313201 R43835
	444584	611496_1	AI168422 D80113 T59074
	444585	611509_1	AW170015 R33479 R67878 AI435489 AI168436 R69800 D51015 F08994 F08984 T16467 AI283968 BE502245 AI917105 R69799 R81389 AI660093
			R81390
70	444711	616797_1	AI188739 AI199794 AI868790
	444715	61692_1	AV650947 AV651027 AV651733
	444750	618592_1	AW242684 AI190795 AW058471 AW612358 BE156035
	444771	6193_1	AB023201 AW862491 F12415 Z42675 T74277 T68970 R12972 R56199 H14683 AW898750 AI686422 H08935 R60625 R56087 AW134976
			BE042973 AI802074 AI458698 AW629209 AW104866 AA336335 AW151449
75	444827	62213_1	R09764 AV651942 AV651629
	444848	622824_1	AW451176 BE551388 AI701475 AI680942 AI199433 AI631918 AI950349
	444870	623844_1	AI200621 AI439729 AW304871 N59474
	444905	624840_1	AW135863 AW006409 AI800007 AI201724
	444922	625418_1	AI921750 AI674408 AI568798 AI686114 AI612728 AI744116 BE326883 AI949058 AI499386 AI825947 AI678940 AW236450 AI202380 AW151821
80	444931	62567_1	AV652066 AA459880 T58512 T58561 AI651255 N49838 H87921 AW264447 AA428067 AA364094 AW955685 D62894 AW341452 AA243652
			AI984618 AI816803 AI871252 AI376942 AI740496 AA452836 AI277917 AI149141 AA456147 AI784566 AI003975 AI245674 AI433703 AI200208
			AI268985 AI382921 AI201946 AW304852 AW262780 AI168633 AI468793 AI659125 AA813519 H88317 AI474943 AI382763 AI758206 AI932757
			AW955686
			AW002844 AI203158 AI655366
	444963	626212_1	AI916973 AI203269 BE045921
	444992	627145_1	R37658 R44530 N63005 R20634 N34919 AW592216 AI204348

5	445020	627991_1	A1205655 AI393391 AI799118
	445038	628439_1	AI635444 AW137083 AI653055 AI206167 AI206286 AI825389
	445049	62852_1	AV652718 AV652415
	445061	628730_1	AI253094 AI480138 AW000921 AI793239 AI820804 AI206494 AI793063 AI792470
	445073	629058_1	AW291389 AI990406 AW002552 AI206867 AW196388
10	445117	630674_1	AI208754 AW664978 AW087492
	445189	632282_1	AI936450 AW592148 AI476512 AI215572
	445205	6326_1	D83776 T76934 F13102 AW381500 R60511 AA304813 AW966698 AW992279 AW793045 AW605075 H16011 AW992123 R76348 BE151815 W94996 AA417845 AI049962 AL045167 AI022987 AA091051 AW949893 N98228 AI076173 AI809048 N47857 AI613421 R40333 W93381 R60512 AW196866 AW272150 R38071 AI678426 F10702 H15905 AA295543 AI689356 AL135488 AA894676 AA248920 AA449736 AI721205 R54137 AA428502 AA448593 AI285385 AW075724 R57655
	445225	633141_1	AI216555 AI697562 AI640297
	445233	63345_1	AV653034 AW875428 AW875755
15	445260	634439_1	AI218133 BE156262 BE156252
	445292	63525_2	AV653264 BE065084 T75514 T75544 N98629 AA778205 AI192865 T75480 W80381 AA682546 AA721100 AA503048 AA702885 AA649271 AA715054 AW149852
	445409	638501_1	AI949081 AI222675 AI630856 AL121471
	445432	63943_1	AV653771 BE089370
	445510	64184_1	AA946676 AA290717 AV654067
20	445564	6435_1	AB028957 AL120001 AI267678 H10928 R19844 AW970334 AA393182 F05472 F11711 H09908 N50250 AI815411 BE463679 D61468 AW970253 D60889 C15548 D61011 D60867 AI815795 AA534831 D81386 AW235039 AI382158 D81174 AA416899 AA852310 H09789 H10929 H09813 F09369 R44721 D51515 Z38456 R14004 T66255 F12148 F12139 AW351702 M85350 AI018713 AW972450 AW972645 AA514964 T66172 F09785 F09776 AA436608 T05327 T07118 AA339352
	445568	6436_2	H00918 AA165336 H15885 AI149852 AI809562 AI365149 AI654827 AW590162 T78758 R18887 H52748 H04859 Z44077 AI927768 AI927758 AI927757 AA985170 AW958395 Z43289 D81295 AA985065 AA379840 AA305419 D81446 AW299583 R68307 AA017267 AA021586 AA058844 AA011038 AA059216 H86492 AA059157 R62754 N99176 H85604 AA059215 AA020967 AI580948 AA348267 AW961810 D60322 AA017348 AA011160 AI241937 AI383112 AW304135 H46107 D62629 D60323 H91991 AI453702 AI362528 R68272 T32807 AI193562 AI359235 AA746048 H00919 AI357382 T16370 AA909430 AI421572 AA927292 AW298053 AI365324 AA634475 AW207262 AW341104 R37302 H04764 AI977740 AA905264 AW593464 AW593449 AA904547 AW593480 AW593404 AI470080 T31617 AA165369 Z39361 F03272 AI423550 AI365991 H01477 AA983881 AA969956 AA318875
	445611	645146_1	AW418497 AW451118 AW235854 AI758099 AW237486 AW269306 AW242392 AW771464 AI262860 AI766090 AI700851 AI733790 AI792591 AI334976 AI307816 AW301240 AI632694 AI244992
	445621	645366_1	AI733818 AI261811 AI245236 AI792639
	445635	645884_1	AI769774 AW295005 AI766749 AW467103 AW299705 AI991407 AW195031 AI245830
35	445660	646976_1	AI702668 AI247286 BE220208
	445688	647796_1	AI248205 W86789 AI810489 AI474340
	445711	648344_1	T79611 AI248791 T79696
	445748	6497_1	U80766 R45968 H17929 R44810 T89020 F10112
	445829	651854_1	AI452457 H95358 AI824534 AI553712 H56682 AI535846 AI261464 AI733816
40	445898	6537_1	AF070623 T80072 H08917 R35413 H14948 T80074 C15452 D81744 F05382 F05380 Z45148 R18285 AI634532 BE549752 AW299752 AW090717 AI693471 H08831 BE217766 AI373383 AW137702 AI241235 R49210 R38766 AA757779 R38765 AI498410 AI693124 AI648374 R14143 AF070526 T80099 AA366440 AA781163 R38778 AA317424 AW241963 AA535053 AI224878 AW470500 AI806061 AA678084 AI681339 R13580 AF070565 F11193 Z44446
	445900	6538_1	H06336 T81273 AF131788 T80341 H06284 R39038 R38884 T20284
	445908	6541_1	N33522 AI334417 AI274841
	445944	6562_1	NM_000929 U03090 AI701153 AW900253 BE222079 BE222806 R32409 AI051138 N54791 AI418243 AI583184 AI769155 AI768971 AW972975 AW008815 AA973633 AI420062 AA526578
	446092	661693_1	H77395 AI276821 AI474228 Z33529
45	446131	662_1	AI279299 AW470350 AI525788
	446139	663406_1	AI375025 AI280244 AI470350 AW451031 AI342721 BE140640
	446190	665642_1	N66336 AI620431 AI308131 T23975 AW051560 AI298642 AI282592 AI334623 AI693443 AW470508
	446209	666485_1	AI283125 AI291693 BE007283
	446242	668327_1	AA985662 N53352 AW371974 AW362930 BE550916 BE172700 AI888088 AW772273 AA401940 AA345071 AW965161 AW965162 AI935241
50	446252	668725_1	AW074281 AA664156 AW677729 AA402095 AI700767 AW269601 AA054585
	446296	67012_1	AI285848 AW274006 AI285847
	446302	670794_1	AB006624 H98087 H89823 W01922 AW846344 AW375619 AW375590 AI656446 AW846513 AW846423 AW846520 AI954621 AW846509
	446364	6746_1	AW846522 AW205215 AW205991 AI361588 AW193731 AA588837 AI631442 AW291638 AI097266 AW408128 AA731997 AA195898 AA361560 BE613425 AA355579 AA424375 R57186 AA694138 H55853 AW403691 AI174809 AA830414 AA830494 AW275865 AW581715 BE179839
			BE162842 BE179852 AW373702 BE179934 BE613295 AW968230 T97115 AA258096 H91376 H80498 T81399 AJ243225 BE464009 AI692806
55			AI042049 BE046527 AI209000 AI188514 AI332988 AI375388 BE550546 AI635540 AI628832 AI683656 AI174519 AI190387 AA773300 AW514965
			AA625929 AI554280 AI283324 AI611631 AI690648 T97001 AI991403 AI689180 AA760975 AA766792 AI440077 AI149764 AI184358 AA424524
			AI039536 AI141238 H81416 T81400 AW196876 AI214990 AW197049 AW965952 R98300 AW500884 BE147950 AW362044 AA534307 AA380314 AA374807 R06924
			AW014174 AW996328 AI298175 T56840
			AI298405 AI457191 AI632887
60			AW576760 AW139364 AI300481 AI299104
			AI743737 R31923 AA376806 AW956333 AA767582 AA909031 AI382417 AA133971 AA039504 BE018194 H38741 AA012970 N47175 H04876
			H03130 AA278514 AW390676 R58333 R64513 AV658563 AV658433 AV658481 AA330472 D63085 R31059 D79916 AA737386 AW886866
			AA328687 AW961394 AW958084 AA479989 R32975 AI336848 D62895 AA291184 AA258032 BE301671 AW515258 D62877 BE218993 AA130246
			AW103896 AA039505 AW627998 AA781243 AA826100 H03942 AA344706 AW965130 AA708612 H04778 R65604 R32976 H38659 AI524495
65			AI472676
			H38026 AA019124 AA053939 H86599 NM_004312 AF033105 S66793 AF076512 U03626 W28132 W27277 W26431 AA047869 H86518 AA019125
			AI307356 AI796352 AW469968 AI767356 AI762913
			AA151730 W05526 D79797 AA449561 AW000891 AI640553 AI631971 AI565810 AW025213 AA640299 AI859413 AI631750 AI631793 AI964068
			AI420725 AI202187 AW300134 BE223003 AI889621 AI421550 AI492458 AW150347 AA151649 AA317639 AI830656 AW580307 AI674988
70			AW769971 AA478767 AA449304 AA935184 AA526157 AI631123 AW067870 AI051366 AI149797 AA393994 H03631 N70512 AW444608 AA644080
			W16856 R69093 BE092770 BE092737 AI339649 BE463403 AI376380 AI361086 R37847 AW079869 AI473395 AI825269 AI337196 AW242952
			AI473262 AI538140 AI767203 AI522180 AI273120 AA643644 AI825749 AI262640 AI796453 AA558703 AI016170 AI799347 AA995841 AW967089
			AB040933 AL157471 BE314014 AA336933 AA359899 AA308673 AW954717 H73422 R14543 Z43766 R19232 AA095202 AA092058 R19840
			AA359596 W07843 T91632 AA348901 T84020 AW959971 T83690 R16418 BE222080 BE327450 AI695033 BE327709 AW613489 AI871647
75			AI871754 BE503552 AW770483 AI299106 BE327132 AI681772 AA887502 BE218416 AI888794 AI697703 N24730 BE327038 AI001790 T84021
			AW291103 AW299281 N81015 AI299101 R41204 AI358195 AI683984 AI300987 AW903049 AW892410 AI220991 AA577472 R45939 AW470555
			AA626318 T91591 N54300 AW138974 Z39826 R12679 H74192 T92028 BE379237 AA367418
80			

446610	68534_1	AV659433 AV659498 AV659434 AA292418
446619	685_1	AU076643 AA594604 AA346866 R18197 AA345192 AA337773 AA089791 R84435 AA337838 AW392167 AA075190 D55416 AW150360 AW366257
5		AA579816 H93048 AW385689 AW385697 AI186216 AW581197 AL037509 AB019562 AA232626 R97905 AW368019 AA242891 AW888502
		AI798331 AW385635 AW581221 T96947 H87989 AA369511 AA075191 R80742 AA366406 W92752 H45586 AI864016 AW888497 BE004992
		AI384110 AI624256 AI627593 W92728 AI682719 AA948208 AA171734 N40517 J04765 AA379957 AA362403 NM_000582 AF052124 AA300290
		AA333447 AA343721 AW889543 BE566767 R76601 R18015 AA100531 AA489963 AA101296 AA363513 AA344088 AA336750 T77505 D56440
		AL110351 AL110331 F12195 R20175 AA336664 H17766 AA363538 AA363590 D28760 AW578517 AA363531 AI814667 AA846899 AA366253
10		AW951285 AA297992 AA327756 AW361609 AW815455 AW815427 AW815428 D54182 AW852200 AA171630 W27018 AW815864 AW379955
		AW378222 AW362610 BE566022 AW021023 C17352 D58435 AA345409 AI623991 AW020967 AI924770 AI799443 AW946393 AA991239 AI571617
		AI935181 AI923999 AI826895 AI860319 AW189873 AW270353 AW023584 AI813811 R99929 AW339056 AA913152 AI636352 AI829394 AW151077
		AW192580 AI570119 AI086391 AW021764 AW519154 AI375193 AW268678 BE465690 AW019983 AW268654 AI573138 AI141809 AI954553
		AI559242 AA568945 AA886417 AW338527 AI635881 BE465666 AI921239 AA968537 AI956027 AA911981 AI827661 AW511046 BE619780
		AI922227 AI811870 AW190131 AW129220 AW512906 AI290757 AI819088 AI623771 AA775616 BE349419 AI126375 H88773 AI241758 AW275157
15		AI337848 AI613425 AI631387 AA922631 AI273483 AI982898 AW168957 AI446481 BE501588 BE048264 AI499922 AW023812 BE220523
		AW973846 BE349276 AI141091 AA976060 AW973845 AA101270 AI582472 AW613675 AI139360 AI282627 AI276044 N22345 AI261875 AE634136
		AI824468 AW887693 N27107 R21504 AI042223 N22067 AW196871 AI581019 BE004973 AA252035 N22087 AA570717 H11250 AI804026
		AA368098 AA021512 H08842 N26275 AA176368 AI758758 AA570371 AA232574 BE221177 AW190221 AW471386 M78225 AI422140 AI624521
20		AI917975 AA300291 AA568657 AI871430 BE465630 N71862 T72587 W92721 H88774 D54383 AW103693 AW089986 AI82689 R42363 R44962
		T98770 AA357374 AW022074 AI356207 T29241 AW089431 AI933875 N66267 N67352 AA121786 AA363910 F09824 T95618 N66888 R80550
		AI280667 AW196719 R59299 AW021049 H73469 AI954311 BE439454 AW079450 AW973850 AA348338 AW896006 AW268145 AA853631 H17650
		R39537 N66873 N67240 H05298 AI784199 R44260 AA904118 AA911756 F04544 AA807809 AA665210 AI696448 T29719 AA837240 T64844
		H08926
25	446645	687609_1 AI336596 AI334319 AW747993
	446672	688977_1 T05514 AI336159
	446818	694276_1 AI342668 AI807327 BE348803 BE219619
	446845	695066_1 AI343645 AI343650 AI343800
	446847	69513_1 T51454 N50080 AA321803 AW964603 H64365
	446854	69546_1 BE268103 BE396714 BE409435 AA248443 AV660636 AW407539 AW207116 AW138993 AI298513 AI806619 AA355016
30	446861	69583_1 AI696519 BE464779 AW296343 BE550149 AW470402 AA129660 T78937 AA342648 N71662 H82431 AI302712 AV660681 R85409 AA962323
		AI680732 AA889147 AA932629 AW103527
	446868	69627_1 AV660737 R52250 AI886394 W07772 AI082824 W86073 AI816793 R44763 AA633473 AI191256
	446895	69756_1 AA166655 AV661067 AV660890
	446901	697809_1 AI347274 AW844024
35	447033	704603_1 AI357412 AI870708 AI590539 W07459
	447039	70488_1 AV661798 BE153774 BE153706 BE153713 BE153531 BE153473 BE153944
	447044	7050_1 AF030107 T94013 H70046 AW662859 AW516010 AI699379 AW054946 AW664784 H70047 T93335 AA728997 AI862711
	447046	7051_1 AA326187 AW949417 NM_005282 U21051 U21051 L36148 AI719098 AI633710 T94021 AI697516 AW206897 AI801140 T93343 AI492409
40	447124	7091_1 AW976438 AF227899 AI079586 AW242991 AA296993 AF083249 AA743290 AA082927 H38607 AA046204 AI458928 AA810515 AI985329
		AW450239 AA279595 AI632699 AI091806 BE221365 AI130893 AA082926 AI017851 AI474175 AA669471 AA169631 AA248905 AL133594 H08612
		AA247824 AA399016 AI268687 AA479433 BE467082 AA961159 AW890022 AW890015 AW899450 AW890140 AW890016 AI656542 AI656530
		AI284462 AW590370 T61838 AA478729 AA047401 N53320 AA834839 AW264473 AW007865 AA249450 AA167427 AI365221 AI701000 AI680921
		AA385375 AW954119 AI860823 C75362 AI492007 AI539819 AW014989 AW628976 AI473662 AW276150 AA047467 N67246 H08613 AI559629
		AI811077 AI039475 AI431949 AA907555 AI915180 AW148492 AI242862 AI365222 BE018520 AA412178 BE302119 AI823337 AA905198 N83376
45		AI382420 AA776507 T94766 W67770 AW369401 AA262427 W84569 AW968527 R20183 AA485189 F06553 BE080982 AW995604 BE080849
		BE080826 BE080978 AA167428 BE080830 AW995687 AA171673 AW995686
	447147	70999_2 AA910353 AI089634 AA316590 W56516 AI338584 W56797 AA902524 AI458315 AI860006 AA643053 AI000711 AI862467 AA429085 AI300871
		AA633432 AA828052 AA501944 AW630767 AA522925 AW176534 AI767351 AA829558 AA492063 AA988763 F21431 AA101077 AA844646
		AW176535 AI000007 AA508501 AI658725 BE163335 AA994678 AI804697 AI804676 AA083680 AA111865 F33483 AA746183 AI245774 AA082817
		AI719665 AW059695 AI718054 AA308466 F24069 AW176539 F32174 AW751579 F20193 Z24864 AA307876 F24671 T32188 AW795069
50		AW795071 T35821 F35579 BE254660
	447153	71004_1 AA805202 AA630626 AI796571 AW290987 AI872596 D60670 BE614381 D61719 D62994 D62993 AI559539 AW059714 D60671 D60264
	447179	710944_1 AW015633 AI689755 AI365278
	447278	715532_1 AI934935 AI831720 AI823793 AI810582 AI371407 AI867956
55	447290	715902_1 AI476732 AI560210 BE049559 AW118381 AI859875 AI371924
	447313	7169_1 U92981 AA962261 AI692733 AI950941 T98902 A11884 R06378 H57717 T97514 AI912004 AI093572 AA478649 W03804 H57718 AA236955
		AI335952 AA872396 AA599748 AI126672 AA700030 T97515 AW129466 AA479190 AA665547 AI265875 N30635 R06377 T84518 AA235940
		AA256641 AA456403 AA454952 BE617735 AW379216 AW770637 AI832118 AW029247 AI355161 AA454953 AA411021 AI086906 AI080714
		AW016448 AI869615 AW002605 AA455934 AI968677 AI991611 AI082287 AI890169 AI637681 AA256642 AA596036
60	447375	719404_1 AI376660 AW303974 AW469703
	447410	720874_1 AI470235 AW207797 AI378278
	447453	722446_1 AW608645 AW608668 AI380017 AW608671 AW608648 AW502702 AW608637 AW608660
	447505	7243_1 AL049266 H70498 BE326381 AI304487 AI634058 AI184322 AA588474 AI018553 W87710 AW592552 H57340 N58055 AI889948 T99770
	447530	725192_1 AW192063 AW152112 AI383250
	447552	726072_1 AI394125 AI391551 AW382947
65	447613	729170_1 AL041057 AI400688 AW503344 AL048930
	447617	729232_1 AI400762 N33555 H96299
	447624	729790_1 AI640326 AW044051 AI470998 AI401392
	447640	730410_1 AI417187 AW572788
	447748	734749_1 AI422023 AI624442 N47903
70	447777	736695_1 AI424223 BE379336
	447816	7382_1 NM_007233 AB007455 AA309750 AA336123 BE393755 R70282 R06495 AA374963 AI745222 AI819254 N33523 AI633581 AA447887 N41502
		AI129548 H48902 AI092418 AI742848 AA573255 AA960987 AI339023 AI742695 AA715097 AI677925 AI004602 AA970396 R06442 AI151125
		AW016754 AA283095 AI266092 N47733
75	447842	73945_1 AW160804 AW068102 AW503854 BE076470 AW340193 AA486291 AA304448 AW958058 AI018381 AI379897 AA758784 AA905905 AI222228
	447849	739671_1 AI538147 AW130519 AW469126 AI434092
	447863	74006_1 AL047611 AA598728 AW294041 AI051281 AI21356 AI823496 AW302591 AW084713 AI760318 AI914147 AI268728 AW970867 AA976025 H15401
		AW204021 N22479 AI275764 AI690077 AA989488 AI149445 D20906 AI813906 AW517681 AI587179 AW675540 AI962562 AI096973 AI984566
		AI690056 AI061100 AI689933 AI281155 N29486 BE328626 AA232274 AA657814 BE302169 AI282478 AW674031 AA492145 AW672954 AA252923
		BE538090 AA034987
80	447972	7454_2 AL137275 AW968082 AW968084 AA256141 AA249820 AB015331 N29303 H53472 W89179 AI800989 N20237 AA004987 N87513 H96441
		AA625489 N31067 AW070638 AI827515 AI521072 N21661 AA741280 AW976755 W88781 AA732045 H53847 AW504018 AI939552 AW873257
		AI369612 AI083817
	447998	746280_1 AI768289 AW087757 R68571 AI457686 AI760288 R66092 R81827



	448045	7471_1	AJ297436 H02338 AA158880 N32011 N32614 AA525838 AA446964 AI677792 AI139599 AW205435 AA640913 AI685741 AI936226 AI094278 AA548812 AI810655 AA702913 AI017464 AA630584 AI597844 AA662112 H96372 AW338346 AA662078 AA543070 AI086213 AW973274 AI221540 AI685668 AW134915 AI696731 R08364 AI391510 AI220820 AA662861 AI623123 AW006591 AI392790 AI972502 AW139444 AI686348 AI801281 AI583077 AI201402 AI674308 AI474807 AA888696 AI972562 NM_005672 AF043498 R68568 AI885281 AW085485 AI459191 H04180 R68360 AI608821 AI467968 BE080204 H49129 AI470042 N51928 N53742 H50480 AI470790 R95850 R92176 AI472167 AI990315 R32175 AW207634 AW191843 AI498708 AI521251 AI580515 R94048 AW614367 AW024839 BE466075 AI521911 AI522109 AW470702 AI830636 AI886317 AI538880 AI669928 W70342 BE467520 AW903775 AI539652 AW576543 AI800374 N48793 AW195208 AI969934 AI565252 C01574 R62583 BE468212 BE614182 BE613935 AI823381 AI765169 C03367 C04878 C04389 C05524 AW978123 AA814608 AI934926 AI093668 AI766081 AI952346 AW337786 BE079720 AI805612 AI739241 AI684958 AI568069 AW004796 AW389191 AW389163 BE302464 H94814 AI989968 AA280673 AW002665 N87730 AI631632 AA781573 AI041464 AI027389 AI023118 BE168062 BE168047 AW504090 AW022662 AW003488 BE168420 AI582633 AA193403 AI215921 AI298868 AI609261 AI337207 AI797444 AA086431 AI189944 AI245672 AI334812 W68643 AW779167 T07006 AA887953 AA912197 BE538788 AI768027 BE219846 AI340047 AI797022 AI300016 N67169 AI349571 AA171895 AI683278 H95351 AI206637 AF052167 AA248646 AW406226 AA879459 AW177671 AW977719 AW183177 AA280002 AA909779 AW194306 AA778243 R95929 AI283116 AI015707 AI277836 BE247754 AA827095 R38723 AW137651 AF288288 AA171910 AA888080 AI628970 AW974621 AA889874 AA013026 AA889471 W32290 AI342569 AA72252 BE219330 AA890448 AA994525 AW296933 AA933950 AI056092 AW295997 R82043 AI695082 AI954726 AI915753 BE463602 AA782213 AI205533 AA843070 AI004717 AI378166 AA779855 AI522078 AI338269 AW025708 AI702757 AI917482 AI271735 AA719712 AI474675 AI871255 AW131633 AA782567 AA889912 AA805733 BE618168 AI798695 T80243 AA112726 T80244 AI580296 AW593969 AI696051 Z20682 BE277929 BE387818 AA128321 BE547690 AI197957 AI130681 AI805319 AW439254 T69668 W57896 W79850 AI276003 AA622624 AI682257 AI271921 AW006128 BE348974 AI190542 AA557401 AI143567 AW274175 AI798043 AI862624 AI031827 AA635631 AA885331 AA542957 AI086401 AA812275 AW303440 AI423118 AI986386 AI191353 AI858948 AA977290 BE207844 AW338627 AI360704 F25322 W72616 AI281963 AW338643 AA766569 AI624153 W74180 AA595903 BE328413 W57897 AI818074 AA126902 AW964041 AA352356 AW874013 AW293034 AA335568 T62817 AI208462 AA483512 AA552610 T69596 AI955937 AI267972 AI014686 F29862 AA678860 AI675117 AI301770 AI927535 AI269744 AI347307 AI246600 H06710 AI955174 AI521559 AW088101 AW090788 AA552632 AI216018 AA912797 AA969209 AI015021 AI475101 AA864270 AA928083 AA476849 AW263104 Z41212 AA886991 AA142963 AI358862 AA775266 AI355522 AA586508 AI568817 AI659173 AI682078 AW615742 AA885179 AA833520 AW301552 BE042035 BE041782 BE043885 AI306902 AI349684 AI581519 AI803868 AW864876 BE181783 AI583921 AI583345 AI609965 BE140902 AI816573 AI587189 D83781 BE004509 AA368157 AW503584 AW501094 AA206525 R18849 AW368940 BE169159 AW389586 AA129386 W68807 BE300086 AW593619 W68609 AI656261 AI952719 N48153 AI269483 AW665558 BE535763 AW511789 AA742226 AW271391 AW795604 D29578 AI934240 AI681503 AI690203 AA133292 AI114476 AI655376 AW235189 AI620743 AL038958 L08807 AA985244 D13540 L07527 X70766 L03535 AA223445 AA579707 AA096486 AW391060 AA995560 S78088 AW393812 AA609602 AW792945 R19952 AW294215 AI657024 AI631734 AI825711 AW292381 AW002402 AI638753 AI633834 AA428229 F26252 AA447961 AA182748 AJ403135 AA868267 AW137656 AI637841 AI651531 AW197348 AW241510 AW593523 AI637873 AW241455 AI657014 AW594035 AI657036 AI638390 AI638743 AI970540 AI654686 AL119995 AA018483 AA001179 AA001429 AI076363 AA001228 AA001640 AI650471 AW241463 AI652696 BE169100 BE169154 AI650640 AA001356 R85361 T97750 AW451361 AI655628 BE465962 AI954638 AI651345 AA927317 AI536927 AA001416 AA017466 AK001566 AA491327 H86389 AA019025 AA020908 AA125749 AA121350 R24015 N72738 N42513 AA299736 AA299645 AI307349 AW592502 AA885018 W93896 AA515336 AW514100 H98082 AA505134 AA757040 H98076 AA928062 R33304 R21201 AI609538 AA932015 AA125870 BE504827 BE044473 AA121288 N29821 AI458019 D81125 AA506104 AA918595 AA911638 AA328421 N63165 AW952423 N58874 H97540 AI990559 AI653696 BE148586 W80363 AA001712 AA677809 AW207260 AI359676 AI076043 AI359698 AI150898 AA350287 AF109301 T56105 AI918864 C00719 AA001917 AA724979 NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 AI961092 AW590412 AI867583 AI656793 AI695961 AW294208 AA164569 AA164568 AI457662 AI056286 AA002153 AI248673 R92031 AA702653 R72032 AI668609 AI668561 H26423 AI820752 R72031 AI733542 H26352 AI668626 AW029612 H42199 N93057 AI668684 AI734229 W24690 AI535663 AI536079 AA010328 AA004346 H72351 AA694220 T83968 AA004353 AI034166 AI671000 AW590375 AW193729 AI867419 AI610700 AI334978 AW004775 AI307251 AA992104 AI631934 AA004648 AW801272 AW801277 AW242077 T60525 AL036624 AI813924 AI674620 C05278 T86420 AA682462 AA004803 AA677124 AW081253 BE075300 AA421642 N41919 N32581 AA993723 AI025682 AI125816 AW992856 AW995620 AI208288 AI151217 AA694484 AI219027 R28671 AK001968 AW993198 AI247444 AA470066 AI693269 AI797080 BE042966 AI681232 AI797034 AW341051 AI681492
5	448067	747652_1	
	448090	748694_1	
	448117	750395_1	
	448134	751036_1	
10	448150	752165_1	
	448405	761605_1	
	448446	763726_1	
	448458	764260_1	
	448466	764440_1	
15	448582	769426_1	
	448587	770043_1	
	448700	77655_1	
	448756	779022_1	
20	448776	77_1	
25			
	448828	783430_1	
30	448835	78401_3	
35			
	448844	784277_1	
	448870	785609_1	
	448889	786366_1	
40	448912	7876_1	
	449011	793518_1	
45	449015	7936_1	
	449138	799277_1	
	449182	801104_1	
	449238	80319_1	
50	449272	803998_1	
	449276	804029_1	
	449311	804513_1	
	449327	804838_1	
	449336	80495_1	
55	449357	80537_1	
	449385	806123_1	
	449396	806281_1	
	449410	80656_1	
	449432	806947_1	
60	449438	80709_1	
	449508	8085_1	
	449529	809101_1	
65	449539	80944_1	
	449579	81032_3	
	449623	81131_1	
	449625	8113_1	
70	449645	811881_1	
	449695	81342_2	
	449729	814504_1	
	449752	814565_1	
	449762	814618_1	
75	449804	81573_1	
	449808	81579_1	
	449815	816054_1	
	449899	81846_1	
	449916	819092_1	
80	449939	81993_1	
	450018	8227_1	
	450048	823416_1	
	450061	823653_1	



5	450068	823750_1	AW207212 AI681598 BE326297
	450101	8243_1	AV649989 U68494 AA384809 AA352233 AW957278 N53336 AA625202 W32180 AA377077 AA376863 AW956335 AW999618 AI222820 AV653102
10	450180	827351_1	AA400615 AI972416 AI628057 D61721 AA069678 AI888572 AA683477 AI521219 N48189 BE551225 AI004949 BE221751 BE048726 AW316594
	450271	830465_1	AI828960 AI432404 AI640515 AI755025 AI276158 AI366073 AI859124 AI953315 AI564279 AW001811 AI936358 R31110 AI830455 AI206719
15	450350	832758_1	N36910 AI748816 AI858679 AI337980 AI138361 AI634975 AI093232 AI445269 AA683358 AW517287 AI684200 AI699398 AI629009 AA173954
	450438	835012_1	AI634799 N36905 AW136500 AI369566 AW132138 AI886386 AI362594 AI474729 AA400505 AA813128 AI915671 AI077826 W32216 AA491979
20	450458	83586_1	T10628 AA830768 AW582766
	450478	836390_1	AW449644 AW451513 AI685929
25	450519	83714_1	H05254 AI685949 AL119495
	450579	839243_1	AI693900 BE467463 AI689896 AI872975 BE326409 AW241810
30	450587	83951_1	T97817 R08788 AI693561 H95238 T85907
	450682	8428_1	AI696071 AW237210 AI916705
35	450737	844673_1	AA009926 BE149301
	450777	84624_1	AW451709 BE219925 AI701402 AI697820 BE219538
40	450785	8465_1	AA010066 AA626198 T07982 Z41240 N53764
	450795	84709_1	AW136774 AI863194 AI824332 BE219232 AI701151 AI796810 AI825016 AI800307 N62724 BE047945 N78448
45	450822	848159_1	AI828854 AW573206 AA010318 AI539832 AW864156 AW864155 AW572826 BE008193 AI873836
	450877	850027_1	Z42993 AF131793 AW021854 Z45654 AW378177 N51799 BE619681 AI973069 AI889304 AA658236 AW975098 AL048032 AA620652 AA648349
50	450895	85055_2	AW172836 AW015349 AI370576 N51711 AI370615 AA639043 AA447223 D62490 Z41325 R39086
	450947	852369_1	AW007152 AI767589 AW469979 AW004781 AW083534 AW571690 AI732392 BE181973 AI865933 AW351817
55	451007	85489_1	AA255646 AA250860 AW966923 T24849 AA527101 AI340241 AI740877 AA262686 AA011069 AI949440 AA281890 AA283910 AA250824
	451065	857520_1	AA852713 M20776 AW068110 X06194 M27447 AI752145 AA853230 AA214439
60	451073	857757_1	AW173371 AA448111 AI250624 AA447612 AA011163
	451078	857963_1	AW771860 AI740668 AI868261
65	451099	8586_1	AI799608 H68482 AI768144 AI742671 R71268 R71222 H75415
	451149	86044_1	N66727 AI333686 AA725067 R49091 Z40664 F03267 AI535727 AI535967 AA781729 T68994 AA770054 AA011536
70	451182	86148_1	AI745400 AI802659 D80023
	451195	861_1	H38108 AA044849 AA046995 AA013117
75	451206	86224_1	AW295132 AI825575 AI758570
	451221	862740_2	AI758905 N66182 N90849 W17076
80	451264	863988_1	AI927694 AI766122 AI760090
	451270	86428_1	R52795 Y08768 U70981 X55302 BE619361 AA298563 AW954333 AI798934 AW629184 AW136614 AW236406 AI358911 R52796 AA909507
85	451325	86591_1	AW001800 AA621766
	451361	86724_1	AL047586 AW840357 AW840354 T31380 AW840504 T35664 AA256196 AA137140 AW954421 Z36755 AW900287 AA247424 AA643796 N78560
90	451403	86852_1	AI753144 AI263010 AA626885 AW300273 AA886718 N59865 AW026173 AI748876 AI720838 AI056930 AI634216 BE221138 AW296259 AI675382
	451421	86908_1	AI677769 AW276137 AA977716 AI078134 AI311733 AI004600 AI984095 AI018092 AI862628 AW044703 N73684 AI302589 AA137069 N73806
95	451426	869162_1	N73811 AI989816 AW571932 AA256268 AI805872 N73713 AA015867 AA053711 AW150861 AW510935 AA348340 AA018642
	451496	87185_1	D52562 AL119854 AI784179 AI336783 AA459272 AI741051 AA016980 AA015987 AA047819 H04297 M85681 R93948 AA937712 R85767
100	451562	874964_1	AA632533 AI804121 AI287661 AI142480 AI222520 AI383874 AI564282 AI985140 BE467954 C15782 AA328883 AI301196
	451604	87727_1	U10492 NM_004527 AA426311 AA424258 AA427812 AI690690 BE296796 AI638033 AW409961 AI968947 AA426033 AA625609 AI202555
105	451640	8784_1	AI682298 AW410298 AI400505 AI707783 AI378323 AI147664 AI279689 AI078582 AI276590 AI375755 AA426312 AA424161 AI588968 AA653542
	451664	87936_1	AA776544 AW410292 AI808644 AI185722 AI382831 AI202409 AI278291 AI811257 AI079324 AI090595 AI473275 AI468493
110	451678	8799_1	H86228 AA059105 AA016076 AA017092 R84699 H81600 H86603 AA059083 AA017088 AA019684
	451700	88072_1	AI949701 AI766901 AI935602 AI830456
115	451704	88106_1	AI768235 R31400 H29082 H23107
	451797	88600_1	AW341392 AW471008 AW148813 AI796475 AI337851 AI186481 AW002414 AI968429 AW043859 AA587218 AA016317 AI370931
120	451805	886324_1	AA021283 W96349 AA017147
	451829	88786_1	AA053854 W96253 AA017300
125	451830	887991_1	AA885569 N94527 AI913655 AA017454 N58859 H98190 AW592090
	451882	888647_1	W16522 AW003230 AW003274 W79989 AI192577 H86814 BE042503 H37762 AA017517 H38845 AA813026
130	451917	889484_1	AW205003 AI796346 AL039596
			AW503407 AA018131 AA046879
135			H04150 AI803260 R49693 R31262 F09911 H40908 H04200
			T65365 H17723 R11944 F11995 AI805949 AW665577
140			AA195601 AL049699 R60408 H17233 BE549033 AA121033 AA126472 AW274871 AW979028 AI810120 AW590698 R60349 AI870609 AI677864
			AI239645 AA677441 AA194966 H17126 AI219946 AI150486 AI191402 AW236095 AI186780 AW023870 AI300201 AI695704 AA828596 AI202230
145			AW386063
			AA889081 AI160840 AI371772 AA055191 N51851 AA019044 BE502387 AI989471 AA046478 W48651 W74505 AA029388 AI831695 AI760955
150			AI00969 AI146540 AI086864 N95838 AA029198 AW194634 W24986 W79217 AI935864 AA029387 AW384925 H51717 AA029197 BE066506
			W51864 N54117 AI471573 W52655 BE246839 AA055280 H70289
155			AA374181 AA333022 R60740 F06765 W79079 AL117615 AA446836 R28530 W40354 AI810111 AA460732 AI767558 AA446837 AA992870
			AW299743 AA653579 AI932333 R60741 AI216371 AW196998 AA186481 AA436726 Z39828 AA181862 N49053 AW299572 AI819526 AI097654
160			AI308869 T94810 AI378276 AA121032 AI308209 H78404 AA126471 N93862 AA461093 N48328 AW295532 AW022896 AI018812 AW118982
			N70124 H78501
165			AI470262 AA019207 R76693
			AI755209 AW131810 AA019248 H67094
170			AW663858 AW137122 AW615084 W53042 AI800886 AA662645 AA019832 AI762870 AA884292 AI708187 AI080352 AW183499 W57697 T16702
			AI355816 AI767731 AA974045 AA885619 AA953054 BE183601 W58129
175			AI968300 AW237144 AI817847
			NM_003729 Y11651 BE278958 BE280706 AW408060 AW238927 AA146802 BE546764 AA281910 AI130008 AA037291 AA304345 AW958055
180			AI378241 AW189994 AA887947 AA380691 AW963766 AW026139 AI702569 AI399815 AI472824 AA843477 AA878646 AA380690 AI016431
			AA635825 AA864189 AI003236 AA744678 AI378170 AA146803 AA767727 AI361091 AI081395 AW516559 N34655 AA829571 AW243654
185			AA962414 AI080717 AA661648 AW189866 AI039395 AW088309 AW304176 AI983339 AA961155 AI264094 BE002221 N51635 Z40195 F01796
			BE280397
190			NM_016117 AF145020 AK002143 BE293167 AK001642 AU077132 AL041966 R51990 BE385500 NM_004253 AF083395 R51989 AA852851
			F11474 AW841910 AW995147 AI762360 AI190566 AA600919 AI046893 D79229 D79903 C75091 Z42599 R70745 AW818441 AW340484
195			AW083311 AW512677 AW903225 AA706745 AI500578 AA604498 H20568 AA747376 AW800682 AI557888 AI246402 AA876333 AA852852
			AA969837 AA513472 AL133608
200			AW964081 AA348837 AA058691 R84846 AA993821 D81352 D60391 AA318900 AA319176 AA020757
			H18433 H11906 N50785 AI819870
205			AI821324 AI821036 T59498
			AW391351 N79473 AI822125 F33906 F33520 AW375647 AW375606 AW846334 AW375641 AW846330 AW846412 AW375578 AW375582
			AW375581 AW846418 AW845534 AW845526 AW846550 AW846550 AW846557 AW846387

5	451927	8898_1	AL355687 AA351769 T78318 H09403 Z42915 AL109792 H09343 F02390 AI267712 AA452540
	451949	890_1	U03884 U12543 S78737 BE161544 AW976728 AW271978 AI795925 BE466312 AW611934 AI636094 AI478535 AW613555 AW611523 AW301626
10	451963	891358_1	AW615383 AI580376 AW271549 BE552450 AI580319 AI474674 AW204788 AA741359 AW611585 AI524801
	452046	8953_1	AI825440 AI954707 BE501174
15	452073	89684_1	AB018345 BE264317 BE268277 AW166019 N28400 AW902780 H12710 BE467863 W33052 AI885753 W55875 AI769435 N94443 AI634704
	452081	89732_1	AI369161 W56303 AA872380 AA927598 N20049 AI827855 AW975152 AA659043 H12711 Z40233 AW803568 AW074724 AI445806 AI358544
20	452092	8980_1	C20725 AL134168
	452148	9014_1	AA625150 AA968818 BE218918 AA935691 AI339742 N21478 AA773849 AA256452 AA257029 AI377372 AA256324 AA256691 AA248726 R21204
25	452161	901998_1	AA022589 AI351915 AA022590 AI480365 R22818 AA906110
	452171	902200_1	AW958859 AI763181 AW016362 AW016353 AA748419 AA827887 AI862780 AI800702 AI222692 AI826606 AI679013 AI301948 AI640774 AI150807
30	452215	9049_1	AA022645 AW589197 AW518961 AI572372 T25735 R92509 AA357893 AA635777
	452259	9073_1	BE245374 AK002072 AA280082 AW601891 AI248500 AA056643 BE140265 AA056538 AI920978 BE001916 Z45294 H06164 N39909 N41582
35			AW795683 AA204713 AI379923 AI806145 N27164 AI220989 AI200124 AW573205 AI220912 AA281331 AA912691 AA417735 AA127174 AI150014
			Z44999 AW401399 AW135675 BE073533 R96977 AW939010 AW813737 AW391015 AI032759 AI215107 AA631682 AA234455 AW664815 N45940
40			AW839240 AA420698 AA470528 AW173159 Z40999 AI633579 AW187998 T32566 AW952986 AI217966 AI630916 AI743488 AI799082 N36779
			AI239633 AA417736 AI187048 N72098 AI421447 AI625533 AA872805 AI039112 AI242444 AA977049 AI247779 AA001636 N26134 AA128214
45			AA234064 AI559104 AA923105 AA207114 AA420658 AA516130 AA643762 AI018134 AW518021 C21393 H89570 AI699310 AI263771 AI249346
			AI401396 AW149222 AA470977 N29810 D62566 AI925627 Z40731 AI954399 AA195030 H13391 H06055 W01144 N42501 R96921
50	452148	9014_1	AF007143 H05113 AI061290 F10985 T77657 F13397 H05578
	452161	901998_1	R43077 AW293944 AI863059
55	452171	902200_1	AI863302 W28704
	452215	9049_1	AK002043 R64048 AI656827 R69653 AI800973 AI028230 AA969948 AI472044 H67896 R63948 AW183559 AW468869 AA367638 AW204416
60			H67941 AA367639
			AA317439 AF110647 NM_007107 R67765 AA171543 AA356723 AA376377 AA332889 AA114187 W02344 D30946 BE562417 N86643 BE001211
65			BE001151 AI909035 AW089566 AA385137 AA424609 AW958982 AA503136 AI953724 AA071284 AA236308 AW087870 R66163 AI808511
			AW971007 AW239354 AA236443 BE044534 AA121207 AI889510 W93528 AI683949 AW474435 F05461 C21379 F05439 AI608772 AW873443
70			AA523526 AW896271 AW896354 AW183743 AW896275 AI392612 AA907761 AI337534 AI687619 AW074837 W93529 AA699320 AI590957
			AW896206 AA686664 AI139278 AI148689 AI288019 AA931436 AA424631 AI311311 AI221545 AI334226 AA424541 AI373801 AI421669 BE008169
75			AA424586 AW592586 AA071356 AI355960 AI093227 AI351606 AI375664 AI051172 AA262962 AI081208 R67045 AI972535 AA227458 AA337272
			AI184399 AI962414 AI918607 AA515476 AI148545 AI334981 AI095116 N50721 AI698503 AI745472 AI221084 AA708788 AI189403 N73309
80			AA338105 W32138 Z43972 AA291997 BE070475 AL134826 W44470 AA397544 AW374093 AI276831 W31785 AI092639 AI027509 AW374092
			N43847 AW388073 AA143181 AA115455 BE002360 AW800643 AW800706 R78699 W44471 AI753555 AW393731 AA171512 W52169 AW885188
85			AA227459 AA293219 BE159082 AW374084 AW886104 BE159088 AA453486 BE081891 AI089896 BE159094 AW385363 Z38420 F01720
			AA453487 AW578866 BE169544 AW977748 AI686557 BE387147 AA356726 AW965463 BE565066
90	452280	90865_2	AI911410 AI797738 AW183539 AA897131 AI393553 AI911411 AA813006
	452291	9090_1	AF015592 AB003698 AW405542 AF005209 AA814975 AA768993 AA291015 AW968900 AL044123 N40295 AA488783 AW574512 AA936081
95			AA131310 W76628 AA488999 N79336 R68530 AA429583 AA131523 AW965175 AI857674 BE551914 AI435106 AW661770 AI656719 AA345059
			AI553954 N62245 AI338118 AI434385 AA431743 AA885165 AA954964 R68236 AA972033 AI672674 AI198936 H96018 AA977604 AA909881
100			AA455048 W73020 AW340789 AI866149
			AK000464 AA316239 AA383204 AA248992 W58683 BE543316 W39634 N39365 H68026 BE548151 BE562984 R72674 AA149092 AA427989
105			AI741236 AA427780 AI684893 AI394428 AI636193 AA505864 W15449 AI363483 AW081776 AA977471 W58684 AI243652 N23764 AI025781
			AA548370 AA505845 AI086660 AW085127 AA149093 AA829516 AI242612 AI687956 AI911165 AI432378 AI784557 AI242697 AI863836 R72606
110			AA427864 AA905233 AI250653 AA952945
			AI885742 AW452581
115	452372	913899_1	AL037405 W32250 W44711 AI885916
	452374	914047_1	H87398 AI160628 H51273 AA858268 H19425 H23422
120	452393	91527_1	NM_007115 M31165 AF086484 W93163 AW959677 AA363579 AW188198 BE500935 AI950438 AW593307 R73532 AA448801 AI914385 W92764
	452401	9158_1	AA909098 AI215056 AA483368 AW665667 AI225126 AA628236 AA558690 AA039722 AW467172 AI803401 AI823971 M31164 AW059953
125			AA507959 AI168135 AW057612 N22156 AA648583 AA448802 AI916126 AI865870 R73533 AA362343 AA039723
			AW854891 AI902513 AW847720 AW847648 AI902512 AW847612 AW847737
130	452492	919516_1	BE063096 BE060997 BE061054 AI904026
	452539	92131_1	AW105321 AA026666 AW080622 AI572798 AI886030 N67618 F09090
135	452542	921410_1	AW812256 AW812257 AI906423 AI906422
	452589	92295_1	BE159915 BE551355 AI291125 AI887813 AA026856 AA026857 AI187932 F25540 F31478 F34444 F18166
140	452594	9230_1	AU076405 NM_000112 U14528 AW882393 AA662725 BE006338 R81077 AW888829 AW968692 R69741 AW969230 AI806609 AW665726 N32897
			AI218845 AI033609 AA741468 AW197706 AA902381 AA687784 AI880386 R80969 AI214493 AA445340 AA468641 AA493529 AA493433
145			N73101 AI285850 AI934051 AA502433 AI557282 AA485135 AW968516 W02106
			AW968557 AA913454 AI088432 N02070 AI524827 AI436094 T05401 AA465676 AW956549 T32513 AA026945
150	452728	929207_1	AI915676 AW044560 T86628 W87347
	452744	9298_1	AI267652 W85764 W90812 AI816033 AL080199 H06580 AW023286 AA772353 BE350762 W90756 AI817455 N80824 AA678493 AI422410 H06525
155			W85765 AI089765 H05093 AA705876 AW044213 H43423 AI375338 AA769792 AI378819
			AW138937 AI919342 AI991480 AI916889
160	452755	930301_1	AW069459 AW139274 AI337988 AI342288 AI369002 AA034020 AI699794 AW028656 AI299410 AI378524 AI669457 AI417487 AA233336
	452768	93077_1	AA233335 AI721188 AA406564 AI810826 AI093515 AA029031 AA490697 AA028109
165			R71338 AI917894 R25452
			AA028167 AA035731 AI700675 BE220448 BE549721 AW887707 AI051312 AW207134 AI377083 AI914607
170	452783	93130_1	R61362 R44837 AI918244 AI934620 R52543
	452786	931432_1	AW471181 AI360916 AI283689 AA458598 BE326346 AW277118 AA551468 AI951683 AI809714 AI809721 AI290496 AI094691 AI767318 AI394533
175	452821	93266_1	AA307690 AW170168 AI970554 AI369846 AW016201 AA909457
			AI796769 AA029141 AW044196 AW137550
180	452843	93406_1	H23230 R41343 Z38417 AI923105
	452850	934353_1	AW905328 AW898982 AW905266 AW905268 AW181935 AA426363 N53641 AW592730 AI335250 AA447514 AI638188 AI830527 AA029326
185	452879	93573_1	BE044339 AW118870 AA431528 AA437157 AA382089 AW905379
			AW962167 AA325477 AA029613
190	452919	93831_1	AA883929 AI803165 AA401248 N22834 AI949123 AI417648 AI084448 AA256613 AI082846 N22363 AA446248 AA029844 AI436001 H84053
	452958	94042_1	H83915 H95930 N75610
195			M85521 AW327262 AW327616 AI769182 AA725234 R43427 H05474 R60056 BE047259 AA483411 AA483400 T16298 AW874660 AA650410
			AA054722 N66755 N62194 AA342241 AA902896 AI051725 AI671131 AA977118 BE327006 AI554330 AA916000 AA594900 T90105 AA933624
200			AI825794 T34734 AA716570 AA811545 AA847865
			AW136440 AI948563 AW005531 AI950053
205	453043	945945_1	AW196690 AW236837 AI948874 BE328040 BE504029 BE502832 BE218326
	453051	946233_1	R63050 AI948886 AI963150
210	453052	946244_1	Z25935 AA031958 AA211009
	453098	94895_1	

5	453111	9497_1	AB014598 NM_014799 AW603770 AW750753 AA317515 AW361871 AA384036 AW843941 AW601924 R58483 AA249449 AI242590 AA320483 N44916 AA327489 AW960584 AA628407 AI741339 AW361193 AA476631 AA909460 AI658618 AF075034 H50094 H20113 AI333679 AI393939 AI095464 AA446957 AI752765 W81624 AI833144 AW269551 AW168800 AI127456 AI751677 AI797200 H50095 AI140404 AA515536 AA515535 AA130966 H20033 AW009268 AI635409 AW237000 AI203260 AW779461 AW613317 AA131047 AI784619 AW015953 AI625021 BE503086 W81365 AA622368 AA235814 AA582130 AI377539 AW084545 AA256629 AI143826 AW611927 AA587621 AA256522 AI682717 AI635936 AW000869 AA601117 AW016188 AI919027 AI474520 AV654908 AI936316 N66466 AA094836
10	453118	950206_1	AW195849 AI953593 BE220224
	453123	950316_1	AI953718 N24412 N92985
	453128	9505_2	AW026516 AI458435 AI167301 AI023608 AA583019 AI250813 AA813631 AI367992 H40557 AI362804 AI222286 AI749644 H20926 AI269168 N49204 AA284358 AA962306 Z25021 H20975 F15203 AA482947
15	453178	95344_1	AA496086 AW341496 AW665989 AA406039 AI633557 AA861411 AA033693 AA034209 AA910471 AA812776 AA705822
	453211	95527_1	W84829 AA033900 AW573557
	453242	95637_1	T98327 AA034014 W90566 AA034013 AA703594 T98273 W90567 AI247668
	453263	95753_1	R91778 AA034133 R15717 T99011 AA458513 R91779 R16082 T99012 R00561
20	453264	95757_1	AA034137 AA699368 AI033840
	453305	960676_1	R39224 T89102 F10202 F10606 AI983216
	453343	96267_1	AA905353 AA035076 D60081 D81399 AI093811 D60080 AA035493 AA771809
	453361	96380_1	AA035197 H14987 H12917
	453362	96381_1	H14988 H05502 AA035198
	453375	964157_1	AI990114 AI990675 AW025802
	453393	96501_1	AW956392 AI247087 AA424155 AI351064 AA377297 AA035332 H93140 AA340205
	453444	967465_1	AL036531 R24983 R18191
	453502	969450_1	AL039786 AL041856
25	453649	9759_1	Y07494 NM_000702 J05096 AL120192 M16795 AA984658 AB018321 AA984659 F00081 AL119335 AW900247 AW900124 AW900139 R20506 AA193018 AW410196 AA324187 F07411 AA233559 AA326820 AA308907 F08479 AL119548 D53757 D55275 D53434 D52673 D53636 F05687
30			AW897161 AW440492 AW514749 M78212 AW440549 R45325 AA193019 AI418529 AL118771 AA233465 AI367523 AA085587 AI927094 AA425484 R72950 AW731602 AA984655 AI361289 F01313 AI937546 AI554659 AI937102 AI970366 AW006698 AI638260 AI674717 BE220583 T28085 AI890537 AW002457 AW237026 BE328374 AW964747 AI499304 AI569412 H88820 AA425300 AA912603 F00806 AA429949 AI620058 H87972 AI091330 AW074608 AW022212 AA635897 AI288877 AI918842 AI359099 AI374669 AI963882 AI291381 AI341416 F33677 AI493690 AI886395 AI990678 AI656810 AA948574 AI359044 AI886332 AA229340 AA228485 H88821 F37110 F35654 R73570 AI610998 F28099 H88154 F32460 N63144 N67333 BE044408 F34665 N71189 N21985 AW966959 W22069 AA016193 R14145 AW900293 AW898414 BE313714 BE313924 BE251744 AA985337 AW905065 AW905054 AI003021 T19576 AW897061 AA326577 AW896688 R88032 H14158 R84491 AW896834 AA351306 AA084378 AW797723
35	453652	97617_1	AW009640 AI692207 AI032859 AI632427 AA737568 AA134747 W45725 AI380939 AA706630 AW243133 AI343674 AI689433 R62896 AA524299 AA312442 AW958688 AI869598 AI476352 AW262542 AI797863 AI801882 AA775620 AA037416 AI150846 AA470732 AI818643 AI125551 AA134746 N48450 AA853411 R62895
40	453687	977759_1	T55674 N32741 AL110337
	453696	97793_1	AI989482 AI636932 AA037612 AI554483 AI299223 F10583 F10582 T03621 C00485
	453736	9792_1	AL118674 NM_014795 AB011141 AI879328 BE247392 AI973112 AL118580 AW068187 AI879705 AA459875 T06966 H98614 N45100 AA676801 AA319442 AW954943 AW384974 D31558 BE046349 AB015341 AA143007 AA044097 AA490798 R57623 R15285 D31109 D31300 D60311 C15061 AW296352 AI755114 AI939494 AI990591 AI675134 AI435119 AW237506 AI338485 AA969266 AW968767 AA775866 AI094145 AI754598 AI741685 AI359739 AI858477 AW020915 AI695283 AI858488 D60310 AA490605 AA045440 AW298036 D60508 AW074458 AA583754 AI468974 AI700924 BE281431 AW972530 N42010 N30289 T87105 W93043 AA993199 AI188535 AI149003 AA039331 AI128458 AI189715 BE302172 AA722699 AI186558 AA505794 AI200158 AI740470 R99925 H53104 H95793 H87367 H87913 T87104 H53211 W93171 AA039416 H96141 AA039250
45	453823	982526_1	AL137967 BE064160 BE064186
	453853	98355_1	AL040600 AA886630 AA602590 AA039568
	453857	9836_1	AL080235 AA031750 D81382 AI480231 AI095947 AI560953 BE010721 AI870290 AA374945 AA125792 D51527 D51556 AI685541 D51559 AW117286 AA195741 AI675138 AW593439 AI201885 T30590 AW952100 D51095 AA523864 W70043 AA987586 AI421515 AI205532 AA127069 AI337367 D51595 AI453785 AW075677 AW088359 C14287 C14284
50	453874	9845_1	AW591783 BE139489 AI755035 AI240724 AW015393 AA603078 AI745223 AA910736 AI674891 AI584134 AA126262 Y11711 AA680137 AA041285 AI015878 AI109790 AI475254 AI468483 D62869 AW770822 AI123663 AW338666 AI248460 AI142682 AW874158 AW005962 AA167223 AI249777 AA910046 AW768845 D79402 AI440216 AI445707 AW707114 AA576834 BE463619 AI131243 AW471376 D79653 D61804 D79381 D79361 D62180 AA011417 W90416 AI085061 AA680158 R95909 D79368 D61969 D61896 W95700 D79303 AW021898 AW021663 D79634 D79682 AA039896 AA126366 D61854 AA482355 AA328081 D79311 AA011468 T57428 H27790 AA247120 AA376930 AW954470 W88516 AA041320 W95699 AA167222 AA368972 AW297739
55	453880	98522_1	AI803166 AA993523 AW021958 AA039755 AI754390 AI760181 R42963 AI143446 AI472813 N66324 AW768725 AI002627 AI275911 AI627496 D63100 Z38648 AI003082 AA489480 D61901 AI287345 AA044830 AW451440 AA216589 AI347579 AI962010 AA486079 AA909305 R63922 H45779
60	453901	986414_1	BE065902 AW749032 AW003637
	453930	9882_1	AA419466 AA143419 W42641 AW328468 AA136997 AA340017 AA381179 AW328544 BE254091 BE543504 AI686155 AI091621 AW055219 AI300170 AI051983 AA716338 H98035 AA635642 AI500292 AA865913 AA393231 AA778614 AI027585 AI028537 AI658634 AI025238 AI423918 AI422134 AA703153 AW000724 AA706734 AI143788 AI024179 AI089503 AI018816 AI077772 AA861355 AW328469 AA929067 AI095004 AI089875 AI024268 AI085709 AI311912 AA994793 AA804222 AI167336 AA632084 AA136886 AI302634 H97410 AA933827 AA732974 AI220913 AI086939 AL133626 AI536823 AW166281 AI140034 AA677713 AW405317 AA399254 AA948296 AA962566 AA416963 AI217557 N30753 D45500 AA989504 AW971081 AI088484 AI244400 AI708246 AA715123 AI085976 AA757217 AA727266 H53100 AA709169 AA143420 AA879177 W57808 F35358 AI363874 AI424396 F22254 AI344220 AA630701 AI334473 AI657138 AA662696 AI658636 AI826325 H49224 AL037735 AI126929 H49410 N79868 N99605 H44756 H43830 AW241813 AA992585 H14627 BE049503 AI800469 N62965 AI375065 N92659 AW614368 AA897465 AA984538 H28691 Z40651 F36840 AA412229 H14920 H53207 F33011 AA657421
65			AL121278 AW204346 AI783831 AA832457 AA834594 AI356646 AI864616 AI739222 AI685036 AA040147 AI088723 AA040084 AI150650 AI914062 N36085 R37504 AI627237 W56371 N34565 AA716465 AI868611 AI457344 AW241352 AA516324 BE382423 BE382689 W56582 AA040811 BE169967 AA040131 AW577540 AW577546 AW577518 AW374021 AW750042 N44089 R36508 AW993372 AW016715 AI632728 AA948453 AI914544 N80867 AI093260 AI042218 AI266049 AI796795 AA974939 BE270561 AA648254 AI080416 AW974437 AI693162 BE397986 AA625406 BE221895 AL121277
70	453931	98831_1	W31790 W02933 C16882 AW297592 AA040896 Z25917
75	454032	99580_1	AA374756 AW861149 W30966 BE004424 AA580682 N59738 AW896886 AA310291 AA174110 Z21254 R76155 AI453090 AW020158 AA040940 N52701 H98193 AA777760 AA933066 AW057724 AW024109 BE219721 R63389 AI493831 N98755 AW304366 N57773 AW079916 AI393583 R01244 AI127416 AI144411 AI251940 AI014530 AA932678 AA700792 AA046237 N49771 R76103 AI674384 AI191111 AA883197 M85697 AI049641 AI018557 AA704274 R55239 AI699295 AW132008 AI814886 Z40520 F04178 AI123623 R38919 AW965736 R01358 H03780 R63444 AW079064 AW022162 AW780345
80	454039	996301_1	AA601518 AA603858 AW453004 AI800450 AA916086 AI139766 AI270587 AA664356 AA618576 AA126614 AI569918 AA436891 AA931725
	454078	99989_1	AI745618 AA776700 AA398533 AA813424 AI130883 AI032288 AW081541 AI268236 AI587015 AI857286 AI004140 AI370031 AA430199 N25288 AW242281 AI683319 AI445766 AI911821 AI926591 AI934183 AA573270 AI565897 AA687634 AA554327 W69579 AI095665 AI597744 AW304844 AA358590 AA705172 AI924827 AW192904 AW664335 BE049444 AA541688 AI476374 AI865731 AI918635 AW075384 AI963606 AI919864 R27785

			AA115447 AA042816 AI922590 AA676733 AI130013 AA722782 AI631988 AW058362 AI375804 AI366906 AA886732 AA694514 AA679037 AA678468 AA430300 AA393105 AW008428 AA042956 AL045796 AA135916 H71919 W69578 H44790 AI939990 AA363371 R59176 AA135927 AA115446 AI446542 R42647 H42641 H44791
5	454086	1003_17	AW885909 BE004454 AW900559 BE090101 BE002768 AI702989 AI903225 BE001507 BE006541 BE006534 BE006539 AW899938 AW996265 AW796248 BE081466 BE081786 BE082026 BE081783 AW868267 AW996372 AA504599 BE081757 BE173468 W55954 N62044 BE003320 M78370 AI694968 BE081701 BE176293 AW996665 AW879193 M62115 AW996285 AA984506 AW351544 AW997605 AW996646 AW997613 BE009330 BE011906 AW996668 AW880515 AW750343 AW373734 BE222875 R17533 T08229 Z44685 AW367704 BE170375 AW390266 BE170379 AI114621 AW886344 AW900604 BE177283 BE006071 T32797 BE177278 BE185088 AW792899 AW352336 AI032798 BE177615 BE003019 BE086939 BE161580 AW885685 N89832 AW363596 N43180 AW363712 BE005286 BE005420 AW902083 AI174898 AI025430 BE002845 AW892938 BE005291 AA855066 W56791 BE010839 BE005429 BE005158 AI718737 AW351878 AA831497 BE003081 AI241798 AI277648 AW351880 AA863129 AW894216 AI244498 AI052045 AW152321 AA984996 AW148429 AI078662 AI767783 AA916731 AI285172 AW366852 W37468 AA843911 AA057577 AI910785 BE045841 AI038598 AI453497 AA782072 AA937973 AW079144 N90907 AI279771 AA771777 AA805878 AI806093 AI022534 AI313233 AA831344 BE465522 AA776822 AA621240 AI188091 W72955 AA903076 AA829334 AA688108 AA994002 N30614 D20363 W35118 W72899 AI200634 AI446756 AI984880 AI620132 T34808 AI872637 AA722738 W60749 AI092298 AW074701 W44771 N29388 N78848 AA130087 AI217530 N80243 AI687217 N90708 AW028901 AI793029 T62951 W93809 AI888887 AI525287 AI368062 AI540483 AA725595 AI858198 AA412668 AA559989 AA682746 AI205938 AW440603 AA053959 AW514317 AI364590 AI114491 AF113016 AL039543 AA031627 AW363091 AW999880 T89332 R78615 AA130086 Z19813 H86291 AI735418 H84067 AI719213 R93868 BE084640 BE172050 AW999185 BE172646 AI184009 AW999083 AW999779 BE172351 AW999962 AW999323 AW999747 AW996428 BE087384 AA329272 W37336 AW902899 BE000118 BE001965 BE086835 BE011011 AA034440 AA090777 BE161366 BE075339 BE007856 AW997518 T62803 N62045 BE082579 AW363675 AI267306 W73218 W20091 AA367038 BE002393 AV656706 BE002210 BE174412 AA313081 AW948382 BE184405 W93920 AA319863 AA031708 AI697809 AA443386 BE003068 AI267480 AI267485 N47937 AF119905 AI207498 AA827878 AA830776 AA845547 BE326302 AA827265 AW879125 AW879051 BE151801 BE003079 AW381919 N87035 W17248 BE010949 AW384754 W56569 BE086396 BE068512 BE081251 AA648757 T31931 T89968 AV647751 R41901 AA948199 N41857 AI279084 T31922 AW869118 AA852080 AA568508 AA258003 AA129158 AI630039 AA467902 R66524 AW263903 AL037363 AW444869 AW853834 AL037918 AA888444 T30729 AI637918 AI365387 AA467848 N56530 AW302175 AW057885 AI762225 AW130889 AI961832 AW073486 BE044094 BE348276 AI824535 AA13645 AI686252 AI271937 BE046039 AI470886 AW612539 AW771110 AW235291 BE246240 W19393 W39023 AI207570 C06356 AA759169 AA813454 N41342 AA894753 AW301229 AI582040 T94789 AA725267 AA493872 AA628866 R57591 AI902976 AA044691 AW275601 BE503540 AI420783 AA090446 AA089806 AW009018 AA746397 W07370 T31530 AI110866 AF075365 AA854301 T94038 AV660253 N87470 Z40528 AA093611 N44064 AA094954 AV660355 AV660048 AA633048 W76595 NM_014086 AA731217 W37091 AI207717 W37335 AA643720 AA682940 BE081340 R78616 T30192 H54908 Z43258 F06414 F05166 F06723 AW864404 BE085063 AW864331 N89375 BE177972 AW999929 AW294720 BE008182 BE008177 BE084766 BE177678 BE000083 AW999190 AW999176 AW992382 AW999773 BE000031 BE173008 BE173002 AW999414 BE000387 AW999494 BE000341 AW999330 AW887498 BE009746 BE093918 AW887427 AA215913 T77314 R61023 R13699 BE410100 D31120 BE384353 BE387905 BE276515 AI929689 AW971616 AW971608 AW971617 AW967819 AW193189 H98230 AA989039 AI868284 AI367862 AI951710 AI216516 AI239959 BE463693 AA906145 AF091077 NM_003916 AB015320 AW162825 H82252 AA724611 AA768208 AA743074 N24872 AA594685 N63563 AI497825 AI186029 AI140289 AI126568 AI095266 AI284962 AA782628 AA732483 AA814540 N21443 AI354794 AI458000 AA719807 N75410 AA904660 AA946626 AI282212 AI130959 N20037 N72992 AW050984 AA126628 AI034045 N25215 AA243506 AI436049 AW051545 AI200619 AA730260 AI218724 AA872419 AA885826 AA907724 N36893 AA128314 AA993331 H95922 N34852 N32939 AW964639 H97150 AA322575 AI458438 H95921 AI267543 AA318887 AW964472 AA476710 AA902555 N48024 AA128258 N30942 H96681 W37207 N94727 N28392 AA890536 N42610 AA129065 N23526 AI823837 AI889006 N39393 AA243505 AA127007 AA453891 N46167 AA093891 N43925 N46490 N79261 N35189 AA453805 AI268958 AI168280 AW341001 AA766913 AA594669 AI47575 AI819223 BE0503760 AI323910 H89971 AI784468 AA774623 N38916 N23402 AW770990 N20973 AI338619 AI379043 N62129 AI265935 H97835 AA262073 N94560 AW500340 BE047591 AW136244 AA046872 AW177821 AW177896 AW177867 AW295069 AW452895 W92612 N30616 N95715 W95237 H20279 AW608930 AW608886 AW386785 AW608880 AW608924 AW876592 AW608893 AW608937 AW386786 BE083970 AA167682 AW608932 AW608888 AW386788 BE083407 AI290593 AA748001 AI034086 AA680056 AI940637 AI940638 AW374283 AI940655 AA809316 AK000625 AA603517 AA554721 AW390779 AW362039 AW170305 AW604129 BE167535 AW602174 AW833977 AW833975 AW833973 AW833976 AW393917 AW393931 AW393924 AA476695 AW373835 R84790 BE079454 BE079543 AW603939 L44407 AA826167 AL046250 AA167708 AW292851 BE348284 AW440289 AA829695 AI872418 AI191432 AI188147 N48830 AF088006 AI352455 AA166945 AA918797 AA923369 BE220983 AW340679 AI825915 AI393175 AA831456 AI206842 AA767426 AI829442 AW272390 AW073367 AI221801 AA205998 AW444790 AI131383 AA149019 AI1619772 W69501 AW069441 AA760763 AW293184 W69500 AI204502 AI862197 AA811517 AA768156 AA507644 AW339567 AI573109 R41696 AI358174 AI522229 AI266707 AA922537 AW663421 AA731024 AA876488 AA166764 AA767889 AA732486 AI580730 AA731023 AI565289 AI364191 AW244047 AI951688 AI356083 AI186830 AI242487 AI598188 AW139199 AA046436 AI741582 AI564355 AI352231 AA885476 AA210643 AA259028 AL120860 AW015304 AI689736 AI912021 AW608948 AW608904 AW608953 AW608909 AW876603 AW386770 AW386784 AW876600 AW386783 AW386778 AW386775 BE002626 AW386763 AA329781 AA258847 AW608892 AW608936 AW805361 AW175822 N46322 N46237 AA082211 AA905105 AA970393 AI650888 AI203926 AI918827 AW603985 AW854350 AA083558 AW07673 Z39772 AA224053 AA114150 AA214275 AA224027 T58431 AA211908 AA669657 AA199744 AA630511 AA164864 T58463 AA214394 AA161378 AA161386 AA205211 AA167824 AA084940 AA223625 AA191190 AA309486 AW961804 BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671 AW902125 AW792853 AW837703 AW837710 AW794878 AW794889 AW794787 AW794993 AW794888 AW794797 BE147919 AW794884 BE147847 AW807605 AW807690 AW807839 AW807752 AW807673 AW807667 AW807955 AW807760 AW807615 AW807898 AW807849 AW807821 AW807832 AW807842 AW807827 AW807822 AW807829 AW807830 AW807825 AW807603 AW807612 AW807908 AW807595 AW807617 AW807678 AW807687 AW807918 AW807921 AW807596 AW807602 AW807688 AW807609 AW807684 AW807770 AW807593 AW807754 AW807679 AW807957 AW807683 AW807763 AW807902 AW807840 AW807819 AW807836 AW807769 AW807685 AW807847 AW807674 AW807686 AW807670 AW807917 AW807677 AW807680 AW807900 AW807669 AW807952 AW807907 AW807846 AW807756 AW807835 AW807608 AW807753 AW807601 AW807956 AW809178 AW809224 AW809150 AW809221 AW809220 AW809195 AW809175 BE150647 AW971143 AW809648 AW809704 AW809643 AW809653 AW809709 AW809949 AW809939 AW810010 AW809705 AW809950 AW809822 AW809667 AW810093 AW810076 AW809673 AW810349 AW809895 AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960 BE006345 BE006344 AW811819 AW812330 D82299 AW850684 AW850150 AW818456 AW818186 AW818191 AW818384 AW819059 AW859016 BE072934 BE072942 AW935690 AW862075 AW858956 AW858941 AW862076 AW862072 AW862074 AW858944 AW935648 AW859012 AW858718 AW859025 AW859017 AW859014 AW859015 AW819131 AW859034 AW859013
10			
15			
20			
25			
30			
35	454117	10206_1	
40			
45	454137 454145 454190 454277 454324	1032652_1 103572_-1 1049996_1 1089764_1 11131_1	
50			
55			
60	454419 454423 454434 454438	118105_1 1183079_1 119085_1 120132_1	
65	454447 454471 454481 454482 454566	1204995_1 1213795_1 1215013_1 1215087_1 1224432_1	
70			
75	454578 454597	1225676_1 1226059_1	
80	454600  454643 454658 454716 454743	1226077_1  1227865_1 1228283_1 1230503_1 1232712_1	

	454747	1233006_1	AW818535 AW818588 AW818651
	454749	1233104_1	AW818649 AW818662 AW818648
	454754	1233580_1	AW819191 AW819252 AW819183 AW819175 AW819177 AW819186 AW819180 BE158470 AW819242 AW819269 AW819244 AW819190
5	454759	1233775_1	AW819265 AW819268 AW819246 BE152602 AW819249 AW819251 AW819263 AW819194
	454769	1234081_1	AW819455 AW819711 AW819553
	454777	1234227_1	AW819848 AW819863 AW819850
	454784	1234630_1	AW820027 BE160390 BE160308 AW820186 AW820162
10	454836	1236509_1	AW820626 AW820621 AW820608
	454864	1237929_1	AW833711 AW833620 AW833699
	454867	1238003_1	AW835775 AW845768 AW845764 AW845773 AW845757 AW845758 AW845780
			AW835924 AW835918 AW835864 AW936632 AW936780 AW835911 AW936775 AW835883 AW936660 AW835887 AW835917 AW835885
			AW835914 AW936773 AW835930 AW835888 AW835921 AW936828 AW835908 AW936820 AW835916 AW835909
	454874	1238494_1	AW836407 BE175600 BE175579
15	454916	1242594_1	BE067246 BE067241 BE067254 BE067249 AW841960
	454936	1245585_1	AW846082 AW846113 AW846127 AW846100 AW846121 AW846101
	454950	1246610_1	AW847460 AW937451 AW937400 AW937379
	454962	1246750_1	AW847645 AW847791 AW854083 AW853945
	455000	1248717_1	AW850283 BE143621
20	455047	1250536_1	AW852530 AW852527 AW852526
	455067	1252050_1	AW854538 AW854418 AW854412
	455092	1252971_1	BE152428 AW855572 AW855607
	455107	1253874_1	BE154113 AW856797 AW856847 AW861128 AW856817
	455110	1253955_1	BE154505 BE154462 BE154454 BE154460 BE154489 BE154496 AW856909 BE154497 BE154565 BE154572 BE154500 BE154472
25	455114	1254106_1	AW857121 AW857123 AW861238
	455121	1254339_1	BE156459 BE156469 BE156468 AW857447
	455189	1259271_1	AW864176 AW864133 AW864185 AW864137
	455201	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
30	455221	1261678_1	AW867751 AW867770 AW867763
	455241	1265809_1	AW876249 AW876253 AW876276 AW876247 AW876278 AW876250 AW876388 AW876430 AW876418 AW876387 AW876411 AW876356
			AW876332 AW876335 AW876348 AW876337 AW876355 AW876338 AW876373 AW876372 AW876313 AW876374 AW876321 AW876317
			AW876303 AW876302 AW876315 AW876153 AW876128 AW876172 AW876370 AW876431 AW876423 AW876225 AW876217 AW876245
			AW876420 AW876211 AW876208 AW876151 AW876223 AW876144 AW876137 AW876149 AW876148 AW876236 AW876194 AW876284
			AW876256 AW876130 AW876389 AW876152 AW876167 AW876175 AW876159 AW876174 AW876164
			AW876538 AW876567 AW876619 AW876629 AW876537 AW876566 AW876547 AW876576 AW876535 AW876564
35	455249	1266140_1	AW876627 AW876630 AW876631 AW876625
	455252	1266222_1	AW977806 AW887923 AW886321
	455275	1272255_1	AW886156 AW887926 AW886324 AW886236 AW887906 AW886304
	455280	1272607_1	U75810 AW890252
	455290	1275447_1	AW893961 AW893998 AW894034 AW894019
40	455310	1278158_1	AW936369 AW936377 AW936355 AW936410 AW936460
	455401	1288141_1	AW983901 AW984485 AW947715
	455464	1292643_1	AW948126 AW948139 AW948196 AW948145 AW948162 AW948134 AW948127 AW948124 AW948153 AW948157 AW948125 AW948131
	455475	1293012_1	AW948158 AW948164 AW948151
45	455488	129372_1	AA102322
	455500	1307364_1	AW963582 BE064169 BE064192 BE152580 AW963587
	455511	1321229_1	BE144762 AW979091
	455540	1323701_1	BE080231 AW993284 AW993293 AW993000
	455544	1324318_1	AW993880 AW993730 AW993732
50	455571	1331885_1	BE003714 BE003721 BE003720 BE003716
	455577	1333898_1	BE006341 BE006307 BE006311
	455614	134100_1	AI693369 AI702140 AA125921
	455675	1349659_1	BE065984 BE065942 BE065955 BE066085
	455678	1349716_1	BE066007 BE066017 BE066074
55	455685	1350393_1	BE066976 BE066928 BE066927
	455688	1350606_1	BE067238 BE067235 BE067240 BE067256 BE067263 BE067236 BE067260 BE067253 BE067248 BE067252
	455696	1351077_1	BE067870 BE067866 BE165133 BE165334 BE165329 BE165332
	455699	1351258_1	BE068121 BE068090 BE068153 BE068128 BE068197 BE068136 BE068140 BE068185 BE068105
	455735	1353881_1	BE161124 BE072284 BE072300 BE072203 BE072274 BE072199 BE161157 BE072314 BE072304 BE161159 BE072302
60	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
	455756	1358603_1	BE079307 BE079309
	455771	1362261_1	BE084820 BE084936
	455780	1364580_1	BE088828
	455791	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
65	455797	1366826_1	BE091833 BE091874 BE091871
	455814	1371429_1	BE141689 BE141690 BE141678 BE141685 BE141686 BE141683 BE141682 BE141679
	455841	1374628_1	BE145836 BE145840 BE145881
	455851	1375451_1	BE146879 BE146914 BE146918
	455866	1377119_1	BE149024 BE149056 BE152826 BE149025 BE149057 BE152819 BE149030 BE149062 BE149023 BE149055
70	455870	137871_1	AW452631 AA130630 AA706431 AA708268 AI694719 BE1504585 H93447 AA130733
	455879	1380017_1	BE153275 BE153189 BE153329 BE153022 BE153030 BE152974
	455880	1380022_1	BE153208 BE153146 BE152981
	455955	1386825_1	BE162394 BE162382 BE162309 BE162303 BE162298 BE162396
	455964	1389912_1	BE166924 BE166921 BE166925 BE166915 BE166970 BE166968
75	455992	1398552_1	BE179015 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997
	456027	142104_1	BE327387 AI800520 AI796001 N72200 AA434212 AA135943 H17771 W00444 AW294967 AI703001 Z20315 AW339782 BE219674 BE219697
	456056	145398_1	AA463550 AW958131 AA329302 AW264037 AI979134 BE163190 AA252163 AA148799 AA148530
	456083	14855_1	U46922 NM_002012 AA256122 T96733 R11128 R05417 T85004 R08282 U76272 AI086356 AI741386 AI338651 AI024929 AI400094 AI401445
80			AI803972 AI493307 AI245155 AA918722 R50713 N35686 AI278165 AW025706 AI885436 R86314 AI582390 AA256123 AI468521 R53094 T89183
			AA621493 AW372683 R05964 AW819303 AI417763 AW393203 BE247001 AA864207 AW819302 AW393209 AW393195 AI870522 R05963
			AA380267 AL117573 R51476 AA131283 AA305730 AW960438 T27291 AW504410 W77831 AA243239 AA426041 AA927639 AW792877 AA055133
			AW291315 AI589104 AI949122 AW025986 AW275328 N51358 AA131190 AA723731 N86864 AA091367 AI738620 AA345291 AA774160 R51372
			AI373904 R37681 W72195 AA476597 AI025596 AI242078 AA384072 BE349121 AI203442 AA885019 AI424214 AI964081 AI219465 AW103904
			AA017216 AW591839 AI890043 BE247650 AW793376 AA224322 AI784198 AW190649 BE247646 AA055073 D19892 AA428076 AA165625

			R34233 AA469355 AI302148 AI690055 AA946756 AI697829 BE218045 AA027985 AI734957 AA436215 AW362506 AA469277 AA436214 AW362508 R79964 AW362504 AW362505 AA027984 AI417795 BE066043 AW967592 AA165661 AA251567 C05877 R19957 R53161 R52318 Z44555 BE066030 AW769414 R35560 H08481 AA017309 H91010 N39092 N48447 AW299698 BE270312 AI333779 R68946 AF154846 AA400924 AF075093 AA626790 AI0202783 H53869 H53499 AI001163 AA714166 L32164 AA768900 AW182419 AW977136 AI915355 AA994468 AI377886 AI654131 AI674302 AW074683 AA224872 AI791642 AA228308 AI821503 AA230172 AA224838 U00803 NM_002031 AW195632 C05922 W28481 AW967500 AW966876 AW976565 AI417020 AI057022 AA251316 AA744820 AI806037 AW966871 AA251713 AF080576 T49825 AA281037 T49826 AK001714 AW960785 AK001831 BE075311 AW273355 AA928445 AI698734 AW977909 AW268863 AI392846 AA811609 AI565035 AW007245 AI754385 AI092244 AA906509 AW438768 AW751668 AA459681 AA861761 AW118314 D63077 AI537049 AA782718 AW050550 AA430988 AA130556 AA383461 AA337522 AA130593 AA258033 AA459485 AK001652 AK001245 AJ010840 AA443492 AA361206 AA384559 AA205216 AI990275 BE075308 AA927343 AA372625 AI572799 BE466582 N30525 AA813191 AA466509 AA854999 N30537 AA463668 BE149580 AA301443 AI366930 AA010769 AA248189 AW043967 AA011050 AI193868 AA508116 N20812 AI190726 AW663652 AI161405 AA909896 H52712 AI081806 AI862934 AI167935 AA460738 AI345960 AA466141 AA346920 BE565501 AA456419 AA953554 AA806622 AI242924 AI619442 AI082684 AA947786 AA601594 BE044119 BE349995 AA091744 AW959301 H70392 AA279143 AA419462 AW135986 BE467356 BE221523 BE468135 AA282464 T70755 AW592167 AA284280 W47266 AW972765 AW069452 W47267 AI186593 AA526308 AA525432 AI868634 BE465909 AI057197 AI968927 AI969377 N21608 W25410 AI792468 AI734237 N28843 N58992 AI820802 N93619 AI668704 AI367790 AI204569 AI827786 AW303478 AI216657 AW592056 AA928804 AA890107 AA292862 AA398885 BE247203 BE244171 AW205198 AI245208 AI284388 BE048356 AW293524 NM_016014 AF151825 AI026799 BE048322 AI568420 AI041696 AI796313 AW003505 AI492609 AI564777 AW590366 AW236586 AI191469 AI571792 AA490835 AA843378 AA843160 AA932149 AA687136 AI829606 AA490836 BE005634 AW965621 F12793 R56751 R52429 T75124 R58675 AI205826 AA258787 BE467912 AI744557 AA554436 AI640749 AI077333 BE221602 AI538508 AA968618 AI671472 AI290360 AI863656 AI910555 AW104195 AI648463 H24708 AA280869 AA279428 AA987634 AA480878 AA836072 AW877911 AA521155 AA305609 AI110686 AF063561 AA480937 AA281170 H96495 BE005402 AW367567 AW367372 AW367351 AW367585 AW601230 AA847183 AA442049 AW896013 BE568756 T09279 T36094 AA287495 Z42413 AA328761 AW139131 AA252554 AA323777 AW950315 AA999676 AI815004 AI203869 AI016834 AW136782 AA999661 AA825909 AW071102 AA826127 AA838505 AA885039 AA287392 AI470496 C01794 AA249575 AL118643 BE538611 R56578 R56014 R17173 AW135076 R45909 AW370767 R77253 U13897 BE165997 AA363946 AA628263 AA628262 S78234 T87689 NM_001256 U00001 M78440 BE280314 BE568566 AI075160 W31156 AA256407 AA255817 R16014 AI203880 AW117283 AA504316 AW105046 AW370478 AI378553 AA732100 AA815109 AW297995 BE501979 AW293480 AA972091 BE082548 N98929 AA255818 AA256301 AI559887 R16115 AA384982 AW949878 AA085260 AL135314 AA211035 AI689616 BE004600 BE004767 BE004597 AW800545 AW197262 AA996213 AW452890 AI458977 AA188660 AA491202 BE327143 AA489098 AW172396 AI399903 AA830687 AI916706 AW860246 AW006356 AI288368 AW193267 AA670452 AA445924 AI276764 AA428407 AA836037 AI886571 AA922445 AA557273 AA599272 AA937432 AW594254 AV650497 AI889557 BE221149 AA934793 AA373059 AA883898 AA491005 T87690 AA167622 AA167635 AA084655 AA207057 AA633879 AA706479 AA706213 AA706197 AA679805 AA683208 AA679343 AA613172 AA679833 AA085131 AA679793 AA601666 AA210946 AA583228 AA601229 AA084718 AA584501 AA224217 AA706452 AA489324 AA587310 AA082786 AA586892 N23070 AA211405 AA082906 AA489789 AA209324 AA206631 AA167636 AA188956 AA666070 AA199718 AA214195 AA113862 AA206791 AA633796 AA223986 AA083048 AA085009 AA085307 AA207042 AA214235 AA166892 AA188689 AA211101 AA706139 AA773961 AA773972 AA189090 AA668591 AA213387 AA206041 AA199719 AA223995 AA085386 AA199670 AA199904 AA199651 AA084336 AA167637 AA666175 AA223978 AA707341 AA214110 AA633741 AA205951 AA214421 AA666402 AA188669 AA161379 AA084747 AA211176 AA6664225 AA169244 AA714142 AA679457 AA668573 AA206000 AA780452 AA454542 AA706364 AA706507 AA706570 AA722308 AA707242 AA704053 AA707423 AA722261 AA703686 AA703777 AA707238 AA706366 AA707433 AA706380 AA703761 AA706572 AA704109 AA706275 AA704117 AA707250 AA774043 AA707349 AA679485 AA214199 AA666241 AA779045 AA668507 AA668597 T03211 AA664313 AA214112 AA668518 AA214159 AA214297 AA085030 AA211088 AA209254 AA214326 AA213476 AA205166 AA223713 AA223626 AA213473 AA199706 AA224108 AA223973 AA167729 AA213641 AA221125 AA199730 AA223972 AA161387 AA668335 AA434073 AA679481 T92447 AA085177 AA633986 T49882 AA214251 AA085153 AA214425 AA223838 AA160951 AA224107 AA214341 AA372581 AA309169 AA199705 AA346242 AA211015 AA224156 AA083161 AA176787 AA224038 AW374738 AA224043 AA209284 AA224039 AA213681 H55496 AA213640 AI267801 AA206853 T82077 BE180566 AA811950 AA397546 AA699372 AA699363 AA399064 AI301740 AL119574 AW504484 BE560671 BE269112 AW897591 T31233 U17279 AW504792 T32181 Z47338 T05711 AL121247 AW504876 AW161725 AI204992 D38743 D38661 AW895130 AA985067 AL120318 AA326654 AW955387 AA776607 D38742 AI267812 AL035910 BE008426 BE008367 AA423862 BE348785 AA249436 AA326809 AA325529 AW361428 N24212 AW302831 AI583363 AW470460 AL038861 AA234531 AI376141 AA194854 W35263 N39248 D52746 D55494 AA083749 D52828 T30063 T31624 D54617 AA112066 BE018814 AW882900 M78702 T31558 T31691 AW859799 AA310616 AW389747 AA317897 T31158 AI077640 AA386250 T10323 D53660 F05613 AL120458 H15866 AW895727 AW895802 AW899191 AA128798 N31267 H14732 BE208125 N64235 H97218 AA236449 BE087062 F11649 F11648 Z42310 T32845 U47717 H43263 Z44143 T05325 T16885 AL138108 H84437 AA197265 N46693 AW020269 AA070847 AW022743 AW885792 M78703 AA486340 T07147 N36340 T35393 AW841129 AI288455 BE005370 AI497892 C14978 AA487674 T30747 AW022976 AA860826 AA730653 AA857741 T08861 N67128 AI127818 AA886918 AI424496 AI004685 D55084 AA747954 AI128832 W23585 Z41668 H84438 AI611575 AI350797 AA502260 AI364537 AA638970 U97105 NM_001386 BE009933 BE546254 BE396357 BE513831 W26313 H10568 T97273 T33131 T07524 AW276666 R15142 T30810 F07479 T33812 H24219 AV647683 AV646892 H29990 N44636 N44265 AW292774 AA398365 R92869 AA403200 N77624 AW607635 H03232 N46965 H94749 AW382351 R02203 BE169946 N56808 AA045401 AA046564 AA658111 N59303 H47303 R09001 AW023738 AW607549 H68307 R73086 W67321 AA126540 R27493 AA400212 AA044323 AA329416 AL037969 N54710 AA101647 D60371 N58245 D61743 H46463 AA126414 BE501495 AI765781 AW237498 BE219266 AA716110 AA031291 AA400123 C16598 AA045283 C16444 D62466 AW189929 AI143224 AA530868 AW194998 AW593426 AA813316 C16384 AI332909 AI335037 D57149 D45498 C16198 C16113 AA705203 AA777104 AI360091 C16168 N89583 W67248 AI469064 H753912 N92420 AI862009 AI093246 AA101648 AI138331 AA296430 AI302151 R25756 N34045 AW338083 AW139636 AI559099 AI184816 AI200476 AI127576 T82460 AI368362 AI435204 AI478453 AI093082 AI469352 AW338517 AI200250 AI031694 AI887286 AI033758 AW080370 AW029140 N32140 N52949 N50055 H47004 R76054 R61887 R73087 AI160363 H64018 W88748 AI081703 AA149098 R40542 N77209 H04380 AA234491 R08896 D57030 AI767209 AA600348 N70842 AA044242 AI888195 AA777676 AI538758 C16174 R38565 AI799219 H74312 F10055 W37697 F10343 AA610106 R52523 R22142 H88895 R77674 R44673 AA045199 R31568 AA505916 AI360773 F10337 AA733180 AI016479 AW183400 AW779199 D58102 H64348 D57909 R26653 AW051234 Z41044 AA876777 F03579 AI680446 AA745688 T24075 T35116 T35115 R02091 Z30229 AI872774 AW772549 AI540411 AI784282 R25646 AA541817 T77442 R26596 BE166424 T77229 R23696 AA399018 AW242359 AI868208 AW020951 AA412180 AI026157 AA838752 AI146272 AA910825 AI266100 N24580 H97503 BE327388 AI697814 W56675 AA423842 AA423880 H40134
5	456189 456208 456273	1620717_1 165094_1 1731_1	
10	456303 456347 456386 456443 456472	176684_1 18004_1 1842693_-1 188540_1 19126_1	
15	456481 456510	192210_1 19507_1	
20			
25	456513 456536 456555 456561	195409_1 198330_1 199748_1 200378_1	
30	456605 456606 456737	203819_1 203847_1 22551_1	
35			
40	456933 457003	256540_2 27203_1	
45			
50			
55	457024 457030	274501_1 27473_1	
60			
65			
70	457039 457040	275248_1 27530_2	
75			
80	457041 457122	275843_1 287827_1	



5	457128	28930_1	AI932995 BE064464 AW371902 AW371841 AI885885 BE064457 AA524113 AA721037 AA504343 AA778099 AI800598 AI693112 AI864633 AI690228 AI400990 AW969089 AW371927 AW371912 AW383562 BE151089 AW383568 BE218503 AW383570 AW371899 BE151097 AW371900 AW293095 AW292008 AA434179 AA714780 R45868 W01182 AW957767 AW119223 AI207864 W01578 AA354403 AA805177 AI613299 AW269636 AA481528 AW079101 AF131777 R60489 T81289 AA481594 BE181020 AA465433 AW808125 T84992 AA749191 AA436837 AA442594 AA443927 AA444106
10	457176	296527_1	AW820035 T20260 T20259 AL049415 AA737756 W46965 W00799 AW340968 AW027417 AW263261 AI420674 AA814921 AA736509 N69991 AW368643 W47065 AI090172 AI924139 BE468071 AA375842 AA375767 AW628849 AI422731 AA494558 AA969233 AI142954 AI161089 AI167233 W94484 AI681576 AA249694 AI695943 AA832347 AA476621 AA937792 AI702870 AA455748 AW195100 AI638530 BE502479 AI383418 AA039630 C20777
15	457314	318637_1	AA479597 Z45151 H28821
20	457460	340038_1	AI143312 AI394343 AW205239 AA523980 AI831223 AI347180 BE263197 AA765781 AI654500
25	457506	34672_1	AF131757 T79901
30	457620	371514_1	AA602711 BE078290
35	457630	373784_1	AI680803 AI703329 AA609004 AI305245 AI457796 AW295787
40	457652	37972_1	AF116656 AI114583 AW838134 AW838525 AW885447 H83251 AW838349 AW838378 AW838175 H83252
45	457653	37979_2	AI820719 AI273515 AW592687 AI263784 AI351926 R46866
50	457741	395767_1	BE044740 AW827360 AW827623 BE161439 BE044718 BE046207 BE046551 AA653908 BE166581
55	457756	3_1	AA126136 H62964 BE245159 AF280094 AA431918 BE386201 AA707576 AI074267 AA969194 AA693596 H62844 AW134991 AA126014 AI077443 AA699881 AI037956 AA961277 AW204185 AI540791 AI273273 AW627957 AA926890 AI014851 AW081056 AA443705 AW137571 BE139390 AI583851 AI583822 AI583814 AW268341 AI590502 AW302642 AI053871 AI254692 AI591255 AI590260 AI583359 AI583341 AI583752 AI224227 AW302089 AW466960 AA810124 AW302684 AI272921 AI141003 AW589738 AA074714 AA621482 AI796501 AW024557 AA621074 T62627 AA639206 AI913538 AA075135 R54613 AA352975 AW206892 AI868280 AW449243 AA907317 AW134573 AI590492 AI610050 AI834309 AI375556 AI284991 AW968038 BE065030 AA670100 AA781546 AI022472 AA846803 AI497780 N68386 AI382890 T78013 AA699327 W87785 W88613 AW976692 AA806542 AA745856 AI373638 AI073389 AI087143 AA764776 AA913318 AW978161 AW978165 AI016938 AI539270 AW294958 AW511089 AA814849 AF074982 R27906 R31333 R31591 R27812 AW979009 AA828038 AA828148 AA393603 Z19481 AA252342 AI807614 AI913804 AA040176 AA971879 H53388 AF085972 AI291424 H53349 AW015078 AA768307 AA127921 AA723700 AA040841 AA993954 AA213655 AA127972 AA913063 BE327712 AI017585 AA988186 AA628183 AI205930 AA833558 AA974107 AI004390 H48931 AA724004 AW296024 AA897109 AI015000 Z40670 BE504110 BE219908 AW468668 AI002334 U48351 AA969182 BE327312 AW138276 BE467567 AI680815 AI422668 AI264628 AF017648 AI872732 AI024855 AI024877 AI084514 N46645 AW183984 AV648310 AV661871 AI928475 AV647819 T55845 AI185703 AI805813 AW292764 AW136139 AI216724 AI305223 AI458577 AI275569 AI362790 AI275996 N48887 AI299789 BE551384 BE281115 T53860 AV659439 AV659421 BE539929 AI554946 AW362008 AW362553 AI683342 AI376781 AW802754 BE619228 AI693417 AI418256 AW627792 F32979 AW295151 AI425004 AW470228 AI693738 H50554 R99198 H50553 R99197 AW001835 AW612725 AW136670 AI798956 BE467368 AA280216 AI216754 BE622057 AL121193 AW853470 AW853450 AW369075 AW369108 AW578479 AW369106 AW361242 AW361190 N79183 N98648 AI458157 BE041652 BE218014 BE622355 AA369340 AA369515 AW962780 AW962704 AI522129 T56009 R53849 AW236702 AI566105 Z40396 AI630223 AI630470 AW865523 AW865128 AW865467 AW865127 AW865466 R15891 R61471 R61469 N69765 AI014624 AA007214 AW592075 H09780 AA709038 AI335898 H11055 AI559229 F09750 T72573 AA935558 AA988654 AA826438 AI002431 AI299721 AW968226 AI139249 AI701692 AA017303 AW469622 AA259148 AA811690 AA807996 AA744260 AA824494 AA731710 T25332 AA258101 AA970887 AW439497 AI826059 AA018402 AA837392 BE551721 H51878 AI823338 C01488 AW813562 AW301478 AW301560 AI889207 AW138410 AI912712 N40186 BE261314 AI243406 AA027322 AI808913 AW028342 W81290 AI571379 AI382808 AA037071 W79688 R48751 N31808 AI870233 R48752 AW024895 AI333754 AW294659 AI204928 AA351653 H51220 R86843 AA993182 U79298 R15294 F05089 Z42963 R17818 T77498 AA332319 W56049 AA331586 AW881873 AW881865 AW881876 R52345 AI652070 AA400044 AA401512 T08151 W05486 N68378 T33846 AI190920 R43021 AI949980 Z39084 T63413 W37269 F01343 R86669 AI621055 AW117593 AI193211 AW297932 AI500709 AA400056

75 Table 30C

80 Pkey: Unique number corresponding to an Eos probe  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
------	-----	--------	-------------

	400462	9929659	Minus	197610-197785
	400608	9887666	Minus	96756-97558
5	400612	9929646	Minus	151513-151662
	400631	8247025	Minus	56203-56313,56424-56482,57073-57185,57513-57593,57747-57941
	400641	8117693	Plus	4786-4992
	400664	8118496	Plus	13558-13721,13942-14090,14554-14679
	400696	8118812	Minus	77737-77899
10	400697	8118812	Minus	79073-79198
	400706	7249204	Minus	78299-78686
	400816	8569993	Plus	161221-162078
	400842	1927148	Plus	90462-90673
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
15	400861	9757506	Plus	163855-164016
	400889	9958234	Minus	169782-170036
	401069	3927852	Minus	45682-45831
	401098	9965518	Minus	85632-86174
	401132	8705350	Minus	85679-85795
20	401189	9690246	Minus	90815-90929
	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
	401240	3355450	Plus	77433-77636
	401324	9863791	Plus	234057-234174
	401365	9796180	Minus	119572-119672
25	401368	8670914	Minus	65508-65662
	401459	9212270	Minus	182001-183323
	401462	6682291	Plus	112763-112909
	401497	7381770	Plus	92607-92813
	401526	7770561	Plus	91570-93177
	401596	3293210	Plus	63639-63890
30	401614	7839924	Plus	17350-17735
	401626	8575943	Minus	238100-238432
	401645	7657839	Minus	34986-35133
	401673	7689903	Minus	122587-122705,122765-123047
35	401694	3540172	Minus	64056-64168
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401878	8099802	Minus	162268-162474,163089-163195
	401887	7229981	Plus	93973-94120
	401899	7230209	Minus	155620-155815
40	401986	4406829	Minus	31137-31293
	401989	4309964	Minus	118611-118821
	401991	4156128	Plus	2398-2513
	402048	8072512	Plus	43936-44078
	402076	8117410	Plus	128316-128627
45	402090	7249154	Minus	104806-104939,106898-107052
	402112	8139750	Plus	10507-10713
	402131	7704961	Minus	33114-33209,33496-33678
	402145	8018280	Plus	113086-114800
	402318	7582559	Minus	12843-13403
50	402333	8844110	Minus	165693-165856
	402341	7656696	Plus	22583-23699
	402369	9558577	Minus	50417-50522
	402451	9796677	Minus	48137-48343
	402528	7630857	Minus	169609-169742
55	402603	9909396	Minus	141663-141852
	402615	9926801	Plus	131390-132157
	402689	8348025	Minus	5885-6209
	402942	9368398	Plus	102152-102386
	403011	6693597	Minus	3468-3623
60	403053	8748888	Plus	146568-146659,147539-147811
	403089	8954241	Plus	171964-172239
	403188	9838289	Minus	157618-157755
	403218	7630969	Plus	58039-58149
	403271	7230852	Plus	134283-134485
65	403281	8072630	Minus	7521-7728
	403306	8099945	Plus	127100-127251
	403310	8139936	Minus	183883-184026
	403317	8318526	Minus	50623-50834
	403329	8516120	Plus	96450-96598
70	403341	8569175	Plus	30699-30910
	403344	8569726	Plus	70823-70990
	403356	8569930	Plus	92839-93036
	403513	7656757	Minus	155310-155436,158402-158535
75	403515	7656757	Minus	173358-179553
	403525	7960440	Plus	152431-153243
	403534	8076917	Minus	46652-47332
	403568	8101145	Minus	85509-85658
	403572	8101156	Minus	1253-1675
	403574	8101156	Plus	5542-6176
80	403623	8569879	Minus	3519-5426
	403625	8569879	Plus	6551-7111
	403637	8671936	Minus	142647-142771,145531-145762
	403678	7331517	Minus	119573-120430
	403691	7387384	Minus	88280-88463



	403776	7770611	Minus	1414-1513,1624-1756
	403780	8076989	Plus	93160-93409
	403786	8083636	Minus	73028-73217
5	403891	7331467	Minus	191508-193220
	403937	7711761	Minus	12609-12773
	404042	9558573	Plus	5140-5208,8633-8763
	404043	9558573	Plus	29042-29135,46597-46699
	404068	3168621	Minus	18123-18766
10	404108	8247074	Minus	63603-64942
	404166	7596822	Plus	86147-86509
	404193	3881948	Minus	94185-94322
	404196	3805917	Minus	67928-68109
	404249	8655533	Plus	64270-64633
15	404367	9965011	Minus	114391-114628
	404404	7272262	Plus	82112-82244
	404414	7382165	Plus	143127-143398
	404416	7382420	Minus	143042-143216,144704-144853,145800-146048
	404420	7407952	Minus	129817-130586
20	404443	7579073	Minus	87198-87441
	404453	7657714	Plus	27768-29179
	404476	8080699	Plus	101841-102043
	404518	8151988	Plus	84494-84603
	404526	8152087	Plus	121918-122123,125198-125348
25	404531	8247909	Plus	20152-20362
	404561	9795980	Minus	69039-70100
	404569	7249169	Minus	104257-104348,104822-104970
	404582	9739220	Plus	53230-53424
30	404587	8698840	Minus	69781-70096
	404588	6456726	Minus	40059-40210
	404593	9944086	Minus	74922-75788
	404595	9958262	Minus	16764-16900
	404638	9796751	Minus	99433-99528,100035-100161
	404652	9796969	Minus	108172-108296
35	404694	9799957	Minus	128092-128227
	404708	9800828	Plus	77522-77658
	404731	7230299	Minus	168609-168781,182951-183081
	404767	7882827	Minus	23244-23759
	404793	7232206	Minus	61087-61590
40	404822	3810614	Plus	7541-8132
	404834	6911603	Minus	37948-38226
	404957	7407927	Plus	147512-148011
	404967	7523744	Minus	89944-90729
	404988	4662677	Minus	72406-72600,72779-72856
45	405001	6015406	Minus	104646-104819
	405008	6088019	Minus	64091-64267
	405090	8072525	Minus	38552-39202
	405120	8099940	Plus	140176-140340
	405229	7249019	Plus	51081-51701
50	405230	7249032	Minus	97493-97682
	405302	2078453	Minus	121688-121840
	405347	2979602	Minus	977-1116
	405443	7408143	Plus	90716-90887,101420-101577
55	405455	7656675	Plus	134112-134671
	405456	7656676	Plus	150052-150208
	405494	8050952	Minus	70284-70518
	405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
	405605	5836195	Minus	117070-117270
60	405608	5815499	Minus	66822-66925
	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405738	9943998	Plus	44370-45410
65	405747	8469069	Minus	153933-154060
	405780	7248203	Minus	48204-48371
	405783	5738434	Minus	27238-27885
	405784	7417368	Minus	77798-78000
	405829	7109593	Minus	15628-16127
70	405920	6758795	Plus	120621-120971
	405935	6758795	Minus	163112-163652
	405970	8247789	Minus	45795-46295
	406005	8247801	Minus	39912-40220
	406018	6758904	Minus	37795-38168
75	406076	9123123	Plus	89972-90319
	406092	9123919	Plus	251370-251797,252168-252882
	406190	7289992	Minus	22395-22901
	406288	7549620	Plus	111718-112008
	406298	5686278	Minus	30084-30770
80	406333	9213235	Plus	64689-64798
	406364	9256114	Minus	50715-50833
	406378	9256142	Minus	126408-126800
	406413	9256407	Plus	43858-44003,46993-47136
	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880

406603 8272659 Minus 39506-39694

## 5 TABLE 31A: ABOUT 1884 GENES UP-REGULATED IN IPF COMPARED TO NSIP

Table 31A lists about 1884 genes whose expression levels are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with non-specific interstitial pneumonia (NSIP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" non-specific interstitial pneumonia sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" non-specific interstitial pneumonia level was set to the 90th percentile amongst non-specific interstitial pneumonia samples.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of IPF (idiopathic pulmonary fibrosis) to NSIP (non-specific interstitial pneumonia)

Pkey	ExAccn	Unigene ID	Unigene Title	R1
450478	AW451709	Hs.271200	ESTs	20.2
405654				16.1
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
403637				11.2
431548	AI834273	Hs.9711	novel protein	10.8
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	10.4
439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
403574				10.1
416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.3
441233	AA972965	Hs.135568	ESTs	9.1
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	8.4
432437	W07088	Hs.293685	ESTs	8.3
407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	8.2
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	8.1
403329				8.0
429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	8.0
441519	AA972740	Hs.127092	ESTs	7.9
453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	7.8
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	7.7
416379	N38857	Hs.203933	ESTs	7.7
428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	7.5
407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	7.2
434683	AW298724	Hs.202639	ESTs	7.2
441802	AA968636	Hs.127877	ESTs	6.9
431242	AA987742	Hs.251278	KIAA1201 protein	6.9
442377	AA993807	Hs.167367	ESTs	6.9
420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	6.8
428908	AW303529	Hs.144955	ESTs	6.8
445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.7
457673	AA551569	Hs.272034	hypothetical protein PRO2822	6.7
458771	AW295151	Hs.163612	ESTs	6.6
426800	AA385085		gb:EST98959 Thyroid Homo sapiens cDNA 5'	6.6
440504	AI948966	Hs.130017	ESTs, Weakly similar to JN0908 H+-transp	6.6
415025	AW207091	Hs.72307	ESTs	6.5
438557	AW364104	Hs.143509	hypothetical protein FLJ21924	6.5
416128	AA173632	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	6.4
457242	AA457011		gb:aa90c11.r1 Stratagene fetal retina 93	6.3
423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	6.3
404793				6.2
435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	6.2
415672	N53097	Hs.193579	ESTs	6.2
455488	AA102322		gb:z190f03.r1 Stratagene colon (937204)	6.2
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	6.1
412282	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	6.1
431622	AW979271	Hs.293184	ESTs	6.1
405523				6.0
424693	BE169810	Hs.47557	ESTs	6.0
436397	AA715013	Hs.169835	ESTs	6.0
456476	AA256753		gb:zs22b12.r1 NCI_CGAP_GCB1 Homo sapiens	5.9
434784	AA649051	Hs.164007	ESTs	5.9
422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	5.9
442849	R10099	Hs.269805	ESTs	5.9
451519	AI800600	Hs.209573	ESTs	5.8
412474	AI791451		gb:ni50c09.y5 NCI_CGAP_Ov2 Homo sapiens	5.8
457081	AA916785	Hs.180610	splicing factor proline/glutamine rich (	5.8
444827	R09764	Hs.20416	ESTs	5.8
404822				5.7
402430				5.7
457900	AW976692	Hs.291665	ESTs	5.7
400292	AA250737	Hs.72472	ESTs	5.7
410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
440172	AA868584	Hs.126154	ESTs	5.7

5	431374	BE258532	Hs.251871	CTP synthase	5.7
	409816	AW500954		gb:UL-HF-BP0p-air-h-12-0-ULr1 NIH_MGC_5	5.6
	447613	AL041057	Hs.33363	DKFZP434N093 protein	5.6
	417919	AI928203	Hs.86379	ESTs	5.6
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.6
10	439063	AF085922	Hs.113968	ESTs	5.6
	406053				5.5
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
	451830	H18433	Hs.21542	KIAA1035 protein	5.5
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.5
15	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	5.5
	459458	AW270957	Hs.254577	ESTs, Weakly similar to B34087 hypotheti	5.5
	416154	Z46122		gb:HSC0VB031 normalized infant brain cDN	5.5
	404561				5.4
	428895	AA437124	Hs.187247	ESTs	5.4
20	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	5.4
	440925	AW511090	Hs.130419	ESTs	5.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
	448477	BE612572		gb:601452090F1 NIH_MGC_66 Homo sapiens c	5.4
25	454039	AW079064	Hs.245540	ESTs	5.3
	459664				5.3
	401497				5.3
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	5.3
30	456680	AL137758	Hs.116072	Homo sapiens mRNA; cDNA DKFZp434H245 (fr	5.3
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	5.2
	411402	BE297855	Hs.69855	NRAS-related gene	5.2
	404957				5.2
	436445	AA922213	Hs.121735	ESTs	5.2
35	442617	AW340093	Hs.130538	ESTs	5.2
	416045	H15990	Hs.31403	ESTs	5.2
	425178	H16097	Hs.161027	ESTs	5.2
	441918	AI733373	Hs.128119	ESTs	5.2
	455464	AW983901		gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.2
40	420929	AI694143	Hs.296251	programmed cell death 4	5.2
	448844	AI581519	Hs.177164	ESTs	5.2
	430686	NM_001942	Hs.2633	desmoglein 1	5.2
	405229				5.1
	417641	AA205015	Hs.54617	hypothetical protein FLJ20060	5.1
45	434167	AA626334	Hs.116153	ESTs	5.1
	450438	AI696071	Hs.253800	ESTs	5.1
	456394	W28506		gb:48f1 Human retina cDNA randomly prime	5.0
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
	417420	T85150	Hs.268814	ESTs	5.0
50	409545	BE296182	Hs.19002	hypothetical protein MGC4675	5.0
	426750	AA383950		gb:EST97403 Thymus II Homo sapiens cDNA	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
	408959	AW890878	Hs.211610	CUG triplet repeat, RNA-binding protein	4.9
	454482	BE147919		gb:RC3-HT0230-160200-016-a08 HT0230 Homo	4.9
55	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	4.9
	452046	AB018345	Hs.27657	KIAA0802 protein	4.9
	407415	AF073328		gb:Homo sapiens tetracycline transporter-	4.9
	450090	AW448940	Hs.202259	ESTs	4.9
	406333				4.9
60	434188	AI765848	Hs.281680	peroxisomal trans 2-enoyl CoA reductase;	4.8
	403344				4.8
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	4.8
	405455				4.8
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	4.8
65	426097	BE327369	Hs.112238	ESTs	4.8
	427768	T78402	Hs.174880	ESTs	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
	415257	F03016	Hs.27513	ESTs	4.8
	441107	AA917075	Hs.190520	ESTs	4.8
70	419519	AI198719	Hs.176376	ESTs	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
	424188	AW954552	Hs.142634	zinc finger protein	4.8
	456987	AI557290	Hs.173536	ESTs	4.8
75	405303				4.8
	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.8
	451620	AW449888	Hs.257224	ESTs	4.7
	421948	L42583	Hs.334309	keratin 6A	4.7
	424780	U39576	Hs.153058	butyrophilin, subfamily 1, member A1	4.7
80	443271	BE568568	Hs.195704	ESTs	4.7
	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	402230				4.7
	422246	AA461032	Hs.5306	hypothetical protein DKFZp586F1122 simil	4.7
	431508	NM_012481	Hs.182979	ribosomal protein L12	4.7
	415236	R41400		gb:yf94b12.s1 Soares infant brain 1N18 H	4.7
	413101	BE065215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo	4.6
	444774	AW052174	Hs.196030	ESTs	4.6

5	444414	AW293214	Hs.8752	transmembrane protein 4	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	436853	BE328074	Hs.148661	ESTs	4.6
	445334	AI610081	Hs.9475	glucose transporter protein 10	4.6
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	4.6
10	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	404638				4.6
	447617	AI400762	Hs.176675	ESTs	4.6
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	4.6
	442360	AI374621	Hs.29055	ESTs	4.6
15	411738	AW859353		gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
	444157	AI125785	Hs.153351	ESTs	4.5
	401365				4.5
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF I [	4.5
	436269	AA707472	Hs.190760	ESTs	4.5
20	459448	AA416773	Hs.275012	EST	4.5
	452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	4.5
	414899	AW975433	Hs.36288	ESTs	4.5
	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	4.5
	444898	AI201548	Hs.308338	ESTs	4.5
25	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.5
	428528	AI004034	Hs.98638	ESTs	4.5
	405605				4.5
	457982	AW856093	Hs.183617	ESTs	4.5
	427731	AA411750	Hs.20943	ESTs	4.4
30	420691	AA829433	Hs.275343	ESTs	4.4
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	4.4
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	4.4
	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
	435747	AI079519	Hs.134398	ESTs	4.4
35	453824	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	4.4
	458865	T05095	Hs.19597	KIAA1694 protein	4.4
	459037	AW439497	Hs.290656	EST	4.4
	403310				4.4
	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
40	427500	AW970017	Hs.293948	ESTs, Weakly similar to S65657 alpha-1C-	4.4
	432020	AJ251509	Hs.272345	phosphodiesterase 11A	4.4
	453043	AW136440	Hs.224277	ESTs	4.4
	456293	AW131715	Hs.311561	ESTs, Weakly similar to CYA7_HUMAN ADENY	4.4
	447879	BE503405	Hs.170437	ESTs, Weakly similar to PRP4_HUMAN SALIV	4.4
45	426646	AA382787	Hs.122713	ESTs	4.4
	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	4.4
	404898				4.4
	435434	AA680387	Hs.187850	ESTs	4.4
	443314	AW771701	Hs.54646	ESTs	4.3
50	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	4.3
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	4.3
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	4.3
	404767				4.3
	445189	AI936450	Hs.147482	ESTs	4.3
55	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	428740	AA433838		gb:zw53e12.r1 Soares_total_fetus_Nb2HF8_	4.3
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H	4.3
	410615	AW772721		gb:hl95c01.x1 NCI_CGAP_Thy8 Homo sapiens	4.3
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.3
60	406073				4.3
	405692				4.3
	436033	H75391	Hs.255748	ESTs	4.3
	410733	D84284	Hs.66052	CD38 antigen (p45)	4.3
	455587	BE007829		gb:QV0-BN0147-280400-213-d03 BN0147 Homo	4.3
65	459084	H01699	Hs.27289	CGI-125 protein	4.3
	401189				4.3
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-hereregulin	4.3
	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
70	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	436659	AI217900	Hs.144464	ESTs	4.3
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	4.3
	439481	AF086294	Hs.125844	ESTs	4.3
75	405287				4.3
	405784				4.3
	436461	AW511956	Hs.293261	ESTs	4.3
	437636	AA764781	Hs.291844	ESTs	4.2
	409629	AW449589	Hs.279724	ESTs	4.2
80	412999	BE046255		gb:hn38g10.x2 NCI_CGAP_RDF2 Homo sapiens	4.2
	403281				4.2
	427531	AA405097	Hs.97957	ESTs	4.2
	451882	AI821324	Hs.100445	ESTs	4.2
	418856	AA362858		gb:EST72900 Ovary II Homo sapiens cDNA 5	4.2
	405494				4.2
	456027	BE327387	Hs.13913	KIAA1577 protein	4.2
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	4.2

5	421106	AA877124	Hs.172844	ESTs	4.2
	409076	N57559	Hs.82273	hypothetical protein	4.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	4.2
	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	4.1
	416614	T83391	Hs.111849	ESTs	4.1
10	454434	AA083558	Hs.261286	ESTs	4.1
	404526	AI912555	Hs.157195	peptide YY, 2 (seminalplasmin)	4.1
	446393	AW014174	Hs.301956	zinc finger protein	4.1
	405302				4.1
	432669	AL043482	Hs.267115	ESTs	4.1
15	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	430484	D82880	Hs.241548	RAS p21 protein activator 2	4.1
	403895				4.1
20	420457	AA482280	Hs.191656	ESTs	4.1
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	458421	AI279978	Hs.22547	ESTs	4.1
	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.1
	411382	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	4.1
25	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	4.1
	430749	AJ242956	Hs.25960	v-myc avian myelocytomatosis viral relat	4.1
	403625				4.1
	401887				4.1
	403667				4.1
30	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	432792	AA448114	Hs.278950	protocadherin beta 1	4.0
	405443				4.0
35	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	4.0
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens	4.0
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.0
	448324	AI571356	Hs.34174	ESTs, Moderately similar to ALU8_HUMAN A	4.0
	456536	AW135986	Hs.257859	ESTs	4.0
40	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.0
	449327	AI638743	Hs.224672	ESTs	4.0
	426062	N57014	Hs.75874	pregnancy-associated plasma protein A	4.0
45	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	4.0
	434849	AW292765	Hs.8053	ESTs	4.0
	400268				4.0
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	4.0
	445414	AV653692	Hs.146105	ESTs	4.0
50	406470				3.9
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (	3.9
	453098	Z25935	Hs.86379	ESTs	3.9
	402867				3.9
	431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
55	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	419091	T85332	Hs.178294	ESTs	3.9
	422591	L07648	Hs.118630	MAX-interacting protein 1	3.9
	426076	AW962714		gb:EST374787 MAGE resequences, MAGG Homo	3.9
60	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	3.9
	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogen	3.9
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	3.9
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.9
65	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
	455993	BE179085		gb:RC0-HT0613-140300-021-d06 HT0613 Homo	3.9
	420111	AA255662		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	403956	W28077	Hs.79389	nel (chicken)-like 2	3.9
70	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru	3.9
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	3.9
	430140	AW296771	Hs.221999	ESTs	3.8
	457042	AI382130	Hs.97703	ESTs	3.8
	450236	AW162998	Hs.24684	KIAA1376 protein	3.8
75	417706	T90797	Hs.268623	ESTs	3.8
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	413071	BE064032		gb:QV3-BT0296-010300-111-b08 BT0296 Homo	3.8
	437354	AA749215	Hs.291886	ESTs	3.8
	403381				3.8
80	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens	3.8
	459429	AA278779	Hs.335696	EST	3.8
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	3.8
	430757	AI458623		gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	3.8
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	433887	AW204232	Hs.279522	ESTs	3.8
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.8
	404043				3.8

	431333	AA708488	Hs.120127	Homo sapiens cDNA: FLJ22769 fis, clone K	3.8
	451073	AI758905	Hs.206063	ESTs	3.8
	417663	R07483	Hs.180461	ESTs	3.8
5	432363	AA534489		gb:nf76g11.s1 NCL_CGAP_Co3 Homo sapiens	3.8
	436975	AA740723	Hs.212644	ESTs	3.8
	405959				3.8
	400631	AF173937	Hs.109494	secreted protein of unknown function	3.7
	425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3.7
10	446158	AI277603	Hs.145990	ESTs, Weakly similar to I38022 hypotheti	3.7
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.7
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.7
	436020	AA778177	Hs.121724	ESTs	3.7
	424989	AA985520	Hs.23575	ESTs	3.7
15	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.7
	441416	AI990139	Hs.148609	ESTs	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	402112	R58624	Hs.2186	eukaryotic translation elongation factor	3.7
	404453				3.7
20	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	453375	AI990114	Hs.240091	ESTs	3.7
	453530	AW021633		gb:df26c02.y1 Morton Fetal Cochlea Homo	3.7
25	406964	M21305		gb:Human alpha satellite and satellite 3	3.7
	432291	AK001108	Hs.274274	hypothetical protein FLJ10246	3.7
	449623	C00719	Hs.120440	EST	3.7
	419691	W03298	Hs.193521	ESTs	3.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.7
30	403271				3.7
	453123	AI953718	Hs.221849	ESTs	3.7
	400462				3.7
	449804	AI535663	Hs.39379	ESTs	3.7
	443305	AI050693	Hs.133318	ESTs	3.7
35	411186	AW621257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.6
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	3.6
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	403296				3.6
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.6
40	436026	AI349764	Hs.217081	ESTs	3.6
	429864	AA480039	Hs.286	ribosomal protein L4	3.6
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	3.6
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.6
	446304	AW104432	Hs.149761	ESTs	3.6
45	441216	BE299830	Hs.192908	ESTs	3.6
	421494	AI763322	Hs.152104	ESTs	3.6
	404476				3.6
	416327	R99822	Hs.36172	ESTs	3.6
	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.6
50	417401	AA426026	Hs.187615	ESTs	3.6
	401200				3.6
	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.6
	426306	AA447310	Hs.164059	Homo sapiens cDNA FLJ13338 fis, clone OV	3.6
	437918	AI761449	Hs.121629	ESTs	3.6
55	447917	AI048037	Hs.164588	ESTs, Moderately similar to neuronal thr	3.6
	421328	BE466506	Hs.3981	ESTs	3.6
	447290	AI476732	Hs.263912	ESTs	3.6
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AI023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	403515				3.6
60	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (fr	3.6
	435554	AF208502	Hs.185708	early B-cell factor	3.6
	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	3.6
	410500	R09442		gb:yf26c09.r1 Soares fetal liver spleen	3.6
65	439326	W07140	Hs.54721	ESTs	3.6
	426296	R14454	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.6
	411311	AW836491		gb:PM3-LT0032-281299-002-f02 LT0032 Homo	3.6
	418019	R68911	Hs.176275	ESTs	3.6
	417490	AA203335		gb:zx56g02.r1 Soares_fetal_liver_spleen_	3.6
70	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	416575	W02414	Hs.38383	ESTs	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	418405	AI868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
	450350	T97817	Hs.174880	ESTs	3.5
75	451704	AI755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.5
	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRN	3.5
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	430533	AA480895	Hs.201552	ESTs, Weakly similar to T17288 hypotheti	3.5
80	457141	AA521410	Hs.41371	ESTs	3.5
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	3.5
	440737	AI375167	Hs.132221	hypothetical protein FLJ12401	3.5
	452728	AI915676	Hs.239708	ESTs	3.5
	423266	AA323875	Hs.193574	ESTs	3.5

5	413543	AA130228	Hs.324611	ESTs, Moderately similar to ALU8_HUMAN A	3.5
	454447	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	3.5
	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	415549	F11942		gb:HSC33F061 normalized infant brain cDN	3.5
10	420910	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (f	3.5
	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	453211	W84829		gb:zh53f04.r1 Soares_fetal_liver_spleen_	3.5
	418717	AI334430	Hs.86984	ESTs	3.5
	400641				3.5
15	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	3.5
	418007	M13509	Hs.83169	matrx metalloproteinase 1 (interstitial	3.5
	440364	AA910460	Hs.128626	ESTs	3.5
	458340	AI457102	Hs.6986	Human glucose transporter pseudogene	3.5
	412281	AI810054	Hs.14119	ESTs	3.5
20	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	3.5
	416616	H68270		gb:yr81h09.r1 Soares fetal liver spleen	3.5
	444338	AI937026	Hs.146642	ESTs	3.4
	436946	AW137748	Hs.125956	ESTs	3.4
	431632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fis, clone HE	3.4
25	403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	3.4
	422093	AF151852	Hs.111449	CGI-94 protein	3.4
	428816	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	3.4
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
	405970				3.4
30	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.4
	416100	H18700	Hs.268799	ESTs	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
	440388	AI693520	Hs.223000	ESTs	3.4
35	421072	AI215069	Hs.89113	ESTs	3.4
	424578	AK001973	Hs.150890	hypothetical protein	3.4
	436331	AI239495	Hs.120189	ESTs	3.4
	444063	AI122614		gb:qa96b05.x1 Soares_fetal_heart_NbHH19W	3.4
	444453	AW379394	Hs.145126	ESTs	3.4
40	404196				3.4
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	3.4
	409555	AW410788	Hs.256185	ESTs	3.4
	417669	T99898		gb:ye68g01.r1 Soares fetal liver spleen	3.4
	416057	AI927382	Hs.29857	ESTs	3.4
45	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	3.4
	447738	AI871000	Hs.161330	ESTs	3.4
	430664	AW969834	Hs.303303	ESTs	3.4
	411377	AW841462		gb:RC6-CN0014-080300-012-B09 CN0014 Homo	3.4
	415769	H94186	Hs.5912	F-box only protein 7	3.4
50	429382	AI791249	Hs.278054	ESTs, Weakly similar to I38022 hypotheti	3.4
	431474	AL133990	Hs.190642	ESTs	3.4
	456908	AI953671	Hs.220994	hypothetical protein FLJ14129	3.4
	442826	AI018777	Hs.131241	ESTs	3.4
	400608				3.4
55	436111	AI803082	Hs.157212	ESTs	3.4
	452807	AA028933	Hs.162434	ESTs	3.4
	436577	W84774	Hs.17643	ESTs	3.4
	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	3.4
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	3.4
60	423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	3.4
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.4
	409623	AW449185		gb:UI-H-BI3-akg-e-05-0-UI.s1 NCI_CGAP_Su	3.4
	416182	NM_004354	Hs.79069	cyclin G2	3.4
	420854	AW296927		gb:UI-H-BW0-ajc-c-07-0-UI.s1 NCI_CGAP_Su	3.4
65	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
	432404	AA535246	Hs.50852	ESTs	3.4
	458695	AV660159	Hs.282284	ESTs, Weakly similar to I38022 hypotheti	3.4
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	3.3
	428766	AA477989	Hs.98800	ESTs	3.3
70	439567	AI056618	Hs.134314	ESTs	3.3
	456231	H73183	Hs.129885	ESTs, Weakly similar to 2004399A chromos	3.3
	454318	AW367764	Hs.7857	erythrocyte membrane protein band 4.1-li	3.3
	411966	AA099113	Hs.118609	ESTs	3.3
	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	3.3
75	437037	T63804		gb:yc21e09.r1 Stratagene lung (937210) H	3.3
	407664	AW063476	Hs.279080	ESTs	3.3
	405780				3.3
	426567	AA381579	Hs.182962	ESTs	3.3
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	3.3
80	403356				3.3
	404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	3.3
	413581	BE150618		gb:RC3-HT0272-110100-013-c06 HT0272 Homo	3.3
	429875	AI091815		gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi	3.3
	433785	BE044593	Hs.112704	ESTs	3.3
	437876	AA770151	Hs.126424	ESTs	3.3
	444870	AI200621	Hs.148504	ESTs	3.3
	453324	W26592	Hs.232089	ESTs	3.3

	437963	BE396279		gb:601309785F1 NIH_MGC_44 Homo sapiens c	3.3
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	3.3
	408813	AI580090	Hs.48295	RNA helicase family	3.3
5	426692	AK001751	Hs.171835	hypothetical protein FLJ10889	3.3
	407456	AJ237589		gb:Homo sapiens mRNA for T-box transcript	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	438456	AA913381	Hs.190513	ESTs	3.3
10	453242	T98327	Hs.18343	ESTs	3.3
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.3
	412040	D86519	Hs.73086	neuropeptide Y receptor Y6 (pseudogene)	3.3
	435070	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	3.3
	444443	AI149286	Hs.55099	rab6 GTPase activating protein (GAP and	3.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	3.3
15	454145	AA046872	Hs.62798	ESTs	3.3
	405264				3.3
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	3.3
	416816	T71168	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	3.3
20	435325	AI038388	Hs.119309	ESTs	3.3
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	428356	AL046991	Hs.10338	ESTs	3.3
	429216	AI369472	Hs.65407	ESTs	3.3
	429106	AA446612		gb:zw85g07.s1 Soares_total_fetus_Nb2HF8_	3.3
25	405720				3.3
	400889				3.3
	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	422094	AF129535	Hs.272027	F-box only protein 5	3.3
	425374	AI904013		gb:MR-BT041-220199-104 BT041 Homo sapien	3.3
30	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
	427374	AI150033	Hs.143686	ESTs	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
	457604	AI004397	Hs.334552	Homo sapiens cDNA FLJ14930 fis, clone PL	3.3
35	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.3
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	3.3
	458885	AA411303	Hs.30022	ESTs, Weakly similar to NAH6_HUMAN SODIU	3.3
	429608	U49250	Hs.210862	T-box, brain, 1	3.2
	437454	AL390159	Hs.269812	Homo sapiens mRNA; cDNA DKFZp761M0415 (f	3.2
40	430503	AA533574	Hs.152274	ESTs	3.2
	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	3.2
	421698	T89677	Hs.324323	ESTs	3.2
	412321	AW936913		gb:RC1-DT0029-030200-012-f08 DT0029 Homo	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
45	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	441705	AI087052	Hs.55993	ESTs	3.2
	403619				3.2
	435608	AW183971	Hs.250896	ESTs	3.2
	426701	AI968103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.2
50	401132				3.2
	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
	409425	U40462	Hs.54452	zinc finger protein, subfamily 1A, 1 (lk	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	443603	BE502601	Hs.134289	ESTs, Weakly similar to KIAA1063 protein	3.2
55	419936	AI792788		gb:cl91d05.y5 NCL_CGAP_Kid5 Homo sapiens	3.2
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	3.2
	406592				3.2
	446530	AV658909	Hs.282642	ESTs	3.2
	454466	AA984138	Hs.155101	ATP synthase, H+ transporting, mitochond	3.2
60	401449				3.2
	431196	AW974436	Hs.154929	ESTs	3.2
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	459459	AA460445		gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_	3.2
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.2
65	427335	AA448542	Hs.251677	G antigen 7B	3.2
	455236	AW875972		gb:CM3-PT0014-071299-051-b05 PT0014 Homo	3.2
	425156	AA351364		gb:EST59099 Infant brain Homo sapiens cD	3.2
	404588				3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
70	444910	AI201849		gb:qs76g04.x1 NCL_CGAP_Pr28 Homo sapiens	3.2
	426660	NM_002719	Hs.171734	protein phosphatase 2, regulatory subuni	3.2
	438315	R56795	Hs.82419	ESTs	3.2
	425523	AB007948	Hs.158244	KIAA0479 protein	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
75	425636	AK001243	Hs.158370	hypothetical protein FLJ10381	3.2
	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	447375	AI376660	Hs.257822	ESTs	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
80	410085	AA428482	Hs.58589	glycogenin 2	3.2
	410536	N39533		gb:yv27d04.s1 Soares fetal liver spleen	3.2
	448495	AW136516	Hs.208515	ESTs	3.2
	405634				3.2
	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoadenylate	3.2



	421581	U89331	Hs.105932	short stature homeobox	3.1
	440633	AI140686	Hs.263320	ESTs	3.1
	453264	AA034137	Hs.271955	ESTs	3.1
5	411656	AW855576		gb:CM4-CT0278-221099-027-d01 CT0278 Homo	3.1
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	3.1
	426591	AA431127	Hs.98685	ESTs	3.1
	446966	C01448	Hs.300511	ESTs	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
10	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.1
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.1
	423657	AL045128	Hs.1691	glucan (1,4-alpha-), branching enzyme 1	3.1
	400816				3.1
	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
15	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
	400315	U46120	Hs.193392	Human expressed unknown mRNA	3.1
	411965	BE467339	Hs.280115	ESTs	3.1
	416316	H58721	Hs.271628	ESTs	3.1
	400613				3.1
20	414819	BE177320	Hs.156148	hypothetical protein FLJ13231	3.1
	434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.1
	418693	AI750878	Hs.87409	thrombospondin 1	3.1
	416258	N45661	Hs.90011	adenylosuccinate synthase	3.1
	405093				3.1
25	415273	Z39840	Hs.22229	ESTs	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	422654	AA314316	Hs.163725	ESTs	3.1
	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	3.1
30	400441	M15530	Hs.99879	B-cell growth factor 1 (12kd)	3.1
	402790				3.1
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	3.1
	447524	D80449	Hs.45177	ESTs	3.1
	448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
35	415979	H16427	Hs.271501	ESTs, Weakly similar to I54374 gene NF2	3.1
	434479	AI138213	Hs.162035	olfactory receptor, family 52, subfamily	3.1
	426724	AA383623	Hs.293616	ESTs	3.1
	418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	3.1
	405608				3.1
	406506				3.1
40	421216	AV649282	Hs.102664	vesicle-associated membrane protein 4	3.1
	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti	3.1
	404288				3.1
	429878	AA460188	Hs.127263	ESTs	3.1
45	439834	AI754576	Hs.124523	ESTs	3.1
	454564	AW807573		gb:MR1-ST0088-021299-004-g01 ST0088 Homo	3.1
	450491	BE045604	Hs.202301	ESTs	3.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	3.1
	400579				3.1
	402953				3.1
50	404285				3.1
	426890	AA393167	Hs.41294	ESTs	3.1
	457770	BE065030	Hs.124179	ESTs	3.1
	435477	BE218708	Hs.117270	hypothetical protein FLJ14345	3.1
55	436391	AJ227892	Hs.146274	ESTs	3.1
	456083	U46922	Hs.77252	fragile histidine triad gene	3.1
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.1
	430101	AF110002	Hs.233363	guanylate cyclase activator 1C	3.1
	449238	AA428229	Hs.331561	muscle-specific RING-finger protein 3	3.1
60	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	3.1
	456323	AW752389	Hs.87296	Homo sapiens cDNA FLJ20269 fis, clone HE	3.1
	429828	AB019494	Hs.225767	IDN3 protein	3.1
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	3.1
	452762	AW501435	Hs.278582	v-akt murine thymoma viral oncogene homo	3.1
	401344				3.1
65	455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	3.1
	455280	AW886156		gb:RC5-OT0078-150300-021-E08 OT0078 Homo	3.1
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.1
	423600	AI633559	Hs.310359	ESTs	3.1
70	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	3.0
	407257	AB006834		gb:Homo sapiens mRNA for HRV Fab N6-VH,	3.0
	457041	AA399018	Hs.250835	ESTs	3.0
	421482	AL135462	Hs.104715	inversin	3.0
	459062	AA059246	Hs.110293	ESTs	3.0
75	436475	R58806	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
	411622	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFp564B176 (fr	3.0
	417489	AW953341	Hs.22573	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
	409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo	3.0
80	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	3.0
	443741	AW451759	Hs.145420	ESTs	3.0
	405090				3.0
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
	445409	AI949081	Hs.147862	ESTs	3.0

	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.0
	406364				3.0
5	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	3.0
	448405	AW207634	Hs.170849	ESTs	3.0
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.0
10	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	3.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.0
	426424	BE081745	Hs.272188	Homo sapiens cDNA FLJ12090 fis, clone HE	3.0
	419505	AA243660	Hs.143061	ESTs	3.0
	403743				3.0
15	415452	F09134	Hs.12839	ESTs	3.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	400227				3.0
20	436219	AK001695	Hs.146589	hypothetical protein FLJ10701	3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439693	AI741816	Hs.125897	ESTs	3.0
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.0
	403513				3.0
25	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.0
	440122	AI733011	Hs.127678	ESTs	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	3.0
	448130	AW271635	Hs.170717	ESTs	3.0
30	420288	AW071225	Hs.245556	ESTs	3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	3.0
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
	404513				3.0
35	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	3.0
	407762	AW235638	Hs.29475	ESTs	3.0
	403396				3.0
	436938	AW139680	Hs.161393	ESTs	3.0
40	458090	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	3.0
	400706				2.9
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.9
	444600	R41398	Hs.6996	ESTs	2.9
	403786				2.9
45	430187	AI799909	Hs.158989	ESTs	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.9
	457503	AW970244	Hs.162188	ESTs	2.9
	446251	AW867156	Hs.282589	ESTs, Weakly similar to I38022 hypotheti	2.9
	406327				2.9
50	434671	R34758		gb:yg61g02.r1 Soares infant brain 1N1B H	2.9
	430175	AA468724		gb:ne09a06.s1 NCI_CGAP_Co3 Homo sapiens	2.9
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	2.9
	449459	BE546846	Hs.195048	ESTs	2.9
55	435934	R19382	Hs.117869	ESTs	2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	414514	BE327365	Hs.280187	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
60	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.9
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	2.9
	456186	W26642		gb:34b8 Human retina cDNA randomly prime	2.9
	412222	AA528283	Hs.292737	ESTs	2.9
65	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.9
	435579	AI332373	Hs.156924	ESTs	2.9
	417027	AA192306	Hs.23926	triadin	2.9
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.9
	445909	BE262656	Hs.32603	hypothetical protein MGC3279 similar to	2.9
70	418343	AA216372	Hs.159501	ESTs	2.9
	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Brn52 Homo sapien	2.9
	403341				2.9
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
75	453830	AA534296	Hs.20953	ESTs	2.9
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.9
	407676	AW064111	Hs.279823	ESTs	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
80	457049	AW631495	Hs.27135	B-cell receptor-associated protein BAP29	2.9
	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	2.9
	456189	H91010	Hs.44940	ESTs	2.9
	441874	AA970389	Hs.128055	ESTs	2.9
	416483	H58311	Hs.165077	ESTs	2.9

	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
	446447	AI300402	Hs.202250	ESTs	2.9
	439953	AA918129	Hs.124638	ESTs	2.9
5	400643				2.9
	436594	AI419982	Hs.156189	ESTs	2.9
	438402	D16902	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.9
	451353	N21043	Hs.42932	ESTs	2.9
	419791	AI579909	Hs.105104	ESTs	2.9
10	415628	F13080		gb:HSC3ID041 normalized infant brain cDN	2.9
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	454747	AW818535		gb:RC1-ST0278-140300-016-f05 ST0278 Homo	2.9
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.9
	457178	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	2.9
15	401526				2.9
	408751	N91553	Hs.258343	ESTs	2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
20	444125	AI124882	Hs.118121	ESTs	2.9
	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.9
	421847	NM_014717	Hs.108884	KIAA0390 gene product	2.8
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.8
	422225	BE245652	Hs.118281	zinc finger protein 266	2.8
25	403011				2.8
	405170				2.8
	435878	R08330	Hs.20152	ESTs	2.8
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	2.8
	400394	AF040257	Hs.283818	Homo sapiens TNF receptor homolog mRNA,	2.8
30	411244	AW833768		gb:QV4-TT0008-130100-077-e06 TT0008 Homo	2.8
	441817	AW969706	Hs.293332	ESTs	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.8
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.8
35	402131				2.8
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	2.8
	438160	AA779332	Hs.122671	ESTs	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
	417877	AI025829	Hs.86320	ESTs	2.8
40	439235	N45513	Hs.46608	ESTs	2.8
	451257	AA016255	Hs.31856	ESTs, Weakly similar to KIAA1453 protein	2.8
	437113	AA744693		gb:ny26c10.s1 NCL_CGAP_GCB1 Homo sapiens	2.8
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.8
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
45	410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.8
	417827	T79366	Hs.108258	actin binding protein; macrophin (microf	2.8
	420206	M91463	Hs.95958	solute carrier family 2 (facilitated glu	2.8
	449676	AW380579	Hs.209657	ESTs	2.8
50	454778	AW820199		gb:QV2-ST0296-190100-029-a07 ST0296 Homo	2.8
	451203	AW070604	Hs.46517	ESTs	2.8
	450180	AW449644	Hs.257182	ESTs	2.8
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.8
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
55	450003	AA777809	Hs.191995	ESTs	2.8
	401602				2.8
	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.8
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.8
	415652	T79213	Hs.272073	ESTs	2.8
60	404076				2.8
	409416	AW388359	Hs.10667	ESTs	2.8
	420814	AA721156	Hs.190440	ESTs	2.8
	426960	AA393713		gb:zt71h04.r1 Soares_testis_NHT Homo sap	2.8
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.8
65	448597	BE613250	Hs.98265	KIAA1877 protein	2.8
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	2.8
	433077	AA314262	Hs.301917	YDD19 protein	2.8
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	447410	AI470235	Hs.172698	EST	2.8
70	414652	AI620599	Hs.72068	ESTs	2.8
	430454	AW469011	Hs.105635	ESTs	2.8
	412417	AA102268	Hs.158622	ESTs	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430660	R11884	Hs.100826	ESTs	2.8
75	401098				2.8
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	2.8
	403549				2.8
	414394	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.8
80	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	2.8
	433513	AI566356	Hs.171437	ESTs	2.8
	446677	AI800311	Hs.156291	ESTs	2.8
	457756	AA126136	Hs.38125	interferon-induced protein 75, 52kD	2.8
	450895	N66727	Hs.10957	ESTs	2.8
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.8

	449358	AA001229	Hs.131436	ESTs	2.8
	422816	AA323586	Hs.93235	ESTs	2.8
	420756	AA411800	Hs.189900	ESTs	2.8
5	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
	451206	H86228	Hs.271780	ESTs, Weakly similar to I38022 hypothe	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	458023	AW978161	Hs.268555	5'-3' exoribonuclease 2	2.8
10	422260	AA315993	Hs.105484	regenerating gene type IV	2.8
	429638	AI916662	Hs.211577	kineclin 1 (kinesin receptor)	2.8
	408936	AL138043	Hs.293549	ESTs	2.8
	411762	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	2.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
15	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	406992	S82472		gb:beta-pol=DNA polymerase beta (exon a	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	445611	AW418497	Hs.145583	ESTs	2.7
20	445747	AI820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	445017	AI205493	Hs.176860	ESTs	2.7
	411726	AW858612		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	2.7
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	2.7
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
25	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
	427134	AA398409	Hs.173561	EST	2.7
	435689	AA694284		gb:zi35c02.s1 Soares_fetal_liver_spleen_	2.7
	429282	N27596	Hs.21342	ESTs	2.7
	435731	AA699581	Hs.186811	ESTs	2.7
30	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
	412174	BE160327	Hs.104572	ESTs	2.7
	403776				2.7
	409526	BE298751	Hs.55014	hypothetical protein FLJ10206	2.7
	410201	AA126129		gb:zm78c07.r1 Stratagene neuroepithelium	2.7
35	427839	AA608823	Hs.98244	ESTs	2.7
	447884	H29505		gb:ym60d10.r1 Soares infant brain 1NIB H	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	422988	AW673847	Hs.97321	ESTs	2.7
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.7
40	434890	AF161345	Hs.283930	Homo sapiens HSPC082 mRNA, partial cds	2.7
	412400	AW948066		gb:RC0-MT0012-290300-031-h10 MT0012 Homo	2.7
	413998	AW103807	Hs.243933	ESTs	2.7
	403677				2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
45	430698	AA492071		gb:ne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	2.7
	432591	AA643238	Hs.146144	ESTs	2.7
	446800	AI341635	Hs.156486	ESTs	2.7
	454938	AW846134		gb:QV0-CT0179-091199-049-d02 CT0179 Homo	2.7
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
50	445233	AV653034	Hs.297559	ESTs	2.7
	448756	AI739241	Hs.171480	ESTs	2.7
	418379	AA218940	Hs.137516	fidgetin-like 1	2.7
	435068	H16262	Hs.31415	ESTs	2.7
	406092				2.7
55	422036	AA302647	Hs.271891	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.7
	441541	AA938663	Hs.199828	ESTs	2.7
	451395	AI082419	Hs.114761	ESTs	2.7
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7
60	423949	AI014546	Hs.130912	ESTs	2.7
	435420	AI928513	Hs.59203	ESTs	2.7
	439418	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	2.7
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	2.7
	447453	AW608645	Hs.18800	hypothetical protein FLJ20281	2.7
65	454767	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	2.7
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	2.7
	402429				2.7
	403760				2.7
	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
70	435448	H17132	Hs.27085	ESTs	2.7
	445706	AA305520	Hs.108812	hypothetical protein FLJ22004	2.7
	422171	U50529	Hs.112434	Novel human gene mapping to chromosome 13	2.7
	459023	AW968226	Hs.60798	ESTs	2.7
	443246	T75157	Hs.337603	ESTs, Weakly similar to T08680 hypothe	2.7
75	404569				2.7
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	422897	AA679784	Hs.4290	ESTs	2.7
	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.7
	449880	AI673006	Hs.231948	ESTs	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
80	415268	R53935	Hs.287827	ESTs, Highly similar to MDR3_HUMAN MULTI	2.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.7
	452512	AW363486	Hs.337635	ESTs	2.7
	440728	AW086077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	2.7

	419481	AI879195	Hs.90606	15 kDa selenoprotein	2.7
	454352	AW389668		gb:RC2-ST0168-071299-013-f06 ST0168 Homo	2.7
	422831	R02504	Hs.332943	ESTs	2.7
5	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.7
	426872	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapie	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	2.7
	446002	AI346468	Hs.145789	ESTs	2.7
10	454716	AW850684		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.7
	406664	L34041	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	2.7
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	2.7
	408691	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	2.7
	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	2.7
15	439451	AF086270	Hs.278554	heterochromatin-like protein 1	2.7
	445225	AI216555	Hs.202398	ESTs	2.7
	427175	H06924	Hs.23782	hypothetical protein FLJ12847	2.7
	411816	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.7
	438135	AI253025	Hs.190426	ESTs	2.7
20	405981				2.7
	406005				2.7
	430762	AI343652	Hs.105667	ESTs	2.7
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.7
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.7
25	434684	AA737282	Hs.190911	ESTs	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
	400844				2.6
	415725	BE219771	Hs.237146	hypothetical protein FLJ12752	2.6
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.6
30	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	430052	AF102850	Hs.227933	Alg5, S. cerevisiae, homolog of	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	417252	AA195014	Hs.85971	ESTs	2.6
35	427167	AI239607	Hs.99196	hypothetical protein MGC11324	2.6
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.6
40	442240	AI791883	Hs.292719	ESTs	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
	410238	N94320	Hs.144225	ESTs	2.6
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	2.6
	440801	AA906366	Hs.190535	ESTs	2.6
45	440274	R24595	Hs.7122	scrapie responsive protein 1	2.6
	411597	AW852925		gb:PM0-CT0248-131099-001-f10 CT0248 Homo	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
	425176	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcr	2.6
50	425492	AL021918	Hs.158174	zinc finger protein 184 (Krueppel-like)	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	426098	NM_014906	Hs.166351	KIAA1072 protein	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
55	445550	AI242754	Hs.137306	ESTs	2.6
	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.6
	436407	T88803	Hs.271507	ESTs, Weakly similar to TIM_HUMAN PROBAB	2.6
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	2.6
60	418282	AA215535	Hs.98133	ESTs	2.6
	442757	AI739528	Hs.28345	ESTs	2.6
	413470	N20934		gb:yx54c11.s1 Soares melanocyte 2NbHM Ho	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	441209	AA922939	Hs.135742	ESTs	2.6
65	458679	AW975460	Hs.143563	ESTs	2.6
	442279	AW867006	Hs.159970	ESTs	2.6
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.6
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	2.6
	404845				2.6
70	411693	AW857271		gb:CM0-CT0307-210100-158-g09 CT0307 Homo	2.6
	438298	H23542	Hs.181788	ESTs	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
	457630	AI680803	Hs.112627	ESTs	2.6
75	424015	N95696	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	2.6
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.6
	413174	AA723564	Hs.191343	ESTs	2.6
	438875	AA827640	Hs.189059	ESTs	2.6
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	2.6
80	423257	AW161039	Hs.125878	synapsin III	2.6
	431086	AI829692	Hs.211561	ESTs	2.6
	409337	H71289	Hs.220535	ESTs	2.6
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	2.6
	410004	AI298027	Hs.5057	carboxypeptidase D	2.6

	455935	BE158687	gb:CM0-HT0395-280100-169-b09 HT0395 Homo	2.6
	403273			2.6
	445955	AA332209	Hs.158196 transcriptional adaptor 3 (ADA3, yeast h	2.6
5	425626	AI537536	Hs.173519 ESTs	2.6
	451531	AA018311	Hs.114762 ESTs	2.6
	428085	AA421081	Hs.12388 ESTs	2.6
	429761	AI276780	Hs.135173 ESTs	2.6
	437958	BE139550	Hs.121668 ESTs, Moderately similar to PC4259 ferri	2.6
10	442666	W74633	Hs.303720 ESTs	2.6
	413088	BE064962	gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	419107	AW085152	Hs.292987 ESTs	2.6
	435766	R11673	Hs.186498 ESTs	2.6
	452879	AW905328	Hs.180842 ribosomal protein L13	2.6
15	440400	AA994364	Hs.125594 ESTs, Weakly similar to T25472 hypotheti	2.6
	440460	H92571	Hs.234478 Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	424146	AA705092	Hs.202368 ESTs	2.6
	439950	AW937417	Hs.293561 ESTs	2.6
	410366	AI267589	Hs.302689 hypothetical protein	2.6
20	417485	AA203304	Hs.32826 CGI-130 protein	2.6
	412566	AW962574	gb:EST374647 MAGE resequences, MAGG Homo	2.6
	416498	U33632	Hs.79351 potassium channel, subfamily K, member 1	2.6
	440397	AA884448	Hs.157239 ESTs	2.6
	451236	AI767406	Hs.207026 ESTs, Weakly similar to B56205 transcrip	2.6
25	411819	AW947884	gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.6
	430357	AW976789	Hs.165607 ESTs	2.6
	432869	AW974094	gb:EST386197 MAGE resequences, MAGM Homo	2.6
	427506	AK000134	Hs.179100 hypothetical protein FLJ20127	2.6
	401614			2.6
30	404531	Z25884	Hs.121483 chloride channel 1, skeletal muscle (Th	2.6
	426698	AA394104	Hs.97489 ESTs	2.6
	440479	AA886461	Hs.208161 ESTs	2.6
	443160	AI467915	Hs.36053 ESTs	2.6
	419323	AI092379	Hs.135275 ESTs	2.5
35	442813	AI018435	Hs.270970 ESTs	2.5
	436195	AK001084	Hs.333498 Homo sapiens cDNA FLJ10222 fis, clone HE	2.5
	433561	BE540937	Hs.20104 hypothetical protein FLJ00052	2.5
	434059	AA649162	Hs.236456 ESTs	2.5
	454836	AW833711	gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
40	458589	AV654623	Hs.288141 hypothetical protein MGC3156	2.5
	459716			2.5
	436340	R42246	Hs.21606 ESTs	2.5
	428020	L19058	Hs.181581 glutamate receptor, ionotropic, kainate	2.5
	416951	AA190926	Hs.190785 ESTs, Moderately similar to S65657 alpha	2.5
	401078			2.5
45	410644	AW902125	gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.5
	411660	AW855718	gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
	425201	AA352111	gb:EST60061 Activated T-cells XX Homo sa	2.5
	455252	AW876627	gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
50	439096	AA830185	Hs.269680 ESTs	2.5
	442627	AI027990	Hs.132303 ESTs	2.5
	457799	AF220188	Hs.236510 uncharacterized hypothalamus protein HTM	2.5
	428799	AI478619	Hs.104677 ESTs	2.5
	450402	BE218027	Hs.89969 ESTs	2.5
55	411156	AW819939	Hs.273629 ESTs	2.5
	431673	AW971302	Hs.293233 ESTs	2.5
	415706	BE182587	Hs.57485 ESTs	2.5
	412882	BE006919	Hs.134106 ESTs	2.5
	441300	R35063	Hs.181536 ESTs	2.5
60	413257	BE075035	gb:PM3-BT0584-260300-002-g05 BT0584 Homo	2.5
	434662	AA641957	gb:ns18d08.r1 NCI_CGAP_GCB1 Homo sapiens	2.5
	455255	AW877139	gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.5
	417137	U46265	Hs.81281 mitochondrial ribosomal protein S21	2.5
	417909	R35614	gb:yg66e08.r1 Soares infant brain 1N1B H	2.5
65	458043	AW979009	Hs.326108 ESTs	2.5
	417006	AW673606	Hs.80758 aspartyl-tRNA synthetase	2.5
	442006	AW975183	Hs.292663 ESTs, Weakly similar to S72482 hypotheti	2.5
	455756	BE079307	gb:RC1-BT0623-120200-011-g09 BT0623 Homo	2.5
	454032	W31790	Hs.194293 ESTs, Weakly similar to I54374 gene NF2	2.5
70	444963	AI916973	Hs.213603 ESTs	2.5
	443526	AW792804	Hs.134002 ESTs	2.5
	454532	AA344685	Hs.58831 regulator of Fas-induced apoptosis	2.5
	428832	AA578229	Hs.324239 ESTs, Moderately similar to ZN91_HUMAN Z	2.5
	442003	AW297497	Hs.201891 ESTs	2.5
75	452768	AW069459	Hs.61539 ESTs	2.5
	411355	AW838479	Hs.22692 ESTs	2.5
	458890	AW865523	gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.5
	400074			2.5
	405241			2.5
80	413096	BE065209	gb:RC1-BT0314-310300-015-b12 BT0314 Homo	2.5
	414349	BE512968	gb:601172296F1 NIH_MGC_15 Homo sapiens c	2.5
	422884	AW860975	Hs.13256 ESTs	2.5
	429515	AL031228	Hs.204370 DNA segment on chromosome 6 (unique, pse	2.5
	431925	AK000890	gb:Homo sapiens cDNA FLJ10028 fis, clone	2.5

	442653	BE269247		gb:601185486F1 NIH_MGC_8 Homo sapiens cD	2.5
	401882				2.5
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hig	2.5
	405336				2.5
5	439492	AF086310	Hs.103159	ESTs	2.5
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.5
	436359	Z83806		gb:H.sapiens mRNA for axonemal dynein he	2.5
	429322	D86984	Hs.199243	KIAA0231 protein	2.5
10	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	2.5
	437107	AA745598	Hs.291840	ESTs, Weakly similar to I78885 serine/th	2.5
	441953	H11695	Hs.322901	disrupter of silencing 10	2.5
	442777	AW341541	Hs.271153	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
15	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
	457824	R84938		gb:yf65f04.r1 Soares retina N2b4HR Homo	2.5
	428550	AW297880	Hs.98661	ESTs	2.5
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.5
	456359	AI967991	Hs.93574	homeo box D3	2.5
20	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.5
	452528	AA742457	Hs.291479	ESTs	2.5
	408444	AW661839	Hs.253204	ESTs	2.5
	440327	R12581	Hs.191146	ESTs	2.5
	410406	AI969703	Hs.1466	glycerol kinase	2.5
25	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.5
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	2.5
	435427	AA682573	Hs.188982	ESTs, Weakly similar to organic anion tr	2.5
	427791	AA412446	Hs.98138	ESTs	2.5
	403509	AF231919	Hs.18759	KIAA0539 gene product	2.5
30	436590	AI393115	Hs.127655	ESTs	2.5
	455556	AW995423		gb:QV0-BN0042-010400-183-g08 BN0042 Homo	2.5
	405869				2.5
	408274	R17315		gb:yg12g11.r1 Soares infant brain 1NIB H	2.5
	448015	AI458065	Hs.23196	ESTs	2.5
35	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
	436154	AA764950	Hs.119898	ESTs	2.5
	406377				2.5
	437030	AA742577	Hs.303781	EST	2.5
	420815	AA280684	Hs.270584	ESTs	2.5
40	418421	R58620	Hs.85050	phospholamban	2.5
	423638	AI003521	Hs.130310	Homo sapiens mRNA for cyclin B3 isoform	2.5
	415425	F08365		gb:HSCZSA121 normalized infant brain cDN	2.5
	404577				2.5
	403568				2.5
45	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.5
	449899	AI610700	Hs.103280	ESTs	2.5
	451078	AI927694	Hs.204470	ESTs	2.5
	453343	AA905353	Hs.121622	ESTs	2.5
	428728	NM_016625	Hs.191381	hypothetical protein	2.5
50	409642	AW450809	Hs.257347	ESTs	2.5
	426235	AI631964	Hs.34447	ESTs	2.5
	452043	H86231		gb:y03f02.r1 Soares retina N2b5HR Homo	2.5
	401992				2.5
55	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	2.5
	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	449311	AI657014		gb:tt49a12.x1 NCL_CGAP_GC6 Homo sapiens	2.5
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
60	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.4
	421583	AA293333		gb:ztl53c09.r1 Soares ovary tumor NbHOT H	2.4
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.4
	454437	AI248173	Hs.191460	hypothetical protein MGC12936	2.4
	419187	AA234852	Hs.44693	ESTs	2.4
65	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypot	2.4
	405547				2.4
	454086	AW885909	Hs.6975	PRO1073 protein	2.4
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	2.4
	416277	W78765	Hs.180145	HSPC030 protein	2.4
70	420976	AI924940	Hs.108082	ESTs, Weakly similar to T31636 hypotheti	2.4
	406468				2.4
	408617	R61736	Hs.124128	ESTs	2.4
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecucl	2.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
75	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypotheti	2.4
	455328	AW896438		gb:PM1-NN0047-040400-001-d09 NN0047 Homo	2.4
	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	2.4
	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.4
	419511	AA429750	Hs.75113	general transcription factor IIIA	2.4
80	437980	R50393	Hs.278436	KIAA1474 protein	2.4
	439999	AA115811	Hs.6838	ras homolog gene family, member E	2.4
	403501				2.4
	446845	AI343645	Hs.156108	ESTs	2.4
	401775				2.4

	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411836	AW901879	Hs.314453	ESTs	2.4
	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo	2.4
5	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypotheti	2.4
	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	428945	AW192803	Hs.98974	ESTs, Weakly similar to S65824 reverse t	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
10	435256	AF193766	Hs.13872	cytokine-like protein C17	2.4
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.4
	458239	BE439877	Hs.283389	ESTs	2.4
	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	2.4
	441262	AI809130	Hs.176906	ESTs	2.4
	402076				2.4
15	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.4
	400587				2.4
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	2.4
	411203	AW872430	Hs.273743	ESTs	2.4
20	447849	AI538147	Hs.164277	ESTs	2.4
	454201	AB023191	Hs.44131	KIAA0974 protein	2.4
	424131	AA335714	Hs.199665	ESTs	2.4
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	2.4
	440385	AA884283	Hs.192136	ESTs	2.4
25	417976	BE565892	Hs.83077	interleukin 18 (interferon-gamma-inducin	2.4
	447179	AW015633	Hs.157299	ESTs	2.4
	412977	AA125910	Hs.191461	ESTs	2.4
	436958	AA740322	Hs.293539	Homo sapiens mRNA for KIAA1758 protein,	2.4
	401361				2.4
30	403891				2.4
	408419	AW250092	Hs.305953	zinc finger protein 83 (HPF1)	2.4
	417002	T79613	Hs.14613	ESTs	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	458570	AW971698	Hs.12627	TJ6 protein	2.4
35	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	459344	AW499533	Hs.257976	ESTs	2.4
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.4
	412114	AW893891	Hs.240833	ESTs, Weakly similar to I38022 hypotheti	2.4
	423296	AW957193	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	2.4
40	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	2.4
	428268	AA424957	Hs.294132	ESTs	2.4
	450947	AI745400	Hs.204662	ESTs	2.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.4
	438142	T90309	Hs.269651	ESTs	2.4
45	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	2.4
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
	433868	AA612960	Hs.337300	ESTs	2.4
	401645				2.4
50	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.4
	453393	AW956392	Hs.110376	ESTs	2.4
	436054	AI076262	Hs.119813	ESTs	2.4
	425433	AA357471		gb:EST66274 LNCAP cells I Homo sapiens c	2.4
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.4
55	420639	AI683116	Hs.25328	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	453369	BE551550	Hs.232630	ESTs	2.4
	405017				2.4
	405385				2.4
60	435633	AI248152	Hs.270047	ESTs	2.4
	457128	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.4
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	2.4
	434544	C05875	Hs.91575	ESTs	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	455219	AW879403		gb:PM0-OT0019-150300-002-d01 OT0019 Homo	2.4
65	458734	AI554946	Hs.158794	ESTs	2.4
	442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	2.4
	444313	AI140494	Hs.197955	KIAA0704 protein	2.4
	440448	AA885428	Hs.125646	ESTs	2.4
	441498	AI379248	Hs.58742	ESTs	2.4
70	438205	AA780365	Hs.122161	ESTs	2.4
	402615				2.4
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.4
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.4
	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
75	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
	449007	AI620433	Hs.193201	EST, Weakly similar to NIP2_HUMAN BCL2/A	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	2.4
	418857	D10216	Hs.89394	POU domain, class 1, transcription facto	2.4
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	2.4
80	458914	BE327696	Hs.280922	ESTs	2.4
	435061	AI651474	Hs.163944	ESTs	2.4
	416458	AA180511		gb:zp53f03.r1 Stratagene NT2 neuronal pr	2.4
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	2.4



	403003			2.4
	405347			2.4
	406091			2.4
5	428402	AW237531	Hs.326876	Homo sapiens SOX6 mRNA, complete cds
	438762	AW844412	Hs.65450	reticulon 4
	455780	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo
	457024	AA397546	Hs.119151	ESTs
	404249			2.4
10	443921	AI091310	Hs.134848	ESTs
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir
	417154	AI674701	Hs.21388	ESTs
	419720	AA249131	Hs.337778	hypothetical protein FLJ11068
	405230			2.4
	405935			2.4
15	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon
	419233	AA458873	Hs.178306	ESTs
	414277	BE269910		gb:601186291F1 NIH_MGC_8 Homo sapiens cD
20	452092	BE245374	Hs.27842	hypothetical protein FLJ11210
	453736	AL118674	Hs.34871	zinc finger homeobox 1B
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo
	434239	AF119910	Hs.283047	hypothetical protein PRO2964
	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapi
25	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p
	445688	AI248205	Hs.153244	ESTs
	451656	BE327088	Hs.212752	ESTs
	423956	W28203	Hs.136169	Homo sapiens clone 25215 mRNA sequence,
	413445	BE141022		gb:MR0-HT0067-201099-002-d10 HT0067 Homo
30	436149	AI754308	Hs.159452	ESTs
	405629			2.3
	432702	AW973953	Hs.293744	ESTs
	433377	AI752713	Hs.43845	ESTs
	444711	AI188739	Hs.148488	ESTs
35	445621	AI733818	Hs.145549	ESTs
	456432	AW966931	Hs.179662	nucleosome assembly protein 1-like 1
	449236	AJ403126	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H
	459024	AA020799	Hs.262869	plasminogen-like
	441037	AA913360	Hs.126468	ESTs
40	431577	T34523	Hs.302040	Homo sapiens DNA sequence from PAC 43401
	438782	AA828380	Hs.126733	ESTs
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo
	429044	AI261490	Hs.145527	ESTs
45	431655	AW971119		gb:EST383206 MAGE resequences, MAGL Homo
	439642	W81441	Hs.153967	ESTs
	441721	AI288259	Hs.127652	ESTs
	443482	AW188093	Hs.250385	ESTs
	403416	AI744626	Hs.151385	KIAA0564 protein
50	416443	N69469	Hs.194225	ESTs
	419714	AA758751	Hs.98216	ESTs
	415511	AI732617	Hs.182362	ESTs
	412344	AW938384	Hs.264190	vacuolar protein sorting 35 (yeast homol
	449264	AI637649	Hs.196105	ESTs
55	451664	AA889081	Hs.153952	5' nucleotidase (CD73)
	441269	AW015206	Hs.178784	ESTs
	402333			2.3
	453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)
	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S
60	404367			2.3
	403696			2.3
	441622	AW450957	Hs.224864	ESTs
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo
	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo
65	428548	AA430058	Hs.98649	EST
	404059			2.3
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H
	413640	BE158118		gb:MR2-HT0378-240200-205-d09 HT0378 Homo
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin
70	435338	AA678071	Hs.194300	ESTs, Weakly similar to I38022 hypotheti
	442710	AI015631	Hs.23210	ESTs
	444206	AW301017	Hs.146492	ESTs
	451250	AA491275	Hs.236940	hypothetical protein FLJ12542
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo
75	458455	AV648310	Hs.213488	ESTs
	458521	AI651039	Hs.148559	ESTs
	407938	AA905097	Hs.85050	phospholamban
	439546	AF088056		gb:Homo sapiens full length insert cDNA
	441274	AW593781	Hs.131357	ESTs
80	454314	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo
	409660	AW452065	Hs.258905	ESTs
	428532	AF157326	Hs.184786	TBP-interacting protein
	411384	AW842115		gb:RC0-CN0026-090200-031-e11 CN0026 Homo
	453687	T55674	Hs.283108	hemoglobin, gamma G

	410140	AL134435	Hs.22269	neurexin 3	2.3
	422443	NM_014707	Hs.116753	histone deacetylase 7B	2.3
	409071	AW316932	Hs.181982	ESTs	2.3
5	421253	AI188102	Hs.31028	ESTs	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypothei	2.3
	448458	AW614367	Hs.171054	ESTs	2.3
	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.3
	443718	AI083580	Hs.221373	ESTs	2.3
10	445568	H00918	Hs.268744	KIAA1796 protein	2.3
	400582				2.3
	411262	AW834480		gb:MR2-TT0014-151199-011-b07 TT0014 Homo	2.3
	401145				2.3
	407440	AF227135		gb:Homo sapiens candidate taste receptor	2.3
15	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo	2.3
	459077	N20370	Hs.235883	ESTs	2.3
	448117	H49129	Hs.172982	ESTs	2.3
	453331	AI240665	Hs.8895	ESTs	2.3
	443751	AI285839	Hs.153324	EST	2.3
20	402038				2.3
	402176				2.3
	456605	AI827786	Hs.259044	ESTs	2.3
	432479	AL042844	Hs.275675	katanin p80 (WD40-containing) subunit B	2.3
	402527				2.3
25	449272	AW137656	Hs.197645	ESTs	2.3
	411024	BE062590		gb:QV1-BT0260-281099-023-f05 BT0260 Homo	2.3
	455608	BE011437		gb:CM4-BN0220-080500-170-f03 BN0220 Homo	2.3
	458818	AI523857	Hs.232257	ESTs	2.3
	419875	AA853410	Hs.93557	proenkephalin	2.3
30	405521				2.3
	436517	BE080932	Hs.135225	ESTs	2.3
	456801	AW961886	Hs.138263	Homo sapiens clone 24528 mRNA sequence	2.3
	430444	AW296421	Hs.121035	ESTs	2.3
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.3
35	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
	419337	AW291112	Hs.209978	ESTs	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothei	2.3
40	454456	AW850984		gb:IL3-CT0220-150200-068-H08 CT0220 Homo	2.3
	454633	AW811380		gb:IL3-ST0143-290999-019-D05 ST0143 Homo	2.3
	457028	AW449838	Hs.97562	ESTs	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.3
	430850	BE144152		gb:MR0-HT0165-060200-006-e02 HT0165 Homo	2.3
45	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	2.3
	421227	R78581	Hs.266308	mosaic serine protease	2.3
	426902	AI125334	Hs.97408	ESTs	2.3
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	2.3
	447475	AI380797	Hs.158992	ESTs	2.3
50	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.3
	430712	AW044647	Hs.196284	ESTs	2.3
	458103	AW780192	Hs.267596	ESTs	2.3
	420959	AA282119	Hs.88975	ESTs	2.3
	444098	AV647969	Hs.109694	KIAA1451 protein	2.3
55	445641	AI245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	2.3
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
	459497	AA825742	Hs.87517	ESTs	2.3
60	412852	BE004117	Hs.37415	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	437539	AA974673	Hs.121419	ESTs	2.3
	421813	BE048255		gb:tz49b05.y1 NCL_CGAP_Brn52 Homo sapien	2.3
	411994	R67298	Hs.109087	Homo sapiens cDNA: FLJ22845 fis, clone K	2.3
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	2.3
65	452463	R36452	Hs.300817	ESTs	2.3
	404936				2.3
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.3
	440836	AW370882	Hs.222080	ESTs	2.3
	405120				2.3
70	400238				2.3
	407809	AW082279	Hs.244106	ESTs	2.3
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	441417	AI733297	Hs.144474	ESTs	2.3
75	445117	AI208754	Hs.147369	ESTs	2.3
	431162	AW971180		gb:EST383268 MAGE resequences, MAGL Homo	2.2
	437036	AI571514	Hs.133022	ESTs	2.2
	455849	BE146866		gb:QV4-HT0222-211099-014-f06 HT0222 Homo	2.2
	447624	AI640326	Hs.62713	ESTs	2.2
80	439780	AL109688		gb:Homo sapiens mRNA full length insert	2.2
	405706				2.2
	447732	AI758398	Hs.161318	ESTs	2.2
	440625	BE539853	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	2.2
	404257				2.2

	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypotheti	2.2
	449133	AI631655	Hs.197919	ESTs	2.2
	456555	AW592167	Hs.293299	ESTs	2.2
5	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiesterase	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	446096	AI276454		gb:ql71a12.x1 Soares_NhHMPu_S1 Homo sapi	2.2
10	448106	AI800470	Hs.171941	ESTs	2.2
	450232	BE300815	Hs.201326	ESTs	2.2
	436134	AK000618	Hs.123784	ESTs	2.2
	448466	AI522109	Hs.171066	ESTs	2.2
	420678	AW593288	Hs.3530	TLS-associated serine-arginine protein 2	2.2
15	430692	X80240		gb:H.sapiens endogenous retrovirus HERV-	2.2
	446453	AV658469	Hs.188646	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	423611	AB011163	Hs.129908	KIAA0591 protein	2.2
	444050	AW138295	Hs.135024	ESTs	2.2
	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
20	422669	H12402	Hs.119122	ribosomal protein L13a	2.2
	403388				2.2
	403780				2.2
	419423	D26488	Hs.90315	KIAA0007 protein	2.2
	424719	H90452		gb:yv01c03.r1 Soares fetal liver spleen	2.2
25	431453	AW753917		gb:RC0-CT0299-291199-031-F02 CT0299 Homo	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	2.2
	427119	AW880562	Hs.114574	ESTs	2.2
	400486				2.2
30	448482	AW294078	Hs.171092	ESTs	2.2
	402621				2.2
	408363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	2.2
	424584	H10692	Hs.13310	ESTs	2.2
35	445061	AI263094	Hs.145227	ESTs	2.2
	431065	AA491286	Hs.128792	ESTs	2.2
	411908	L27943	Hs.72924	cytidine deaminase	2.2
	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
40	422677	AL046388	Hs.208206	hypothetical protein FLJ21162	2.2
	455534	AW991925		gb:PM3-BN0011-130100-002-b07 BN0011 Homo	2.2
	400163				2.2
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	409206	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	2.2
45	410556	R32158		gb:yh67a07.s1 Soares placenta Nb2HP Homo	2.2
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	2.2
	439482	W70045	Hs.58089	ESTs	2.2
	447877	AI435184	Hs.164252	ESTs	2.2
	418297	R91254		gb:yp94e12.s1 Soares fetal liver spleen	2.2
50	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	414000	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.2
	432762	NM_014099	Hs.278924	PRO1768 protein	2.2
	437606	AA761594	Hs.122440	ESTs	2.2
55	438550	AW976002	Hs.258402	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
	444540	AI693927	Hs.265165	ESTs	2.2
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.2
	456481	AA258033	Hs.108110	DKFZP547E2110 protein	2.2
60	435138	BE314734		gb:601152976F1 NIH_MGC_19 Homo sapiens c	2.2
	412887	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.2
	454204	AW816498		gb:QV0-ST0236-171299-075-b02 ST0236 Homo	2.2
	408253	AW807476	Hs.21051	Homo sapiens mRNA for FLJ00012 protein,	2.2
	432887	AI926047	Hs.162859	ESTs	2.2
65	448063	AI459108	Hs.159818	ESTs	2.2
	416171	H23896	Hs.125790	leucine-rich repeat-containing 2	2.2
	433098	AW190593	Hs.151143	ESTs	2.2
	409781	AW812266	Hs.15220	zinc finger protein 106	2.2
	423441	R68649	Hs.278359	absent in melanoma 1 like	2.2
70	423646	H02364		gb:yj35d06.r1 Soares placenta Nb2HP Homo	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
75	437334	AL353947	Hs.283780	hypothetical protein DKFZp761N1814	2.2
	431917	D16181	Hs.2868	peripheral myelin protein 2	2.2
	400843				2.2
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.2
80	449560	AA001767	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	408940	M58583	Hs.662	cerebellin 1 precursor	2.2
	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.2
	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.2
	459495	BE544158		gb:601076707F1 NIH_MGC_12 Homo sapiens c	2.2
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	2.2

	444547	AV650207	Hs.282437	ESTs, Weakly similar to I38022 hypotheti	2.2
	417156	N49476	Hs.166563	replication factor C (activator 1) 1 (14	2.2
	416761	H85422	Hs.108556	ESTs	2.2
5	408867	AA437199	Hs.655	cell division cycle 25C	2.2
	406748	AW339106	Hs.217493	annexin A2	2.2
	427443	AA402713	Hs.97872	ESTs	2.2
	452843	AI796769	Hs.208320	ESTs	2.2
	427473	AW274439	Hs.252709	ESTs	2.2
10	433919	AA746311		gb:oa56d12.r1 NCL_CGAP_GCB1 Homo sapiens	2.2
	431058	AW968865		gb:EST380941 MAGE resequences, MAGJ Homo	2.2
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	2.2
	415250	F02614	Hs.27319	ESTs	2.2
	440253	AI651329	Hs.160289	ESTs	2.2
15	434470	AA634818	Hs.298138	ESTs	2.2
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	2.2
	432463	AA548518	Hs.186733	ESTs	2.2
	400861				2.2
	407287	AI678812		gb:tu59d08.x1 NCL_CGAP_Gas4 Homo sapiens	2.2
20	414817	AW902892	Hs.23782	hypothetical protein FLJ12847	2.2
	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	2.2
	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	2.2
	442952	AI743261	Hs.131860	ESTs	2.2
25	425187	AW014486	Hs.22509	ESTs	2.2
	408221	AA912183	Hs.47447	ESTs	2.2
	411480	AW848022		gb:IL3-CT0214-231299-053-A09 CT0214 Homo	2.2
	459681				2.2
	414784	NM_000344	Hs.288986	survival of motor neuron 1, telomeric	2.2
30	442726	AW136066	Hs.19145	ESTs	2.2
	450433	AW444538	Hs.231863	ESTs	2.2
	437642	AL079309		gb:Homo sapiens mRNA full length insert	2.2
	406298				2.2
	409723	AW885757	Hs.257862	ESTs	2.2
35	433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
	446534	AI307356	Hs.175225	ESTs	2.2
	403764				2.2
40	442735	R91949		gb:yq06h06.s1 Soares fetal liver spleen	2.2
	455221	AW867751		gb:MR0-SN0038-290300-001-a03 SN0038 Homo	2.2
	405965				2.2
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	2.2
45	441679	BE502267	Hs.65596	ESTs	2.2
	432781	NM_014133	Hs.278940	PRO0618 protein	2.2
	448470	AW026226	Hs.309479	ESTs	2.2
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.2
	443180	R15875	Hs.258576	claudin 12	2.2
	422213	AA306385	Hs.133160	ESTs	2.2
50	423119	AA322201	Hs.131976	ESTs	2.2
	450192	AA263143	Hs.24596	RAD51-interacting protein	2.2
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	2.2
	400734				2.2
	430499	AW969408	Hs.231991	ESTs	2.2
55	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.2
	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
60	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
	436640	AA724411	Hs.156065	ESTs	2.2
	436802	N34486	Hs.170504	ESTs	2.2
	443994	AI094805	Hs.135522	ESTs, Weakly similar to S38038 hypotheti	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	446412	AW135313	Hs.150098	ESTs	2.2
65	448390	AL035414	Hs.21068	hypothetical protein	2.2
	449939	T86420	Hs.272139	ESTs	2.2
	412700	BE222433	Hs.201262	ESTs, Weakly similar to I38022 hypotheti	2.2
	453125	AW779544	Hs.115497	hypothetical protein FLJ22655	2.2
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
70	452864	AA033714	Hs.287629	hypothetical protein FLJ14260	2.2
	452441	BE222078	Hs.113069	ESTs	2.2
	402395				2.2
	459659				2.2
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.2
75	438432	AW444990	Hs.258800	ESTs, Weakly similar to I38022 hypotheti	2.2
	409446	AI561173	Hs.67688	ESTs	2.2
	408764	BE087164	Hs.302415	ESTs	2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
80	436992	AA741074	Hs.120750	ESTs	2.2
	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
	444199	AI128931	Hs.260681	ESTs, Moderately similar to ALUF_HUMAN !	2.2
	446009	AI989885	Hs.231926	ESTs	2.2
	435510	BE143837		gb:MR0-HT0164-151299-012-b08 HT0164 Homo	2.1

	403691				2.1
	458333	AI000792	Hs.108209	ESTs	2.1
	454560	AW807281		gb:MR4-ST0062-240300-003-g01 ST0062 Homo	2.1
5	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.1
	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protei	2.1
	406941	X58140		(NONE)	2.1
	445712	AI458246	Hs.167451	ESTs	2.1
10	451270	AW341392	Hs.235795	ESTs	2.1
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	2.1
	437073	AI885608	Hs.94122	ESTs	2.1
	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	2.1
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.1
15	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence	2.1
	405233				2.1
	446512	H30351	Hs.207982	ESTs	2.1
	403188				2.1
	404443				2.1
20	433645	AI821746	Hs.190258	ESTs, Moderately similar to ALU6_HUMAN A	2.1
	414456	H74314		gb:yu56e10.r1 Soares fetal liver spleen	2.1
	433479	AW511459	Hs.249972	ESTs	2.1
	455482	AW948353		gb:RC0-MT0015-130400-031-d07 MT0015 Homo	2.1
	446364	AB006624	Hs.14912	KIAA0286 protein	2.1
25	452004	AI827815	Hs.277359	ESTs	2.1
	405059				2.1
	425457	AW964212		gb:EST376285 MAGE resequences, MAGH Homo	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
30	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	432774	AA564946	Hs.156280	ESTs	2.1
	436349	AI445255	Hs.115315	ESTs	2.1
	445532	BE138944	Hs.146200	ESTs	2.1
	456313	AA225741		gb:nc17b10.s1 NCI_CGAP_Pr1 Homo sapiens	2.1
35	412818	NM_003337	Hs.811	ubiquitin-conjugating enzyme E2B (RAD6 h	2.1
	450271	AI693900	Hs.200920	ESTs	2.1
	401521				2.1
	422880	AF228704	Hs.121524	glutathione reductase	2.1
	448871	BE616709	Hs.159265	kruppel-related zinc finger protein hckr	2.1
40	449233	BE048401	Hs.196511	ESTs	2.1
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle	2.1
	457003	S78234	Hs.172405	cell division cycle 27	2.1
	417448	AA203135	Hs.130186	ESTs	2.1
	402103				2.1
45	450579	AW136774	Hs.48614	ESTs	2.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.1
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	2.1
	415333	H24415	Hs.13273	KIAA0592 protein	2.1
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotr	2.1
50	434985	AA658229	Hs.291228	ESTs	2.1
	414729	BE466928	Hs.281901	ESTs	2.1
	400510				2.1
	420844	AA595522		gb:nh22c09.s1 NCI_CGAP_Pr1 Homo sapiens	2.1
	427434	BE538374	Hs.301732	hypothetical protein MGC5306	2.1
55	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino	2.1
	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.1
	453853	AL040600	Hs.188083	ESTs	2.1
	459108	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	2.1
	430118	AI377255	Hs.183287	ESTs	2.1
60	455964	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.1
	437981	AA774445	Hs.192095	ESTs, Weakly similar to KIAA1397 protein	2.1
	439957	AI453184	Hs.66357	ESTs	2.1
	423734	H02217		gb:yj38d11.r1 Soares placenta Nb2HP Homo	2.1
	450721	AI732271	Hs.25567	ESTs	2.1
65	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	2.1
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	2.1
	432919	AL079800		gb:DKFP434O2330_r1 434 (synonym: htes3)	2.1
	434791	AA649235	Hs.116457	ESTs, Weakly similar to NIP3_HUMAN BCL2/	2.1
	445273	AI218441	Hs.153846	ESTs	2.1
	400514				2.1
70	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.1
	439391	AW975638	Hs.293490	ESTs, Weakly similar to I38022 hypotheti	2.1
75	428414	AL049980	Hs.184216	DKFZP564C152 protein	2.1
	429430	AI381837	Hs.155335	ESTs	2.1
	449689	AF228421	Hs.23889	DKFZP564A032 protein	2.1
	430909	AF034632	Hs.248126	G protein-coupled receptor 38	2.1
	453116	AI276680	Hs.146086	ESTs	2.1
80	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	2.1
	423019	AI640185	Hs.283626	ESTs	2.1
	414007	AI733895	Hs.103813	ESTs	2.1
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	2.1
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	2.1

	421279	AW664878	Hs.106645	ESTs	2.1
	443167	AI202009	Hs.132087	ESTs	2.1
	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.1
5	448078	AI460117	Hs.170464	ESTs, Highly similar to A53933 myosin I	2.1
	436858	BE545498		gb:601070344F1 NIH_MGC_12 Homo sapiens c	2.1
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.1
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.1
	407401	AF029325		gb:Homo sapiens laminin beta-4 chain pre	2.1
10	426336	AA375802		gb:EST88135 HSC172 cells II Homo sapiens	2.1
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	2.1
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens c	2.1
	406504				2.1
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	2.1
15	415186	AA160945	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.1
	416175	H24230	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	442095	AI733162	Hs.128470	ESTs	2.1
	451878	AI821027	Hs.8429	ESTs	2.1
20	449178	AI633748	Hs.197597	ESTs	2.1
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	2.1
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	2.1
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	2.1
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	2.1
25	441543	AI733014	Hs.269715	ESTs	2.1
	403065				2.1
	428811	AA436052	Hs.99487	ESTs	2.1
	451803	BE541174	Hs.252058	ESTs, Moderately similar to PC4259 ferri	2.1
	442906	AW296888	Hs.170939	ESTs	2.1
30	409171	R17126		gb:yg09c11.r1 Soares infant brain 1N1B H	2.1
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	2.1
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	2.1
	412039	AW887384		gb:RC0-OT0089-130300-021-d07 OT0089 Homo	2.1
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	2.1
35	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.1
	455022	AW850845		gb:IL3-CT0220-111199-028-D11 CT0220 Homo	2.1
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	2.1
	422942	AF054839	Hs.122540	tetraspan 2	2.1
	400451				2.1
40	406668	T62745	Hs.184411	albumin	2.1
	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	404834				2.1
	448732	BE614063	Hs.334689	KIAA1838 protein	2.1
	423453	AW450737	Hs.128791	CGI-09 protein	2.1
45	421447	AB005216	Hs.104481	Nck, Ash and phospholipase C binding pro	2.1
	408774	AW270899	Hs.254569	ESTs, Weakly similar to B34087 hypotheti	2.1
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.1
	405732				2.1
	417848	AA206581	Hs.39457	ESTs, Weakly similar to JC5314 CDC28/cdc	2.1
50	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.1
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	2.1
	426953	AI769281	Hs.97439	ESTs	2.1
	440454	AI733037	Hs.129990	ESTs	2.1
55	433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D1	2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
	441963	AI733307	Hs.128002	ESTs	2.1
	439498	AA908731	Hs.58297	CLLL8 protein	2.1
60	456224	AW292905	Hs.128770	ESTs	2.1
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	2.1
	444702	AI220122	Hs.326560	hypothetical protein MGC2780	2.1
	417787	R14948	Hs.23883	ESTs	2.1
	400612				2.1
65	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	451067	BE172186		gb:MR0-HT0559-110300-005-h11 HT0559 Homo	2.1
	455032	AI830890	Hs.192422	ESTs	2.1
70	417945	R29072		gb:F1-101D 22 week old human fetal liver	2.1
	438268	AA782163	Hs.293502	ESTs	2.1
	424754	R09692		gb:yf23b12.r1 Soares fetal liver spleen	2.1
	404599				2.1
	459655				2.1
75	402455				2.1
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	2.1
	421987	AI133161	Hs.286131	CGI-101 protein	2.1
	400339	X57131	Hs.248209	H2A histone family, member F, pseudogene	2.1
	438206	AA780385	Hs.187885	ESTs	2.1
80	458451	AW297181	Hs.195922	ESTs	2.1
	447534	AW953935	Hs.30837	ESTs	2.1
	417687	AI828596	Hs.250691	ESTs	2.1
	412717	W00973	Hs.334728	ESTs	2.1
	405759				2.1

	406413				2.1
	442081	AA401863	Hs.22380	ESTs	2.1
	457938	AI373638	Hs.133900	ESTs	2.1
5	420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 fis, clone PL	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	2.1
	411421	BE272110	Hs.21177	ESTs	2.1
	437825	AA769123	Hs.291947	ESTs	2.1
10	437083	AW082597	Hs.244862	ESTs	2.1
	409466	AA436207	Hs.226666	ESTs, Moderately similar to I54374 gene	2.1
	433523	H29882	Hs.162614	ESTs	2.1
	446868	AV660737	Hs.135100	ESTs	2.1
	445882	AI948717	Hs.225155	ESTs, Weakly similar to A46302 PTB-assoc	2.1
15	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.1
	406817	AI936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
	410486	AW235094	Hs.69233	zinc finger protein	2.1
	411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
	412446	AI768015	Hs.92127	ESTs	2.1
20	457289	AW573204	Hs.137078	ESTs	2.1
	400335	Y13187	Hs.248067	Homo sapiens dmd gene, intron 11	2.0
	435959	AW296243	Hs.118375	ESTs	2.0
	448188	AW001835	Hs.13323	hypothetical protein FLJ22059	2.0
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	2.0
25	420430	AI703192		gb:wd92h04.x1 NCI_CGAP_Lu24 Homo sapiens	2.0
	445717	AW664658	Hs.149332	ESTs	2.0
	451862	H09260	Hs.32333	ESTs	2.0
	459686				2.0
	441996	BE349537	Hs.38383	ESTs	2.0
30	412194	AW900282	Hs.115412	hypothetical protein FLJ13881	2.0
	444229	AV648613	Hs.282397	ESTs	2.0
	441635	AI908538	Hs.133000	ESTs, Weakly similar to S26689 hypotheti	2.0
	421387	AF059566	Hs.103983	solute carrier family 5 (sodium iodide s	2.0
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.0
35	428209	AA424197	Hs.98947	ESTs, Weakly similar to S33496 trypsin [	2.0
	443520	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	2.0
	409248	AB033035	Hs.51965	KIAA1209 protein	2.0
	444518	AI160278	Hs.146884	ESTs	2.0
	422237	M13149	Hs.1498	histidine-rich glycoprotein	2.0
40	409316	U28251	Hs.53237	ESTs, Highly similar to Z169_HUMAN ZINC	2.0
	402725				2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
45	425008	AW675764	Hs.174248	ESTs	2.0
	427271	AW195922	Hs.188758	connexin 59	2.0
	444102	AV647953	Hs.83077	interleukin 18 (interferon-gamma-inducin	2.0
	445829	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
50	457652	AF116656	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.0
	429540	M85776		gb:EST02297 Fetal brain, Stratagene (cat	2.0
	459456	AA486036	Hs.190124	ESTs	2.0
	409840	AW502122		gb:UI-HF-BR0p-ajr-c-08-0-UI.r1 NIH_MGC_5	2.0
	441025	AA913880	Hs.176379	ESTs	2.0
	457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.0
55	445627	AW818475	Hs.7363	ESTs	2.0
	440299	AI871778	Hs.250112	ESTs	2.0
	401236	H24185	Hs.92918	hypothetical protein	2.0
	429996	N90822	Hs.48969	ESTs	2.0
60	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	2.0
	411537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	2.0
	433449	AW772282		gb:hn71b05.x1 NCI_CGAP_Kid11 Homo sapien	2.0
	454197	BE140966		gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
	445297	BE544163	Hs.87128	hypothetical protein FLJ23309	2.0
	403977				2.0
65	458948	AI695359	Hs.280943	ESTs	2.0
	418663	AK001100	Hs.41690	desmocollin 3	2.0
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	2.0
	426536	AI949749	Hs.44441	ESTs	2.0
	442765	BE567353	Hs.99480	ESTs	2.0
70	400859				2.0
	405829				2.0
	411863	BE075244	Hs.12420	ESTs	2.0
	415258	AW752247	Hs.293853	ESTs	2.0
75	416093	R60685	Hs.268698	ESTs, Moderately similar to ALUC_HUMAN !	2.0
	416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
	457039	H29990	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.0
	444292	AI139794	Hs.146569	ESTs	2.0
80	431360	NM_000427	Hs.251680	loricrin	2.0
	407644	D16815	Hs.37288	nuclear receptor subfamily 1, group D, m	2.0
	412029	AW886238		gb:RC5-OT0078-280300-022-F01 OT0078 Homo	2.0
	438522	AA809431	Hs.258886	ESTs	2.0
	422634	NM_016010	Hs.118821	CGI-62 protein	2.0

	418790	H95693		gb:yt95d11.s1 Soares_pineal_gland_N3HPG	2.0
	442950	AI500417	Hs.46764	ESTs	2.0
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.0
5	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	402674				2.0
	408733	AW264812	Hs.254290	ESTs	2.0
	408767	AA057279	Hs.211928	ESTs	2.0
	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
10	418205	L21715	Hs.83760	tropoin I, skeletal, fast	2.0
	404604				2.0
	413627	BE182082	Hs.246973	ESTs	2.0
	402341				2.0
	438090	AA777534	Hs.191992	ESTs	2.0
15	421303	T06464		gb:EST04353 Fetal brain, Stratagene (cat	2.0
	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.0
	401986				2.0
	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0
	417756	Z43056		gb:HSC12B021 normalized infant brain cDN	2.0
20	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.0
	433755	AW085934	Hs.120868	ESTs	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
	435648	H24347	Hs.27524	ESTs	2.0
	447555	AI391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	2.0
25	458175	AW296024	Hs.150434	ESTs	2.0
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothe	2.0
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	2.0
	447678	BE385257	Hs.336457	Homo sapiens dopamine receptor interact	2.0
	448150	AI472167	Hs.302739	ESTs	2.0
30	453445	AL036532	Hs.91453	ESTs	2.0
	444420	AI148157	Hs.146766	ESTs	2.0
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	2.0
	413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo	2.0
	428231	U17989	Hs.183105	nuclear autoantigen	2.0
35	455873	BE152239		gb:QV4-HT0316-091199-028-f12 HT0316 Homo	2.0
	430970	AI018210	Hs.144083	ESTs	2.0
	412277	BE277592	Hs.73799	guanine nucleotide binding protein (G pr	2.0
	413025	AA805265	Hs.291646	ESTs	2.0
	424083	AF055018	Hs.139137	Homo sapiens clone 24442 mRNA sequence	2.0
40	427654	AA410183	Hs.137475	ESTs	2.0
	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.0
	423942	AF209704	Hs.135723	glycolipid transfer protein	2.0
	430340	AA476777		gb:zw94g11.r1 Soares_total_fetus_Nb2HF8_	2.0
	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.0
45	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.0
	400285				2.0
	405966				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
50	415105	D60166		gb:HUM089G11B Clontech human fetal brain	2.0
	434531	AA642007	Hs.116369	ESTs	2.0
	447153	AA805202	Hs.315562	ESTs	2.0
	447185	AW377092	Hs.99601	hypothetical protein FLJ12553	2.0
	455696	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo	2.0
55	456510	AK001652	Hs.99423	ATP-dependent RNA helicase	2.0
	400617	AF151064	Hs.36069	hypothetical protein	2.0
	418647	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	2.0
	401785				2.0
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	2.0
60	420777	AA280223	Hs.130865	ESTs	2.0
	439509	AF086332	Hs.58314	ESTs	2.0
	430203	L36140	Hs.235069	RecQ protein-like (DNA helicase Q1-like)	2.0
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	2.0
	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	2.0
65	437620	AW976930	Hs.128760	ESTs	2.0
	407528	X64990		gb:H.sapiens mRNA HTPCRX16 for olfactory	2.0
	402048				2.0
	403623				2.0
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	2.0
70	417531	NM_003157	Hs.1087	serine/threonine kinase 2	2.0
	422600	BE143586	Hs.87	retinoblastoma-like 1 (p107)	2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.0
	433153	AA578512		gb:nh22e11.s1 NCI_CGAP_Pr1 Homo sapiens	2.0
75	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
	435373	AW665538	Hs.117689	ESTs	2.0
	442988	AI026130	Hs.131683	ESTs	2.0
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.0
80	454423	AW603985		gb:RC4-CN0048-140100-011-a04 CN0048 Homo	2.0



Table 31B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

	Pkey	CAT number	Accession
5			
10	407764	1014849_1	BE008347 BE008320 BE083307 BE083311 AW075968
	408274	104999_1	R17315 Z43964 AA053547
	408691	1074933_1	AW250525 BE265117
	409171	1104879_1	R17126 R38456 H02771
	409206	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659
15	409623	1144047_1	AW449185 AW449665 BE220971
	409699	1149033_1	BE154650 BE154785 AW468343 BE154816 BE154667
	409816	1155396_1	AW500954 AW501111 AW501394
	409840	1156071_1	AW502122 AW502125 AW501663 AW501720
	410201	118365_1	AA126129 AA126033 AA082561
20	410483	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
	410500	1206323_1	R09442 AW846115 AW846108 AW751967 AW846083 AW846087 AW846090
	410536	1207322_1	N39533 AW753094 AW753093
	410556	1208157_1	R32158 AW754055 AW754054 AW754053 AW754045 AW857320
	410615	1212203_1	AW772721 AW873372 H89212
	410626	1212621_1	BE407727
25	410644	1213795_1	AW902125 AW792853 AW837703 AW837710
	410672	1214882_1	AW794600 AW794730
	410845	1223881_1	AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280
			AW807283
30	410888	1225955_1	AW861207 AW809508
	410901	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786
			AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960
	410934	1227240_1	AW811114 AW811095 AW811087 AW811124 AW811054 AW811094 AW811157
	410999	1228809_1	AW813004 AW812962 AW812961
35	411004	1228975_1	AW813242 BE146089 AW813195 AW813173 AW813206 BE145953 BE146212 AW813196 AW854582 AW813241 BE061582
	411018	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
	411024	1229310_1	BE062590 AW813565 BE147101
	411093	1231970_1	BE067650 AW817053
	411186	1235090_1	AW821257 AW821267 AW821283
40	411244	1236407_2	AW833768 AW833631 AW833435 AW833533 AW833554 AW833543 AW833557
	411262	1236998_1	AW834480 AW834531 AW834637 AW834618 AW834653 AW834487
	411311	1238530_1	AW836491 AW836461 AW836673
	411377	1242238_1	AW841462 BE156657 BE156668 BE092475
	411382	1242594_1	BE067246 BE067241 BE067254 BE067249 AW841960
45	411384	1242702_1	AW842115 AW842111 AW842103
	411417	1245075_1	AW845481 AW845474 AW850849
	411459	1246724_1	BE142707 BE142852 BE142723 BE142905 AW847712 AW847792 AW847858 AW847852 AW847654 AW847608 BE142961
	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
			AW848905 AW848214
50	411480	1247089_1	AW848022 AW848704 AW848168 AW848959 AW848476 AW848699 AW848700 AW848761
	411518	1248692_1	AW850246 AW850251 AW850302
	411537	1248899_1	BE073250 BE073378 BE073379 AW850533 AW850529
	411597	1250843_1	AW852925 AW852922
	411656	1252973_1	AW855576 AW855650 AW855578 AW855577 AW855642 AW855619 AW855624 AW855621
55	411660	1253078_1	AW855718 AW855740 AW855748
	411688	1254076_1	AW953440 T08189 AW857085
	411693	1254206_1	AW857271 AW857308 AW857296 AW857258
	411726	1255048_1	AW858612 AW861964 AW858600 AW861945 AW858445 AW861901 AW858546 AW861921 AW858395 AW861968 AW858394 AW858401
			AW858404 AW858399
60	411738	1255755_1	AW859353 AW859365 AW859362 AW859356 AW859351 AW859354 AW859355 AW859361 AW859348 AW859364 AW859372 AW859352
			AW859349 AW859367 AW859360 AW859374 AW859350
	411745	1256160_1	AW867826 AW859896
	411762	1256906_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860988 AW860925 AW860922 AW860986 AW860984 AW860989
	411772	1257386_1	BE170301 AW861539 AW904851 BE154336 BE154090 BE154275
65	411816	1259632_1	AW864609 AW864592 AW864594
	411819	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
	411880	1263110_1	AW872477 BE088101 T05990
	411940	1266262_1	AW876686 AW876717 AW877215 AW876691 AW876722 AW877218 AW876694 AW876725
	412029	1272597_1	AW886238 AW886229 AW886244 AW887891 AW886289 AW886146
	412039	1273497_1	AW887384 AW887372 AW887461 AW887315
70	412147	1279411_1	AW895984 AW895982 AW895983 AW895918 AW895772 AW895843 AW895847 AW895653 AW895652 AW895648 AW896054 M85583
	412209	1283610_1	AW901456 AW901450 AW901441
	412236	1284501_1	AW902583 AW902585 AW902695 AW902568 AW902580 AW902692 AW902684 AW902595 AW902573 AW902681
	412282	1287679_1	BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
	412303	1288130_1	AW936336 AW936339
75	412321	1288608_1	AW936913 AW936959 AW936918 AW936909
	412323	1288770_1	AW937143 AW937150 AW937141 AW937151 AW937132 AW937160 AW937191 AW937174 AW937195 AW937173 AW937159 AW937139
			AW937171 AW937142 AW937145 AW937165 AW937163 AW937164 AW937137 AW937179 AW937156 AW937140 AW937135 AW937170
	412329	1288943_1	AW937445 AW937457 AW937364 AW937374 AW937395
80	412400	1292900_1	AW948066 AW948106 AW948020 AW948047 AW948011 AW948033 AW948034 AW948041 AW948028 AW948048 AW948046 AW948056
			AW948025 AW948053 AW948043 AW948032 AW948037 AW948050 AW948060 AW948059 AW948051 AW948027 AW948038 AW948052
			AW948036 AW948031 AW948030 AW948035 AW948039 AW948026 AW948044 AW948049 AW948042 AW948054 AW948055 AW948013
			AW948058 AW948045 AW948057 AW948029 AW948003 AW948016 AW948123 AW948008 AW948001 AW948022 AW948014 AW948023
			AW948004 AW948000 AW948018

5	412474	129869_1	AI791451 AI791288 BE019234 BE296601 AA111939
	412566	1306469_1	AW962574 BE073261
	412879	1334272_1	BE092219 BE092361 BE006789
	412887	1334741_1	BE007420 BE007419 BE007421 BE007422
	412999	1343220_1	BE046255 BE046611 BE046716 BE046732 BE046273
10	413071	1348162_1	BE064032 BE064039 BE064027 BE064040 BE064045 BE063868 BE063890
	413087	1348720_1	BE064655 BE153953
	413088	1348732_1	BE064962 BE064979 BE064853 BE064857 BE064856 BE064977 BE064960 BE064860 BE064815 BE064957 BE064804 BE064816 BE064850
			BE064806 BE064796 BE064818 BE064975 BE064819 BE064810 BE064668 BE065059
	413096	1349078_1	BE065209 BE065364 BE065110 BE065111
15	413101	1349154_1	BE065215 BE155544 BE155541 BE155540 BE155542 BE155543
	413252	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
	413257	1355963_1	BE075035 BE074999 BE075006 BE075005 BE075032 BE075008 BE075037
	413445	1370833_1	BE141022 BE141513 BE141532 BE141488 BE141481 BE141526 BE141516 BE141471 BE141478 BE141476 BE141475 BE141021 BE141533
			BE141464 BE141490 BE141472 BE141480
20	413470	1371600_1	N20934 BE141875 BE141877
	413488	1373234_1	BE144017 BE185527 BE144023
	413499	1373910_1	BE144884 H97942
	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	413581	1378335_1	BE150618 BE150616 BE150626
25	413640	1381286_1	BE158118 BE158034 BE154709 BE154825
	413646	1381488_1	BE155042 BE155040 BE154987 BE155012
	413758	1386900_1	BE162391
	413875	1396766_1	BE176776 H85072
	413986	140720_1	Z43567 H24159 AA134240
30	414277	1432122_1	BE269910 BE296510 BE295925 BE269325
	414349	1437515_1	BE512968
	414366	1438636_1	BE549143 BE390613 BE277344
	414456	1447655_1	H74314 BE299593
	414539	1460320_1	BE379046 BE395459
35	414546	1460704_1	BE379492 BE391967
	414605	1465790_1	BE390440
	414955	1509869_1	C15506 D80541 D80506
	415105	1522674_1	D60166 D60893 D60101
	415131	1523680_1	D61119 D81508 D81734
40	415236	1531080_1	R41400 H06659 Z38637 F02023 T16516
	415318	1533859_1	T06544 Z44549 F05465 R61128
	415425	1536408_1	F08365 Z43395 R54298
	415549	1539692_1	F11942 T78047 R13266
	415628	1540769_1	F13080 R34751 T75411
45	415635	1540853_1	F13168 R21289 T77628
	416035	1567254_1	H42314 H43080 H45217 H15384
	416154	1573965_1	Z46122 H23303 R56554 H23055 T80310 R13090 Z45524
	416458	159583_1	AA180511 AA649022 AW974566
	416548	1600181_1	H62953 N76608 N72413
50	416616	1604113_1	H68270 H68271 R07781
	416972	163668_1	BE019670 AA191284 AA191255
	417428	1679519_1	N87579 T93706
	417490	168397_1	AA203335 R11393
	417563	168749_1	AA203701 R86895
55	417669	1692157_1	T99898 T92080 T91447 R07806 R07779
	417756	1697154_1	Z43056 R13398 T80474
	417909	1707657_1	R35614 R24837 R52440
	417945	1711126_1	R29072 R29717 R29699 R29709 R29751 R29609 R29060 R29718 R29057 R29591 R29683 R29575 R28913 R28910
	418297	1736343_1	R91254 T97156 R58711
60	418647	177521_1	AA226198 AA226513 AA383773
	418790	179028_1	H95693 W02322 AA228140 H95692
	418856	179649_1	AA362858 AW863761 AA229428
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
	419637	186639_1	W27493 AA248063 AA249685 AA429679
65	419936	189181_1	AI792788 BE142230 AA252019
	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	420430	193538_1	AI703192 AW901259 AA278523 AA262062
	420621	195113_1	AA278808 BE082076 BE081812 BE081581
	420844	196986_1	AA595522 AA280981 BE464358
70	420854	197072_1	AW296927 AI684514 AI263168 AA281079
	421065	198936_1	AA329711 AA287436 AA283148
	421303	201039_1	T06464 C17931
	421338	201378_1	AA287443 AA419385 BE084078 AI478347
	421583	204220_1	AA293333 AI820910 AA293403
75	421813	207654_1	BE048255 AA313083 AA298419
	422977	223410_1	AA631498 AI017191 AA491211 AA761823 AA714555 AA768099 AA808286 AI934069 AA570223 AA574389 AA582438 AI745346 AW964510
			AA319642 AW853758 H56414
	423121	225175_1	AW864848 AA322213 AA322209 AW961624
	423532	229362_1	BE090503 BE090490 BE090483 BE090501 BE090500 BE090365 BE090505 BE090509 BE090499 BE090502 BE090504 BE090497 AA327285
80	423646	230597_1	H02364 AA329065 AW958111 AW961436
	423734	231479_1	H02217 AA330235 AW955673
	423841	232507_1	AW753967 AA370795 AA331630 AW962550
	423867	232732_1	AA331886 AW962659 AW962655 T89841
	423871	232749_1	AA331906 AA332484
	424719	242889_1	H90452 AA345767 AW964302 H90399
	424754	243305_1	R09692 R09414 AA346353
	424872	244505_1	AA347923 AA347928 AW961769

	425156	247338_1	AA351364 H19138 R12960
	425201	247933_1	AA352111 AW962247 AA429695
	425374	250946_1	AI904013 AI904015 AA356332
5	425433	251775_1	AA357471 AA360564 AW962961
	425457	252038_1	AW964212 AA357832 AA357831
	425541	252945_1	AA359119 AW963014 D79884
	425798	256586_1	AA364002 AI522307
	426076	260504_1	AW962714 AA369277 AA369278
10	426336	265003_1	AA375802 AA375642 AW963815
	426497	268121_1	AA379913 AA379981 AW963523
	426750	271252_1	AA383950 AA383958 AW966432
	426800	272088_1	AA385085 AW966617 T87798
	426960	273843_1	AA393713 AA400726
	428679	294049_1	AA431765 AA432015
15	428740	294655_1	AA433838 AA450385 AA683244
	429106	299886_1	AA446612 AA456438 AA476655
	429540	305828_1	M85776 AA454535 AA456208 H90189
	429875	310034_1	AI091815 AA460162 AA460761
20	430175	314040_1	AA468724 AA468772 AA468643 AW969231
	430340	316229_1	AA476777 T86049
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
	430553	319868_1	AW392821 AW392809 AW843258 AW843049 AW603156 BE165656 AW821728
	430692	32200_1	X80240 AI064750 AI133594
25	430698	322100_1	AA492071 AA484229 AW969850
	430757	322947_1	AI458623 AA639708 AA485409 R22065 AA485570
	430850	324651_1	BE144152 AA937952 AA487799
	431058	327401_1	AW968865 AA491199 C17148
	431071	327550_1	AA491379 H86020 AW969148
30	431162	328726_1	AW971180 AA551515 AA493610 AW089533
	431169	328799_1	AW971240 AA493843 AA493723
	431453	333457_1	AW753917 BE152926 AA505333 BE155673
	431655	336189_1	AW971119 AA574265 AA513268
	431822	338082_1	AA516049 AW004922
35	431925	33905_1	AK000890 BE182413 AW890890 AW844179 BE178934
	432189	342819_1	AA527941 AI810608 AI620190 AA635266
	432363	345469_1	AA534489 AW970240 AW970323
	432779	354024_1	AW979241 AA565006 AA847102
	432869	355475_1	AW974094 AA569074 AA602574
40	432919	356290_1	AL079800 AA570294 L25459
	433153	359936_1	AA578512 AA595535 BE177533
	433347	36388_1	AF023130 AF181250 AA984703 AA694303 AA351792
	433449	366532_1	AW772282 AA592974
	433919	377243_1	AA746311 AA927492 AA617995
45	434098	380006_1	AA625499 AA625269 AA625184
	434138	380572_1	AA625804 AW418787 AW074833 AI675642 AI393368
	434662	390415_1	AA641957 AW749897 AW749866 AW749887 AW749890
	434671	390655_1	R34758 AA642317
	435079	399783_1	AA664192 H60250 T71388
50	435138	401159_1	BE314734 AA666393
	435463	406582_1	AA682507 AW851124
	435510	407286_1	BE143837 AW749652 AA683327
	435634	409239_1	T82384 R05307 AA693714
	435689	409755_1	AA694284 H68267 H68264
55	436359	41847_1	Z83806 AJ132091 AJ132090
	436720	425676_1	AW975902 AA729344 AI557342
	436858	428095_1	BE545498 AA830720 AI873015 AA732679
	437037	431828_1	T63804 T63768 AA742849
	437113	433234_1	AA744693 AW750059
60	437642	43997_1	AL079309 AA281819
	437963	44635_1	BE396279
	438005	447553_1	BE151746 BE336853 D63271 T94955 AA774994
	438993	467651_1	AA828995 AA834879 AI926361
	439037	46803_1	AF075084 H53157 H53054
65	439546	47360_1	AF088056 W76297 W72448
	439780	47673_1	AL109688 R23665 R26578
	442653	54812_1	BE269247 BE270032 BE270800 BE566840
	442735	550247_1	R91949 AI016237 BE072329
	443764	579650_1	F23283 AI084941 F35774
	444063	590989_1	AI122614 AW869134
70	444910	624951_1	AI201849 BE069007 AW946544
	445432	63943_1	AV653771 BE089370
	446096	661959_1	AI276454 AI633717 AI275116
	446901	697809_1	AI347274 AW844024
75	447884	740749_1	H29505 R18575 Z43580 T48738 AI435454 BE004683
	448477	76475_1	BE612572 AL040190 F08514
	449311	804513_1	AI657014 AW594035 AI657036 AI638390
	450024	82296_1	AA005129 AA679084 AA694399
	451067	85759_1	BE172186 AA059279 AA020815 AA013437
80	452043	89532_1	H86231 AA021632 H38271
	452542	921410_1	AW812256 AW812257 AI906423 AI906422
	453211	95527_1	W84829 AA033900 AW573557
	453530	97021_1	AW021633 AA036730 AI866854
	453823	982526_1	AL137967 BE064160 BE064186

	453901	986414_1	BE065902 AW749032 AW003637
	454186	1049791_1	BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581 BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460 BE141749 AW177598
5	454190	1049996_1	AW177821 AW177896 AW177867
	454197	1050392_1	BE140966 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969 BE141673 BE141650 BE141674 BE141550 BE141688 AW178241 BE140994 BE141666 BE140998 BE141008 BE140988 BE141011 BE140975 BE141667 BE141675 BE141657 BE141681 BE141656 BE141672 BE141680 AW178237 BE141012 BE140990 BE141658 BE141648 BE141013 BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646 BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671 AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141556
10	454204	1050597_1	AW816498 AW808791 AW808515 AW808379 AW808532 AW808605 AW808977 AW808816 AW178676 AW178486 AW808514 AW178483 AW178485 AW809007 AW808524
15	454314	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659
	454352	1129667_1	AW389668 AW389657 AW609198 AW389649
	454423	1183079_1	AW603985 AW854350
	454447	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
	454456	1207088_1	AW850984 AW752836 M86124
	454482	1215087_1	BE147919 AW794884 BE147847
20	454560	1223940_1	AW807281 AW807092 AW807425 AW807330 AW807174 AW807171 AW807274 AW807278 AW807367
	454564	1224407_1	AW807573 AW807566 AW807572
	454566	1224432_1	AW807605 AW807690 AW807839 AW807752 AW807673 AW807667 AW807955 AW807760 AW807615 AW807898 AW807849 AW807821 AW807832 AW807842 AW807827 AW807822 AW807829 AW807830 AW807825 AW807603 AW807612 AW807908 AW807595 AW807617 AW807678 AW807687 AW807918 AW807921 AW807596 AW807602 AW807688 AW807609 AW807684 AW807770 AW807593 AW807754 AW807679 AW807957 AW807683 AW807763 AW807902 AW807840 AW807819 AW807836 AW807769 AW807685 AW807847 AW807674 AW807686 AW807670 AW807917 AW807677 AW807680 AW807900 AW807669 AW807952 AW807907 AW807846 AW807756 AW807835 AW807608 AW807753 AW807601 AW807956
25	454597	1226059_1	AW809648 AW809704 AW809643 AW809653 AW809709 AW809949 AW809939 AW810010 AW809705 AW809950 AW809822 AW809667 AW810093 AW810076 AW809673 AW810349 AW809895
30	454633	1227504_1	AW811380 AW811385
	454716	1230503_1	AW850684 AW850150
	454747	1233006_1	AW818535 AW818588 AW818651
	454754	1233580_1	AW819191 AW819252 AW819183 AW819175 AW819177 AW819186 AW819180 BE158470 AW819242 AW819269 AW819244 AW819190 AW819265 AW819268 AW819246 BE152602 AW819249 AW819251 AW819263 AW819194
35	454767	1234028_1	BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202 AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784
	454778	1234343_1	AW820199 AW820434 BE174743
	454784	1234630_1	AW820626 AW820621 AW820608
40	454790	1234752_1	AW820852 AW820773 AW821088
	454836	1236509_1	AW833711 AW833620 AW833699
	454864	1237929_1	AW835775 AW845768 AW845764 AW845773 AW845757 AW845758 AW845780
	454938	1245635_1	AW846134 AW846467 AW846468 AW846386 AW846461 AW846211 AW846179 AW846205 AW846320 AW846379 AW846367 AW846561 AW846556
45	454962	1246750_1	AW847645 AW847791 AW854083 AW853945
	455022	1249160_1	AW850845 BE144010 AW855164
	455121	1254339_1	BE156459 BE156469 BE156468 AW857447
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455170	1256906_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
50	455201	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
	455219	1261640_1	AW879403 AW867707
	455221	1261678_1	AW867751 AW867770 AW867763
	455236	1265662_1	AW875972 AW875983 AW875974 AW876000 AW875966 AW876050
	455252	1266222_1	AW876627 AW876630 AW876631 AW876625
55	455255	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	455275	1272255_1	AW977806 AW887923 AW886321
	455280	1272607_1	AW886156 AW887926 AW886324 AW886236 AW887906 AW886304
	455310	1278158_1	AW893961 AW893998 AW894034 AW894019
	455328	1280063_1	AW896438 AW896534 AW896500 AW896540 AW896446
	455464	1292643_1	AW983901 AW984485 AW947715
60	455482	1293183_1	AW948353 AW948351 AW948331 AW948303 AW948336 AW948305 AW948299 AW948346 AW948352
	455488	129372_1	AA102322
	455511	1321229_1	BE144762 AW979091
	455534	1322942_1	AW991925 AW991919
65	455540	1323701_1	BE080231 AW993284 AW993293 AW993000
	455556	1325658_1	AW995423 AW995373
	455571	1331885_1	BE003714 BE003721 BE003720 BE003716
	455587	1335046_1	BE007829 BE007815 BE007822 BE007996 BE007835 BE007837 BE007824 BE007836 BE007827
	455608	1337389_1	BE011437 BE011402 BE011395 BE011428 BE011407 BE011421 BE011406
	455675	1349659_1	BE065984 BE065942 BE065955 BE066085
70	455688	1350606_1	BE067238 BE067235 BE067240 BE067256 BE067263 BE067236 BE067260 BE067253 BE067248 BE067252
	455696	1351077_1	BE067870 BE067866 BE165133 BE165334 BE165329 BE165332
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
	455756	1358603_1	BE079307 BE079309
	455778	1364506_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
75	455780	1364580_1	BE088828
	455849	1375441_1	BE146866 BE146865 BE146867
	455851	1375451_1	BE146879 BE146914 BE146918
	455866	1377119_1	BE149024 BE149056 BE152826 BE149025 BE149057 BE152819 BE149030 BE149062 BE149023 BE149055
	455873	1379498_1	BE152239 BE152242 BE152230
80	455880	1380022_1	BE153208 BE153146 BE152981
	455935	1384144_1	BE158687 BE158688
	455964	1389912_1	BE166924 BE166921 BE166925 BE166915 BE166970 BE166968
	455992	1398552_1	BE179015 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997

455993 1398665\_1 BE179085 BE179084 BE179086 BE179264  
 456186 1618618\_1 W26642 H88394  
 456313 177240\_1 AA225741 AI734056 AI820965 AI732153 AA259201 AA225731  
 456394 1843275\_-2 W28506  
 456407 184986\_1 AW968614 AA243209 AA281411  
 456476 191761\_1 AA256753 AW628680  
 457242 307984\_1 AA457011 AI978850  
 457824 41515\_6 R84938 AL047151 AA310309 AW063200 AI569528 AI307823 N49975  
 458804 75803\_1 AL157625 N72696 BE622492  
 458890 812733\_2 AW865523 AW865128 AW865467 AW865127 AW865466  
 459160 920051\_1 AI904723 AI904725 AI904729 AI904722 AI904758 AI904736  
 459201 925883\_1 AW391177 W45021

TABLE 31C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400451	8113550	Minus	82189-82320
400462	9929659	Minus	197610-197785
400486	8569885	Plus	181108-181605
400510	9796540	Minus	139633-139910,140469-140979
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
400579	9887603	Plus	21323-21526
400582	9887609	Plus	88642-88726,89716-89866
400587	9887626	Plus	25435-25588,25668-25747
400608	9887666	Minus	96756-97558
400612	9929646	Minus	151513-151662
400613	9864507	Plus	92278-92472
400641	8117693	Plus	4786-4992
400643	8117693	Plus	12818-13016
400706	7249204	Minus	78299-78686
400734	8118979	Plus	122853-123971
400816	8569993	Plus	161221-162078
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
400859	9757499	Minus	91888-92018,98131-98294,99474-99570
400861	9757506	Plus	163855-164016
400889	9958234	Minus	169782-170036
401078	3687273	Plus	105052-105171
401098	9965518	Minus	85632-86174
401132	8705350	Minus	85679-85795
401145	2547238	Plus	17599-17776
401189	9690246	Minus	90815-90929
401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
401344	9926411	Minus	82478-82602,86952-87110
401361	9958052	Plus	153093-154106
401365	9796180	Minus	119572-119672
401449	8574316	Minus	144928-145030
401497	7381770	Plus	92607-92813
401521	7705251	Plus	9127-9234
401526	7770561	Plus	91570-93177
401602	7689963	Plus	101096-101253
401614	7839924	Plus	17350-17735
401645	7657839	Minus	34986-35133
401694	3540172	Minus	64056-64168
401775	9966311	Minus	110228-110340
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
401882	8139716	Plus	86466-87077
401887	7229981	Plus	93973-94120
401986	4406829	Minus	31137-31293
401992	4153858	Plus	31452-31649
402038	7684482	Minus	100751-100885
402048	8072512	Plus	43936-44078
402076	8117410	Plus	128316-128627
402103	7249203	Plus	14453-15414
402131	7704961	Minus	33114-33209,33496-33678
402176	7543687	Minus	10-750
402230	9966312	Minus	29782-29932
402333	8844110	Minus	165693-165856
402341	7656696	Plus	22583-23699
402395	9929693	Minus	131016-131998
402429	9796372	Minus	57622-57793,59282-59402,59624-59827
402430	9796372	Minus	62382-62552
402455	9796753	Minus	139640-139779,140568-140660
402527	9800806	Plus	4722-4916,17858-18037,19964-20140,24423-24605,26699-26881

	402615	9926801	Plus	131390-132157
	402621	9930950	Plus	130806-131036
	402674	8077108	Minus	39290-39502
5	402725	8979991	Plus	107231-107383
	402790	4835258	Minus	147744-147861
	402867	5596716	Plus	52806-53106,53500-53818
	402953	9408724	Minus	122603-122743
	403003	5441423	Minus	79403-79560,79712-80021
10	403011	6693597	Minus	3468-3623
	403065	8954197	Minus	71615-71773,73930-74144
	403188	9838289	Minus	157618-157755
	403271	7230852	Plus	134283-134485
	403273	8018055	Plus	133809-134099
15	403281	8072630	Minus	7521-7728
	403296	8096530	Minus	35913-36520
	403310	8139936	Minus	183883-184026
	403329	8516120	Plus	96450-96598
	403341	8569175	Plus	30699-30910
20	403344	8569726	Plus	70823-70990
	403356	8569930	Plus	92839-93036
	403381	9438267	Minus	26009-26178
	403388	9438331	Plus	112733-113001,114599-114735
	403396	9438367	Minus	952-1160
25	403501	7534005	Minus	108903-110438
	403513	7656757	Minus	155310-155436,158402-158535
	403515	7656757	Minus	173358-179553
	403534	8076917	Minus	46652-47332
	403549	8081591	Minus	137150-137362
30	403568	8101145	Minus	85509-85658
	403574	8101156	Plus	5542-6176
	403619	8569810	Plus	62501-62653
	403623	8569879	Minus	3519-5426
	403625	8569879	Plus	6551-7111
35	403637	8671936	Minus	142647-142771,145531-145762
	403667	6850483	Minus	1344-1442,1545-1697
	403677	7331517	Minus	55008-55083,62860-63051
	403691	7387384	Minus	88280-88463
	403696	3135242	Minus	143467-143634
40	403743	7652003	Minus	136463-136646
	403760	7712202	Minus	45910-46260,47563-47824
	403764	7717105	Minus	118692-118853
	403776	7770611	Minus	1414-1513,1624-1756
	403780	8076989	Plus	93160-93409
45	403786	8083636	Minus	73028-73217
	403891	7331467	Minus	191508-193220
	403895	7381715	Minus	3502-4002,4070-4308
	403977	7657840	Minus	115573-115820
	404043	9558573	Plus	29042-29135,46597-46699
50	404059	3548785	Plus	104326-106788
	404076	9931752	Minus	3848-3967
	404196	3805917	Minus	67928-68109
	404249	8655533	Plus	64270-64633
	404257	9367215	Plus	15262-16227
55	404285	2326514	Plus	32282-32416
	404288	2769644	Plus	3512-3691
	404367	9965011	Minus	114391-114628
	404443	7579073	Minus	87198-87441
	404453	7657714	Plus	27768-29179
60	404476	8080699	Plus	101841-102043
	404513	8151941	Minus	112837-113339
	404561	9795980	Minus	69039-70100
	404569	7249169	Minus	104257-104348,104822-104970
	404577	4020145	Plus	17991-18420
65	404588	6456726	Minus	40059-40210
	404599	8705107	Plus	110443-110733
	404604	9212537	Minus	72019-72509
	404638	9796751	Minus	99433-99528,100035-100161
	404767	7882827	Minus	23244-23759
70	404793	7232206	Minus	61087-61590
	404822	3810614	Plus	7541-8132
	404834	6911603	Minus	37948-38226
	404845	7958980	Minus	47174-47326,52928-53146,53312-53602
	404898	7331420	Minus	177015-177328
75	404936	6850774	Plus	191519-191664
	404957	7407927	Plus	147512-148011
	405017	6532084	Plus	35551-35690
	405059	7656683	Plus	349-822
80	405090	8072525	Minus	38552-39202
	405093	8072575	Plus	95878-96020
	405120	8099940	Plus	140176-140340
	405170	9966524	Plus	37047-37198
	405229	7249019	Plus	51081-51701
	405230	7249032	Minus	97493-97682

	405233	7249045	Plus	9588-10065
	405241	7249178	Minus	69927-70526
	405264	7329374	Plus	28556-28684
5	405287	3928029	Plus	89802-89999
	405302	2078453	Minus	121688-121840
	405303	2078453	Minus	130607-130802
	405336	6094635	Plus	33267-33563
	405347	2979602	Minus	977-1116
10	405385	6552772	Plus	48332-48454
	405443	7408143	Plus	90716-90887,101420-101577
	405455	7656675	Plus	134112-134671
	405494	8050952	Minus	70284-70518
	405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
15	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
	405547	1054740	Plus	124361-124520,124914-125050
	405605	5836195	Minus	117070-117270
	405608	5815499	Minus	66822-66925
	405629	4508116	Minus	101678-101866
20	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405706	4165003	Plus	44307-44431,49619-49802
	405720	9797144	Plus	13409-13861
25	405732	7534017	Plus	146981-147316
	405759	3288022	Minus	18283-18399
	405780	7248203	Minus	48204-48371
	405784	7417368	Minus	77798-78000
	405829	7109593	Minus	15628-16127
	405869	6758731	Minus	89867-90358
30	405935	6758795	Minus	163112-163652
	405959	6758815	Plus	1-642
	405965	8247786	Minus	179930-180373
	405966	8247788	Minus	51762-51978
	405970	8247789	Minus	45795-46295
35	405981	8247790	Plus	4771-5338
	406005	8247801	Minus	39912-40220
	406053	6758997	Plus	30921-31532
	406073	9119150	Plus	60495-60610
40	406091	9123919	Minus	197370-197935
	406092	9123919	Plus	251370-251797,252168-252882
	406298	5686278	Minus	30084-30770
	406327	9212407	Plus	168241-168492
	406333	9213235	Plus	64689-64798
45	406364	9256114	Minus	50715-50833
	406377	9256135	Plus	126826-126979,129755-129942
	406413	9256407	Plus	43858-44003,46993-47136
	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
	406470	9795562	Minus	15532-15697
50	406504	7711360	Minus	107068-107277
	406506	7711374	Minus	6843-8077F
	406592	4567182	Plus	352560-352963

55

Table 32A lists about 969 genes upregulated in lung fibrosis relative to normal body tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

60

Table 33A lists about 800 genes upregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

65

Table 34A lists about 703 genes upregulated in idiopathic pulmonary fibrosis (IPF) relative to hypersensitivity pneumonitis (HP) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

70

Table 35A lists about 323 genes upregulated in hypersensitivity pneumonitis (HP) relative to idiopathic pulmonary fibrosis (IPF) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

75

Table 36A lists about 52 genes upregulated in non-specific interstitial pneumonitis (NSIP) relative to hypersensitivity pneumonitis (HP) or idiopathic pulmonary fibrosis (IPF). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

80

Table 37A lists about 206 genes downregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 38A lists about 207 genes upregulated in lung fibrosis relative to normal tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

TABLE 32A: About 969 genes upregulated in lung fibrosis relative to normal body tissues

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.  
 R2: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	22.45	28.63
406964	M21305		FGENES predicted novel secreted protein	16.10	7.65
431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	15.83	14.86
442275	AW449467	Hs.54795	ESTs	15.74	21.96
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	13.83	34.53
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	12.40	7.38
431089	BE041395		ESTs, Weakly similar to unknown protein	12.38	6.05
421110	AJ250717	Hs.1355	cathepsin E	11.86	6.49
457200	U33749	Hs.197764	thyroid transcription factor 1	11.38	9.79
425211	M18667	Hs.1867	progastricisin (pepsinogen C)	10.89	15.94
443709	AI082692	Hs.134662	ESTs	10.84	8.27
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	10.06	8.92
445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	9.96	5.43
432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	9.90	7.87
421798	N74880		N-acylsphingosine amidohydrolase (acid c	9.38	8.35
400269			Eos Control	9.03	6.48
444325	AW152618	Hs.16757	ESTs	8.31	6.76
416402	NM_000715	Hs.1012	complement component 4-binding protein,	8.14	5.51
413048	M93221	Hs.75182	mannose receptor, C type 1	7.70	4.09
432985	T92363	Hs.178703	ESTs	7.56	7.83
443324	R44013	Hs.164225	ESTs	7.06	4.47
449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	6.90	2.89
408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88	4.00
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56	4.25
421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46	4.47
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.30	13.57
409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	6.28	3.38
441835	AB036432	Hs.184	advanced glycosylation end product-speci	5.99	13.26
446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.88	4.10
415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	5.88	3.35
442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	5.87	5.69
414812	X72755	Hs.77367	monokine induced by gamma interferon	5.84	3.34
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.72	5.90
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	5.59	6.89
436954	AA740151	Hs.130425	ESTs	5.58	4.72
446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	5.48	5.33
421340	F07783	Hs.1369	decay accelerating factor for complement	5.48	2.69
420656	AA279098	Hs.187636	ESTs	5.45	3.99
432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	5.38	3.65
408380	AF123050	Hs.44532	diubiquitin	5.37	3.11
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	5.30	3.98
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.29	4.00
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	5.28	2.48
442832	AW206560	Hs.253569	ESTs	5.20	3.78
407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	5.11	3.81
433293	AF007835	Hs.32417	hypothetical protein MGC4309	5.11	2.88
424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.07	3.46
428043	T92248	Hs.2240	uteroglobin	5.06	9.46
431745	AW972448	Hs.163425	ESTs	5.04	4.16
444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04	3.68
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	5.02	4.26
419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	4.97	3.35
428927	AA441837	Hs.90250	ESTs	4.92	3.15
432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.79	3.05
442994	AI026718	Hs.16954	ESTs	4.76	2.65
416030	H15261	Hs.21948	ESTs	4.76	4.26
438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.73	3.24
453142	AA033648	Hs.7473	ESTs	4.66	2.92
424917	AI636208	Hs.96901	hypothetical protein FLJ23049	4.64	4.88
439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	4.60	2.60
432810	AA863400		ESTs	4.54	2.42
418259	AA215404		ESTs	4.54	2.54
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	4.48	4.86
424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.46	3.62
423575	C18863	Hs.163443	intron of periostin(OSF-2os)	4.44	3.41
428667	AI375550	Hs.346868	nucleolar protein p40; homolog of yeast	4.42	3.41



	429228	AI553633		ESTs	4.32	2.98
	432435	BE218886	Hs.282070	ESTs	4.30	2.26
	446932	AA961459	Hs.125644	ESTs	4.30	2.81
5	408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30	2.39
	409435	AI810721	Hs.95424	ESTs	4.30	2.60
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	4.29	2.48
	452561	AI692181	Hs.49169	KIAA1634 protein	4.23	2.26
	427698	AW972594	Hs.335499	ESTs	4.22	3.49
10	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	4.22	13.34
	446608	N75217	Hs.257846	ESTs	4.20	3.62
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.18	3.14
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.16	2.64
	445885	AI734009	Hs.127699	KIAA1603 protein	4.16	3.99
15	430280	AA361258	Hs.237868	interleukin 7 receptor	4.13	2.79
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFp564K143 (fr	4.12	2.19
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	4.12	3.02
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.08	3.13
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.08	3.48
20	432731	R31178	Hs.287820	fibronectin 1	4.06	2.66
	439398	AA284267	Hs.221504	ESTs	4.06	2.86
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.05	3.51
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04	2.44
	436120	AI248193	Hs.119860	ESTs	4.04	3.11
25	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.03	2.69
	421462	AF016495	Hs.104624	aquaporin 9	4.00	2.51
	443257	AI334040	Hs.11614	HSPC065 protein	4.00	2.61
	421659	NM_014459	Hs.106511	protocadherin 17	4.00	3.00
	424273	W40460	Hs.144442	phospholipase A2, group X	3.98	2.30
30	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.97	3.36
	450656	AA010539	Hs.18912	ESTs	3.96	4.37
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.94	2.44
	424527	AW138558	Hs.334873	ESTs, Weakly similar to I54374 gene NF2	3.93	3.08
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.92	3.53
35	452416	AA026115	Hs.114777	ESTs	3.92	2.90
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	3.90	5.06
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ111041 fis, clone PL	3.90	2.00
	453204	R10799	Hs.191990	ESTs	3.90	2.22
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	3.81	3.82
40	422173	BE385828	Hs.250619	phorbol-like protein MDS019(CEM15)	3.80	2.23
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.78	2.86
	406672	M26041	Hs.198253	major histocompatibility complex, class	3.78	3.70
	457411	AW085961	Hs.130093	iroquois-class homeobox protein IRX2	3.76	2.56
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.76	2.76
45	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74	2.83
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.72	2.55
	428820	AA436187	Hs.172631	integrin, alpha M (complement component	3.71	2.25
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	3.70	2.26
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	3.69	7.71
50	417412	X16896	Hs.82112	interleukin 1 receptor, type I	3.68	2.17
	426174	AA547959	Hs.115838	ESTs	3.65	2.93
	408727	AL137259	Hs.47115	hypothetical protein DKFp434D0513	3.64	2.62
	435990	AI015862	Hs.131793	ESTs	3.62	2.27
	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	3.62	3.48
55	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	3.61	3.18
	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.60	3.05
	426116	AA868729	Hs.144694	ESTs	3.60	2.80
	419235	AW470411	Hs.288433	neurotrimin	3.58	2.88
	424054	AA334511	Hs.26638	membrane-spanning 4-domains, subfamily A	3.56	2.58
60	422667	H25642		ESTs	3.55	2.44
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.54	3.98
	414142	AW368397	Hs.334485	hemicentin (fibulin 6)	3.54	3.30
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.54	3.11
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	3.53	2.38
65	417318	AW953937	Hs.240845	ESTs	3.52	2.02
	456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	3.50	3.21
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.48	2.35
	430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo	3.48	2.13
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.47	2.93
70	424711	NM_005795	Hs.152175	calcitonin receptor-like	3.47	2.69
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.46	2.31
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	3.46	2.37
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.45	2.07
	447183	AI554733	Hs.173182	ESTs	3.42	2.01
75	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	3.40	3.49
	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFp761E2423 (f	3.40	2.42
	413714	AI560944	Hs.71428	ESTs	3.38	2.52
	407361	AA744622	Hs.292545	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.36	2.13
80	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36	2.41
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	3.36	2.06
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.35	2.42
	410606	AW418779	Hs.114889	ESTs	3.35	2.39
	450726	AW204600		retinoic acid receptor, alpha	3.34	6.35
	430573	AA744550	Hs.136345	ESTs	3.33	1.94

	421585	U95626	Hs.302043	chemokine (C-C motif) receptor-like 2(	3.32	2.75
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.31	2.22
	454076	AW204712	Hs.61957	ESTs	3.31	1.95
5	452039	AI922988	Hs.172510	ESTs	3.30	2.95
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30	2.37
	430414	AW365665	Hs.120388	ESTs	3.30	2.48
	417958	AA767382	Hs.193417	ESTs	3.30	2.04
	423001	AA320014	Hs.208603	ESTs	3.29	2.62
10	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28	2.35
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	3.28	2.05
	424238	AA337401	Hs.137635	ESTs	3.28	2.45
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	3.27	2.63
	448869	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.26	2.67
15	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5	3.26	2.04
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22	2.36
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22	3.87
	422109	S73265	Hs.1473	gastrin-releasing peptide	3.20	2.79
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	3.20	2.30
20	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18	2.42
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.18	2.12
	438568	R98865	Hs.11135	major histocompatibility complex, class	3.18	3.86
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	3.18	2.99
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	3.17	2.02
25	446094	AK001760	Hs.13801	KIAA1685 protein	3.17	2.42
	442048	AA974603		gb:op34f05.s1 Soares_NFL_T_GBC_S1 Homo s	3.17	2.27
	406685	M18728		gb:Human nonspecific crossreacting anti	3.17	2.80
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.16	1.95
	424943	AU077260	Hs.153924	death-associated protein kinase 1	3.16	2.18
30	436805	AA731533	Hs.270751	ESTs	3.16	1.95
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.15	3.63
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	3.14	1.74
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.13	3.35
	420729	AW964897	Hs.290825	ESTs	3.12	2.09
35	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12	2.06
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	3.12	2.58
	451820	AW058357	Hs.199248	ESTs	3.10	2.26
	440028	AW473675		ESTs, Weakly similar to T17227 hypotheti	3.10	3.01
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10	2.32
40	437866	AA156781		metallothionein 1E (functional)	3.10	1.80
	428513	BE220806	Hs.184697	plexin C1	3.10	2.11
	438607	AW080237	Hs.252884	ESTs	3.10	2.20
	445034	AW293376	Hs.143659	ESTs	3.08	2.81
	458332	AI000341		ESTs	3.08	1.87
45	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.08	1.87
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08	1.94
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.07	2.12
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	3.07	2.16
	425509	AF079363	Hs.158213	sperm associated antigen 6	3.06	2.75
50	431087	H12723	Hs.290791	ESTs	3.06	2.41
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	3.06	2.64
	449328	AI962493		ESTs	3.06	2.78
	422900	AA641201	Hs.222051	ESTs	3.05	1.87
55	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.05	1.99
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	3.05	2.49
	437527	AI241019	Hs.145644	ESTs	3.04	2.17
	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	3.04	1.78
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	3.02	2.43
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	3.02	1.77
60	411252	AB018549	Hs.69328	MD-2 protein	3.02	1.95
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02	2.24
	420683	AA830168	Hs.271305	ESTs	3.01	2.14
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00	2.13
	410434	AF051152	Hs.63668	toll-like receptor 2	3.00	2.60
65	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	3.00	1.94
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.00	1.81
	435800	AI248285	Hs.118348	ESTs	3.00	1.89
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	3.00	2.08
	449057	AB037784	Hs.22941	KIAA1363 protein	3.00	2.18
70	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	2.99	2.46
	436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	2.99	2.76
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.99	2.16
	444020	R92962	Hs.35052	ESTs	2.98	2.21
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.98	2.08
75	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	2.98	2.40
	457675	AF119917	Hs.306574	Homo sapiens PRO3098 mRNA, complete cds	2.96	2.03
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	2.96	1.74
	429950	AW081608	Hs.105053	ESTs	2.96	2.40
	420394	AB023161	Hs.97403	KIAA0944 protein	2.95	2.46
80	406698	X03068	Hs.73931	major histocompatibility complex, class	2.95	4.13
	419038	AW134924	Hs.190325	ESTs	2.94	1.72
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94	2.93
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	2.94	1.94
	400880			NM_000611*:Homo sapiens CD59 antigen p18	2.94	1.74

5	430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypot	2.94	2.12
	419034	NM_002110	Hs.89555	hemopoietic cell kinase	2.93	2.25
	439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobulin, fa	2.93	3.72
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.92	1.91
	419981	AA897581	Hs.128773	ESTs	2.92	2.18
10	400419	AF084545		Target	2.92	1.83
	435176	AA744875	Hs.189413	ESTs	2.91	2.15
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	2.90	2.25
	444339	T96555	Hs.31562	ESTs	2.90	3.16
	429272	W25140	Hs.110667	ESTs	2.90	2.43
15	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.90	2.29
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	2.90	2.40
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	2.88	2.47
	421554	AW137676	Hs.97775	ESTs	2.88	3.37
	422770	AL117544	Hs.120021	DKFZP434I092 protein	2.88	2.00
20	434658	AI624436	Hs.310286	ESTs	2.88	2.06
	440248	AA876138		ESTs	2.86	2.24
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.86	4.32
	430515	AA746503	Hs.283313	ESTs	2.86	2.96
	446063	AI720140	Hs.151079	ESTs	2.86	2.47
25	438177	BE327015		ESTs	2.86	1.70
	429083	Y09397	Hs.227817	BCL2-related protein A1	2.85	2.06
	417105	X60992	Hs.81226	CD6 antigen	2.85	3.00
	433230	AW136134	Hs.220277	ESTs	2.84	1.97
	438676	AA813745	Hs.123446	ESTs	2.84	2.62
30	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.82	4.33
	420252	AW270404	Hs.193161	ESTs	2.82	3.22
	415788	AW628686	Hs.78851	KIAA0217 protein	2.82	1.78
	428065	AI634046	Hs.157313	ESTs	2.81	2.47
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.81	2.67
35	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.78	3.39
	435517	AA928626	Hs.130177	ESTs	2.78	2.36
	439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFzP434A041	2.78	1.82
	434158	T86534	Hs.14372	ESTs	2.78	1.96
	428923	BE047698	Hs.188785	ESTs	2.78	2.07
40	413786	AW613780	Hs.13500	ESTs	2.78	1.97
	406387			Target Exon	2.77	4.22
	421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	2.76	3.24
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.76	2.11
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	2.76	1.94
45	417728	AW138437	Hs.24790	KIAA1573 protein	2.76	1.78
	435154	AA668764		ESTs	2.76	2.10
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.76	2.21
	423387	AJ012074		vasoactive intestinal peptide receptor 1	2.76	2.36
	432060	AW971364	Hs.324775	ESTs	2.75	2.02
50	434164	AW207019	Hs.148135	serine/threonine kinase 33	2.74	2.48
	423706	U95218	Hs.131924	G protein-coupled receptor 65	2.74	1.93
	442703	AL044949	Hs.116298	ESTs	2.74	1.89
	450247	AF123303	Hs.24713	hypothetical protein	2.74	1.73
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	2.74	2.85
55	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.74	1.88
	409196	NM_001874	Hs.334873	carboxypeptidase M	2.73	1.86
	422389	AF240635	Hs.115897	protocadherin 12	2.72	2.26
	444324	AI301330	Hs.143838	ESTs	2.72	1.74
	417831	H16423	Hs.82685	CD47 antigen (Rh-related antigen, integr	2.72	2.40
60	428769	AW207175	Hs.106771	ESTs	2.72	2.19
	404277			NM_019111:Homo sapiens major histocompa	2.72	3.12
	409653	AW451693	Hs.220826	ESTs	2.72	2.62
	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	2.72	2.25
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	2.72	2.09
65	444381	BE387335	Hs.283713	hypothetical protein BC014245	2.71	2.26
	443547	AW271273		hypothetical protein FLJ12666	2.71	1.74
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.70	2.39
	402674			Target Exon	2.70	1.95
	438068	AI927209	Hs.306210	Homo sapiens cDNA: FLJ23133 fis, clone L	2.70	2.23
70	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	2.69	2.11
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.69	2.28
	428656	AB037798	Hs.188790	KIAA1377 protein	2.68	1.91
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.68	3.95
	443951	F13272		ferritin, light polypeptide	2.68	2.66
75	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.68	1.74
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	2.68	1.78
	446423	AW139555	Hs.150120	ESTs	2.68	2.29
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.67	2.07
	431779	AW971178	Hs.268571	apolipoprotein C-I	2.67	3.00
80	458124	AW005548	Hs.124590	ESTs	2.67	3.78
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	2.66	1.64
	445745	AB007924	Hs.13245	KIAA0455 gene product	2.66	1.64
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.65	1.92
	432231	AA339977	Hs.274127	CLST 11240 protein	2.64	4.23
	442200	AW590572	Hs.235768	ESTs	2.64	2.46
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	2.64	2.00
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.63	3.23

	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.63	2.48
	411213	AA676939	Hs.69285	neuropilin 1	2.62	1.73
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.62	2.69
	446570	AV659177	Hs.127160	ESTs	2.61	2.44
5	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	2.60	3.39
	434792	AA649253	Hs.132458	ESTs	2.60	1.74
	426782	R14614	Hs.33846	ESTs	2.60	2.36
	425371	D49441	Hs.155981	mesothelin	2.60	6.97
	447720	AL038765	Hs.161304	ESTs	2.59	3.06
10	444623	AI183829	Hs.202111	ESTs	2.59	2.77
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	2.58	2.01
	444542	AI161293	Hs.280380	aminopeptidase	2.58	2.31
	439549	AW937885	Hs.137314	ESTs	2.58	2.37
15	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	2.58	2.56
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.56	2.47
	433308	AA582718	Hs.291650	ESTs	2.56	2.01
	443885	H91806	Hs.15284	ESTs	2.55	1.71
	408170	AW204516	Hs.31835	ESTs	2.55	1.59
20	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.54	1.63
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.54	2.98
	428791	AA435661	Hs.264750	ESTs	2.53	2.29
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.53	3.91
	447357	AI375922	Hs.159367	ESTs	2.52	2.83
25	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	2.52	1.90
	424105	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1	2.52	3.45
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	2.52	1.98
	438698	AW297855		ESTs, Weakly similar to I38022 hypotheti	2.52	1.98
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	2.52	2.41
30	424049	AB014524	Hs.138380	KIAA0624 protein	2.51	2.19
	438543	AA810141	Hs.192182	ESTs	2.51	2.06
	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	2.51	2.14
	424806	AA382523	Hs.105689	MSTP031 protein	2.51	2.11
	438580	AA811262	Hs.299202	ESTs	2.50	1.83
35	434445	AI349306	Hs.11782	ESTs	2.50	3.13
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	2.50	1.76
	413638	H71252		gb:ys12h12.s1 Soares fetal liver spleen	2.50	2.00
	421281	AI299139	Hs.17517	ESTs	2.50	2.40
	441384	AA447849	Hs.288660	retinoic acid induced 3	2.50	2.75
40	436772	AW975688		metallothionein 1E (functional)	2.49	1.80
	433102	AI343966	Hs.158528	ESTs	2.49	2.25
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.48	2.09
	445612	N94126	Hs.12969	hypothetical protein	2.48	2.28
	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	2.48	1.87
45	433854	AA610649	Hs.333239	ESTs	2.48	2.09
	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	2.48	2.75
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.48	2.01
	440594	AW445167	Hs.126036	ESTs	2.48	1.57
	450295	AI766732	Hs.210628	ESTs	2.48	1.99
50	431316	AA502663	Hs.145037	ESTs	2.48	1.80
	438564	AA381553	Hs.198253	major histocompatibility complex, class	2.48	2.80
	439593	BE073697	Hs.124863	ESTs	2.48	1.89
	422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	2.47	3.74
	453134	AA032211	Hs.118493	ESTs	2.46	2.72
55	417169	R13550	Hs.21388	ESTs	2.46	1.88
	434411	AA632649	Hs.201372	ESTs	2.46	1.95
	440381	AA917808	Hs.190495	ESTs	2.46	2.09
	448782	AL050295		KIAA0758 protein	2.46	2.69
	404240			NM_018950:Homo sapiens major histocompat	2.45	2.83
60	450843	AI741483	Hs.205383	ESTs	2.44	2.25
	434137	AA907734	Hs.124895	ESTs	2.44	2.55
	438315	R56795	Hs.82419	ESTs	2.44	1.94
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44	1.61
	439402	W02753	Hs.103002	ESTs	2.44	1.90
65	445903	AI347487	Hs.132781	class I cytokine receptor	2.44	2.32
	437323	AA371145	Hs.194397	leptin receptor	2.44	1.70
	433923	AI823453	Hs.146625	ESTs	2.44	1.58
	442201	AW516704	Hs.208726	ESTs	2.43	1.68
	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	2.43	3.22
70	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	2.43	2.21
	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	2.43	2.13
	406973	M34996	Hs.198253	major histocompatibility complex, class	2.43	2.68
	428055	AA420564	Hs.101760	ESTs	2.42	2.05
	428970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	2.42	2.79
75	433138	AB029496	Hs.59729	semaphorin sem2	2.42	1.68
	415757	AA830854	Hs.187810	ESTs	2.42	2.02
	438507	AA809052		ESTs	2.42	2.08
	450811	AI739486	Hs.245497	ESTs	2.42	1.97
	424027	AW337575	Hs.201591	ESTs	2.42	2.76
80	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.41	3.15
	435978	AF272899	Hs.135118	Homo sapiens PR-domain zinc finger prote	2.41	2.08
	426291	U58913	Hs.169191	small inducible cytokine subfamily A (Cy	2.40	1.76
	416370	N90470	Hs.203697	CD38 antigen (p45)	2.40	1.97
	415688	AA166963		gb:zo86d01.s1 Stratagene ovarian cancer	2.40	1.63

	445633	AI453386	Hs.17287	ESTs, Weakly similar to S26689 hypotheti	2.39	1.99
	431300	AA502346		gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens	2.39	1.79
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	2.39	1.84
5	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.39	2.21
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	2.38	2.09
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.38	1.78
	437479	R61866	Hs.101277	ESTs	2.38	3.00
	445784	AI253155	Hs.146065	ESTs	2.38	1.61
10	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	2.38	2.25
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.37	1.55
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	2.37	2.41
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	2.37	1.61
	418262	Z38968		ESTs	2.37	2.05
15	420943	AI718702	Hs.279930	major histocompatibility complex, class	2.37	2.00
	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.37	2.05
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.37	1.67
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.36	1.88
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.36	2.61
20	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	2.36	2.84
	427250	R35941	Hs.25418	ESTs	2.36	2.15
	452194	AI694413		olfactory receptor, family 2, subfamily	2.36	3.41
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	2.36	3.05
	407242	M18728		gb:Human nonspecific crossreacting antig	2.35	2.34
25	418875	W19971	Hs.233459	ESTs	2.35	1.95
	425023	AW956889	Hs.154210	EDG-1 (endothelial differentiation, sph	2.35	1.85
	432608	AI492660	Hs.170935	ESTs	2.35	2.06
	408048	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2	2.35	1.91
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	2.35	2.34
30	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	2.35	2.13
	410577	X91911	Hs.64639	glioma pathogenesis-related protein	2.34	1.73
	422099	AA156022	Hs.111518	hypothetical protein	2.34	1.80
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	2.34	2.24
	427541	AI798983	Hs.82921	solute carrier family 35 (CMP-sialic aci	2.33	2.62
35	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	2.32	2.52
	431848	AI378857	Hs.271605	ESTs, Highly similar to AF175283 1 zinc	2.32	2.50
	446354	AW449650		ESTs	2.32	2.21
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.32	4.34
	423961	D13666	Hs.136348	perioslin(OSF-2os)	2.31	2.19
40	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	2.31	2.34
	457250	AA811987	Hs.125779	ESTs	2.31	1.66
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	2.31	2.96
	426839	M74782	Hs.172689	interleukin 3 receptor, alpha (low affin	2.30	2.12
	422746	NM_004484	Hs.119651	glypican 3	2.30	2.16
45	439920	H05430	Hs.288433	neurotrimin	2.30	4.06
	414942	C14898	Hs.192986	ESTs	2.30	2.02
	419092	J05581	Hs.89603	mucin 1, transmembrane	2.29	3.08
	424878	H57111	Hs.221132	ESTs	2.29	1.84
	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.29	2.76
50	411605	AW006831		ESTs	2.29	1.58
	416965	N26223	Hs.160436	ESTs	2.29	4.71
	428713	AA432067		ESTs, Moderately similar to CYA4 RAT ADE	2.29	1.73
	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	2.28	1.90
	420380	AA640891	Hs.102406	ESTs	2.28	2.82
55	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.28	1.52
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28	2.09
	447160	AA330310	Hs.24181	ESTs	2.28	1.71
	421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	2.27	1.98
	453686	AL110326	Hs.304679	ESTs, Moderately similar to Z195_HUMAN Z	2.27	1.91
60	452114	N22687	Hs.8236	ESTs	2.27	1.88
	417355	D13168	Hs.82002	endothelin receptor type B	2.26	1.63
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.26	1.84
	442262	BE170651	Hs.8700	deleted in liver cancer 1	2.26	1.86
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	2.26	1.72
65	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26	1.70
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.26	1.56
	414221	AW450979		gb:UL-H-BI3-ala-a-12-0-UL.s1 NCI_CGAP_Su	2.26	2.12
	435272	AA906415	Hs.110041	ESTs	2.25	2.15
	414991	C17898		gb:C17898 Human placenta cDNA (TFujiwara	2.24	3.58
70	424623	AW963062	Hs.270737	ESTs	2.24	1.87
	424665	AW368576	Hs.139851	caveolin 2	2.24	2.15
	422426	W79117	Hs.58559	ESTs	2.22	3.33
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.22	2.39
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.22	3.28
75	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.22	1.59
	446142	AI754693	Hs.145968	ESTs	2.22	1.88
	410503	AW975746	Hs.188662	KIAA1702 protein	2.22	1.56
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.22	2.49
	437629	AW574774	Hs.121692	ESTs	2.22	1.70
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	2.21	1.64
80	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.20	2.73
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	2.20	2.58
	429496	AA453800	Hs.192793	ESTs	2.20	2.97
	425516	BE000707	Hs.29567	ESTs	2.20	1.58

5	422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (f	2.19	1.92
	423526	AB011086	Hs.129739	KIAA0514 gene product	2.19	2.85
	436485	X59135	Hs.156110	immunoglobulin kappa constant	2.19	2.01
	426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.19	2.53
	443441	AW291196	Hs.92195	ESTs	2.18	1.73
10	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	2.18	2.53
	408705	AA312135	Hs.48967	HSPCO34 protein	2.18	1.54
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.18	1.93
	430915	AA488953		gb:aa55e05.r1 NCI_CGAP_GCB1 Homo sapiens	2.18	1.57
	418791	AA935633	Hs.194628	ESTs	2.17	2.05
15	432620	AA777749	Hs.5978	LIM domain only 7	2.17	1.75
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	2.17	2.01
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.17	3.12
	424450	AL137526		dynein intermediate chain 2	2.17	4.14
	426410	BE298446	Hs.305890	BCL2-like 1	2.16	2.19
20	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.16	1.70
	421077	AK000061	Hs.101590	hypothetical protein	2.16	1.60
	424563	AA446932	Hs.151428	ret finger protein 2	2.16	1.83
	405102			C15001220*.gil4469558[gb]AAD21311.1] (AF	2.16	1.78
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	2.15	1.87
25	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	2.15	1.65
	418067	AI127958	Hs.83393	cystatin E/M	2.15	2.40
	436372	AW972301	Hs.310286	ESTs	2.15	2.35
	418728	AW970937	Hs.293843	ESTs	2.14	2.58
	450400	AI694722	Hs.279744	ESTs	2.14	2.06
30	409031	AA376836		ESTs	2.14	2.14
	435143	R12375	Hs.194600	ESTs	2.14	1.69
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	2.14	2.03
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	2.14	1.57
	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	2.14	1.68
35	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.14	2.04
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.13	1.72
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	2.13	1.68
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.13	2.47
	452353	C18825	Hs.29191	epithelial membrane protein 2	2.12	2.31
40	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.12	2.76
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	2.12	2.11
	437581	N59284	Hs.288010	ESTs	2.12	2.85
	410976	R36207	Hs.25092	hypothetical protein MGC10744	2.12	2.04
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.12	2.00
45	423069	W15613	Hs.1613	adenosine A2a receptor	2.12	1.72
	432860	AW974077	Hs.283349	ESTs	2.12	1.75
	449509	AA001615	Hs.84561	ESTs	2.12	1.84
	456062	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	2.11	4.42
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.11	1.65
50	459680	H96982	Hs.42321	ESTs	2.11	2.20
	449677	AA002071		gb:zh85d01.s1 Soares_fetal_liver_spleen_	2.10	2.12
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	2.10	2.48
	443021	AA368546	Hs.8904	Ig superfamily protein	2.10	2.42
	437838	AI307229		ESTs	2.10	1.67
55	429421	AL031658		Human DNA sequence from clone RP1-310O13	2.10	1.91
	407202	N58172	Hs.109370	ESTs	2.10	1.68
	443669	AI140462	Hs.134587	ESTs	2.10	1.64
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	2.10	1.71
	408410	AA447438	Hs.44697	ATPase, Class V, type 10C	2.10	2.05
60	436293	AI601188	Hs.120910	ESTs	2.10	2.01
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	2.10	1.66
	427876	AI494291		ESTs	2.10	2.48
	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	2.09	3.11
	434987	AW975114		ESTs	2.09	1.69
65	433735	AA608955	Hs.109653	ESTs	2.09	1.78
	433226	AW503733	Hs.9414	KIAA1488 protein	2.09	1.62
	425787	AA363867	Hs.155029	ESTs	2.09	1.85
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.08	3.41
	442369	AI565071		ESTs	2.08	1.60
70	430478	NM_014349	Hs.241535	apolipoprotein L, 3	2.08	2.39
	434421	AI915927	Hs.34771	ESTs	2.08	1.66
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.08	1.72
	431728	NM_007351	Hs.268107	multimerin	2.08	1.51
	444929	AI685841	Hs.161354	ESTs	2.08	3.14
75	408873	AL046017		calmodulin 2 (phosphorylase kinase, delt	2.08	2.09
	437634	AW293046	Hs.255158	ESTs	2.08	1.66
	400277			Eos Control	2.08	1.46
	443601	AI078554	Hs.42658	ESTs	2.08	1.87
	432212	AW137742		ESTs	2.08	2.84
80	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	2.07	1.48
	406122			Target Exon	2.06	2.75
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	2.06	1.66
	408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-102O5 from Y	2.06	1.70
	421057	T58283		Homo sapiens cDNA: FLJ22063 fis, clone H	2.06	1.78
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.06	2.30
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	2.06	2.31
	449444	AW818436		solute carrier family 16 (monocarboxylic	2.06	1.41

	421464	AA291553	Hs.190086	ESTs	2.06	2.61
	424831	H61453		ESTs	2.06	2.12
	434542	AA769310		hypothetical protein FLJ13164	2.06	1.44
5	418323	NM_002118	Hs.1162	major histocompatibility complex, class	2.05	2.61
	418836	AI655499	Hs.161712	ESTs	2.05	1.73
	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	2.05	1.99
	400750			Target Exon	2.05	1.75
	406851	AA609784		major histocompatibility complex, class	2.05	3.94
10	414936	C14774		gb:C14774 Clontech human aorta polyA mRNA	2.05	2.41
	453459	BE047032	Hs.257789	ESTs	2.04	1.86
	443450	N66045	Hs.133529	ESTs	2.04	2.46
	430015	AW768399		ESTs	2.04	1.63
	429399	AA452244	Hs.16727	ESTs	2.04	1.51
15	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	2.04	1.73
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	2.04	1.46
	421757	Z20897	Hs.296259	paraaxonase 3	2.04	2.13
	441942	AF182645	Hs.8024	IK cytokine, down-regulator of HLA II	2.04	1.82
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	2.04	1.67
	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	2.04	3.23
20	414154	AW205314	Hs.323060	ESTs	2.03	2.96
	449987	AW079749	Hs.184719	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.03	1.59
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	2.03	2.01
	406645	M57466	Hs.814	major histocompatibility complex, class	2.03	2.49
25	414516	AI307802		ESTs, Weakly similar to T43458 hypotheti	2.02	1.56
	417032	AA192469	Hs.271838	ESTs	2.02	1.48
	414875	H42679	Hs.77522	major histocompatibility complex, class	2.02	2.79
	414522	AW518944	Hs.76325	Immunoglobulin J chain	2.02	1.84
	410511	AA743475	Hs.285655	ESTs	2.02	1.87
30	423533	NM_014339	Hs.129751	interleukin 17 receptor	2.02	2.26
	437259	AI377755	Hs.120695	ESTs	2.02	2.34
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	2.02	1.86
	426722	U53823	Hs.171952	occludin	2.02	1.57
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	2.02	1.79
35	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.02	1.97
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	2.02	2.09
	449317	AW293413	Hs.132906	19A24 protein	2.02	1.84
	439556	AI623752	Hs.163603	ESTs	2.02	1.62
	443031	AW134696	Hs.49418	ESTs	2.01	1.58
40	444838	AV651680	Hs.208558	ESTs	2.01	1.69
	453108	AI311457	Hs.99472	ESTs	2.01	1.64
	432967	AA572949	Hs.207566	ESTs	2.01	1.83
	441390	AI692560	Hs.131175	ESTs	2.01	1.63
	448076	AJ133123	Hs.20196	adenylate cyclase 9	2.01	1.80
45	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.01	2.32
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	2.01	1.90
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.01	1.90
	415443	T07353	Hs.7948	ESTs	2.00	1.54
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	2.00	2.74
50	404394			ENSP00000241075:TRRAP PROTEIN.	2.00	2.99
	459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	2.00	1.89
	437204	AL110216		ESTs, Weakly similar to I55214 salivary	2.00	1.46
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	2.00	1.37
	440667	BE076969	Hs.7337	hypothetical protein FLJ10936	2.00	1.51
55	431193	AW749505	Hs.296770	KIAA1719 protein	1.99	2.01
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	1.99	2.11
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	1.98	1.79
	417072	BE243915	Hs.81118	leukotriene A4 hydrolase	1.98	2.47
	429073	AA446167	Hs.47385	ESTs	1.98	1.92
60	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.98	2.94
	420838	AW118210	Hs.42321	ESTs	1.98	1.67
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	1.97	2.10
	430702	U56979	Hs.278568	H factor 1 (complement)	1.97	1.84
	456804	AI421645	Hs.139851	caveolin 2	1.97	1.58
65	439195	H89360		gb:yw28d08.s1 Morton Fetal Cochlea Homo	1.97	1.93
	459299	BE094291	Hs.155651	hepatocyte nuclear factor 3, beta	1.97	2.28
	413836	W92003	Hs.70614	ESTs	1.97	1.80
	400417	X72475		Target	1.97	1.75
	427814	W28383	Hs.180900	Williams-Beuren syndrome chromosome regi	1.96	1.46
70	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	1.96	2.18
	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	1.96	2.06
	455615	BE045344	Hs.274923	ESTs, Moderately similar to unnamed prot	1.96	2.21
	414572	AU077174	Hs.288181	cathepsin H	1.96	2.65
	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	1.95	1.71
75	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	1.95	2.88
	451609	AL046019	Hs.209276	ESTs	1.94	3.26
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	1.94	2.94
	430887	N66801	Hs.260287	KIAA1841 protein	1.94	1.62
	414700	H63202	Hs.38163	ESTs	1.94	1.72
80	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	1.94	1.56
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	1.93	2.22
	425252	AW391162		calreticulin	1.92	2.14
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	1.92	2.19
	425810	AI923627	Hs.31903	ESTs	1.92	1.76

	433618	AA602539	Hs.345494	ESTs	1.92	1.84
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.92	2.27
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.92	1.76
5	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	1.92	1.72
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	1.91	1.83
	426780	BE242284	Hs.172199	adenylate cyclase 7	1.91	1.67
	452386	R12499	Hs.20468	ESTs	1.91	2.64
	438670	AI275803	Hs.123428	ESTs	1.91	3.12
10	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.91	1.82
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.90	2.06
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.90	1.85
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	1.90	1.65
	428166	AA423849	Hs.79530	M5-14 protein	1.90	1.70
15	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	1.89	3.22
	449271	AW338067	Hs.7869	Homo sapiens cDNA FLJ11946 fis, clone HE	1.88	2.07
	436576	AI458213	Hs.77542	ESTs	1.88	2.25
	437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.88	2.41
	449618	AI076459	Hs.15978	KIAA1272 protein	1.88	1.63
20	430634	AI860651	Hs.26685	calcyphosine	1.88	3.01
	440663	AW452976	Hs.247112	hypothetical protein FLJ10902	1.88	1.65
	440099	AL080058	Hs.6909	DKFZP564G202 protein	1.88	1.78
	414662	AL036058	Hs.76807	major histocompatibility complex, class	1.88	2.37
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	1.87	2.07
25	414464	AI870175	Hs.13957	ESTs	1.87	2.68
	427792	M63928	Hs.180841	tumor necrosis factor receptor superfam	1.87	2.25
	415801	R24219	Hs.278443	Fc fragment of IgG, low affinity Iib, re	1.87	2.05
	430027	AB023197	Hs.227743	KIAA0980 protein	1.87	1.70
	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.87	2.18
30	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	1.86	2.87
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	1.86	2.31
	420361	N92054	Hs.194718	zinc finger protein 265	1.86	1.63
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.86	2.13
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.85	1.77
35	442434	AA995787	Hs.129583	ESTs	1.85	2.15
	422735	AA169685	Hs.119529	Niemann-Pick disease, type C2 gene	1.85	2.77
	444083	AI123195		gb:oo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.84	1.73
	449679	AI823951	Hs.129700	tolloid-like 1	1.84	1.57
40	418183	NM_001772	Hs.83731	CD33 antigen (gp67)	1.84	2.02
	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.84	1.72
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	1.84	2.47
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	1.84	2.29
	455508	AW976165		gb:EST388274 MAGE resequences, MAGN Homo	1.84	1.69
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	1.83	2.12
45	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.83	1.59
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	1.83	1.57
	417086	AA194446		ESTs, Weakly similar to S55024 nebulin,	1.83	1.45
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	1.83	2.18
	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	1.83	1.75
50	438596	AA829427	Hs.243081	ESTs	1.83	2.83
	436486	AA742221	Hs.120633	ESTs	1.82	2.14
	433365	AF026944	Hs.293797	ESTs	1.82	2.50
	449943	AF104266	Hs.24212	latrophilin	1.82	2.08
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.82	2.37
55	421563	NM_006433	Hs.105806	granulysin	1.82	2.48
	449161	N53431	Hs.47647	ESTs, Weakly similar to T00057 hypotheti	1.81	2.81
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	1.81	2.66
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.81	2.50
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	1.81	2.05
60	432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	1.80	3.13
	428677	AI657119	Hs.120036	troponin I, cardiac	1.80	2.94
	409485	S80990	Hs.252136	ficolin (collagen/fibrinogen domain-cont	1.80	2.28
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.80	1.56
	425458	H89317	Hs.182889	ESTs	1.80	2.21
65	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	1.80	1.41
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	1.80	2.20
	430570	AI417881	Hs.292464	ESTs	1.80	1.62
	439425	AF086244	Hs.114659	ESTs	1.80	2.37
	408688	AI634522	Hs.152925	KIAA1268 protein	1.80	2.13
70	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	1.80	1.80
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PNO099 son3 prot	1.79	1.57
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.79	2.18
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.79	1.68
	403421			NM_016369*:Homo sapiens claudin 18 (CLDN	1.79	2.47
75	430423	AI190548	Hs.143479	ESTs, Weakly similar to hypothetical pro	1.79	2.92
	416384	AU076903	Hs.79283	selectin P ligand	1.79	1.87
	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	1.78	1.69
	422003	AA361760	Hs.296326	ESTs	1.78	2.05
	412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140	1.77	1.82
	432987	AI864771	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	1.77	2.03
80	441602	AI655043	Hs.133456	ESTs	1.77	2.01
	458194	AW383618		ESTs, Moderately similar to ALU2_HUMAN A	1.76	2.35
	432565	AA553477	Hs.152428	ESTs	1.76	2.63
	421071	AI311238	Hs.104476	ESTs, Weakly similar to CGHU1E collagen	1.75	2.59



	408989	AW361666	Hs.49500	KIAA0746 protein	1.75	1.66
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.75	1.54
	430903			C5001632*gi10645308 gb AAG21430.1 AC00	1.75	3.20
5	421461	AW291023		ESTs, Weakly similar to A46010 X-linked	1.74	2.67
	430850	BE144152		gb:MR0-HT0165-060200-006-e02 HT0165 Homo	1.74	2.52
	424377	AF081675	Hs.146322	killer cell lectin-like receptor subfam1	1.74	2.15
	443884	N20617	Hs.194397	leptin receptor	1.74	1.51
	423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	1.74	1.63
10	448262	AW880830	Hs.186273	ESTs	1.73	2.57
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.73	1.87
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.73	2.21
	412896	AW804157	Hs.308026	major histocompatibility complex, class	1.72	2.37
	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	1.72	2.16
15	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	1.72	1.52
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	1.71	1.55
	438606	NM_014859	Hs.6336	KIAA0672 gene product	1.71	1.57
	434795	BE620794	Hs.4147	translocating chain-associating membrane	1.71	2.21
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	1.71	1.46
20	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	1.71	2.49
	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	1.71	1.57
	423857	N48902	Hs.133481	Homo sapiens mRNA; cDNA DKFZp564O0862 (f	1.71	1.56
	408393	AW015318	Hs.23165	ESTs	1.70	1.43
	432409	AA806538	Hs.130732	KIAA1575 protein	1.70	1.54
25	440817	AI341423	Hs.288433	neurotrophin	1.70	2.17
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.69	2.54
	453691	H12235	Hs.226505	ESTs	1.69	2.07
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	1.68	1.54
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.68	2.29
30	434951	AF161442	Hs.191591	Homo sapiens HSPC324 mRNA, partial cds	1.68	2.24
	444301	AK000136	Hs.10760	asporin (LRR class 1)	1.68	1.44
	407775	NM_004914	Hs.38772	RAB36, member RAS oncogene family	1.68	2.03
	437119	AI379921	Hs.177043	ESTs	1.68	4.21
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1.68	2.28
35	453498	BE181412	Hs.23245	hypothetical protein FLJ11767	1.68	2.76
	428289	M26301	Hs.2253	complement component 2	1.67	2.40
	404854			Target Exon	1.67	1.76
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	1.67	2.32
	410048	W76467	Hs.343874	proline oxidase homolog	1.67	3.03
40	407857	AI928445	Hs.92254	synaptotagmin-like 2	1.66	1.51
	447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	1.66	2.01
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	1.66	2.05
	421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	1.66	2.20
	433350	BE563152	Hs.10362	Homo sapiens cDNA: FLJ20944 fis, clone A	1.66	2.11
45	417451	AW007280	Hs.115537	putative dipeptidase	1.65	2.11
	443791	N64458	Hs.143345	ESTs	1.65	2.11
	440475	AI807671	Hs.24040	potassium channel, subfamily K, member 3	1.65	2.04
	431743	AW972642	Hs.293055	ESTs	1.64	2.64
	400328	X87344		transporter 2, ATP-binding cassette, sub	1.64	2.43
50	451876	T63141		gb:yb99a12.s1 Stratagene lung (937210) H	1.64	2.02
	417321	N68722	Hs.191368	ESTs	1.64	2.53
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.64	2.01
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.63	2.17
	432176	AW090386	Hs.112278	arrestin, beta 1	1.63	2.04
55	450708	AA376654		eukaryotic translation initiation factor	1.62	2.05
	429570	BE242256	Hs.2441	KIAA0022 gene product	1.62	1.39
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	1.62	1.57
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	1.62	1.44
	452424	AI964028	Hs.48353	ESTs	1.62	2.53
60	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	1.62	1.38
	416316	H58721	Hs.271628	ESTs	1.62	1.39
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam1	1.62	2.67
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.62	2.45
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	1.62	1.51
65	438089	W05391		nuclear receptor subfamily 1, group I, m	1.61	1.45
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.61	1.52
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.61	2.40
	444009	AI380792	Hs.135104	ESTs	1.60	2.15
	436057	AJ004832	Hs.5038	neuropathy target esterase	1.60	2.60
70	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	1.60	2.57
	433614	W07475	Hs.277101	cytochrome c oxidase subunit IV isoform	1.60	3.30
	410494	M36564	Hs.64016	protein S (alpha)	1.59	1.42
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	1.59	2.02
	446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.59	2.52
75	419918	X80700	Hs.93728	pre-B-cell leukemia transcription factor	1.59	2.04
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	1.59	1.98
	434308	N51517	Hs.47282	ESTs	1.58	2.29
	447341	AF106941	Hs.18142	arrestin, beta 2	1.58	2.09
	454315	AW373564	Hs.251928	BANP homolog, SMAR1 homolog	1.58	2.10
80	423281	AJ271684	Hs.126355	C-type (calcium dependent, carbohydrate-	1.57	1.75
	433671	AW138797	Hs.132906	19A24 protein	1.57	2.05
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	1.57	2.71
	436906	H95990	Hs.181244	major histocompatibility complex, class	1.57	2.24
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	1.57	1.43

5	406825	AI982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.57	2.37
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.56	1.61
	423329	AF054910	Hs.127111	teklin 2 (testicular)	1.56	2.51
	424909	S78187	Hs.153752	cell division cycle 25B	1.55	2.00
	431921	N46466	Hs.58879	ESTs	1.54	3.04
10	437400	AB011542	Hs.5599	EGF-like-domain, multiple 5	1.54	1.44
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfam	1.54	3.04
	415078	AA311223	Hs.283091	found in inflammatory zone 3	1.53	2.61
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.53	2.18
	401854			Target Exon	1.53	2.08
15	406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.52	1.52
	433815	AI696602	Hs.112757	ESTs	1.52	2.57
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.52	1.36
	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	1.51	1.43
	414763	U97276	Hs.77266	quiescin Q6	1.50	2.07
20	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	1.50	1.46
	412870	N22788	Hs.82407	CXC chemokine ligand 16	1.50	2.83
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.50	2.04
	432894	AW167668	Hs.279772	brain specific protein	1.50	2.25
	457941	AI004525	Hs.14587	ESTs, Weakly similar to AF151859 1 CGI-1	1.49	2.22
25	442743	AI801351	Hs.302110	ESTs, Weakly similar to MUC2_HUMAN MUCIN	1.49	2.09
	419542	AA366037	Hs.90911	solute carrier family 16 (monocarboxylic	1.49	2.40
	433124	U51712	Hs.13775	hypothetical protein SMAP31	1.49	1.39
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.49	1.39
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.48	1.76
30	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.48	1.41
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	1.48	1.44
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.47	1.31
	427872	AA835058		Human DNA sequence from clone RP1-261G23	1.47	2.50
	449853	AF006823	Hs.24040	potassium channel, subfamily K, member 3	1.47	2.21
35	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	1.47	1.50
	415149	X12451	Hs.78056	cathepsin L	1.46	1.84
	447217	BE465754	Hs.17778	neuropilin 2	1.46	1.40
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid melaph	1.46	2.16
	445672	AI907438	Hs.282862	ESTs	1.46	2.01
40	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.46	2.10
	458208	AI380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	1.46	1.60
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	1.45	1.40
	419577	L36531	Hs.91296	integrin, alpha 8	1.45	1.40
	439620	AA838727	Hs.124405	ESTs, Weakly similar to A46010 X-linked	1.45	1.57
45	423804	AW403448	Hs.16725	interferon-stimulated transcription fact	1.45	2.10
	424658	NM_002406	Hs.151513	mannosyl (alpha-1,3-)-glycoprotein beta-	1.44	2.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	1.44	1.45
	431573	AW971070	Hs.291160	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.44	1.40
	409524	AW402151	Hs.54673	tumor necrosis factor (ligand) superfami	1.43	2.01
50	406787	AW090702	Hs.240615	tubulin alpha 1	1.42	1.86
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.42	1.95
	406422			Target Exon	1.41	2.02
	421341	AJ243212		deleted in malignant brain tumors 1	1.41	1.47
	421195	BE464560	Hs.133017	ESTs	1.41	2.42
55	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	1.41	2.05
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.41	1.34
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	1.40	2.10
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.40	3.64
	411890	AW872477		gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens	1.40	3.24
60	432133	AB033088	Hs.272567	KIAA1262 protein	1.40	2.78
	428833	AI928355		ESTs	1.40	2.02
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.39	1.55
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	1.39	2.09
	427732	NM_002980	Hs.2199	secretin receptor	1.38	2.44
65	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	1.38	1.85
	407568	AA740964	Hs.62699	ESTs	1.38	3.13
	422573	AW297985	Hs.295726	integrin, alpha V(vitronectin receptor	1.38	1.38
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	1.37	1.12
	457918	AL359590	Hs.162604	hypothetical protein DKFZp762M186	1.36	2.01
70	423696	Z92546	Hs.131819	Sushi domain (SCR repeat) containing	1.36	2.54
	416700	AW498958	Hs.343475	cathepsin D (lysosomal aspartyl protease	1.36	2.04
	407244	M10014		fibrinogen, gamma polypeptide	1.36	1.29
	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	1.35	1.34
	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	1.35	2.47
75	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	1.34	1.66
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	1.34	1.92
	436982	AB018305	Hs.5378	spondin 1, (F-spondin) extracellular mat	1.34	1.86
	427507	AF240467	Hs.179152	toll-like receptor 7	1.34	2.11
	446967	AI699629	Hs.156781	ESTs	1.34	3.75
80	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.34	2.18
	456637	AW161450	Hs.109201	CGI-86 protein	1.33	1.78
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.33	1.95
	417785	X59812	Hs.82568	cytochrome P450, subfamily XXVIIA (stero	1.32	2.05
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unnamed protein	1.32	2.08
	436986	AA740983	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.32	2.06
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	1.32	2.08
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	1.31	1.29

5	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	1.30	1.25
	413474	T86312	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.30	1.92
	406659	AA663985	Hs.277477	major histocompatibility complex, class	1.30	2.22
	451049	AA013353		gb:ze28h10.s1 Soares retina N2b4HR Homo	1.30	2.12
	436494	AA720997	Hs.128295	ESTs	1.29	2.30
	438374	AA321866	Hs.6193	hypothetical protein FLJ14590	1.28	2.34
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	1.28	2.39
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.28	1.69
10	428458	AA428820	Hs.251399	neurogranin (protein kinase C substrate,	1.27	2.00
	443180	R15875	Hs.258576	claudin 12	1.26	1.25
	421764	AI681535	Hs.148135	serine/threonine kinase 33	1.26	2.01
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.26	1.21
	433283	BE041135	Hs.175622	ESTs	1.24	3.05
15	426759	AI590401	Hs.21213	ESTs	1.23	1.20
	436446	AW016809	Hs.119021	ESTs	1.23	1.20
	421467	AA291590	Hs.97252	ESTs	1.22	1.54
	431353	AA828032		ESTs	1.22	3.00
	427403	AA402107	Hs.257146	ESTs, Moderately similar to I38022 hypot	1.22	1.91
20	453037	AA045175	Hs.17914	ESTs	1.22	2.40
	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.22	2.26
	439941	AI392640	Hs.18272	amino acid transporter system A1	1.22	1.22
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	1.21	1.49
	400496			ENSP00000224716*:GTP-binding protein SAR	1.20	1.25
25	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	1.20	1.44
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.19	2.06
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.18	2.02
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2B (p1	1.17	1.14
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	1.14	1.16
	440555	D31292	Hs.6853	hypothetical protein FLJ22167	1.14	2.19
30	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.13	1.12
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.12	2.43
	432798	AA565309	Hs.194015	ESTs	1.10	2.23
	411274	NM_002776	Hs.69423	kallikrein 10	1.10	1.09
35	438856	N40027	Hs.7473	ESTs	1.09	1.52
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	1.09	1.07
	448253	H25899	Hs.201591	ESTs	1.08	2.10
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.08	2.08
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.06	1.58
40	449321	AA001150	Hs.132937	ESTs	1.06	2.06
	418693	AI750878	Hs.87409	thrombospondin 1	1.06	1.02
	402333			Target Exon	1.03	1.03
	421814	L12350	Hs.108623	thrombospondin 2	1.02	1.02
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	2.36
45	458158	AW296778	Hs.144734	Human DNA sequence from clone RP3-416F21	1.00	2.73
	406517			nel (chicken)-like 2	1.00	2.07
	442526	AW277221		ESTs	1.00	2.21
	446164	AW273539		hypothetical protein FLJ23577	1.00	2.52
	449122	AI631310	Hs.196955	ESTs	1.00	2.23
50	438038	AI732629		ESTs, Weakly similar to TA2R HUMAN, BETA	1.00	2.04
	429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	1.00	2.02
	453672	U73531	Hs.34526	G protein-coupled receptor	1.00	2.57
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	1.00	2.64
	438909	AF085839		gb:Homo sapiens full length insert cDNA	1.00	2.23
55	423609	AA328348	Hs.218289	ESTs	1.00	2.19
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	1.00	2.28
	436284	AA708016	Hs.190389	ESTs	1.00	2.22
	440932	AI801509	Hs.182080	ESTs	1.00	1.66
	403420			Target Exon	1.00	1.86
60	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	1.00	2.02
	425916	NM_006786	Hs.162200	urotensin 2	1.00	2.11
	419721	NM_001650		aquaporin 4	1.00	2.26
	421761	AL120297	Hs.108043	Friend leukemia virus integration 1	1.00	1.86
	425781	AF001622	Hs.159523	class-I MHC-restricted T cell associated	1.00	1.96
65	415094	D59513	Hs.330778	ESTs	1.00	2.32
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	2.26
	420727	H75701	Hs.99886	complement component 4-binding protein,	1.00	1.84
	430049	AW277085	Hs.99619	ESTs	1.00	1.87
	446868	AV660737		ESTs	1.00	1.79
70	418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	1.00	1.44
	436391	AJ227892	Hs.146274	ESTs	1.00	1.30
	413059	BE151498		gb:RCO-HT0295-291199-031-E11 HT0295 Homo	1.00	1.42
	427739	AW196755	Hs.98105	NYD-SP14 protein	1.00	2.41
	452788	AW294571	Hs.136040	ESTs	1.00	2.23

TABLE 32B:

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826

5	421798	3042_4	BC017829 AW276646 AI984209 AA663933 AA634104 AA551528 AA634041 AA298038 BG483990 T89297 BF853958 H64685 T90329 T60644 T57747 BF852694 T92529 BG482852 BF883064 BF883066 N74880 AA829796 N90716
	400269	2726_1	X65018 BC022318 NM_003019 BE465060 AI732255 BF446634 AI820677 AI002217 AI924488 BI821373 BI770406 BI823937 BI820265 BI489632 BG482911 AA617783 AI807697 AW205576 T94427 AA487101 T94513 BI819407 BI822450 BI820618 BI824619 BG542824 BG537862
10	432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	432810	101919_1	BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017 AI286003 AI147163 AA626033 AI539156 AA565542 AI094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 AI991439 R46187 BE929954 AA333976 D63102 BF744491
15	418259	133853_1	BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI934445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240
	429228	215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633
20	459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	422667	224778_1	AI758223 AW469334 BF940841 AW080348 AI270363 AI055892 BE464168 BF431797 BE350144 BF448739 AI693409 BF432999 D62848 AA398070 AI383375 AW611490
25	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	430709	1234627_1	AW969880 AA484613 AA501874 R34356
30	450726	666520_1	AI732297 AW204600 T95017
	442048	750422_1	AW340495 AI984319 AA974603
35	406685	0_0	M18728
	440028	598730_1	AW473675 AI190744 W69997 AW104913 AI221098 W69996 AA885487 AA861491
40	437866	34267_1	U52054 AL581000 AA156850 AW293839 BI335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161 BM194134 AW966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF446960 AA837481 AV755539 AW468444 AW468002 AA811830 AA581806 AI866686 AI572124 AA687333 D20160 AA7812489 AU185248 AU186004 AA156781 AI536733 BM144850 AI471883 AA040926 BF507639 AA043777 AW874142 BE832523 BE163972 BI022546 BI021204 AI000341 AI766341 AW873274
	458332	1139685_1	AA602964 AA609200
45	407192	2200202_1	AI884781 AI652306 AI651694 AI638744 AI962493
	449328	3030726_1	AA534222 AA632632 T81234
50	432340	1619980_1	AF119847 AA437261 AA436987 AI132965
	434194	62680_1	AK001125 AU120581 AU146612 AW301393
55	436198	28727_1	AA876138 AI239602 AI698953
	440248	2616908_1	AW975183 AA973583 AI365103 AI699495 AI301787
60	442006	1239046_1	AK024965 AU158033 AA978370 R79120 BE327015 AA779740 R79121
	438177	9337_12	AW972063 AA668764 AA804491 AW665688 AA765069
65	435154	126605_1	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356
	423387	2612_2	AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138 AV645808 AA701657 AW271273 AI796734 AI472316 AI017531 AI061178 BF109096 AA548964 N83805 AA131648 AA156589 BE708349 AW952494 D30877 AV684717 Z24837 F00167 BF576150 T63841 R78995 N87474
70	444314	1027984_1	AW749625 AW749626 AW749644 AI140497
	443951	MH1768_18	AI334106 R63583 AI028079 AI140098 AI911625 AI890637 F34815 T65959 N40935 W52768 AA854747 AA861945 AA878472 AA778270 W32249
75	432639	1237887_1	AA026061 W52662 W15352 W79670 W95384 T94283 AA002155 R82052 BE825493 BE825520
	438698	598828_1	AW973785 H60163 AA557608
80	413638	1525406_1	AW975851 AI911033 AI540093 AA932284 AW297855 AA829228 AA814442 AW105017
	436772	1239464_1	H71252 BE154642 BE154668
85	448782	34980_1	AA156151 Z25109 C05177 AW975688 AA731063 N67084
			AB018301 AL050295 BF513128 AW385080 AL551708 AI352542 AI829703 AI819388 AW629019 AW073189 AW273857 AW118768 AI453845 AI452494 AA886341 AI057144 AA904647 AI423547 AW263913 AI094774 AI434419 AI039546 AI002491 AI240412 Z25099 AA995178 AW050649 AW026140 AI796309 AI584012 BE166666 AI767991 AI309041 AA724059 AI695284 AI245095 T63971 Z40627 BE166681 BG570071 BF921915 BI562702 BG506502 AV658066 R48378 AA121543 AI096938 AA618131 H40993 R48277 AI352281 BG540263 BG538901 N95226 AI356752 AI221152 Z28777 R16574 AW966449 AA044116 AW797518 BI010405 AA044288 AI093508 BE140169 T64039 BG433106 AW130367 AW130361 N73937 AA127680 AW044037 AI096437 AA384077 BF941499 T93764 BG003285
90	438507	2729_4	BG698329 AI417878 AI080171 AI190332 AI092344 AI357100 AA744522 AA412653 AA977007 BF438628 AA743264 AA365279 AW073197 BI493198 AA169355 BI493197 AI283051 BF436642 AA809052 AI833263
	415688	1235745_1	AW971218 AA493942 AA166963
95	431300	1529181_1	BE159863 AA502346 AU186097 R86267 H71358
	418262	5824_2	AK055180 AA490810 AI420925 AI473832 AA127397 AA127409 AW820078 AI214567 AA876961 AA283985 AI904240 D20426 BC015835 N28408 Z42826 AI927925 AW590850 AW195543 AI675823 W84675 AA767204 AW207335 AI051690 AI434786 AI051699 AW139875 BF195790 AI250256 AI767042 AI521899 AA829382 AA526451 AI971192 R08173 N20059 AA215409 Z38968 H13200 H01182 R82482 AW972928 BF242637 H01273 H13567 R82532
100	452194	90339_1	AI694413 AW994700 AI912946 N73548 AI082035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043 AI709339
	446354	831448_1	AI701583 AI291038 AW449650
105	406687	0_0	M31126
	411605	10026_3	BG256892 H10532 N46614 R52610 AW977696 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09686 BI838226 BF034269 AA429173 BE741829 AW867495 AI123683 AW006831 BE831162 AW452753 AV742717 W86152 BF115102 AI633815 BF921562 AA094230 BE092587 W86151 AA526153 AI672156 BF914496 R12579 BF852352 AA699780 T57386 BF903022 R09933 AA678298
110	428713	21322_7	AA432067 AW572442
	414221	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
115	414991	1785136_1	D78831 C17898 D78863
	447197	2176805_1	R36075 R36167 AI366546
120	430915	197844_1	BG425760 BF997600 N48516 W73454 BF816344 BF997601 AA488953
	424450	1674_1	NM_023036 AJ295276 AF250288 AL137526 AW517074 AI870459 AI215420
125	409031	9531_1	BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258

			AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798 BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 BI496876 AI264159 BM128481 AI624657 AI689301 AI969467 AA861685 AA251595 AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302 BE883520 BI057842 AA215702 AA215703 AA368006 BE006876 BE066555 AA002232 T99209 AA002071 AI308202 AI307229 AA769348 AW341668 AI201382 AW104364 AA648367 AA897604 AW977914 AA811957 AI352198 AL040620 BG427950 AA826016 AI903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823 AI494291 AI582807 AA417018 AA608841 AW975114 AI096634 AI767001 AA658364 AW517542 AA993566 AI521958 AI565071 AI864217 AL046017 AW504804 AA532433 AI634701 AI126421 AW151275 AA620782 AA933047 AI828223 AI624555 AI624489 AV749032 BI495751 AI672286 AA342944 AV748076 AV747586 AA058597 H56073 W87367 R71630 H84499 AI866297 D25918 AV746788 N78995 H63752 H82985 R46600 BE786692 R71128 AA608909 R29728 BG534018 Y00281 NM_002950 BC010839 BC007995 BG675232 BM468552 AI555484 BG831516 BF035300 BG677277 BF852972 BE314901 BF850656 AI371816 AA292474 AA375747 AA308414 BM454544 BI333370 BM049921 BI461428 BI465007 BI223401 BE856245 AW821164 BF914775 BF914761 AU125835 BI222678 BI091137 BF340536 BM462798 BI224452 BG707915 AL569160 AA443815 AW572867 AW363410 BF739268 BG010283 BI013120 BF818845 BF763468 AA305165 AI630370 AA039826 R24906 H02046 T96891 BF981330 AW936510 AA478169 H04587 BG166574 BI869342 BE562482 BE539637 AA165089 AL579118 AI553699 BE044054 AW117440 AI520674 BF435417 AW245648 AI952404 T29534 AU153459 AU152168 AW591591 AU146918 AI933187 AA478013 AU148143 AI224471 AI640728 AI871537 AW264752 N83787 AI189357 AV756134 AI471659 AU147466 AA779206 AU149419 AU149104 AU159135 AA312221 AW445119 AW021912 AI799771 F04407 AI285530 AI914643 AW068751 AA513325 AA164627 AA639285 AA569644 T96892 AI923594 BF439180 BI770936 BF032438 AU154884 AA682793 AW072992 AU158815 AI884444 AL048031 AU158922 AU152546 AI695187 AL048033 AI245650 AU148507 AW467451 BE536868 BF913001 BF062707 AL573082 AW067993 AA523354 BE86727 AI890705 AU159092 AI982693 AI817553 AA236729 AI687858 BG163767 AI524675 AI678155 AA127100 AI762661 AU159718 AI469720 AA483627 AW131696 R26868 AI199885 AW875614 AW938694 AW578974 BI763988 BG819168 BE874767 BG978292 BE162948 AL555483 AW189719 T56783 AI018819 AI476552 BI492837 AI824440 BG996262 AA932887 AI380726 R79530 AA622108 AI262575 T56782 R27437 BE784153 AW129549 AI675567 AI866759 BG987935 AW972351 AW182936 AI478370 AA528309 BG997292 AW137742 AI632006 AA775020 AA961625 W86628 BF112014 AI275423 AI680786 BE222349 AA830545 BF224127 H99396 N81017 N81016 AI525205 T58283 U59185 NM_004696 AV734324 AI245349 AA369517 H88760 D79128 AA970406 H01059 H88761 H03446 BG620383 AU135008 AU136895 AU158158 AU155762 R73608 R65751 R23756 N74630 AW078687 BE439761 BE786351 R68994 BE785867 AW297502 AW297553 BG431545 AW814843 BF382644 BG429539 BE929862 BF811258 H61453 AA838765 AI693104 AA721107 AF392454 AK023074 AI884890 AI814455 AW966220 BF736545 AA026021 AA286843 AA251918 BG197710 AA026294 AA337356 BC010422 AK023226 NM_022776 BM459496 AA769310 AI826460 AU153650 AU160375 AW166211 AW292992 BF433338 AI823888 AI684798 AI655985 AW770982 AI400454 AI276257 AA639510 AI689818 AW772604 AA807639 AU130298 AU132028 BF900889 BF904822 AY007102 AU143256 BG621460 AA829630 AI864665 AI084922 AA025234 AI360060 AA766554 AA026295 AA825817 AA251762 BE180751 BM464530 AV715833 AA779447 AI452519 AW418525 AA435643 D25894 AA435651 AA286844 N64369 AI702262 BG288063 BE170545 BM466232 BE299160 AA169573 AL567428 BF217285 BE967276 AA609784 R97304 C14774 C17911 D79033 BC017171 BC012195 NM_007126 AF100752 AI137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AI531791 AI435581 BF793112 AI577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BF759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA843319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60656 AK057782 AI146454 BG703115 AI765980 AI948611 AA889263 AA947457 BG547193 H11947 Z38147 F10426 BF447329 H11946 T74968 F06195 BG548563 AI004988 AA148735 AI307802 AI439791 BE041453 AI984904 AA148734 F12823 BG623239 N58315 AI524952 AL110216 AI816283 AI688476 AA928351 AW157672 AI288740 BE468242 AI452476 AI291665 AW192364 BE503635 AW592672 AA857393 AW162770 AI680660 AI879565 AI347717 BF880800 AI266646 AA834381 AI291667 AI264567 Z38449 T03352 AI929432 BE673697 AI124770 AI350389 AA910378 R54042 AV746670 AW089037 AV729218 H28971 R38549 AI692560 BE671562 BE669916 BE672206 BF445152 BF445151 AI914323 AI684406 AA932348 BE670597 AA932080 AF086037 H89360 H89546 AW182329 AA613792 T05304 AW858385 AK056513 AL553942 AL553941 BG924307 BE879339 AA576941 BG054674 BF431361 BE467806 BF445874 BE138798 AA425029 BF084265 BE814324 BM466426 BE819467 AW594593 AA341536 AI823511 BI792998 AW296213 AW800506 AW378236 BE819553 AW341342 BE146513 BE146525 BE146515 AW295699 BE146518 BE146516 BF349828 AL520587 AW803944 BE931092 BF375188 BG676709 BF832746 BG696737 AW391179 AI582980 AW582217 AW814484 BE672215 AW391162 AW814336 AW814302 AW814444 AL520586 AI333134 AI378333 AW243412 BE350482 AI628661 AI925481 AI246159 AW593633 AI273558 AI494388 AA806280 AW005606 BE048135 AW341024 AA969419 AA912778 AA621100 AA479920 AI867584 AI290391 BE348490 BF340755 AI225038 AI867592 BG113588 AI656808 AW196841 BF087184 AA335354 AW957546 BF340833 BF037221 BE146523 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445 AW978796 AA767373 AW173343 AA836163 N27563 AA905328 R97032
5			
10	418304	1093209_1	
	449677	79505_1	
	437838	2512601_1	
	429421	117617_1	
15	410730	114639_1	
	427876	1373914_1	
	434987	121985_1	
	442369	2691713_1	
	408873	105337_1	
20			
	400277	170_1	
25			
30			
35	432212	629625_1	
	421057	265006_1	
	449444	2735_1	
40	424831	1272834_1	
	434542	11990_1	
45			
	406851	0_0	
	414936	1782849_1	
	430015	713_2	
50			
55			
60	431843	445334_1	
	414516	60847_1	
65	459557	859794_1	
	437204	28243_1	
70	439195	21979_1	
	433891	647290_1	
	425252	38271_1	
75			
80	409745	MH1944_5	
	437751	643238_1	

444083	10908_12	B1836699 A1123195
455508	1239880_1	AW976165 C04000
417086	1154_2	AK056605 AK056969 AW380724 AA195950 F21243 Z17422 AA176595 AA176955 AA194350 BC005933 BC017866 AA196396 Z24810 AA181361 AA193115 AA086465 F25194 F30130 AA180013 AJ346143 F20589 F20620 F29371 F32439 F25153 F32146 F26110 F28506 F25307 F27533 F20375 F32370 AA653078 BF574897 Z24852 F00172 T30560 AW449825 AI620346 BG986374 BE706521 C02691 AL596834 F31902 F26078 AA670099 BF475555 F30818 F37524 AJ346558 F28050 F17933 F31637 C03413 AI092152 AA180743 AA085730 F21998 F20854 F18944 F31180 F37937 F37738 AA193162 Z17344 AA192546
409208	10117_2	AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372 AA989341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF881946
440638	371165_1	BC009500 AI376551 AA897445 T87714
458194	506272_1	AI692525 AW005307 AW383618 AI689861 AI342712 AA906899
421461	128918_1	AA291529 AI629027 AI890447 AA677465 BF001179 AI301102 AW452003 AA704419 AA706883 T68871 AW291023
430850	296806_1	BE144152 AA487799 BF916865 AA937952
400328		
451876	2328579_1	T63141 AI821021 BF370092 BF370127 BF370060 T62998
450708	12745_1	AK055196 AW952031 AI694545 AI742403 AW874431 AW204731 AI887383 BE220997 AA011287 AA115112 AI306385 AW571707 BF433009 AW197042 AI367086 H23002 H11743 R37085 Z39208 AI002267 H10206 T23948 W74801 R51633 R37677 R59986 H10833 BG012000 R13817 H22794 Z43122 H10257 BG984543 H10875 BG984542 AA318232 BF849799 W76367 AA376654 R18795 AA114979 AA303838 AW139819
452203	2630_1	AI674165 AI686172 W94102 R67170 H11820 BG015023
		BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556892 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470
		BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AI571889
		AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377
		AL154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222
		BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198
		AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054
		AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927
		H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
		BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA089472 AV654440
		AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664
		H91240 R60548 N41701
		BI826340 BI868674 R12615 AW887767 BF439409 AI424995 BG059893 AA417003 AI220270 AA418740 AI190974 Z39070 AA742556 AA835058
		AA694436 R20520 AA418795 BG460307 BI560147
		AI990640 AI380016 BM273298 BM273060
		NM_007329 AF159456 AJ243212 AJ297935 AA295769 NM_017579 AJ243224 AI492875 AI796676 AI749838 AA918144 AI814590 AI923531
		BF513992 AI720725 AI150879 AI279072 AW612904 AI492104 AI284510 AI141231 AA613554 AW662148 AW769047 AA565985 AW612888
		AU100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569 T89953 BE934311
		BE088101 T05990 AW872477
		AI928355 AI709178 AA436447 AI431274 BF946000
		BE091833 BE091874 BE091871
		W92422 AA013353
		AW977507 AA503803 AA767137 AA828032 AA828033
		AA019761 AA017656 AA017374
		AF150283 AW182000 AW277221 AV735848
		AK026817 AI559708 AW273539 AW892986
		AI732629 AI732831 AA776249
		AF085839 R69254 R69137 AW188788
		AW971240 AA493723 AA493843
		AK026728 AL138136 BF059437 AI657037 AL600872 C15206 C14676 AA001003 AL157562 BG706081 H24162 BF841047 H15952 Z45355
		AL157565 AV721762 AW953127 AA324171 BF476417 R52508 N54211 R46734 BG485659 BF810747 BE766227 AL538364 R19964 T15657
		AW197333 R16235 R40826 BG152309 AV729035 R45066 AA016969 BE504976 BF593783 N51085 R61284 BE702264 AI216994 Z41068 N72577
		R37645 AW237014 AW197630 AI359402 AA707906 AL119885 H23480 T16037 AI950756 T62597 T91664 R40195 D60186 H23014 T89715 H05749
		H24054 AA001565 H15041 C15205 D59987 R13787 R61283 H23479 H07874 R14070 R52555 R21139 H05856 AA348655 AL120460 T62525
		AV725241 AA046875 AI361912 H13341 BG150488 AL119338 Z42792 F05895 H07966 F06492 R59866 D31594 H09436 R35726 BI917845
		BG704196 BF735198 AL036526 BG569879 AW195713 R59867 AA016968 H09087 BE841173 AW893631
		AK074473 BC017997 BI831060 BF971101 AI886394 AI082824 AV708785 W86073 W07772 AV660737 AI816793 R52250 BG183529 AA633473
		AI191256 R44763 R19947 BF571346 W86257
		BE063078 BE151503 BE151498

TABLE 32C:

65

Pkey:

Ref:

Strand:

Nt\_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

70

Pkey

Ref

Strand

Nt\_position

400880

9931121

Plus

29235-29336,36363-36580

402474

7547175

Minus

53526-53628,55755-55920,57530-57757

406387

9256180

Plus

116229-116371,117512-117651

404277

1834458

Minus

91665-91946

75

402674

8077108

Minus

39290-39502

404240

5002624

Minus

116132-116407,116653-116922

405102

8076881

Minus

120922-121296

406122

9144087

Minus

30940-31386

400750

8119067

Plus

198991-199168,199316-199548

80

404394

3135305

Minus

37121-37205,37491-37762,41053-41140,4132

403421

9665041

Minus

126609-126773,139986-140205

403903

7710671

Minus

101165-102597

404854

7143420

Plus

14260-14537

401854	7770538	Plus	151483-151637,151902-152008,152146-15231
406422	9256411	Plus	163003-163311
400496	9743564	Plus	41515-41695
402333	8844110	Minus	165693-165856
406517	7711431	Plus	7151-7402
403420	9664969	Plus	159835-159938

10 TABLE 33A: About 800 genes upregulated in lung fibrosis relative to normal lung

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: 90th percentile of lung fibrosis Als divided by 90th percentile of normal lung Als, where the minimum value for the numerator and denominator was set to 50

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
20	406964	M21305		FGENES predicted novel secreted protein	16.10
	431089	BE041395		ESTs, Weakly similar to unknown protein	12.38
	421110	AJ250717	Hs.1355	cathepsin E	11.86
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	11.62
25	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.90
	444381	BE387335	Hs.283713	hypothetical protein BC014245	8.58
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	8.26
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	8.24
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.72
	408380	AF123050	Hs.44532	diubiquitin	7.24
30	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	7.15
	456034	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCI_CGAP_Su	7.12
	453355	AW295374	Hs.31412	myopodin	6.96
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.83
35	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	6.72
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	6.72
	438089	W05391		nuclear receptor subfamily 1, group I, m	6.62
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56
	421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46
40	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	6.32
	439195	H89360		gb:yyw28d08.s1 Morton Fetal Cochlea Homo	6.29
	444301	AK000136	Hs.10760	asporin (LRR class 1)	6.28
	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	6.13
	423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	6.11
45	430702	U56979	Hs.278568	H factor 1 (complement)	6.10
	424878	H57111	Hs.221132	ESTs	6.00
	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	6.00
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	5.94
	408491	AI088063	Hs.7882	ESTs	5.94
50	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	5.92
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	5.92
	407857	AI928445	Hs.92254	synaptotagmin-like 2	5.90
	433230	AW136134	Hs.220277	ESTs	5.86
55	412719	AW016610	Hs.816	ESTs	5.86
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.82
	426759	AI590401	Hs.21213	ESTs	5.72
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.72
	421814	L12350	Hs.108623	thrombospondin 2	5.71
	430887	N66801	Hs.260287	KIAA1841 protein	5.70
60	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	5.62
	436954	AA740151	Hs.130425	ESTs	5.58
	411573	AB029000	Hs.70823	KIAA1077 protein	5.55
	432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	5.38
	410606	AW418779	Hs.114889	ESTs	5.38
65	410800	BE280421	Hs.94499	ESTs	5.32
	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	5.28
	406687	M31126		matrix metalloproteinase 11 (stromelysin	5.26
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	5.22
	412622	AW664708	Hs.171959	ESTs	5.22
70	439941	AI392640	Hs.18272	amino acid transporter system A1	5.18
	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	5.15
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	5.13
	425177	AF127577	Hs.155017	nuclear receptor interacting protein 1	5.12
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	5.11
75	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04
	452239	AW379378		protein tyrosine phosphatase, receptor t	4.97
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	4.96
	443884	N20617	Hs.194397	leptin receptor	4.94
	444040	AF204231	Hs.182982	golgin-67	4.94
80	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	4.93
	440687	AL080222	Hs.7358	hypothetical protein FLJ13110	4.92
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	4.92
	432435	BE218886	Hs.282070	ESTs	4.92

	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	4.90
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	4.90
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.90
5	415992	C05837	Hs.145807	hypothetical protein FLJ13593	4.82
	430027	AB023197	Hs.227743	KIAA0980 protein	4.78
	408393	AW015318	Hs.23165	ESTs	4.76
	449509	AA001615	Hs.84561	ESTs	4.72
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	4.72
10	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	4.72
	433226	AW503733	Hs.9414	KIAA1488 protein	4.68
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	4.68
	442994	AI026718	Hs.16954	ESTs	4.66
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	4.66
15	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.66
	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	4.65
	433586	T85301		gb:yd78d06.s1 Soares fetal liver spleen	4.64
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	4.64
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	4.64
20	418113	AI272141	Hs.83484	SRV (sex determining region Y)-box 4	4.62
	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	4.62
	450086	AW016343	Hs.233301	ESTs	4.61
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	4.60
25	442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	4.59
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.58
	418259	AA215404		ESTs	4.54
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.54
	432810	AA863400		ESTs	4.54
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.53
30	436100	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	4.52
	412652	AI801777		ESTs	4.52
	438899	AF085833	Hs.135624	ESTs	4.52
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	4.52
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	4.52
35	443324	R44013	Hs.164225	ESTs	4.51
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	4.51
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.51
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	4.50
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	4.50
40	436865	AW880358	Hs.339808	hypothetical protein FLJ10120	4.46
	452561	AI692181	Hs.49169	KIAA1634 protein	4.46
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	4.45
	442048	AA974603		gb:op34f05.s1 Soares_NFL_T_GBC_S1 Homo s	4.44
	436120	AI248193	Hs.119860	ESTs	4.44
45	423575	C18863	Hs.163443	intron of periostin (OSF-2os)	4.44
	429697	AW296451	Hs.24605	ESTs	4.44
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	4.43
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	4.43
	414462	BE622743	Hs.301064	araplatin 1	4.42
50	428698	AA852773	Hs.334838	KIAA1866 protein	4.42
	420838	AW118210	Hs.42321	ESTs	4.41
	458584	AF217518	Hs.8360	PTD012 protein	4.40
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	4.40
	400076			Eos Control	4.38
55	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	4.38
	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (f	4.36
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.36
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.36
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.34
60	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	4.34
	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	4.33
	409342	AI077058	Hs.54089	BRCA1 associated RING domain 1	4.33
	429228	AI553633		ESTs	4.32
	426458	D83032	Hs.169984	nuclear protein	4.30
65	408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30
	432476	T94344	Hs.326263	ESTs	4.29
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.28
	436446	AW016809	Hs.119021	ESTs	4.27
	439556	AI623752	Hs.163603	ESTs	4.26
70	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-li	4.26
	428411	AW291464	Hs.10338	ESTs	4.26
	434936	AI285970	Hs.183817	ESTs	4.23
	413048	M93221	Hs.75182	mannose receptor, C type 1	4.23
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.22
75	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	4.22
	409977	AW805510	Hs.97056	hypothetical protein FLJ21634	4.22
	441297	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.21
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	4.20
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	4.20
80	423578	AW960454	Hs.222830	ESTs	4.20
	446608	N75217	Hs.257846	ESTs	4.20
	424238	AA337401	Hs.137635	ESTs	4.19
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	4.18
	420674	NM_000055	Hs.1327	butyrylcholinesterase	4.18



	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.18
	439593	BE073597	Hs.124863	ESTs	4.17
	442369	AI565071		ESTs	4.16
5	445885	AI734009	Hs.127699	KIAA1603 protein	4.16
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.16
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	4.16
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	4.15
	407347	AA829847		gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens	4.14
10	409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.13
	430168	AW968343	Hs.145582	DKFZP434I1735 protein	4.12
	451184	T87943		transcription factor 7-like 2 (T-cell sp	4.12
	426174	AA547959	Hs.115838	ESTs	4.12
	431562	AI884334	Hs.11637	ESTs	4.12
15	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.12
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.12
	449437	AI702038	Hs.100057	Homo sapiens cDNA: FLJ22902 fis, clone K	4.12
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homolog	4.10
	444020	R92962	Hs.35052	ESTs	4.10
20	439424	AI478667	Hs.118183	hypothetical protein FLJ22833	4.10
	416987	D86957	Hs.80712	KIAA0202 protein	4.10
	457121	AI743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	4.09
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	4.09
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.08
25	431193	AW749505	Hs.296770	KIAA1719 protein	4.08
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	4.08
	433308	AA582718	Hs.291650	ESTs	4.08
	445756	AA290690	Hs.300776	ESTs	4.08
	431745	AW972448	Hs.163425	ESTs	4.08
30	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	4.07
	440099	AL080058	Hs.6909	DKFZP564G202 protein	4.06
	439398	AA284267	Hs.221504	ESTs	4.06
	432731	R31178	Hs.287820	fibronectin 1	4.06
	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	4.05
35	433626	AF078859	Hs.86347	hypothetical protein	4.05
	428055	AA420564	Hs.101760	ESTs	4.04
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04
	413243	AA769266	Hs.193657	ESTs	4.02
	431214	AA294921	Hs.348024	v-rat simian leukemia viral oncogene hom	4.02
40	453753	BE252983	Hs.35086	ubiquitin specific protease 1	4.02
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	4.02
	434404	AW445034	Hs.256578	ESTs	4.02
	407604	AW191962		collagen, type VIII, alpha 2	4.02
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	4.02
45	436772	AW975688		metallothionein 1E (functional)	4.00
	443257	AI334040	Hs.11614	HSPC065 protein	4.00
	450187	AA736788	Hs.78521	KIAA1717 protein	3.98
	433913	AI694106	Hs.72325	ESTs, Weakly similar to I38022 hypotheti	3.98
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	3.98
50	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	3.98
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.98
	426818	AA554827	Hs.292996	DKFZp434A0131 protein	3.98
	440118	AB040893	Hs.6968	KIAA1460 protein	3.98
	413836	W92003	Hs.70614	ESTs	3.97
55	442647	AL038436	Hs.31388	ESTs	3.96
	449188	AW072939	Hs.347187	myotubularin related protein 1	3.96
	450656	AA010539	Hs.18912	ESTs	3.96
	410817	AI262789	Hs.93659	protein disulfide isomerase related prot	3.94
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.94
60	408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypotheti	3.94
	407879	AA045464	Hs.6557	zinc finger protein 161	3.93
	438146	Z36842	Hs.57548	ESTs	3.93
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.93
	429355	AW973253	Hs.292689	ESTs	3.92
65	437210	AA311443	Hs.293563	Homo sapiens mRNA; cDNA DKFZp586E2317 (f	3.92
	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	3.92
	452416	AA026115	Hs.114777	ESTs	3.92
	413873	AI310151	Hs.173524	ESTs	3.91
	400196			Eos Control	3.91
70	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.90
	453204	R10799	Hs.191990	ESTs	3.90
	454076	AW204712	Hs.61957	ESTs	3.90
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.90
	437158	AW090198		KIAA1150 protein	3.90
	443970	AI280341	Hs.166571	ESTs	3.90
75	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	3.90
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.90
	444057	AA316896	Hs.257267	FYVE and coiled-coil domain containing 1	3.89
	411495	AP000693	Hs.70359	KIAA0136 protein	3.88
80	438452	AI220911	Hs.288959	hypothetical protein FLJ20920	3.88
	410297	AA148710		lumican	3.88
	427698	AW972594	Hs.335499	ESTs	3.88
	436769	AA748675		ESTs	3.86
	417819	AI253112	Hs.133540	ESTs	3.86

5	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ly	3.86
	425838	NM_014071	Hs.159613	nuclear receptor coactivator RAP250; per	3.86
	422173	BE385828	Hs.250619	phorbol-in-like protein MDS019 (CEM15)	3.86
	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109260A B cell	3.85
	445693	AW800444	Hs.76507	LPS-induced TNF-alpha factor	3.85
10	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	3.85
	412636	NM_004415		desmoplakin (DPI, DPII)	3.84
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	3.84
	418876	AA740616		gb:ny97f11.1.s1 NCL_CGAP_GCB1 Homo sapiens	3.84
	436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypotheti	3.84
15	430317	AB020645	Hs.239189	glutaminase	3.84
	442806	AW294522	Hs.149991	ESTs	3.84
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.82
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	3.82
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	3.82
20	430573	AA744550	Hs.136345	ESTs	3.82
	453394	AW960474	Hs.40289	ESTs	3.81
	431266	AW149321	Hs.105411	ESTs	3.80
	434987	AW975114		ESTs	3.80
	452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	3.79
25	435176	AA744875	Hs.189413	ESTs	3.78
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	3.77
	430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo	3.77
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.76
	441989	AA306207	Hs.286241	protein kinase, cAMP-dependent, regulato	3.76
30	417228	AL134324	Hs.7312	ESTs	3.76
	418546	AA224827		gb:nc32g04.s1 NCL_CGAP_Pr2 Homo sapiens	3.76
	450779	AW204145	Hs.156044	ESTs	3.75
	412408	D51103	Hs.73851	ATP synthase, H transporting, mitochondr	3.75
	443879	Z28462	Hs.9927	Homo sapiens mRNA; cDNA DKFZp564D156 (fr	3.75
35	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.75
	429494	AA769365	Hs.126058	ESTs	3.75
	447118	AB014599	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro	3.75
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	3.74
	419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	3.74
40	448121	AL045714	Hs.128653	hypothetical protein DKFZp564F013	3.74
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.73
	414883	AA926960		CDC28 protein kinase 1	3.72
	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.72
45	452250	BE618654	Hs.28607	hypothetical protein A-211C6.1	3.72
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	3.72
	438607	AW080237	Hs.252884	ESTs	3.72
	408221	AA912183	Hs.47447	ESTs	3.72
	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.70
50	419900	AI469960	Hs.170698	ESTs	3.70
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	3.70
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	3.70
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.70
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	3.70
55	447846	AA324057	Hs.77955	Homo sapiens cDNA: FLJ23527 fis, clone L	3.70
	436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	3.70
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.69
	408495	W68796	Hs.237731	ESTs	3.69
	424452	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypotheti	3.68
60	448479	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphorylas	3.68
	431974	AW972689	Hs.200934	ESTs	3.68
	416354	NM_000633	Hs.79241	B-cell CLL/lymphoma 2 (BCL2)	3.68
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	3.68
	413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	3.67
65	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	3.67
	419111	AA234172	Hs.137418	ESTs	3.67
	423979	AF229181	Hs.136644	CS box-containing WD protein	3.66
	418875	W19971	Hs.233459	ESTs	3.66
	451690	AW451469	Hs.209990	ESTs	3.66
70	423032	AI684746	Hs.119274	RAS p21 protein activator (GTPase activa	3.66
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.66
	428347	AI264161	Hs.183773	golgi autoantigen, golgin subfamily a, 4	3.66
	426779	AA384577	Hs.93714	ESTs, Weakly similar to T00365 hypotheti	3.66
	435335	AI693150	Hs.137928	ESTs	3.66
75	410577	X91911	Hs.64639	glioma pathogenesis-related protein	3.66
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	3.65
	429105	D87077	Hs.196275	KIAA0240 protein	3.64
	407813	AL120247	Hs.40109	KIAA0872 protein	3.64
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	3.64
80	451678	AA374181	Hs.26799	DKFZP564D0764 protein	3.64
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.64
	452408	AA306477	Hs.29379	hypothetical protein FLJ10687	3.64
	441466	AW673081	Hs.54828	ESTs	3.63
	414013	AA766605	Hs.47099	hypothetical protein FLJ21212	3.62
	420056	AW043684	Hs.99804	ESTs	3.62
	424886	H88584	Hs.96900	hypothetical protein; KIAA1830 protein	3.62
	431774	BE348813	Hs.268561	hypothetical protein FLJ10726	3.62

	435990	AI015862	Hs.131793	ESTs	3.62
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	3.62
	414715	AA587891	Hs.904	amylase-1,6-glucosidase, 4-alpha-glucanot	3.62
5	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	3.62
	417008	AA191708	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	3.62
	413823	AI341417	Hs.29406	ESTs	3.61
	435354	AA678267	Hs.117115	ESTs	3.60
	427832	AF038362	Hs.180930	TBP-associated factor 172	3.60
10	427846	AW499770	Hs.180948	KIAA0729 protein	3.60
	426116	AA868729	Hs.144694	ESTs	3.60
	457635	AV660976	Hs.3569	hypothetical protein	3.60
	443998	AI620661	Hs.296276	ESTs	3.60
	417867	AW952547	Hs.194603	ESTs, Moderately similar to I38022 hypot	3.58
	418182	AW016405	Hs.16648	ESTs	3.58
15	434941	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	3.58
	424831	H61453		ESTs	3.58
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.58
	421823	N40850	Hs.28625	ESTs	3.58
20	414781	D50917	Hs.77293	KIAA0127 gene product	3.57
	427393	AB029018	Hs.177635	KIAA1095 protein	3.57
	415664	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.56
	425465	L18964	Hs.1904	protein kinase C, iota	3.56
	417124	BE122762	Hs.25338	ESTs	3.56
25	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	3.56
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	3.55
	421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	3.55
	410390	AA876905	Hs.125286	ESTs	3.54
	442073	AW973443	Hs.8086	RNA (guanine-7-) methyltransferase	3.54
30	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	3.54
	441499	AW298235	Hs.101689	ESTs	3.54
	453256	AI565587	Hs.32556	KIAA0379 protein	3.54
	414142	AW368397	Hs.334485	hemocentin (fibulin 6)	3.54
	438023	AF204883	Hs.6048	FEM-1 (C.elegans) homolog b	3.54
35	412245	AI952669	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.54
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.53
	446682	AW205632	Hs.211198	ESTs	3.52
	431392	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	3.52
	433430	AI863735		ESTs	3.52
40	420394	AB023161	Hs.97403	KIAA0944 protein	3.52
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.52
	443547	AW271273		hypothetical protein FLJ12666	3.52
	420676	AI434780	Hs.4248	vav 2 oncogene	3.51
	410690	AA322979	Hs.130266	ESTs	3.50
45	459645	AA074346		ESTs	3.50
	401403			Target Exon	3.50
	451166	T98171	Hs.185675	ESTs	3.50
	418836	AI655499	Hs.161712	ESTs	3.50
	421462	AF016495	Hs.104624	aquaporin 9	3.50
50	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	3.50
	432401	NM_013330	Hs.274479	NME7	3.49
	408392	U28831	Hs.44566	KIAA1641 protein	3.49
	425836	AW955696	Hs.90960	ESTs	3.48
	452327	AK000196	Hs.29052	hypothetical protein FLJ20189	3.48
55	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.48
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	3.48
	422960	AW890487		cadherin 13, H-cadherin (heart)	3.48
	430570	AI417881	Hs.292464	ESTs	3.48
	406387			Target Exon	3.47
60	416585	X54162	Hs.79386	leiomodulin 1, smooth muscle (LMOD1) (Thy	3.46
	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	3.46
	412240	H72176		hypothetical protein FLJ13159	3.46
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.46
	443634	H73972	Hs.134460	ESTs	3.46
65	422963	M79141	Hs.13234	ESTs	3.46
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	3.46
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	3.46
	425100	AF051850	Hs.154567	supervillin	3.45
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.45
70	444250	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	3.44
	428386	R17298	Hs.295923	seven in absentia (Drosophila) homolog 1	3.44
	447764	NM_003776	Hs.19500	nuclear localization signal deleted in v	3.44
	411251	R19774	Hs.22835	HHGP protein	3.44
	432648	AA557952		gb:n17c05.s1 NCI_CGAP_HSC1 Homo sapiens	3.44
75	428708	NM_014897	Hs.190386	KIAA0924 protein	3.44
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	3.43
	451743	AW074266	Hs.23071	ESTs	3.42
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	3.42
	448705	H05072	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	3.42
80	414489	AI620677	Hs.73105	ESTs	3.42
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.41
	435841	R28522	Hs.186937	ESTs	3.41
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	3.40
	451198	AW964541		hypothetical protein FLJ21127	3.40

	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	3.40
	436023	T81819	Hs.302251	ESTs	3.40
	449656	AA002008	Hs.188633	ESTs	3.40
5	437739	AW579216	Hs.264610	ESTs, Moderately similar to Ibd1 [H.sapi	3.40
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	3.40
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	3.40
	456505	AA504595		ESTs	3.40
	439867	AA847510	Hs.161292	ESTs	3.40
10	442113	BE622187		ESTs, Weakly similar to I38022 hypotheti	3.40
	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (f	3.40
	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	3.40
	421263	AB020638	Hs.103000	KIAA0831 protein	3.40
	410300	AW903988	Hs.62119	hypothetical protein FLJ14800	3.39
15	440028	AW473675		ESTs, Weakly similar to T17227 hypotheti	3.39
	454070	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	3.38
	432572	AI660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN !!!!	3.38
	442426	AI373062	Hs.332938	hypothetical protein MGC5370	3.38
	428412	AA428240	Hs.126083	ESTs	3.38
20	448772	AW390822	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.38
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.38
	413714	AI660944	Hs.71428	ESTs	3.38
	415663	AW296841	Hs.313332	ESTs	3.38
	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	3.37
25	421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.37
	440214	AA247118	Hs.7049	hypothetical protein FLJ11305	3.37
	440980	AL042005	Hs.1117	tripeptidyl peptidase II	3.36
	411975	AI916058	Hs.144583	ESTs	3.36
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	3.36
30	414783	AW069569		inactive progesterone receptor, 23 kD	3.36
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.36
	411213	AA676939	Hs.69285	neuropilin 1	3.36
	420613	AI873871	Hs.7041	ESTs, Weakly similar to A47582 B-cell gr	3.35
35	417534	NM_004998	Hs.82251	myosin IE	3.35
	431698	AI92369		ESTs	3.35
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.35
	441623	AA315805		desmoglein 2	3.34
	420729	AW964897	Hs.290825	ESTs	3.34
40	440010	AA534930	Hs.127236	hypothetical protein FLJ12879	3.34
	448369	AW268962	Hs.111335	ESTs	3.34
	452820	N46161	Hs.35274	ESTs	3.34
	453271	AA903424	Hs.6786	ESTs	3.34
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.34
45	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.34
	443291	AA325633	Hs.136102	KIAA0853 protein	3.33
	418720	AI381687	Hs.39526	ESTs	3.33
	452107	AB020681	Hs.27973	KIAA0874 protein	3.33
	439943	AW083789	Hs.124620	ESTs	3.33
50	433282	BE539101		hypothetical protein	3.33
	410344	AW978436	Hs.62515	KIAA0494 gene product	3.33
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	3.32
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.32
	434210	AA665612		ESTs	3.32
55	431923	AI741770	Hs.292690	ESTs, Weakly similar to I38022 hypotheti	3.32
	453199	AI336266	Hs.32353	mitogen-activated protein kinase kinase	3.32
	419534	AA443691	Hs.90858	Homo sapiens clone 25023 mRNA sequence	3.32
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	3.32
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	3.32
60	422092	AB007883	Hs.111373	KIAA0423 protein	3.32
	412262	W26406		seven in absentia (Drosophila) homolog 1	3.32
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.32
	446094	AK001760	Hs.13801	KIAA1685 protein	3.32
	446493	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.32
65	420339	AW968259	Hs.186647	ESTs	3.31
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.31
	432331	W37862	Hs.274368	MSTP032 protein	3.31
	433697	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.31
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	3.31
70	430950	AA489525		ESTs	3.30
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	3.30
	417958	AA767382	Hs.193417	ESTs	3.30
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.30
	419543	AA244170		gb:nc05h02.s1 NCI_CGAP_Pr1 Homo sapiens	3.30
75	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30
	452039	AI922988	Hs.172510	ESTs	3.30
	443798	R07848	Hs.188522	ESTs	3.29
	449378	AW664026	Hs.59892	ESTs	3.29
	455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	3.28
80	420126	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	3.28
	444291	AI598022	Hs.193989	TAR DNA binding protein	3.28
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	3.28
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	3.28
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28

	425657	T89839	Hs.119471	ESTs	3.28
	406672	M26041	Hs.198253	major histocompatibility complex, class	3.28
	419905	AW248229	Hs.93659	protein disulfide isomerase related prot	3.27
5	425332	AA633306	Hs.127279	ESTs	3.27
	418529	AW005695	Hs.250897	TRK-fused gene	3.27
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.27
	433618	AA602539	Hs.345494	ESTs	3.27
	408630	AA748009	Hs.173328	ESTs	3.26
10	415914	AA306033	Hs.78915	GA-binding protein transcription factor,	3.26
	415102	M31899	Hs.77929	excision repair cross-complementing rode	3.26
	432626	AA471098	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	3.26
	429493	AL134708	Hs.145998	ESTs	3.26
	445860	AA332145	Hs.13392	lethering factor SEC34	3.26
15	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	3.26
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.26
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	3.26
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	3.26
	436758	AW977167	Hs.155272	ESTs	3.26
20	438011	BE466173	Hs.145696	splicing factor (CC1.3)	3.26
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	3.25
	426860	U04953	Hs.172801	isoleucine-tRNA synthetase	3.25
	437830	AB020658	Hs.5867	KIAA0851 protein; suppressor of actin 1	3.25
	453368	W20296	Hs.288178	Homo sapiens cDNA FLJ11968 fis, clone HE	3.25
25	409939	AA463437	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	3.25
	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	3.24
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	3.24
	418283	S79895	Hs.83942	cathepsin K (pseudosostosis)	3.24
	414405	AI362533		KIAA0306 protein	3.24
30	445893	AI610702	Hs.202613	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.24
	434423	NM_006769	Hs.3844	LIM domain only 4	3.24
	408951	AW407227	Hs.227591	hypothetical protein FLJ11088	3.24
	408949	AF189011	Hs.49163	putative ribonuclease III	3.24
	410337	M83822	Hs.62354	cell division cycle 4-like	3.24
35	409010	AI648675		Homo sapiens, Similar to RIKEN cDNA 1700	3.24
	400419	AF084545		Target	3.24
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	3.24
	422461	NM_003417	Hs.117077	zinc finger protein 264	3.24
	441604	AI683049	Hs.201282	ESTs	3.24
40	411960	R77776	Hs.18103	ESTs	3.23
	414895	AW894856	Hs.116278	Homo sapiens cDNA FLJ13571 fis, clone PL	3.23
	430522	N75750	Hs.242271	KIAA0471 gene product	3.23
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	3.23
	405268			ENSP00000223174*:KIAA0783 PROTEIN.	3.23
45	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.22
	427196	AW967522	Hs.191593	ESTs	3.22
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	3.22
	417727	AL133623	Hs.82501	similar to mouse Xrn1 / Dhm2 protein	3.22
	410853	H04588	Hs.30469	ESTs	3.22
50	411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	3.22
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22
	427480	BE148769	Hs.334477	hypothetical protein FLJ11328	3.22
	444623	AI183829	Hs.202111	ESTs	3.21
55	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	3.21
	435874	AA868688	Hs.93102	ESTs	3.20
	443801	AW206942	Hs.253594	intron of: trichorhinophalangeal syndro	3.20
	434982	AW975084		gb:EST387190 MAGE resequences, MAGN Homo	3.20
	430929	AA489166	Hs.156933	ESTs	3.20
60	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	3.20
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	3.20
	422109	S73265	Hs.1473	gastrin-releasing peptide	3.20
	451119	AA805417	Hs.64753	ESTs	3.20
	414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	3.20
65	432676	AI187366		gb:qf29c01.x1 Soares_testis_NHT Homo sap	3.19
	428820	AA436187	Hs.172631	integrin, alpha M (complement component	3.19
	422040	AA172106	Hs.110950	Rag C protein	3.18
	437838	AI307229		ESTs	3.18
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.18
70	420789	AI670057	Hs.199882	ESTs	3.18
	419135	R61448	Hs.106728	ESTs, Weakly similar to KIAA1353 protein	3.18
	446019	AI362520		histone deacetylase 3	3.18
	430848	AW021726	Hs.345490	gb:df27e02.y1 Morton Fetal Cochlea Homo	3.18
	425375	AA631977	Hs.155995	KIAA0643 protein	3.18
75	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.18
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18
	453111	AB014598	Hs.31720	hephaestin	3.18
	454042	H22570		hypothetical protein FLJ20093	3.18
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.18
80	447183	AI554733	Hs.173182	ESTs	3.18
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	3.18
	431831	AW023204	Hs.302743	ESTs	3.18
	420664	AI681270	Hs.99824	BCE-1 protein	3.18
	451582	AI963026	Hs.289958	ESTs, Weakly similar to putative p150 [H	3.17

	432954	AI076345		ESTs	3.17
	444990	AI912410	Hs.27475	Homo sapiens cDNA FLJ12749 fis, clone NT	3.17
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	3.17
5	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.17
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.17
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.16
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.16
	420623	BE245485	Hs.99437	Homo sapiens mRNA; cDNA DKFZp586G1924 (f	3.16
10	451475	T19093	Hs.26450	KIAA0725 protein	3.16
	452066	AA772149	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p	3.16
	429556	AW139399	Hs.98988	ESTs	3.16
	448514	AB020626	Hs.301866	KIAA0819 protein	3.16
	443732	AI188803	Hs.153944	ESTs	3.16
15	436805	AA731533	Hs.270751	ESTs	3.16
	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	3.16
	417511	AL049176	Hs.82223	chordin-like	3.16
	423595	R82826	Hs.220702	ESTs	3.16
	445837	AI261700	Hs.145544	ESTs	3.16
20	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	3.16
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.16
	414183	AW957446	Hs.301711	ESTs	3.16
	433194	AB040883	Hs.83243	KIAA1450 protein	3.16
	453915	AA588721	Hs.286218	ribosomal protein L44	3.15
25	407725	BE388094	Hs.21857	ESTs	3.15
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.14
	440937	AF202724	Hs.7531	KIAA0810 protein	3.14
	449057	AB037784	Hs.22941	KIAA1363 protein	3.14
	446126	AW085909		pleckstrin homology domain interacting p	3.14
30	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.14
	419145	N99638		gb:za39g11.r1 Soares fetal liver spleen	3.14
	418757	AI864193	Hs.169728	hypothetical protein FLJ13150	3.14
	430000	AW205931	Hs.99598	hypothetical protein MGC5338	3.14
	437296	AA350994	Hs.20281	KIAA1700	3.14
35	441381	H22195	Hs.31874	ESTs	3.14
	457250	AA811987	Hs.125779	ESTs	3.14
	422900	AA641201	Hs.222051	ESTs	3.14
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.14
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.14
40	419355	AA428520	Hs.90061	progesterone binding protein	3.14
	409509	AL036923	Hs.322710	ESTs	3.14
	417308	H60720	Hs.81892	KIAA0101 gene product	3.14
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	3.14
	429160	AW663083	Hs.144469	ESTs	3.14
45	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.14
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (U	3.14
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	3.14
	451518	AW340925	Hs.174918	ESTs	3.14
	435702	AI033647	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3.13
50	439208	AK000299	Hs.180952	dynactin 4 (p62)	3.13
	451838	AW005866	Hs.193969	ESTs	3.13
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zip	3.13
	446945	AI193115	Hs.16611	tumor protein D52-like 1	3.13
	453920	AI133148	Hs.36602	I factor (complement)	3.13
55	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.13
	417105	X60992	Hs.81226	CD6 antigen	3.12
	433854	AA610649	Hs.333239	ESTs	3.12
	408089	H59799	Hs.42644	thioredoxin-like	3.12
	453686	AL110326	Hs.304679	ESTs, Moderately similar to Z195_HUMAN Z	3.12
60	426167	AF039023	Hs.167496	RAN binding protein 6	3.12
	452195	AA994712	Hs.116878	ESTs	3.12
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	3.12
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12
	424001	W67883	Hs.137476	paternally expressed 10	3.12
65	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.12
	433401	AF039698	Hs.284217	serologically defined colon cancer antig	3.12
	409245	AA361037		tRNA isopentenylpyrophosphate transferas	3.12
	414290	AI568801	Hs.71721	ESTs	3.12
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	3.12
70	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	3.11
	448873	NM_003677	Hs.22393	density-regulated protein	3.11
	428471	X57348	Hs.184510	stratifin	3.11
	436288	AI361722	Hs.192410	ESTs	3.10
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.10
75	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	3.10
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.10
	412340	AA101809	Hs.182685	ESTs	3.10
	438716	AA814903	Hs.155113	ESTs	3.10
	419440	AB020689	Hs.90419	KIAA0882 protein	3.10
80	433017	Y15067	Hs.279914	zinc finger protein 232	3.10
	428513	BE220806	Hs.184697	plexin C1	3.10
	437866	AA156781		metallothionein 1E (functional)	3.10
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	3.10
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10

	435445	AA737345	Hs.294041	ESTs	3.10
	420997	AK001214	Hs.100914	hypothetical protein FLJ10352	3.09
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	3.09
5	406122			Target Exon	3.09
	435272	AA906415	Hs.110041	ESTs	3.09
	410726	AI623859	Hs.15936	ESTs	3.09
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.08
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.08
10	417538	AW050865	Hs.275711	hypothetical protein MGC2452	3.08
	434938	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	3.08
	434733	AI334367	Hs.159337	ESTs	3.08
	434421	AI915927	Hs.34771	ESTs	3.08
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08
15	424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	3.08
	458332	AI000341		ESTs	3.08
	445034	AW293376	Hs.143659	ESTs	3.08
	446570	AV659177	Hs.127160	ESTs	3.08
	429920	AW473208	Hs.115572	ESTs, Weakly similar to I38022 hypotheti	3.08
20	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	3.06
	419038	AW134924	Hs.190325	ESTs	3.06
	451079	AI827988	Hs.240728	ESTs, Moderately similar to PC4259 ferri	3.06
	417386	AL037228	Hs.82043	D123 gene product	3.06
	453108	AI311457	Hs.99472	ESTs	3.06
25	449328	AI962493		ESTs	3.06
	428656	AB037798	Hs.188790	KIAA1377 protein	3.06
	425509	AF079363	Hs.158213	sperm associated antigen 6	3.06
	447957	NM_014821	Hs.20126	KIAA0317 gene product	3.06
	417226	AW505054	Hs.4283	ESTs	3.05
30	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	3.05
	426279	AI648520	Hs.169084	tubby like protein 3	3.05
	433814	AA609738	Hs.16525	ESTs	3.05
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	3.05
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	3.04
35	441789	D52059	Hs.7972	KIAA0871 protein	3.04
	456437	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.04
	438771	NM_016289	Hs.6406	MO25 protein	3.04
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	3.04
	416240	NM_001981	Hs.79095	epidermal growth factor receptor pathway	3.04
40	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	3.04
	424776	AI867931	Hs.164595	ESTs	3.03
	408409	AW838181	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.03
	429693	BE254962	Hs.211612	SEC24 (S. cerevisiae) related gene famil	3.03
	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	3.03
45	431625	AW750627	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	3.03
	451144	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	3.02
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.02
	408683	R58665	Hs.46847	TRAF and TNF receptor-associated protein	3.02
	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (	3.02
50	440603	AL121733	Hs.7299	Novel human gene mapping to chromosome 1	3.02
	415443	T07353	Hs.7948	ESTs	3.02
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02
	406685	M18728		gb:Human nonspecific crossreacting antig	3.02
	446013	AI360167	Hs.152774	ESTs	3.02
55	433902	AW292820	Hs.144906	ESTs	3.02
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.02
	432505	AW274526	Hs.277721	KIAA0049	3.01
	440040	BE219431	Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.01
	433255	AI274270	Hs.96840	KIAA1527 protein	3.01
60	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.01
	417258	N58885		gb:yy60a09.s1 Soares_multiple_sclerosis_	3.00
	435800	AI248285	Hs.118348	ESTs	3.00
	444838	AV651680	Hs.208558	ESTs	3.00
	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	3.00
65	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	3.00
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.00
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	3.00
	410434	AF051152	Hs.63668	toll-like receptor 2	3.00
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00
70	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.98
	450247	AF123303	Hs.24713	hypothetical protein	2.98
	417865	AW086059	Hs.6529	ESTs, Weakly similar to I78885 serine/th	2.98
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.98
	438543	AA810141	Hs.192182	ESTs	2.98
75	415503	U36601	Hs.78473	N-deacetylase/N-sulfotransferase (hepara	2.98
	429138	AB020657	Hs.197298	NS1-binding protein	2.98
	447881	BE620886		GCN1 (general control of amino-acid synt	2.96
	425481	AW978162		ESTs	2.96
	453315	BE544203	Hs.24831	ESTs	2.96
80	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	2.95
	433208	AW002834	Hs.24095	ESTs	2.95
	442495	AI184717		ESTs	2.94
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.94
	408170	AW204516	Hs.31835	ESTs	2.94

5	430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypot	2.94
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94
	407361	AA744622	Hs.292645	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.94
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.93
	436005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 fis, clone OV	2.93
	449458	AI805078	Hs.208261	ESTs	2.93
	449317	AW293413	Hs.132906	19A24 protein	2.92
	411118	N27944	Hs.221476	ESTs, Weakly similar to AF108460 1 ubinu	2.92
10	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	2.91
	416311	D80529		gb:HUM081H05B Human fetal brain (TFujiwa	2.91
	433068	NM_006456	Hs.288215	sialyltransferase	2.90
	429272	W25140	Hs.110667	ESTs	2.90
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	2.90
15	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.88
	426782	R14614	Hs.33846	ESTs	2.88
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	2.88
	413882	AA132973	Hs.184492	ESTs	2.88
	421554	AW137676	Hs.97775	ESTs	2.88
20	446488	AB037782	Hs.15119	KIAA1361 protein	2.84
	421391	AW304350	Hs.191958	immunoglobulin superfamily receptor tran	2.84
	424527	AW138558	Hs.334873	ESTs, Weakly similar to I54374 gene NF2	2.82
	419284	AW820869	Hs.215658	ESTs, Moderately similar to ZN91_HUMAN Z	2.82
	415788	AW628686	Hs.78851	KIAA0217 protein	2.82
25	448481	W15284	Hs.74832	ESTs	2.82
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.80
	443441	AW291196	Hs.92195	ESTs	2.80
	422725	AA315703	Hs.199993	ESTs, Weakly similar to ALUB_HUMAN !!!!	2.80
	431926	AW972724		gb:EST384816 MAGE resequences, MAGL Homo	2.80
30	420406	AA741024	Hs.88378	ESTs	2.79
	437678	AA829860	Hs.122834	ESTs	2.78
	440115	R41808	Hs.144924	ESTs, Weakly similar to B Chain B, Solut	2.78
	439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	2.78
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.77
35	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.76
	435154	AA668764		ESTs	2.76
	432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.75
	442703	AL044949	Hs.116298	ESTs	2.74
	419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.74
40	435861	AF254956	Hs.16608	candidate tumor suppressor protein	2.72
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.70
	438441	AW664960	Hs.205319	ESTs	2.70
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.67
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-ii	2.66
45	416239	AL038450	Hs.48948	ESTs	2.62
	434792	AA649253	Hs.132458	ESTs	2.60
	424852	AI222779	Hs.144848	ESTs	2.58
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.57
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	2.56
50	450571	AF158240	Hs.60397	ESTs	2.56
	442435	AI986208	Hs.244760	ESTs, Highly similar to B34087 hypotheti	2.56
	424148	BE242274	Hs.1741	integrin, beta 7	2.56
	445784	AI253155	Hs.146065	ESTs	2.53
	408072	BE005566	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	2.52
55	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.52
	450295	AI766732	Hs.210628	ESTs	2.48
	440381	AA917808	Hs.190495	ESTs	2.46
	433923	AI823453	Hs.146625	ESTs	2.44
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44
60	429670	L01087	Hs.211593	protein kinase C, theta	2.44
	437908	AI082424		ESTs	2.43
	438676	AA813745	Hs.123446	ESTs	2.37
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28
	444969	AI203334	Hs.160628	ESTs	2.28
65	446423	AW139655	Hs.150120	ESTs	2.27
	435517	AA928626	Hs.130177	ESTs	2.27
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.00
	429073	AA446167	Hs.47385	ESTs	1.98
70	433834	AA620742	Hs.130786	ESTs	1.72
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	1.52
	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigen	1.30
	402550			Target Exon	1.09
75	TABLE 33B:				
	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
80	Pkey	CAT Number	Accession		
	431089	125941_2	BC940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826		
	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945		
	407192	2200202_1	AA602964 AA609200		



5	438089	22448_4	BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 R83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701 AF086037 H89360 H89546 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 M31126 AW749625 AW749626 AW749644 AI140497 BG034853 AW173315 AW303375 BG190225 BG939153 BF057308 AA600736 AI751258 AI090486 BE939504 AW631492 AI768270 AI862133 AA417652 BE378218 AA599207 AW794702 AA024968 AA446024 AI148235 AI191710 BI493797 AI272646 BI493796 AA634323 AI754332 AA258414 C05155 AI218226 AI039656 AI350380 AI084698 AI754989 AI673545 AI432010 AI751035 AA375571 AA446297 BG216743 BC011194 AW517087 AA601054 T85512 BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240 BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017 AI286003 AI147163 AA626033 AI539156 AA565542 AI094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 AI991439 R46187 BE292954 AA333976 D63102 BF744491 AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981 AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60656 AW340495 AI984319 AA974603 BG676155 BM000951 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633 AA993566 AI521958 AI565071 AI864217 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 T23514 AI655785 Z99386 AV716301 BE222333 AI949687 BF732426 AI949086 AV721430 AW577332 N66315 BE672030 AI084440 AI250908 N50901 AA757364 BF515264 AI186231 BE466036 AW631313 AA993514 N54411 BG057515 AW013895 N77963 AA708723 AI273295 N59093 AA522665 AI871574 AA505521 AA812256 AA553841 AW467057 W68650 AI168772 AA988308 AA910057 AI868258 AA918322 AI335847 AA621494 AA904390 AI760007 AU146694 AV758440 BM142562 N66507 AI674563 AW628584 AI263902 BF223368 AI090490 AI452918 N71423 AA062767 T94332 AA016003 BG681608 AA082426 AA029451 N71873 BF437845 T54154 AV741757 AI174783 R12271 R83569 AK074129 AL138071 AI806793 AI453544 AI084616 BF062435 BE672932 AI828296 BF062464 AI803443 AI264326 AI280956 AI743547 AW295227 AW139967 AI972561 AI863570 AW062752 AW062756 AW062753 AW176904 AW062755 AW062750 AW062749 AW176886 AI751694 BG251391 AA043621 W30872 BI524827 N94581 AI084614 AA776976 AI377572 AI751695 AI016576 AW439994 AW194255 AW627763 AA668249 AI079870 AW022524 AI968540 AI248360 AA702490 AA043262 AA631511 AW176883 AW751767 AW176887 AW062748 AW062745 AW176862 AW176815 AW176814 AW176846 AW176841 AW176871 AW176874 AW176819 AI927437 AW191962 R36548 AA853713 AW196059 AA618567 AW176881 AW062754 AW062751 AW062746 AW176888 AW751772 AW176859 AW751765 AW751762 AW176833 AW176873 AW751745 AA694513 AA780815 AW176857 AW176834 AW176839 AW751771 AW176878 AW176843 AW176842 AW751755 AW176847 AW176812 AW176830 AW176849 AW176844 AW176877 AW751757 AW176850 AW176851 AW751758 AW751746 AW176858 AW176853 AW751766 AW176845 AW176872 AW176840 AW176876 AW176852 AW751754 AW176836 AW176856 AW751773 AW751760 AW751751 AL138070 AA639738 AL602588 AA853712 AA317570 R38469 AW291569 AA156151 Z25109 C05177 AW975688 AA731063 N67084 AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW403993 R39847 BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AI928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355 AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI450479 AI016166 AA779515 AA661791 BM474307 BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893 AI989299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299 R70463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI624611 BG271780 AI497723 H88862 D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z39807 BF954386 AW975804 AA748675 AA731006 M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI063306 BG990973 BI040954 BF919911 AU140155 AI751766 AI43518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 BI603116 BE149760 BE705967 BE075966 BF705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE719915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181
---	--------	---------	---

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654  
AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320  
AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474  
BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763  
BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406  
BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012  
BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442  
BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090  
BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653  
BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487  
AA740616 AA654854 AA229923  
AW975114 AI096634 AI767001 AA658364 AW517542  
AW969880 AA484613 AA501874 R34356  
T59708 AA224827 T59843 BE156903  
AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360  
AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871  
AI075239 AI339996 AA701623 AI139549 AI366880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887  
AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 AA954344 N49682 AI457100 AW589407  
AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363  
AK001125 AU120581 AU146612 AW301393  
AI130992 AW969537 AA503835  
H61453 AA838765 AI693104 AA721107  
AA961586 AI863735 AA588325  
AV645808 AA701657 AW271273 AI796734 AI472316 AI017531 AI061178 BF109096 AA548964 N83805 AA131648 AA156589 BE708349  
AW952494 D30877 AV684717 Z24837 F00167 BF576150 T63841 R78995 N87474  
AW232984 AA724304 AA074346 AA074368  
BF090249 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119  
AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260  
AA534222 AA632632 T81234  
BF963346 BI460763 BI599382 AI188089 AI505500 AW959185 AA187681 AI692282 AU153608 BI493898 BI493899 AI97349 BE550679 AI701137  
AA744561 AA082682 BE218816 AW511501 BF447881 AI859101 BF059295 AI914038 AI346564 AI685003 AI676076 AI125336 AW469637 T10225  
AI831296 R53451 AI453440 AA983739 AW470873 AI348290 BE857670 D55901 Z43908 T34429 F07305 AK074340 AI538118 BG201484 AI334192  
T35535 AW176751 BI496132 BI496133 AA469961 H72176 BF326265 AI770016 AI693177 BF223634 BF963661 BF962265 BI034894 AI475851  
N69071 AI910707 BE219038 AI918036 BE670589 BM193515 AI338497 AA805525 AA487625 AA830336 AW749368 AW104323 AI628055 AI932332  
AI272788 AI568649 AW162414 AW161923 T23854 AA610763 AA912188 AW339028 Z39946 T10224 F03171 AI205478 AI638791 F02580 F01551  
AW207551 AA421030 BE246012 BI034937 BI035373 BF939581 H19984 BE867247 H92677 N55988 BF957332 I18615 R16442 BF956229  
BF961886 R12698 AA101186 AA365932 R53452 BF062714 BF959364 H41634 AW086187 H19985 BF054881 F02581 H18616 H41527 AW003446  
BE243443 H92276 AW954002 BI670132  
AA677593 AA618150 AA557952  
AK024780 NM\_024549 AA5440385 AW965502 BF477855 AI149742 BE669424 BE349941 AI376717 AA977493 AW592564 AA884111 AA865463  
N51840 BF593777 AA044645 AW512183 BF059034 AI984320 AA733139 AI884563 AI559673 AI421262 AI052068 AI085891 BI963100 AA479883  
AI271696 AI539839 AI370924 AI147781 AA535765 BI966896 AA877448 AW152259 AA938992 AA996022 AI800410 AA613303 AA588323 R53623  
AW571973 AI203770 BI494224 BI494225 D45504 AA705824 AI625183 AA437118 AA640325 AA235528 AA731411 AA626263 AI560519 AW071114  
AW005691 AI055933 AA971813 AA334937 N58441 AA536020 AW874174 AI565960 AW607532 H44547  
BC017965 AW969075 AA279982 AA504511 AI219979 AA504595 AI245579 AA278181 BG485019 BI049312  
AK074156 AI401548 BE002083 BE002085 BE002084 BG113650 AW580909 AA632959 BG610861 BG436183 BF438017 AI568608 AI095503  
AI204208 AW244158 BE622614 N52349 BE042940 AI095858 AA976119 AA835838 AI620854 AA456105 AA971569 AI246289 AI335636 AA994082  
AI250060 AI095710 AA605125 AA291672 BE463947 N52870 AA287553 AI149093 AA581802 W31684 AA610159 BF247061 BG258954 BE176866  
BE177041 AA332106 BE967020  
AW473675 AI190744 W69997 AW104913 AI221098 W69996 AA885487 AA861491  
BE972667 AW069569 AI392889 H85161 AI074962 AA423935 BE671254 AA912627 H39845 H69083 AA280259 N67746 AA155722  
BM423504 BE075913 AI492369 AI831729 AA807134 AI057292 BF059751 AA918209 BE858647 AW016707 AI675289 AI452916 BF593014  
AI480099 AI522283 AI628681 AI470402 BF056360 AW236830 AA514206 BF055812 AI796201 BF055617 BF054627 AI288301 AA705763  
BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853  
AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424  
AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AI497784 AW189392 W37448  
AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306  
AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522  
BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595  
BI094458 BE706702 BG496559 BF248373 BG494800  
BC015150 BM471660 BM478941 BI759769 BI094332 BE005819 BE005834 BM023432 BE179013 BE675522 AI680275 AA515794 AA256503  
F01634 AF002990 BG288697 AI091615 AW002917 AI631085 AW182664 BE501232 AI922188 BF838783 AI631078 BE464544 AI376986 AW503774  
AA424131 AW511849 AA872189 BF084885 AI432024 AI491908 BF197906 AA580599 AI274418 AW269225 AW058288 AI611346 AA236200  
C00417 BE669699 AI468149 BM460137 AI685282 AI902714 BG990066 BF894391 T83393 T84298 BF809721 BE925494 AV755948 BF928512  
BF894494 BF808642 AA256710 BF894347 BE928708 H06072 AA199607 BI859300 AI983233 AI521122 BE168896 BE302846 X76770 BC000927  
NM\_032632 BG707103 BG913857 BG613824 BG613257 BM313077 BI561132 BI461426 BE389811 BE391509 BE164646 AA746371 AV750611  
BE175813 AA332040 BG200997 BG485576 AL043706 AV716994 BF903156 AW820369 AU132824 BF941136 BE543211 AA521432 AW837568  
BF809623 AW614670 AU129338 AW880782 AA371070 BG615427 BI667976 BI598706 BI599341 BE869166 BG502432 NM\_020144 AF218840  
BI461106 BI562235 BI462594 BI458753 BF195561 BF832738 BE890146 AI678629 AL135238 AU129571 AW500045 AA382478 AW502738  
BI561031 BE280153 BF087226 BM480024 AW804395 BE707050 R72668 BF038881 BF895070 BG036594 BE551809 BF326901 BG286526  
AW962888 BE544939 AW363399  
AK057015 AI026834 BE857936 AA149091 AI742972 AW439172 AI253168 AA255613 BF513175 AI005006 T03406 AW338149 AA836442  
AA420530 R88566 AI611672 AA433916 AA442855 BF063008 AA812568 AI889706 AA715313 AA768539 AA767620 AA665471 AA404380  
AA665612 BF056442 AA706388 AI650676 AA627448 AI141769 H78227 AW901852 H78221 BE701982 BF689273 AA397464 N33072 R60218  
AW968247 H14833 AA768305 AA043348 R56470 BF739832 R51827 AI474963 BG494574 AA149090 BF238154 AI802210 BE000129 BF734513  
R41964 H21055 R85253 R17705 R40844 BF790218 BG388356 BF003037 AA703138 AA377348 W24822  
AK056051 AI971258 AI681134 AU146134 AI803300 AA917325 AA923663 BF895068 AI304442 AI167464 AI284188 AA054272 AA829262 AI351910  
T90930 AI886230 U70056 AU119916 BF446537 BE503207 BE502849 AI698102 AA258553 AV718529 AV719917 BF724133 BI438668 AI804000  
BE349103 AI912294 BE645117 AA227954 AA446520 AA879147 AA281770 AW136872 AA807907 AI439589 AI339626 AI383274 AA418512  
BE771804 BF894509 AA455093 AI379061 AI150855 BF769906 R17298 AW30138740 BF808607 BE674633 AV700132 AA227789 AA253099  
AW975199 AA935418 T74315 F12666 AA022923 T89028 AA258606 W26406 BE838620 AV700706 AA101321 R41382 H14479 AA253044 R54810  
R42784 R44804 R41278  
AI525877 AA489525 AW088177

5	419543 455657 414405	251903_1 1490185_1 112689_1	AI018087 AA244170 AA244355 BE065209 BE065364 BE065110 BE065111 AL047596 AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090696 AI927369 AI669226 AI369437 AI371075 AW612409 AI686711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 D81020 BF575223 AI356183 D79312 AI375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545
10	409010	10331_1	AL575207 AL551714 BM014781 BG542863 BG771232 AA429722 AI377511 AI770155 AA716665 BG003427 AA810811 AA442760 AA128610 AA059411 AI796263 AI494075 AI572127 AA420992 BF436083 AI648675 AA878813 BI488614 BG700886 AA128609 AV702879 AA731146 AI580336 AI373224 AA919169 AI758175 AA976350 BG701414 BF057794 AW135598 AA062583 BI549631 AI185077 AA933879 AW024454 AA193289 AA045194 BG928396 BE855883 BF435859 AA196423 AW237471 R99289 D61992 BE856637 BF368270 AA194235 N51319 AA363499 N63065 BG548812 BF027898 BG779448
15	411962 434982 432676 437838 446019	2307710_1 121871_1 3503_22 2512601_1 658727_1	AA099050 AA099526 T47733 AW975084 T90204 AA658177 AI187366 AA618478 AA558869 AI308202 AI307229 AA769348 AI362520 D25917 AI670784 AI742347 AW269789 AI270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827
20	454042	30254_1	AJ420458 AI018523 AA708686 BF949633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI654847 AW874199 AI206120 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366468 N64350 AA779107 AW025969 R49056 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202561 AA788851 AI494436 BF856114 H22570 AI076345 AI887648 AA572691
25	432954 446126	2159612_1 610_2	BF946219 BF946218 BF851494 AL536879 AA457150 AI590194 AI582629 AA464515 AA916242 AA337109 AA336509 N46906 AA336322 AA336407 AA337222 AA319240 BI026817 BI027058 AI536880 AI693827 AA651730 AI701013 BM068789 AW339506 AA293021 BF891108 AI458885 AW361203 AW974652 AI761251 AI655763 AA628063 BE047125 AW085916 AI129587 N52070 AW172361 AA052951 AW085909 AI000008 AA962570 AI371342 AI364207 AA464514 AI962506 AI824603 AW376300 AA058439 AW361192 AV656660 N50282 BF820514 BF891008 H40784 BF891112 BE708029 AW043567 AA056762
30	419145 409245	248375_1 3199_2	BM456602 AV706711 BF379357 H90994 AA234435 AA558020 BF351723 AA328271 R94815 N99638 BG223375 AW973750 N59599 AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857 AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R66856 H01374 BI257369 BI259830 AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024 BF093291 AW021929 H22650 AA459715 BG496341 BE697763 BI254209 BG499543 H42946 BI059780 BI086741 H87896 H87599 BF691752 BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF909744 AW966003 AV714014 BI492868 BI495144 AA921845 AI693426 AI652147 AI435449 N47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897 AW665247 AW340077 N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AI080245 AA884954 AI125702 AI382934 AA931835 AI358631 AW439905 AI027833 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI768667 AA948472 AI819214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AI492769 D56771 AA095911 BE222062 D56772 AW372265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI492848 HI6217 H21980 H22651 H88179 H87354 H44052 H25165 H44128
35	437866	34267_1	U52054 AL581000 AA156850 AW293839 BI335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161 BM194134 AW966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF446960 AA837481 AV755539 AW468444 AW468002 AA811830 AA581806 AI866686 AI572124 AA687333 D20160 AA812489 AU185248 AU186004 AA156781 AI536733 BM144850 AI471883 AA040926 BF507639 AA043777 AW874142 BE832523 BE163972 BI022546 BI021204 AI000341 AI766341 AW873274
40	458332 459513 449328 406685 417258 447881	1139685_1 417837_1 3030726_1 0_0 400835_1 44623_1	AV704062 BE162284 AI032946 BF360636 AI884781 AI652306 AI651694 AI638744 AI962493 M18728 BG116781 BI914326 BI030196 N58885 N63406 AV683374 N58892 BG110501 AA333708 AA359583 AW963123 N95562 N95696 N95587 AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
45	425481 440638 442495 416311 431926 435154 437908	334120_2 371165_1 928718_1 1280744_1 1237041_1 126605_1 13268_11	AL520496 AW978162 AI610475 AI688890 AW470054 AA609426 AI167391 AA815231 AA358241 BG009500 AI376551 AA897445 T87714 AI184717 AW518883 AF121173 AA179446 AA357794 D81719 D80529 C14833 AW972724 AA877998 AA522631 AU185388 AW972063 AA668764 AA804491 AW665688 AA765069 AI740586 AA771806 BE500996 AW204531 AI082424 AI033879 BF093176 AA771764 D38676

TABLE 33C:

65

Pkey:

Ref:

Strand:

Nt\_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

70

Pkey	Ref	Strand	Nt_position
401403	7710966	Plus	146180-146294
406387	9256180	Plus	116229-116371,117512-117651
405268	4156151	Minus	24404-24521
406122	9144087	Minus	30940-31386
402550	7652009	Minus	80413-80673

75

80 TABLE 34A: About 703 genes upregulated in idiopathic pulmonary fibrosis relative to hypersensitivity pneumonitis or non-specific interstitial pneumonitis

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number  
Unigene Title: Unigene gene title

R1: 90th percentile of IPF AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50

R2: 90th percentile of IPF AIs divided by 90th percentile of NSIP AIs, where the minimum value for the numerator and denominator was set to 50

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
5	405443			Target Exon	9.66	7.50
10	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.23	3.66
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.63	3.03
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	4.84	2.81
	406964	M21305		FGENES predicted novel secreted protein	4.73	5.69
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.34	4.34
15	407244	M10014		fibrinogen, gamma polypeptide	4.14	5.88
	421823	N40850	Hs.28625	ESTs	4.12	1.80
	419875	AA853410	Hs.93557	proenkephalin	3.90	2.01
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.88	2.90
	418310	AA814100	Hs.86693	ESTs	3.66	2.84
20	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	3.60	3.13
	438315	R56795	Hs.82419	ESTs	3.49	3.70
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.47	1.38
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	3.46	3.46
	434233	AF119903	Hs.138453	hypothetical protein PRO2834	3.28	2.51
25	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	3.26	3.26
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	3.19	2.12
	420185	AL044056	Hs.251385	ESTs	3.18	3.01
	420195	N44348		Homo sapiens cDNA FLJ11177 fis, clone PL	3.16	3.16
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	3.08	3.18
30	408221	AA912183	Hs.47447	ESTs	3.07	1.98
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.02	2.36
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.98	1.72
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.87	1.48
	422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (f	2.80	2.66
35	445745	AB007924	Hs.13245	KIAA0455 gene product	2.78	1.65
	407938	AA905097	Hs.85050	phospholamban	2.78	2.46
	423575	C18863	Hs.163443	intron of perlestin (OSF-2os)	2.78	1.55
	446659	AI335361	Hs.226376	ESTs	2.74	1.56
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	2.74	1.85
40	437620	AW976930		ESTs	2.72	2.72
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.67	2.05
	416585	X54162	Hs.79386	leiomodrin 1, smooth muscle (LMOD1) (Thy	2.66	1.47
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.66	2.66
	430712	AW044647		ESTs	2.62	2.62
45	453111	AB014598	Hs.31720	hephaestin	2.61	1.72
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.59	1.27
	414290	AI568801	Hs.71721	ESTs	2.59	1.23
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.58	2.58
	412639	AW961284	Hs.203838	ESTs	2.58	2.29
50	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.57	1.74
	429757	AW452355	Hs.256037	ESTs	2.57	1.60
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57	1.00
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.56	1.12
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.56	1.25
55	411880	AW872477		gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens	2.54	2.54
	401645			C16001440:gil12330704[gb]AAG52890.1[AF3	2.53	3.38
	401673			C16001416:gil12743112[ref]XP_010131.2]	2.47	2.83
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.46	1.18
	416316	H58721	Hs.271628	ESTs	2.42	3.44
60	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.40	1.69
	451149	AL047586		RNA binding motif protein 8B	2.40	1.95
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.40	1.61
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	2.40	2.40
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.39	1.27
65	405120			C4001445:gil12697999[dbj]BAB21818.1[AB	2.38	2.38
	432224	AW189460	Hs.208358	ESTs	2.38	2.00
	418663	AK001100	Hs.41690	desmocollin 3	2.38	2.38
	412622	AW664708	Hs.171959	ESTs	2.37	1.63
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.37	1.52
70	442767	AI017208	Hs.131149	ESTs	2.36	1.22
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.35	1.79
	411800	N39342	Hs.103042	microtubule-associated protein 1B	2.35	1.18
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.34	2.34
	444009	AI380792	Hs.135104	ESTs	2.34	2.07
75	435143	R12375	Hs.194600	ESTs	2.33	1.68
	402333			Target Exon	2.33	3.15
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.33	1.10
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.32	1.30
	452242	R50956	Hs.159993	glycosyltransferase	2.32	1.45
80	418693	AI750878	Hs.87409	thrombospondin 1	2.32	2.32
	428411	AW291464	Hs.10338	ESTs	2.32	1.54
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.31	1.98
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.31	2.49
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.31	1.32

5	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.30	2.30
	456536	AW135986	Hs.257859	ESTs	2.28	2.28
	428166	AA423849	Hs.79530	M5-14 protein	2.27	1.88
	456936	M81349	Hs.1955	serum amyloid A4, constitutive	2.25	2.16
	417728	AW138437	Hs.24790	KIAA1573 protein	2.25	1.37
10	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.24	2.42
	409159	AW673312	Hs.50848	hypothetical protein FLJ20331	2.24	2.24
	404942			splicing factor, arginine/serine-rich 9	2.24	2.64
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.24	2.46
	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	2.24	1.94
15	421574	AJ000152	Hs.105924	defensin, beta 2	2.23	1.36
	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	2.22	1.37
	421948	L42583	Hs.334309	keratin 6A	2.20	2.20
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.19	1.61
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.18	2.40
20	431089	BE041395		ESTs, Weakly similar to unknown protein	2.16	2.46
	447333	BE090580	Hs.70704	hypothetical protein dJ616B8.3	2.16	2.00
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.16	1.26
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.16	1.99
	403362			NM_001615: Homo sapiens actin, gamma 2,	2.16	1.61
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.15	2.11
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.15	2.24
	402641			C1002296:gi 6677817 ref NP_033126.1  rep	2.14	2.14
	418236	AW994005	Hs.337534	ESTs	2.14	2.14
	413059	BE151498		gb:RC0-HT0295-291199-031-E11 HT0295 Homo	2.14	2.14
30	432437	W07088	Hs.293685	ESTs	2.14	2.14
	428398	AI249368	Hs.98558	ESTs	2.14	2.14
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.12	1.43
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	2.12	1.93
	436391	AJ227892	Hs.146274	ESTs	2.12	2.12
35	417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.11	2.17
	407443	AF227138		gb:Homo sapiens candidate taste receptor	2.11	2.36
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.10	1.29
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.10	2.10
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	2.10	2.00
40	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.10	1.37
	450271	AI693900	Hs.200920	ESTs	2.09	2.34
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.09	1.40
	458208	AI380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	2.08	2.00
	405600			C12001673:gi 9631264 ref NP_048045.1  or	2.07	1.97
45	434654	AI825942	Hs.139366	Homo sapiens clone L5 polyadenylated HER	2.07	2.52
	439261	AI126020	Hs.145674	basic transcription factor 3	2.05	1.45
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	2.04	2.04
	457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RDF1 Homo sapiens	2.04	2.04
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	2.02	1.33
50	412505	AA974491	Hs.21734	ESTs	2.02	2.02
	443180	R15875	Hs.258576	claudin 12	2.02	2.02
	431605	AW972407	Hs.124370	gb:EST384498 MAGE resequences, MAGL Homo	2.02	2.02
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	2.02	2.17
	452571	W31518	Hs.34665	ESTs	2.02	2.09
55	405061			Target Exon	2.01	2.52
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.01	2.41
	402327			Target Exon	2.00	2.44
	418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	2.00	2.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.00	2.00
60	438634	AW340400	Hs.126728	ESTs	1.99	2.43
	416127	N49843	Hs.79022	GTP-binding protein overexpressed in ske	1.97	1.41
	423961	D13666	Hs.136348	periostin(OSF-2os)	1.96	1.48
	430397	AI924533	Hs.105607	bicarbonate transporter related protein	1.96	1.31
	411010	AW813339		gb:MR3-ST0192-101299-013-c05 ST0192 Homo	1.96	2.73
65	439628	W81007	Hs.58628	ESTs	1.96	1.28
	444301	AK000136	Hs.10760	asporin (LRR class 1)	1.96	1.58
	431726	NM_015361	Hs.268053	KIAA0029 protein	1.95	1.72
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.95	1.87
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	1.95	1.06
70	417562	AW888754	Hs.134126	crystallin, gamma S	1.95	2.14
	424480	AA341442	Hs.205299	ESTs	1.94	1.94
	404342			C7002192:gi 7299207 gb AA54404.1  (AE0	1.92	1.32
	443320	AI051607	Hs.16335	ESTs	1.91	2.18
	449780	AA443241		ribosomal protein L44	1.90	1.76
75	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	1.89	2.16
	434416	AA805903	Hs.59498	cell division cycle 2-like 5 (cholinese	1.89	2.04
	457505	AL044659	Hs.43791	ESTs	1.89	2.34
	425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pl	1.88	1.26
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	1.88	1.88
80	428231	U17989	Hs.183105	nuclear autoantigen	1.88	1.88
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	1.88	1.88
	404429			Target Exon	1.88	2.18
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	1.88	3.04
	406641	AJ235667		gb:Homo sapiens mRNA for immunoglobulin	1.86	2.57
	417059	AL037672	Hs.81071	extracellular matrix protein 1	1.86	1.48
	454565	BE141231		gb:MR0-HT0075-081199-003-a09 HT0075 Homo	1.86	1.21
	415115	AA214228	Hs.127751	hypothetical protein	1.85	1.23

5	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	1.85	1.45
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	1.84	1.44
	403344			NM_000341:Homo sapiens solute carrier fa	1.84	1.84
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	1.84	2.33
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.84	2.02
10	401593			Target Exon	1.83	2.34
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	1.83	2.12
	406461			hypothetical protein, clone 24751	1.83	2.01
	455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.83	1.26
	400609			C10001147:gi12698926[jgb]AAK01739.1[AF33	1.82	2.08
15	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	1.81	1.14
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.81	1.22
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	1.81	2.10
	426521	AF161445	Hs.170219	hypothetical protein	1.81	2.08
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.81	1.64
20	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	1.80	1.34
	439606	W79123	Hs.58561	G protein-coupled receptor 87	1.80	1.80
	459189	AI909090		gb:IL-BT198-010499-007 BT198 Homo sapien	1.80	1.80
	412429	AV650262	Hs.75765	GRO2 oncogene	1.80	2.55
	402674			Target Exon	1.80	3.41
25	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.79	1.57
	454824	AW833646		gb:QV4-TT0008-161199-033-d09 TT0008 Homo	1.78	1.94
	401677			BAI1-associated protein 3	1.78	2.28
	426291	U58913	Hs.169191	small inducible cytokine subfamily A (Cy	1.78	1.53
	430028	BE564110	Hs.227750	Target CAT	1.78	1.59
30	445988	BE007663	Hs.13503	inactivation escape 2	1.78	2.10
	452272	AW292249	Hs.252739	hypothetical protein DKFZp434P0316	1.78	2.08
	418205	L21715	Hs.83760	troponin I, skeletal, fast	1.78	2.70
	400425	AY004252	Hs.287385	PR domain containing 12	1.77	2.02
	400419	AF084545		Target	1.77	2.67
35	447169	AI989803	Hs.157289	ESTs	1.77	2.21
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	1.77	2.12
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	1.76	2.54
	432808	NM_015985	Hs.278973	angiopoietin-3	1.76	1.76
	437400	AB011542	Hs.55599	EGF-like-domain, multiple 5	1.75	2.00
40	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.75	1.47
	444986	AI204197		ESTs	1.75	2.48
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	1.74	1.69
	413524	BE145837		gb:MR0-HT0208-101299-202-c07 HT0208 Homo	1.74	1.74
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	1.74	2.26
45	405579			C22000151:gi16806921[ref]NP_004165.1[ so	1.74	2.12
	405797			CX001015:gi11322384[emb]CAC16687.1[ (AJ	1.73	2.66
	405159			ENSP00000243337*:CDNA FLJ13984 fis, clon	1.73	2.01
	450569	AW192334	Hs.38218	ESTs	1.73	2.08
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	1.73	1.24
50	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	1.73	2.52
	454231	AW450669	Hs.45068	hypothetical protein DKFZp434I143	1.73	1.64
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	1.72	1.37
	422259	AA307584		gb:EST178498 Colon carcinoma (HCC) cell	1.72	1.72
	456034	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	1.72	1.34
55	451862	H09260	Hs.32333	ESTs	1.71	2.16
	403520			Target Exon	1.71	1.39
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	1.71	2.26
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	1.70	1.70
	418387	R18085	Hs.22279	gb:yg16b12.r1 Soares infant brain 1NIB H	1.70	1.70
60	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.70	1.87
	402538			C1001634:gi12621136[ref]NP_075245.1[ Ba	1.69	1.57
	414844	AA296874	Hs.77494	deoxyguanosine kinase	1.69	2.06
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.69	1.63
	446553	AB021179	Hs.15299	HMBA-inducible	1.68	2.02
65	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	1.68	2.12
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	1.68	2.03
	433930	AA620338		ESTs	1.68	2.28
	404151			Target Exon	1.68	1.80
	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	1.67	2.18
70	430070	AF197927	Hs.231967	ALL1 fused gene from 5q31	1.66	2.16
	400496			ENSP00000224716*:GTP-binding protein SAR	1.66	2.13
	413464	AL121500		ESTs	1.66	2.03
	411188	BE161168		gb:PM0-HT0425-170100-002-a10 HT0425 Homo	1.66	2.12
	446281	H69416	Hs.14606	hypothetical protein FLJ20271	1.65	2.28
75	443282	T47764	Hs.132917	ESTs	1.65	2.04
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.65	1.67
	453355	AW295374	Hs.31412	myopodin	1.65	1.66
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.54
	437929	T09353	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	1.65	2.04
80	410295	AA741357		nidogen (enactin)	1.64	2.30
	437767	AA830103	Hs.293331	ESTs	1.64	1.26
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	1.64	3.38
	450795	AW173371	Hs.60435	ESTs	1.64	1.64
	421847	NM_014717	Hs.108884	KIAA0390 gene product	1.64	2.75
	403010			C21000152:gi16226483[sp]Q52118[YMOS_ERWS	1.64	2.03
	406387			Target Exon	1.64	1.78
	440423	AW293995	Hs.192277	ESTs	1.63	2.05

	444381	BE387335	Hs.283713	hypothetical protein BC014245	1.63	2.07
	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.63	1.65
	442424	AI342715	Hs.129569	ESTs, Moderately similar to B34087 hypot	1.62	2.40
5	402885			Target Exon	1.62	1.18
	408786	AA773187	Hs.294027	ESTs	1.62	1.59
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	1.62	1.63
	414684	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart,	1.62	2.10
	406838	AA827569	Hs.153	ribosomal protein L7	1.61	1.41
10	441600	AA939347	Hs.127223	Homo sapiens cysteine knot protein (ZSIG	1.61	2.32
	420693	NM_001972	Hs.99863	elastase 2, neutrophil	1.60	2.37
	412649	NM_002206	Hs.74369	integrin, alpha 7	1.60	1.23
	432331	W37862	Hs.274368	MSTP032 protein	1.60	1.23
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.60	1.69
15	400279			NM_004581*:Homo sapiens Rab geranylgeran	1.60	1.56
	437865	AI472305	Hs.19565	ESTs	1.60	2.42
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	1.60	1.29
	442993	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1	1.60	2.11
	410684	AA088500	Hs.170298	ESTs	1.59	1.46
20	433149	BE257672	Hs.42949	hypothetical protein HES6	1.59	2.22
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	1.59	1.41
	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.59	1.26
	427654	AA410183	Hs.137475	ESTs	1.59	2.83
	411662	D60541	Hs.285519	Homo sapiens cDNA FLJ11904 fis, clone HE	1.59	2.18
25	440383	AA884208	Hs.30484	ESTs	1.58	2.19
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.58	1.58
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.58	1.47
	407857	AI928445	Hs.92254	synaptotagmin-like 2	1.58	1.51
	411573	AB029000	Hs.70823	KIAA1077 protein	1.57	1.29
30	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	1.57	1.17
	428471	X57348	Hs.184510	stratifin	1.57	1.55
	429249	X81479	Hs.2375	egf-like module containing, mucin-like,	1.57	1.19
	407966	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.57	2.12
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.57	1.05
35	430469	AW603667	Hs.288742	Homo sapiens cDNA: FLJ22712 fis, clone H	1.56	1.56
	445511	AA846512		Homo sapiens cDNA FLJ14459 fis, clone HE	1.55	2.08
	404501			nucleoside phosphorylase	1.55	2.54
	429107	AI470451	Hs.99075	ESTs	1.55	2.05
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	1.55	1.45
40	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	1.54	2.61
	458091	AF150286		gb:AF150286 Human mRNA from cd34 stem ce	1.54	1.54
	439280	AI125436	Hs.123654	ESTs	1.54	2.06
	428096	AW291771	Hs.42239	Homo sapiens, clone IMAGE:3868989, mRNA,	1.53	1.55
	414221	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCI_CGAP_Su	1.53	1.39
45	451712	AA019290	Hs.110489	ESTs	1.53	1.99
	402487			Target Exon	1.53	2.02
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.53	1.29
	452887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	1.53	1.21
	410253	T51823		ESTs	1.52	2.03
50	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	1.52	1.37
	432985	T92363	Hs.178703	ESTs	1.51	1.48
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.51	1.15
	429259	AA420450	Hs.292911	Plakophilin	1.51	1.31
	429289	AI400746	Hs.62187	phosphatidylinositol glycan, class K	1.51	1.19
55	441457	AW996651	Hs.43838	ESTs	1.51	2.08
	433365	AF026944	Hs.293797	ESTs	1.51	2.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.51	1.21
	424386	BE146577	Hs.285132	ESTs	1.50	1.53
	429655	U48969	Hs.211582	myosin, light polypeptide kinase	1.50	1.29
60	442391	AW450544	Hs.220751	ESTs	1.50	1.65
	414341	D80004	Hs.75909	KIAA0182 protein	1.50	2.10
	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	1.50	2.16
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.50	1.50
	443878	AW292499	Hs.139709	hypothetical protein FLJ12572	1.50	1.37
65	430152	AB001325	Hs.234642	aquaporin 3	1.50	1.43
	447752	M73700	Hs.105938	lactotransferrin	1.49	0.91
	404455			opioid receptor, kappa 1	1.49	1.36
	424106	AA412442	Hs.98132	ESTs	1.49	1.30
	433095	AK001092	Hs.302480	Homo sapiens cDNA FLJ10230 fis, clone HE	1.49	2.02
70	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.48	1.50
	456256	AB000450	Hs.82771	vaccinia related kinase 2	1.48	1.42
	439310	AF086120	Hs.102793	ESTs	1.48	1.48
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	1.48	1.15
	437981	AA774445	Hs.145365	ESTs, Weakly similar to KIAA1397 protein	1.48	2.36
75	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	1.47	1.21
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	1.47	1.25
	453864	AW021407	Hs.21068	hypothetical protein	1.47	2.18
	401067			ENSP00000252105*:CDNA FLJ12240 fis, clon	1.47	1.81
80	456054	BE313241		gb:601151545F1 NIH_MGC_19 Homo sapiens c	1.47	1.99
	402324			C19001982:gil3043638[dbj]BAA25483.1[ AB	1.47	2.03
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	1.47	1.29
	457734	BE394365	Hs.38750	hypothetical protein FLJ11526	1.47	2.26
	402013			Target Exon	1.46	2.42
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	1.46	2.09

5	430920	U96402	Hs.248132	goosecoid-like	1.46	2.46
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	1.46	2.02
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.46	1.43
	427719	AI393122	Hs.134726	ESTs	1.46	1.46
	433430	AI863735		ESTs	1.46	1.15
10	423790	BE152393		gb:CM2-HT0323-171199-033-a08 HT0323 Homo	1.46	2.36
	444083	AI123195		gb:oo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.45	2.29
	433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypotheti	1.45	1.50
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	1.45	1.17
	456664	AW963354	Hs.334409	metallothionein 1G	1.45	2.20
15	438158	AI796556	Hs.187884	ESTs	1.45	1.18
	409883	AW452419	Hs.296098	ESTs	1.45	2.00
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.45	1.27
	413048	M93221	Hs.75182	mannose receptor, C type 1	1.45	1.36
	457462	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	1.45	2.08
20	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	1.44	1.28
	401116			Target Exon	1.44	2.19
	419618	AA528295		gb:nh26e06.s1 NCI_CGAP_Pr3 Homo sapiens	1.44	2.30
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	1.44	2.03
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.43	1.48
25	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.43	1.51
	418742	AW451197	Hs.113418	ESTs	1.43	1.24
	418335	R63267	Hs.28399	ESTs	1.43	1.14
	408404	AW192518		gb:xl45h08.x1 NCI_CGAP_Pan1 Homo sapiens	1.43	2.08
	448175	BE296174	Hs.225160	hypothetical protein FLJ13102	1.43	2.29
30	431846	BE019924	Hs.271580	uroplakin 1B	1.43	2.12
	459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	1.43	2.00
	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	1.43	1.33
	442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (	1.43	1.10
	454843	AW834536	Hs.258549	gb:MR2-TT0014-241199-012-f06 TT0014 Homo	1.43	1.55
35	410281	AF076612	Hs.166186	Homo sapiens clone 23928 mRNA sequence	1.43	1.38
	402998			NM_002463*:Homo sapiens myxovirus (influ	1.42	2.16
	443709	AI082692	Hs.134662	ESTs	1.42	2.22
	435259	AA152106	Hs.4859	cyclin L ania-6a	1.42	2.01
	454407	AW578420	Hs.118843	gb:RC1-CT0249-120100-022-b04 CT0249 Homo	1.42	1.76
40	453359	AA448787	Hs.24872	ESTs	1.42	1.33
	434126	AI138589	Hs.118205	ESTs	1.41	2.06
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	1.41	1.46
	442316	Z75331	Hs.8217	stromal antigen 2	1.41	2.20
	438330	AW450572	Hs.257316	ESTs	1.41	2.20
45	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	1.41	2.02
	455885	BE153524		gb:PM0-HT0339-241199-002-C03 HT0339 Homo	1.41	1.33
	405550			C7001981*:gil565157[gb]AAB31881.1  T-cel	1.41	1.24
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	1.41	1.99
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	1.40	2.64
50	431022	AA490815	Hs.208351	ESTs	1.40	1.26
	439781	AA845538		glial cells missing (Drosophila) homolog	1.40	2.72
	429379	NM_014840	Hs.200598	KIAA0537 gene product	1.40	1.05
	435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprote	1.40	1.26
	430702	U56979	Hs.278568	H factor 1 (complement)	1.39	1.18
55	451331	AK002039		Homo sapiens cDNA FLJ11177 fis, clone PL	1.39	1.26
	459198	AI086347	Hs.151138	ESTs	1.39	1.22
	442344	AI022925	Hs.79368	epithelial membrane protein 1	1.39	1.35
	402917			ENSP00000202587*:Bicarbonate transporter	1.39	1.44
	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	1.39	2.08
60	437158	AW090198		KIAA1150 protein	1.38	2.07
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	1.38	1.24
	433911	AI923092	Hs.8899	ESTs	1.38	2.15
	402504			C1003823*:gil4826521[emb]CAB42853.1  {AL	1.38	1.38
	409465	AW393810	Hs.78054	gb:QV4-TT0008-251099-016-e11 TT0008 Homo	1.37	2.22
65	449426	T92251	Hs.198882	ESTs	1.37	2.38
	405491			Target Exon	1.37	2.74
	406685	M18728		gb:Human nonspecific crossreacting antig	1.37	1.34
	442410	AW996503	Hs.197680	ESTs	1.37	1.56
	407701	AW375009	Hs.164407	ESTs	1.36	2.02
70	400818			Target Exon	1.36	2.10
	406475			C15000508*:gil2558825[gb]AAC53387.1  {AF	1.36	2.78
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	1.36	1.41
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	1.36	2.20
	444195	AB002351	Hs.10587	KIAA0353 protein	1.35	0.94
75	447918	AI129320	Hs.115175	ESTs, Highly similar to JC5818 gamma-act	1.35	1.22
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	1.35	1.40
	412992	AI423369	Hs.75111	protease, serine, 11 (IGF binding)	1.35	1.24
	401025			NM_004055*:Homo sapiens calpain 5 (CAPN5	1.35	1.30
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	1.34	2.12
80	425308	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	1.34	1.02
	402308			Target Exon	1.34	1.21
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	1.34	1.40
	407242	M18728		gb:Human nonspecific crossreacting antig	1.34	1.22
	410741	Z11695	Hs.324473	mitogen-activated protein kinase 1	1.34	2.05
	439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobin, fa	1.34	1.12
	431254	NM_006069	Hs.251385	murine retrovirus integration site 1 hom	1.33	1.21
	405213			Target Exon	1.33	2.03



5	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1.33	1.05
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthase	1.33	2.09
	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	1.33	1.32
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	1.33	1.18
	430385	AA113437		N-myc downstream-regulated gene 3	1.32	1.48
10	447731	AA373527	Hs.19385	CGI-58 protein	1.32	2.22
	400740			hypothetical protein FLJ14280	1.32	2.01
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	1.32	1.32
	440274	R24595	Hs.7122	scrapie responsive protein 1	1.32	1.32
	406867	AA157857	Hs.182265	keralin 19	1.32	1.42
15	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	1.32	2.30
	443144	BE246335		hypothetical protein MGC14797	1.32	2.03
	432810	AA863400		ESTs	1.32	4.01
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.31	1.24
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	1.31	2.17
20	440099	AL080058	Hs.6909	DKFZP564G202 protein	1.31	1.53
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	1.31	1.31
	438874	HQ2780		gb:yj41a11.1 r1 Soares placenta Nb2HP Homo	1.31	2.03
	402825			Target Exon	1.31	1.24
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	1.31	1.45
25	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	1.31	1.19
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	1.31	1.12
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	1.30	2.06
	447409	AF060168		gb:Homo sapiens AS10 protein mRNA, parti	1.30	2.16
	400221			NM_002082*:Homo sapiens G protein-couple	1.30	2.02
30	437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.30	2.44
	450008	H52970	Hs.36688	WAP four-disulfide core domain 1	1.30	1.19
	441591	AF055992	Hs.183	Duffy blood group	1.29	1.03
	405973			Target Exon	1.29	1.32
	424604	AW865388	Hs.151076	KIAA1243 protein	1.29	0.92
35	410899	AW809716		gb:MR4-ST0124-241199-026-h09 ST0124 Homo	1.29	2.06
	405818			CX001073:gi 4176497 emb CAA20116.1} (AL0	1.29	2.05
	402621			Target Exon	1.29	3.06
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	1.28	2.35
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.28	1.44
40	453331	AI240665		ESTs	1.28	2.36
	439791	H77774	Hs.35755	ESTs	1.28	2.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.28	3.00
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	1.28	1.28
	446526	H89616		Homo sapiens cDNA FLJ13357 fis, clone PL	1.28	1.28
45	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	1.28	1.28
	418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	1.28	2.10
	407711	AI085846	Hs.25522	KIAA1808 protein	1.28	1.23
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	1.28	1.19
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	1.27	1.24
50	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.27	2.08
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	1.27	2.05
	444418	AL034417	Hs.11169	Gene 33/Mig-6	1.27	1.98
	427809	M26380	Hs.180878	lipoprotein lipase	1.27	1.09
	414690	BE410103	Hs.12313	hypothetical protein FLJ14566	1.27	1.36
55	439919	AA970710	Hs.128064	ESTs	1.27	2.28
	401311			Target Exon	1.27	2.05
	444235	AW207346	Hs.143202	ESTs	1.27	2.00
	430858	AF007190		Homo sapiens SIB 297 intestinal mucin (M	1.26	1.23
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	1.26	2.40
60	400161			Eos Control	1.26	1.33
	444239	R57988	Hs.10706	epithelial protein lost in neoplasm beta	1.26	1.20
	438369	T77886	Hs.83428	nuclear factor of kappa light polypeptid	1.26	1.26
	441944	AW855861	Hs.8025	Homo sapiens clone 23767 and 23782 mRNA	1.26	1.12
	431142	AA852596	Hs.250641	tropomyosin 4	1.26	1.23
65	434229	R56378	Hs.181223	hypothetical protein PRO2801	1.26	2.04
	406733	AA976565	Hs.297753	vimentin	1.26	1.29
	422292	AI815733	Hs.114360	transforming growth factor beta-stimulat	1.25	1.16
	424137	AA335769	Hs.16262	ESTs	1.25	1.27
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	1.24	1.50
70	424408	AI754813	Hs.146428	collagen, type V, alpha 1	1.24	1.29
	433750	H15448	Hs.31330	Homo sapiens clone HQ0319	1.24	1.27
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.24	1.13
	438357	AI042101	Hs.294107	ESTs	1.24	2.04
	409959	BE349470		mucin 6, gastric	1.23	2.22
75	439897	NM_015310	Hs.6763	KIAA0942 protein	1.23	2.44
	421982	AF206019	Hs.110347	REV1 (yeast homolog)- like	1.23	2.14
	407207	T03651	Hs.336780	tubulin, beta polypeptide	1.23	1.32
	416956	AA810664	Hs.101660	hypothetical protein MGC5391	1.23	2.39
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev9)	1.23	1.06
80	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	1.23	1.51
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.23	1.01
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.22	1.41
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.22	1.17
	421341	AJ243212		deleted in malignant brain tumors 1	1.22	1.09
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.22	1.52
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	1.22	2.55
	423189	M59371	Hs.171596	EphA2	1.22	1.15

	401899		Target Exon	1.22	1.22
	403579		Target Exon	1.22	2.34
	415954	AA171850	ESTs	1.22	2.24
5	429171	AI743173	ESTs, Weakly similar to ARL2_HUMAN ADP-R	1.21	1.14
	444071	AI627808	ESTs	1.21	2.23
	424344	AF036973	Hs.145477 HCGIV-6 protein	1.21	2.15
	434051	AF116622	gb:Homo sapiens clone FLB4217 mRNA seque	1.21	1.25
	422311	AF073515	Hs.114948 cytokine receptor-like factor 1	1.21	1.39
10	404600		Target Exon	1.21	1.29
	429751	M55210	Hs.214982 laminin, gamma 1 (formerly LAMB2)	1.21	1.03
	430392	NM_000627	Hs.241257 latent transforming growth factor beta b	1.21	1.21
	422687	AW068823	Hs.119206 insulin-like growth factor binding prote	1.21	1.23
	424855	AW204725	Hs.25560 ESTs	1.20	1.98
15	418890	AA232134	Hs.190028 ESTs	1.20	1.33
	413232	BE073258	Hs.133988 hypothetical protein FKSG28	1.20	2.18
	414154	AW205314	Hs.323060 ESTs	1.20	1.34
	416784	AA334592	Hs.79914 lumican	1.20	1.27
	410933	C15974	gb:C15974 Clontech human aorta polyA mRN	1.19	2.05
20	415388	AF018081	Hs.78409 collagen, type XVIII, alpha 1	1.19	1.11
	406731	AI559131	gb:U31907.x1 NCI_CGAP_U11 Homo sapiens	1.19	1.19
	447563	BE536115	Hs.160983 EST	1.19	1.14
	405531		Target Exon	1.19	2.02
	400363	NM_001403	eukaryotic translation elongation factor	1.19	1.21
25	426611	BE178050	Hs.171271 catenin (cadherin-associated protein), b	1.19	1.18
	427676	AA394062	Hs.300772 tropomyosin 2 (beta)	1.18	1.16
	413929	BE501689	Hs.75617 collagen, type IV, alpha 2	1.18	1.20
	413856	D13639	Hs.75586 cyclin D2	1.18	1.20
	427111	AA351026	Hs.173594 serine (or cysteine) proteinase inhibito	1.18	1.12
30	422287	F16365	Hs.114346 cytochrome c oxidase subunit VIIa polype	1.18	1.05
	412758	Y07818	Hs.74566 dihydropyrimidinase-like 3(ULIP)	1.18	1.06
	446868	AV680737	ESTs	1.18	1.18
	417613	AV654351	Hs.82306 destrin (actin depolymerizing factor)	1.18	1.17
	405542		Target Exon	1.18	1.98
35	419908	AW971327	Hs.293315 ESTs	1.17	2.02
	434095	AA011117	Hs.3745 milk fat globule-EGF factor 8 protein	1.17	1.19
	407230	AA157857	Hs.182265 keratin 19	1.17	1.35
	448413	AI745379	Hs.42911 ESTs	1.17	2.87
	426653	AA530892	Hs.171695 dual specificity phosphatase 1	1.17	1.39
40	424572	M19650	Hs.179600 2',3'-cyclic nucleotide 3' phosphodiester	1.17	2.08
	440109	AK001138	Hs.333149 hypothetical protein FLJ10276	1.17	1.06
	405131		C1002509:gi 9938010 ref NP_064684.1  odo	1.17	2.22
	422354	U20982	Hs.1516 insulin-like growth factor-binding prote	1.17	1.19
	442124	R66412	Hs.129013 Homo sapiens cDNA FLJ14309 fis, clone PL	1.17	1.11
45	400080		Eos Control	1.16	2.53
	431924	AK000850	Hs.272203 Homo sapiens cDNA FLJ20843 fis, clone AD	1.16	2.00
	412802	U41518	Hs.74602 'aquaporin 1 (channel-forming integral pr	1.16	1.30
	429207	AA447941	Hs.123423 ESTs	1.16	1.27
	415149	X12451	Hs.78056 cathepsin L	1.16	1.12
50	400231		Eos Control	1.16	1.17
	416653	AA768553	Hs.193145 metallothionein 1E (functional)	1.16	1.16
	422813	AV656571	Hs.121068 transmembrane 4 superfamily member 6	1.16	1.10
	439318	AW837046	Hs.6527 G protein-coupled receptor 56	1.16	1.15
	422424	AI186431	Hs.296638 prostate differentiation factor	1.16	1.21
55	432745	AI821926	gb:nt78f05.x5 NCI_CGAP_Pr3 Homo sapiens	1.15	2.00
	412477	AA150864	microsomal glutathione S-transferase 1	1.15	1.23
	430361	AI033965	Hs.239926 sterol-C4-methyl oxidase-like	1.15	2.31
	424512	X53002	Hs.149846 integrin, beta 5	1.15	1.15
	449924	W30681	Hs.146233 Homo sapiens cDNA: FLJ22130 fis, clone H	1.15	1.24
60	414682	AL021154	Hs.76884 inhibitor of DNA binding 3, dominant neg	1.15	1.07
	456076	BE243877	ATPase, Na <sup>+</sup> transporting, beta 3 polypep	1.15	2.00
	403026		Target Exon	1.15	2.32
	422545	X02761	Hs.287820 fibronectin 1	1.15	1.17
	412719	AW016610	Hs.816 ESTs	1.15	1.05
65	421848	X15880	Hs.108885 collagen, type VI, alpha 1	1.15	1.14
	422087	X58968	Hs.111301 matrix metalloproteinase 2 (gelatinase A	1.15	1.16
	413936	AF113676	Hs.297681 serine (or cysteine) proteinase inhibito	1.14	1.13
	449845	AW971183	Hs.6019 DnaJ (Hsp40) homolog, subfamily C, membe	1.14	2.07
	430202	T85775	gb:yd60g02.r1 Soares fetal liver spleen	1.14	1.14
70	418806	AA485970	Hs.191718 ESTs	1.14	2.14
	424017	AA333789	gb:EST37925 Embryo, 9 week Homo sapiens	1.14	2.16
	422003	AA361760	Hs.296326 ESTs	1.14	1.17
	437272	AW975957	gb:EST388066 MAGE resequences, MAGN Homo	1.14	2.17
	438367	N79688	Hs.204354 ras homolog gene family, member B	1.14	1.23
75	453152	AK001933	Hs.31945 hypothetical protein FLJ11071	1.13	2.36
	406849	AA454809	Hs.172928 collagen, type I, alpha 1	1.13	1.33
	422110	AI376736	Hs.111779 secreted protein, acidic, cysteine-rich	1.13	1.06
	425335	BE394327	Hs.296267 follistatin-like 1	1.13	1.08
	434795	BE620794	Hs.4147 translocating chain-associating membrane	1.13	1.08
80	417426	NM_002291	Hs.82124 laminin, beta 1	1.13	1.11
	452924	AW580939	Hs.97199 complement component C1q receptor	1.13	1.01
	416379	N38857	Hs.34145 ESTs	1.12	1.12
	421464	AA291553	Hs.190086 ESTs	1.12	2.01
	442420	AI024834	Hs.131729 ESTs	1.12	1.15

	405369			NM_005569*:Homo sapiens LIM domain kinas	1.12	1.99
	421730	AW449808	Hs.334534	glucosamine (N-acetyl)-6-sulfatase (Sanf	1.12	2.08
	405932			C15000305:gi 3806122 gb AAC69198.1  (AFO	1.11	2.01
5	453542	AW836724		Homo sapiens mRNA expressed only in plac	1.11	2.00
	437585	AW976857		ESTs	1.11	2.01
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.11	1.05
	449931	AW875786	Hs.25734	ESTs, Weakly similar to BING1 [H.sapiens	1.11	1.03
	407085	Z70759		gb:H.sapiens mitochondrial 16S rRNA gene	1.10	1.12
10	447191	NM_014521	Hs.17667	SH3-domain binding protein 4	1.10	1.04
	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.10	1.07
	432675	AI791855	Hs.105884	ESTs	1.10	2.30
	432731	R31178	Hs.287820	fibronectin 1	1.09	2.12
	430763	AA485468		DNA fragmentation factor, 45 kD, alpha p	1.09	2.10
15	438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	1.09	1.04
	405156			NM_003213*:Homo sapiens TEA domain famil	1.09	2.19
	409031	AA376836		ESTs	1.09	2.22
	422608	AW160644	Hs.118695	potassium voltage-gated channel, subfamI	1.09	2.26
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.09	1.28
20	410577	X91911	Hs.64639	glioma pathogenesis-related protein	1.08	2.64
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	1.07	1.02
	452219	AA024860	Hs.61224	ESTs	1.07	2.08
	430108	AA465294		ESTs	1.07	2.11
	402174			Target Exon	1.07	2.11
25	416952	AI767736	Hs.290070	gelsolin (amyloidosis, Finnish type)	1.07	1.00
	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fis, clone H	1.07	1.13
	442670	BE410050	Hs.11859	hypothetical protein FLJ13188	1.07	2.21
	442310	AF033199	Hs.8198	zinc finger protein 204	1.06	2.04
	405536			NM_005805:Homo sapiens 26S proteasome-as	1.06	2.20
30	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	1.06	1.06
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	1.06	1.06
	425371	D49441	Hs.155981	mesothelin	1.06	1.27
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	1.06	2.37
	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.06	1.05
35	409407	AW967370	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	1.05	2.00
	406109			Target Exon	1.05	2.04
	418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	1.05	2.67
	403162			C2000231*:gi 9802031 gb AAF95597.1 AF239	1.05	2.07
40	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	1.05	1.07
	407225	J04617		eukaryotic translation elongation factor	1.05	1.02
	416955	AW889150	Hs.80595	NM_004552*:Homo sapiens NADH dehydrogena	1.05	1.10
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	1.04	2.12
	410276	AI554545		angiotensin-2	1.04	1.04
45	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.04	1.04
	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.03	1.05
	406773	AA812424	Hs.76067	heat shock 27kD protein 1	1.03	1.10
	452082	N51905	Hs.125133	hypothetical protein FLJ22501	1.03	2.01
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	1.03	2.24
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	1.02	1.00
50	408339	R97502	Hs.30443	sentrin/SUMO-specific protease	1.02	2.19
	400247			Eos Control	1.02	2.04
	430030	BE300094	Hs.227751	lectin, galactoside-binding, soluble, 1	1.01	1.01
	442275	AW449467	Hs.54795	ESTs	1.01	1.04
	406786	AW161678	Hs.111334	ferritin, light polypeptide	1.01	1.06
55	439403	BE265745		ESTs, Weakly similar to ALUC_HUMAN !!!!	1.01	2.11
	428043	T92248	Hs.2240	uteroglobin	1.00	1.06
	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.02
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	2.16
	450724	R55428		gb:yj79b05.r1 Soares breast 2NbHBst Homo	1.00	0.99
60	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	1.00	1.08
	432077	AL134685		gb:DKFZp547M126_r1 547 (synonym: hfbr1)	1.00	2.05
	427687	AW003867	Hs.1570	histamine receptor H1	1.00	1.00
	435256	AF193766	Hs.13872	cytokine-like protein C17	1.00	1.00
	420026	AI831190	Hs.166676	ESTs	1.00	1.00
65	455128	AW861555	Hs.314372	EST	1.00	1.00
	410685	AA497117	Hs.58893	ESTs, Moderately similar to ALU1_HUMAN A	1.00	1.00
	401404			Target Exon	1.00	1.00
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	1.00	1.00
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	1.00	1.00
70	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	1.00	1.00
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, alp	1.00	1.00
	447947	N33033	Hs.270215	ESTs	1.00	1.00
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	1.00	1.00
	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	1.00	1.00
75	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheri	1.00	1.00
	444963	AI916973	Hs.213603	ESTs	1.00	1.00
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	1.00	1.00
	442849	R10099	Hs.269805	ESTs	1.00	1.00
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	1.00	1.00
80	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	1.00	1.00
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	1.00	1.00
	459045	N69101	Hs.40730	ESTs	1.00	1.00
	455500	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	1.00	1.00
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	1.00	1.00

5	429932	AI095005	Hs.21586	ESTs	1.00	1.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	1.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	1.00	1.00
	431374	BE258532	Hs.251871	CTP synthase	1.00	1.00
	443162	T49951	Hs.9029	DKFZP434G032 protein	1.00	1.00
	432128	AA127221	Hs.296502	ESTs	0.99	2.33
	451838	AW005866	Hs.193969	ESTs	0.98	3.26
	438414	AA806794	Hs.131511	ESTs	0.97	3.61
10	435872	AA701357	Hs.192759	ESTs	0.97	0.96
	425211	M18657	Hs.1867	progastricin (pepsinogen C)	0.97	1.08
	424001	W67883	Hs.137476	paternally expressed 10	0.96	2.25
	418869	AW516565		gb:xq01d05.x1 Soares_NHCeC_cervical_tumo	0.96	2.07
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	0.94	2.18
15	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	0.94	1.31
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	0.94	2.12
	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	0.94	2.19
	452239	AW379378		protein tyrosine phosphatase, receptor t	0.94	0.79
	403167			Target Exon	0.94	2.06
20	402209			Target Exon	0.92	2.04
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	0.92	0.74
	424090	X99699	Hs.139262	XIAP associated factor-1	0.91	2.11
	432816	N38913	Hs.221575	ESTs	0.91	2.15
	451779	AW968616	Hs.296234	ESTs, Weakly similar to T31613 hypotheti	0.91	2.14
25	406851	AA609784		major histocompatibility complex, class	0.89	1.04
	427698	AW972594	Hs.335499	ESTs	0.89	0.90
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-II	0.88	2.42
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.87	1.14
	426024	Z43405	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	0.87	2.04
30	400986			NM_024085*:Homo sapiens hypothetical pro	0.87	2.10
	430353	AW952337		citrate synthase	0.86	2.28
	404975			uncharacterized hypothalamus protein HT0	0.86	2.50
	406673	M34996	Hs.198253	major histocompatibility complex, class	0.86	1.94
	431323	AW970623		gb:EST382705 MAGE resequences, MAGK Homo	0.80	2.08
35	404926			Target Exon	0.79	2.01
	432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	0.77	0.86
	437601	AA761546	Hs.248844	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	2.10
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	0.76	2.66
	406646	M33600	Hs.308026	major histocompatibility complex, class	0.76	1.09
40	442195	NM_001430		endothelial PAS domain protein 1	0.76	2.00
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.76	0.78
	413916	N49813	Hs.75615	apolipoprotein C-II	0.73	2.06
	453716	AA037675	Hs.152675	ESTs	0.73	2.10
	437802	AI475995	Hs.122910	ESTs	0.70	2.08
45	422282	AF019225	Hs.114309	apolipoprotein L	0.68	2.95
	410361	BE391804	Hs.62651	guanylate binding protein 1, interferon-	0.54	2.11
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	0.53	0.53

TABLE 34B:

50	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
55	Pkey	CAT Number	Accession
	442006	1239046_1	AW975183 AA973583 AI365103 AI699495 AI301787
	420195	28714_1	AK002039 AL117524 AV714494 AW954901 AL045243 BF955185 AU137860 AW880615 AW880496 AA256290 BE767078 N44348 AI886676 AA455877 N66571 AA999864 AU157344 AI817146 R54821 BE223107 AA455880 AI355752 BF589210 N63487 AI924033 AI923020 AI306145 AI919421 AI584169 AI250173 AI440227 AA669696 AW244040 AI358104 AI570333 AI418315 N94787 R72348 N94780 BF944396 BF754698 AW005707 N98831 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N63481 BE838574 BF909132 BI084973 BG257295 BG818471 BE348449 AI420623 AW271213 BE048764 W44682 AI887849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 BI045196 AW880645 437620 9575_20 AW976930 AW292808 AW451796 BF514112 AI806378 AI658903 AI769457 AW593455 AI625525 AI538551 AI660509 AA761825 AA973287 AA861483 W73065 AI735361 W60499 W76653 BG959557 AW044647 AI670953 AI656180 AA484715 AI659205 BF923472 430712 301999_1 BE088101 T05990 AW872477 411880 1139083_1 AF231512 AW300273 BG779015 AW510935 AI989816 AA137069 AI748876 AW150861 AI862628 AI805872 AI675382 BE855437 AW044703 451149 4941_2 AI677769 AA886718 AI753144 AA626885 AI018092 AI263010 AW026173 BE221138 AA256268 AW571932 AW276137 AI634216 AW296259 AA977716 AI302589 AA348340 AI720838 AI311733 AA015867 N73713 AL047586 AW840354 AA256196 AW840357 AW840504 T35664 Z36755 AW954421 AA247424 AI056930 T31380 BI910428 H88489 BG675223 AA443427 BE879501 AA478530 R72977 AA298568 BF792417 AA356982 BF922499 BE764808 BE565636 BF903986 BF331881 N42207 BG623760 BG611090 BF735387 BE697757 BE697755 BE718853 N78560 AI984095 AA137140 AA053711 N59865 AI078134 AA643796 T57803 AA018642 N66799 AI004600 BG896323 BF895104 N73684 N73806 N73811 AW900287 AA018641 459702 539529_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 417563 2243443_1 AA203701 R86895 431089 125941_2 BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826 455797 1511159_1 BE091833 BE091874 BE091871 413059 1488711_1 BE063078 BE151503 BE151498 417430 40161_2 AW872732 AW827432 AA199662 AA610519 R54983 432222 539529_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 458208 45807_4 AI990640 AI380016 BM273298 BM273060 80 457741 120741_1 BI017968 BE044740 BI017768 AW827360 BF380597 BI017970 BF746974 BF380582 BF380592 BF908552 BF907924 BF380784 BF380651 BF380634 BE166581 BE161439 BF908606 BI017961 BE044718 AW827623 BF907758 BI017967 AW827621 AA653908 BI017765 BI017955 BI017960 BI017798

5	411010	1066474_1	AW813381 AW816094 AW813357 AW814469 AW813293 AW816099 AW813295 AW813425 AW813331 AW813325 AW813351 AW813427 AW813339
	449780	31099_2	BG721806 BG623574 AA367501 BG436403 BG619828 BG570704 BF086115 BF086118 R78932 BG620860 BG571920 BF997723 AA368244 BG620631 BG621967 BG435818 BG620442 BG621518 H12650 BG573175 H61600 R67494 H01715 D78811 BG435953 BF107266 D79043 R67255 H01310 BG570941 BG570693 R21776 AA327133 R32578 R30775 BG570963 T86946 H61601 W86279 BF991104 R21732 BF990905 BG622861 BE929694 AI090290 BE929277 BE929284 AA367783 AA082581 D78839 H78318 N91085 BE929344 D63217 BE929334 H53536 R80360 H54070 C17064 AW962470 R00900 BG619698 BG623946 H94918 BE929345 AA004267 BF957177 BG620685 BF086421 T87029 C17044 H60972 BG573514 AA131924 D78838 BG003560 C18615 W86323 R09737 R02529 AA367502
10	406641	0_0	AJ235667 AJ235668 AJ235669 AJ235670
	454565	1061836_1	BE141160 BE141231 BE141793 BE141791 BE141167 BE141807 BE141806 BE141805 AW807591 AW807590 AW807586 AW807583 BE141803 AW845918 BE141207 BE141158
15	455657	1490185_1	BE065209 BE065364 BE065110 BE065111
	459189	MH1945_5	AV683451 AK057494 BG718853 BM152866 BG309826 BE709644 AI864727 BI045181 BI459637 AI909102 AI909090 BG722507 BI023834
20	454824	1073655_1	AW833783 AW833646 AW833525 AW833351 AW833526 AW833825
	444986	704733_1	AW268472 AI204197 AW592537
25	413524	1518859_1	BE145894 BE145837 BM263472
	422259	140437_1	BF821471 AW795791 BF844843 BF821371 AA307584 AW795790 BF833724 BE154067 BE064709
30	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	426603	1299162_1	AA994657 AA382291
35	456235	1979764_1	AA203637 AA832266 H67452
	433930	19851_15	AW873618 AA620338
40	413464	415532_1	AL527514 AI732432 AA133309 AI225224 AV700997 BF589361 AW291763 AL121500 AA129708
	411188	1072487_1	AW821260 BE162466 BE161168
45	410295	2817_1	BG402852 BG545066 AA150252 AL036760 AA452480 AI033256 W68776 W93372 N31248 AI052219 AI367635 W69374 N88610 R58194 BI524854 BI497111 BF940043 AI129268 AI359798 AI056480 AA121421 AI042150 AW449003 AI418180 AI419420 AI356058 BF832243 AI349330 AI359448 W76647 BF477170 AA099163 BF994549 AW608256 AA045418 H03770 AL574791 AW069455 BE302148 AW022281 AW960273 AA121268
			AI336371 AI989381 AI131425 AI147483 AI311537 AW338638 AI141649 AA709414 AI187177 AA780884 AI333805 AA045312 AI623918 AI349421 W63753 W70299 AA557276 AA299007 N98212 W74064 N24823 T54892 AA054724 W73059 AI869152 N93462 W71889 AI537432 R71628
50			AA303089 AI498550 T60941 AV706417 AW067848 AI150677 AW338118 AI336313 AA826256 AI139518 AA662948 AA902723 AI970175 W68682 AI089380 AI148372 H99951 AW183001 AI270317 AA532767 AA044727 AA931652 R82469 AA150261 W67788 H67495 R80715 AW149812 N78914 AI862034 W61122 AW023118 W69375 T88917 T47984 N21531 R35646 AA055544 H15534 AA688295 AA090586 AA044764 BF994641 R79547 N21313 BF674610 H02874 AW975323 R16904 AA328030 AA054671 R79546 BF832310 AI249109
	400279	2140_1	Y08200 NM_004581 BC003093 BE733834 BI753321 BG773890 BF091906 BI917541 AI023762 AA587230 BF435086 AI264262 AI687392 AI810536 AW589886 AI244419 AA749261 AA553435 AW205689 AI765770 AI765431 C02465 AW305347 AI818456 AA322111 AW381845 AW381829 AV749407 AA811636 AU159893 AA603065 AA652542 AI468678 R49616 AW381863 BE389867 BE182387 BF087771 AA527551 AA134051
55	445511	9560_8	AA831504 AA134052 AI871759 AW089048 BI913532 AA367709 BG828155 BF093014
			BM471219 BE093160 BG171761 BI254009 AI905474 AA453162 AA829759 AI086559 AA776022 AI377446 BF589018 AA452822 AW614566
60			AA443880 AA476733 AW970674 AI393291 AA988283 AI905528 AW384956 D78656
	458091	452694_1	AF150286 AV739062 AA835857
65	414221	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	410253	132134_1	AA774785 AA584875 AA577705 AA683178 AA083204 AW362057 T92332 T51823 T02858 AA083375 T92381
70	407102	7177_2	AW945170 BF930905 F33652 BG057818 AI368018 AI421485 AI300352 AI378525 AI264177 AI276281 AI245302 AI281050 AI190036 AW451438 AW242903 AA910870 F22289 F19647 F22375 AW473816 BF445785 AA774528 F33447 C01077 AW772227 F17759 H42812 R09701 AA349096 R48772 H42892 H42537 R47898 N28263 H25721 F32386 H43971 R48205 F21390 H45809 AA007629 R47897 R83734 H45844 AW983653 H43970 H42536 H24495 R48875 H42961 H22079 R86018
	456054	1263570_1	BF314481 BE313241 BI196333 BE383148
75	409368	110612_1	AA071059 AA085201 AA085020
	433430	2181751_1	AA961586 AI863735 AA588325
80	423790	886344_1	BE152393 AA330984 BE073904 BF176271
	444083	10908_12	BI836699 AI123195
85	419618	252691_1	BG168298 AA247945 AA528295 AW971284
	408404	658475_1	BF308898 BE298629 BE298765 AW192518 BE299614 BE300025 BF307463
90	459557	859794_1	BG623239 N58315 AI524952
	455885	1524553_1	BE153524 BE153576 BE153583
95	451385	85022_1	AA019761 AA017656 AA017374
	439781	2592493_1	AA845538 AA890229
100	451331	28714_1	AK002039 AL117524 AV714494 AW954901 AL045243 BF955185 AU137860 AW880615 AW880496 AA256290 BE767078 N44348 AI886676 AA455877 N65571 AA999864 AU157344 AI817146 R54821 BE223107 AA455880 AI355752 BF589210 N63487 AI924033 AI923020 AI306145 AI919421 AI584169 AI250173 AI440227 AA669696 AW244040 AI358104 AI570333 AI418315 N94787 R72348 N94780 BF944396 BF754698 AW005707 N98831 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N63481 BE838574 BF909132 BI084973 BG257295 BG818471 BE348449 AI420623 AW271213 BE048764 W44682 AI887849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 BI045196 AW880645
	437158	59575_1	AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602
105			AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI880606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847
	406685	0_0	M18728
110	430385	MH497_8	NM_032013 AB044943 AF308609 BI769254 AI819262 AA845639 AI289073 BE670187 AA207127 T33098 AA633492 BE328324 AI083620 AI204945 AA903471 AI372602 AI049836 AI049737 BF000101 AI686167 BF436896 AI659189 T32971 AA311302 AW733149 AI435981 T03438 AA879206 AI972177 T33083 AA613910 AI971019 AI027140 AA853739 AI620528 AI637519 AI972307 BF054861 AK027665 BF082751 AI598127 T33663
			AA204743 BE086660 F12132 T26372 BF765338 AA323106 AA322907 BI037062 BE315235 AV722868 BE254381 T66212 BE566142 T09034 AA406202 BF843940 AI743855 AA113356 BG990683 BE086729 BE535539
115	443144	16112_3	AB058726 AI651414 BE245990 BE245765 BF439734 AA648422 AA040639 AI340155 AA255928 AA278365 BE766296 AA280771 AL555562 AI474638 AI863068 BI260946 AK027039 BG615852 AI698039 AA252016 AA258886 BE905205 AW501167 BF514117 BI857400 AW297001
			AI624923 AA125900 AW272165 AA190967 AA280729 AA035532 AW129692 AA125899 BG528645 BE614599 BE464693 AI560128 AA551511 AI351149 AL555561
120	432810	101919_1	BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017
			AI286003 AI147163 AA626033 AI539156 AA565542 AI094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 AI991439 R46187 BE929954 AA333976 D63102 BF744491
125	438874	52147_1	AF075017 R66779 R22463 H02780
	400221	9287_3	NM_002082 L16862 BG828886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823182 H16710
130	437751	643238_1	AW978796 AA767373 AW173343 AA836163 N27563 AA905328 R97032



5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

BG290073 BI667399 BM451469 BI667173 BI602139 BG532171 BI669216 BI544727 BG721852 AV716503 AV701327 BM090738 BI492000  
 AI308856 BI544904 AL599813 AV715829 AV716505 AV714587 AV717902 BF668072 AV716385 BI461927 BM090954 AV717826 BG503676  
 AV647719 BG501392 BG428433 BE895629 BM313117 AW021050 BG435032 BM152910 AA313503 AA872377 BG574714 AV712054 AV732696  
 AA252476 AV712759 AL599643 BE790872 BG654930 W73337 AW675377 AV760376 AV725139 AV716379 AA887165 BE830003 AW023796  
 AL599291 AI902948 BG944042 F00781 AA352483 BG217897 N33888 AW581924 BG654730 D31410 AA353088 D31288 AA295029 H95170  
 BE935104 AU139980 BG772963 BG776470 BG532512 BG105449 BI545421 AV715456 AW386083 BG699714 AL535832 AL514940 BG190861  
 BG210593 AW999254 H95138 AA353863 BE764809 N50375 BE091363 BG701255 BI860846 BI832485 BG168150 BG028647 BE546301  
 BG900321 BI909737 BG702363 BG614141 BG611137 BG700121 BF031492 N85802 AV715940 N51590 BG993478 BE172016 AW893622  
 AK056692 AF086220 AI375066 AA284293 W32566 AW797961 AA960897 AA504145  
 BF060834 BI019048 AW862002 AK056737 AA429538 AW063311 AW440655 AW231970 AA428584 AA995028 AW854593 AA984131 AA552874  
 AA564758 AA528743 BG927275 BE045117 AW975234 AA664937 BF749390 BG928948 AA984546 BE009153 AV732487 BE078167 AW872716  
 AW063245 AA578441 AI820704 AI732283 R55428 BF999154 BF880485  
 AL134685 AW972760 AA525319 AA526644 AA525342 AA526632 AA525296 AV739423 AW972755  
 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526  
 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360  
 AW852530 AW852526 AW852527 AL597969  
 AW811114 AW811095 AW811094 AW811124 AW811157 AW811054 AW811087  
 AW810001 BF374633 AW809694 AW809672 BF374748 BF374562 AW810209 AW810092 AW809786 AW810428 AW810429 AW809884 BF374650  
 BF374641 BF374764 BF374744 AW810552 BF374678 BF374653 BF374579 AW810168 AW810170 BF374611 BF374676 BF374667 AW810353  
 BF374682 AW810154 BF374688 BF374565 BF374757 BF374637 BF374743 BF374719 AW809664 BF374643 BF374680 BF374714 BF374708  
 BF374716 AW810432 BF374691 BF358066 AW810006 AW810345 AW809960  
 AW963582 BE064192 BE064169 BE152580 AW963587  
 AV704306 BF368780 AW867826 AW859896  
 AA229762 AA230035  
 AW972670 AA525808 H28359 H28383  
 BG034853 AW173315 AW303375 BG190225 BG939153 BF057308 AA600736 AI751258 AI090486 BE939504 AW631492 AI768270 AI862133  
 AA417652 BE378218 AA599207 AW794702 AA024968 AA446024 AI148235 AI191710 BI493797 AI272646 BI493796 AA634323 AI754332  
 AA258414 C05155 AI218226 AI039656 AI350380 AI084698 AI754989 AI673545 AI432010 AI751035 AA375571 AA446297 BG216743  
 AA609784 R97304  
 BC010106 AL560552 AU133296 AU133086 BE268567 BE268523 BI544879 BE398161 BG473088 BI544445 BE258021 BE296339 BE255040  
 BE263020 BG706790 AL598627 AW952337 BG758113 AW512753 BE267666 BE253415 BI225718 BE268350 BE258245 BI224965 AW772605  
 BG723903 BE397282 BI196341 BG702880 AI878949 AL600437 AA416759 BE259917 AI031582 BF512142 AI088248 BE560328 AI802623  
 AI288613 AL597585 AW768553 AI816352 BF732831 BI225687 AA833686 AA722593 AA807750 AW068064 AA405187 AI923236 N51593 AL527710  
 BG282576 AL525927 AL525971 BI869547 AI064725 R91856 H46814 H20112 W01682 AW848870 AW848585 AW376662 AW848985 AW848937  
 AW848862 AW848581 AW848512 AW848176 AW752623 AW752618 AW376822 AW376821 AW376684 AW376623 AW376622 BE706047  
 AW752602 AW752691 AW752674 AW752652 AA379167 AW752610 AW752684 AW752613 AW752660 AW848709 AW848576 AW848915  
 AW848981 AW848980 AW848979 AW848978 AW848973 AW848916 AW848713 AW848708 AW848642 AW848641 AW848639 AW848573  
 AW848493 AW848492 AW848489 AW848488 AW848487 AW848353 AW848352 AW848220 AW752698 AW752697 AW752682 AW752681  
 AW752680 AW752679 AW752664 AW752651 AW752638 AW752637 AW752636 AW752628 AW752626 AW752624 AW752619 AW752596  
 AW752608 AL582019 BE875587 AL529175 AW965868 BG686208 AA259073 BE696973 AA459543 AA358314 W40564 BF926427 AW849000  
 AW848718 AW848515 AW848507 AW848444 AW848440 AW848232 AW848222 AW752657 AW376786 AW376781 AW376615 AW376614  
 BI752581 AA534520 AI748906 AA047799 AI014753 AL514460 AL581982 BG743146 W24171 H20102 H11227 AW752607 AW006596 AW130378  
 BE716519 AW752661 AW848289 BF349557 AW752612 AW752632 AW848910 NM\_004077 AF047042 AL560606 BI765896 BI196831 BI855656  
 BE906674 BG749937 BE535486 BE019810 AA313713 AA992542 AA332541 AA682985 AA356125 BE140478 BG750945 BI457548 BG025661  
 BF326302 AA325019 BG980676 AA337465 AA321974 BG949285 BG427585 R23979 BG611485 BE560678 W16977 N50379 BG824101 BG471750  
 BI463171 W04691 AU099360 BG471590 BM011999 BE262945 BE559801 BF756438 BE881957 BE314546 BG911831 BG150811 BG112017  
 AA157518 T92368 AW752620  
 AW970623 AA502839 AA502819  
 U81984 NM\_001430 BE907085 BI333232 AI021986 AU138476 C18601 U51626 AU100517 BI054387 AU076970 BE786454 BG010080 AW377189  
 BF998789 AA368139 R11396 T83613 BG006324 BI012404 BG001643 BF757957 AL549361 AL544018 BE002870 BE929314 BE090199 AL046650  
 BI053717 BE929315 BI054967 BF960055 BF925432 R05421 BF922073 T70331 BI004403

TABLE 34C:

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405443	7408143	Plus	90716-90887,101420-101577
401645	7657839	Minus	34986-35133
401673	7689903	Minus	122587-122705,122765-123047
405120	8099940	Plus	140176-140340
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
402333	8844110	Minus	165693-165856
404942	7382153	Plus	92095-92252
403362	8571772	Plus	64099-64260
402641	9958129	Minus	122596-125136
405600	5923640	Plus	26662-27225
405061	7656744	Minus	132492-132932
402327	7656695	Minus	108675-108770,109801-109910
404342	9838093	Plus	115854-116033
404429	7407979	Plus	31352-31498
403344	8569726	Plus	70823-70990
401593	7230957	Plus	10368-10572,11293-12356
406461	9756020	Minus	158842-159136
400609	9887671	Minus	92037-92247
402674	8077108	Minus	39290-39502
401677	9965537	Minus	62856-63086,63603-63884
405579	6456174	Plus	100996-101542
405797	1934909	Minus	5599-5681,5821-6104

5	405159	9966252	Plus	79659-79804
	403520	7684483	Minus	97621-98084
	402538	9801137	Minus	96314-96539
	404151	7534014	Minus	69038-69399
	400496	9743564	Plus	41515-41695
	403010	3132346	Plus	78385-79052
	406387	9256180	Plus	116229-116371,117512-117651
	402885	9926751	Plus	71919-72049
10	404501	7229859	Minus	37270-37526
	402487	9797538	Plus	75677-75843
	404455	7677926	Minus	26927-27611
	401067	5764724	Minus	153366-153509
	402324	7630361	Plus	26052-26803
15	402013	7407997	Plus	174540-174634,175449-175568
	401116	9966559	Plus	123579-124447
	402998	2996643	Minus	17175-17373
	405550	1552494	Plus	91720-92115
	402917	7406502	Minus	1034-1177,3143-3266
20	402504	9797871	Plus	12366-12614
	405491	5801645	Plus	81857-82045
	400818	8569994	Plus	172644-172765,173085-173200
	406475	9797684	Plus	125417-125563,128052-128180
	401025	8117518	Minus	179287-179483,181044-181166,181844-18203
25	402308	7340295	Minus	92080-93638
	405213	6692345	Minus	50267-51151
	400740	7329267	Minus	79920-80510,80576-80746
	402825	6165330	Minus	78572-78807
	405973	8247789	Plus	103859-104254
30	405818	4071056	Plus	29055-29196
	402621	9930950	Plus	130806-131036
	401311	9212516	Minus	180124-180754
	401899	7230209	Minus	155620-155815
	403579	8101179	Minus	36167-36365
35	404600	8705107	Plus	118354-118444,118649-118792
	405531	9665194	Plus	35602-35803
	405542	9857564	Plus	71331-72183
	405131	8516051	Minus	136764-137594
	403026	7670575	Plus	56521-56840
40	405369	2078469	Minus	34183-34357,35686-35751
	405932	7767812	Minus	123525-123713
	405156	9966228	Plus	146733-146860,147899-147961,153127-15325
	402174	8575912	Plus	253499-253674
	405536	9795661	Plus	164091-164162,164397-164516,166720-16679
45	406109	9127147	Minus	58328-58485
	403162	9838085	Plus	82652-83613
	401404	7710968	Plus	136474-136646
	403167	9838127	Plus	162599-162935
	402209	8576119	Minus	53315-53472
50	400986	8085497	Minus	63140-63319
	404975	3419864	Minus	86096-86605
	404926	7341919	Minus	150411-151484

55

TABLE 35A: About 323 genes upregulated in hypersensitivity pneumonitis relative to idiopathic pulmonary fibrosis or non-specific interstitial pneumonitis

60

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: 90th percentile of HP AIs divided by 90th percentile of IPF AIs, where 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.

65

R2: 90th percentile of HP AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.

70

75

80

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
402550			Target Exon	4.03	4.70
421563	NM_006433	Hs.105806	granulysin	3.37	2.70
424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	3.31	2.42
417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	3.09	1.51
411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	2.99	1.28
416350	AF188625	Hs.189507	phospholipase A2, group IID	2.71	1.43
406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	2.70	1.53
459705	BE082764	Hs.270252	ESTs, Weakly similar to androgen recepto	2.70	1.14
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.69	2.99
452194	AI694413		olfactory receptor, family 2, subfamily	2.63	2.67
447709	U97145	Hs.19317	GDNF family receptor alpha 2	2.63	1.52
410910	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.59	1.00
454671	AW812929	Hs.336908	ESTs	2.50	2.34
441859	AW194364	Hs.94814	interleukin-4 induced gene-1 protein (FI	2.45	1.90
422398	AI476149	Hs.334489	hypothetical protein FLJ21992	2.45	1.36
403244			C2002870*:g[82698]pir[JQ0985 hydroxypr	2.40	1.53



5	415462	R52692	Hs.12698	ESTs	2.40	1.00
	447028	AI973128	Hs.167257	brain link protein-1	2.33	1.64
	412394	AW984150		gb:PM2-HN0008-170300-001-h09 HN0008 Homo	2.32	1.00
	450165	AA007235	Hs.63931	ESTs	2.32	1.32
	431093	AB031038	Hs.301704	eomesodermin (Xenopus laevis) homolog	2.30	1.81
10	444090	S69115	Hs.10306	natural killer cell group 7 sequence	2.28	1.69
	413682	BE156991		gb:RC3-HT0371-290100-013-e02 HT0371 Homo	2.27	1.59
	441320	AI768724		fibulin 1	2.27	1.87
	456766	R87310	Hs.7740	oxysterol binding protein-like 1	2.27	1.36
	420340	NM_000734	Hs.97087	CD3Z antigen, zeta polypeptide (TIT3 com	2.26	1.98
15	459721	AI299050	Hs.143835	gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	2.25	1.82
	405452			Target Exon	2.25	1.29
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.25	5.80
	401447			Target Exon	2.25	1.55
	423066	Y18264	Hs.123094	sal (Drosophila)-like 1	2.24	1.51
20	441704	AI458766	Hs.192125	ESTs	2.24	1.00
	405097			ENSP00000175238*:A disintegrin and metal	2.24	1.00
	408544	AW293825		ESTs	2.22	1.95
	413454	BE141162		gb:MR0-HT0076-021299-001-d03 HT0076 Homo	2.20	2.26
	444404	M31525		major histocompatibility complex, class	2.20	1.37
25	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.19	2.88
	436063	AK000028		ribosomal protein S24	2.19	1.42
	429212	NM_001504	Hs.198252	G protein-coupled receptor 9	2.18	1.22
	400712			Target Exon	2.18	1.00
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	2.17	1.79
30	403478			NM_022342:Homo sapiens kinesin protein 9	2.17	1.80
	418747	AJ249977	Hs.88049	protein kinase, AMP-activated, gamma 3 n	2.17	1.76
	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquinone oxidore	2.16	1.44
	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.16	2.12
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	2.15	2.88
35	456057	AA947457	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.15	2.50
	444346	AI142274		ESTs	2.15	2.38
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.14	1.93
	451318	AA029888	Hs.95071	ESTs	2.14	1.16
	458935	Y16521	Hs.24812	CDP-diacylglycerol synthase (phosphatida	2.13	1.52
40	417105	X60992	Hs.81226	CD6 antigen	2.13	2.61
	408219	BE061111	Hs.254211	gb:QV0-BT0041-011199-039-f02 BT0041 Homo	2.13	1.94
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.11	2.66
	443711	N67861	Hs.49390	ESTs	2.10	1.00
	423234	AA323534	Hs.296162	AD037 protein	2.10	1.52
45	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.09	3.74
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	2.08	1.84
	405827			Target Exon	2.08	1.00
	406909	L20777	Hs.73885	gb:Human MHC class I HLA-G gene (HLA-A33	2.08	2.29
	437295	AW779318	Hs.88417	ESTs	2.07	1.72
50	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	2.07	1.00
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.07	2.16
	423901	AA333006		gb:EST37064 Embryo, 8 week I Homo sapien	2.07	1.50
	405075			Target Exon	2.07	1.15
	457423	AK000642	Hs.265018	hypothetical protein FLJ20635	2.07	2.67
55	406267			Target Exon	2.07	1.30
	423365	AA324992	Hs.257168	ESTs	2.06	1.70
	449970	AI678058	Hs.201227	ESTs	2.06	2.48
	430733	AW975920	Hs.121036	ESTs	2.06	1.00
	446323	AI288274	Hs.345792	ESTs	2.06	1.00
60	402240			Target Exon	2.05	1.94
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.05	1.44
	424463	AW195353	Hs.119903	ESTs	2.04	1.32
	400107			Eos Control	2.04	2.42
	404811			NM_021096:Homo sapiens calcium channel,	2.03	2.18
65	403589			Target Exon	2.03	1.57
	404088			Target Exon	2.03	1.00
	414991	C17898		gb:C17898 Human placenta cDNA (TFujiwara	2.03	2.04
	429073	AA446167	Hs.47385	ESTs	2.03	3.10
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfami	2.02	1.92
70	401897			C17001987:gi 7303380 gb AAF58438.1  (AE0	2.02	1.55
	431094	AW972276	Hs.116195	ESTs	2.02	1.00
	424899	AL119387	Hs.119062	ESTs	2.01	2.41
	419711	C02621	Hs.159282	ESTs	2.01	1.92
	459019	AA017156	Hs.40719	hypothetical protein KIAA1164	2.01	1.76
75	405453			NM_005748*:Homo sapiens YY1-associated f	2.01	1.24
	402516			Target Exon	2.01	1.00
	457365	AA577297	Hs.303249	EST	2.01	2.36
	407928	NM_002262	Hs.41682	killer cell lectin-like receptor subfami	2.01	2.62
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	2.00	1.64
80	406266			Target Exon	2.00	2.46
	419409	AW297831	Hs.143792	hypothetical protein MGC2656	2.00	1.60
	435028	AW193035	Hs.187370	ESTs	2.00	1.55
	404696			NM_013443:Homo sapiens CMP-NeuAC;(beta)-	2.00	1.21
	403533			Target Exon	2.00	1.17
	411673	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	2.00	1.00
	424148	BE242274	Hs.1741	integrin, beta 7	1.99	3.66
	419833	AA251131	Hs.220697	ESTs	1.99	1.69

5	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	1.99	1.84
	426416	AW612744	Hs.169824	killer cell lectin-like receptor subfam	1.98	2.56
	449317	AW293413	Hs.132906	19A24 protein	1.98	2.44
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	1.97	2.51
	422109	S73265	Hs.1473	gastrin-releasing peptide	1.97	3.32
10	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.96	1.86
	406303			C16000922.gij7499103 pir  T20903 hypothe	1.96	2.16
	438676	AA813745	Hs.123446	ESTs	1.95	3.62
	404240			NM_018950:Homo sapiens major histocompat	1.95	2.06
	404056			Target Exon	1.94	2.60
15	425508	AA991551	Hs.97013	Homo sapiens, Similar to RIKEN cDNA 2310	1.93	3.24
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	1.93	2.35
	416941	BE000150	Hs.48778	niban protein	1.92	2.24
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.92	5.44
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	1.92	6.08
20	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	1.90	5.52
	446608	N75217	Hs.257846	ESTs	1.90	4.63
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.89	1.50
	414812	X72755	Hs.77367	monokine induced by gamma interferon	1.89	4.93
	422994	AW891802	Hs.296276	ESTs	1.88	3.30
25	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.88	2.17
	433671	AW138797	Hs.132906	19A24 protein	1.88	1.83
	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	1.86	3.12
	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of	1.86	1.88
	432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TIT3	1.84	1.65
30	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheli	1.83	2.46
	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	1.82	2.07
	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	1.82	2.63
	436485	X59135	Hs.156110	immunoglobulin kappa constant	1.82	2.75
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.81	4.56
35	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.80	5.10
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.79	1.89
	429670	L01087	Hs.211593	protein kinase C, theta	1.78	3.34
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.78	3.55
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.78	1.97
40	406672	M26041	Hs.198253	major histocompatibility complex, class	1.76	2.12
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.75	1.55
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	1.73	2.04
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (tazaro	1.73	1.56
	414512	AL044336	Hs.6831	golgi phosphoprotein 1	1.73	2.00
45	426752	X69490	Hs.172004	titin	1.73	2.62
	444793	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	1.72	2.30
	452334	D60471	Hs.13390	gb:HUM111D09B Clontech human fetal brain	1.72	2.12
	446227	AI281459	Hs.270114	ESTs	1.72	2.48
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	1.72	2.72
50	423799	AW026300	Hs.132906	19A24 protein	1.71	2.40
	458332	AI000341		ESTs	1.70	3.71
	408380	AF123050	Hs.44532	diubiquitin	1.70	2.71
	437644	AA748575	Hs.136748	lectin-like NK cell receptor	1.70	2.58
	402736			NM_024852:Homo sapiens hypothetical prot	1.69	2.10
55	438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2	1.69	1.39
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	1.68	2.02
	426202	BE266484	Hs.82916	chaperonin containing TCP1, subunit 6A (	1.68	2.14
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	1.68	3.30
	420440	NM_002407	Hs.97644	mammaglobin 2	1.67	2.42
60	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.67	1.49
	415823	R81864	Hs.205103	ESTs	1.65	2.16
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	1.65	1.58
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	1.63	1.94
	444929	AI685841	Hs.161354	ESTs	1.63	2.16
65	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.63	1.74
	418196	AI745649	Hs.26549	KIAA1708 protein	1.62	2.76
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.62	4.42
	438568	R98865	Hs.11135	major histocompatibility complex, class	1.62	1.74
	430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	1.62	1.85
70	433934	AW273261	Hs.216292	ESTs	1.62	2.00
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	1.61	2.00
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	1.61	1.46
	415349	AI766697	Hs.13231	ESTs	1.60	2.00
	406656	M16714	Hs.89643	major histocompatibility complex, class	1.60	1.47
75	456974	M12529	Hs.169401	apolipoprotein E	1.60	1.63
	416401	N80139	Hs.268916	ESTs	1.59	1.68
	439372	AF088033	Hs.159225	ESTs	1.59	2.04
	434666	AF151103	Hs.112259	T cell receptor gamma locus	1.59	4.08
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	1.58	3.06
80	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	1.58	2.37
	431903	AB029488	Hs.272100	SMS3 protein	1.57	2.14
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	1.57	2.28
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	1.56	1.46
	412472	AW975398	Hs.293836	ESTs	1.56	2.26
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	1.56	2.38
	412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.55	1.67
	449835	AW979300	Hs.293813	ESTs	1.55	2.16

	405545		Target Exon	1.55	2.64	
	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypothe	1.55	3.81
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.54	2.14
5	424243	AI949359	Hs.143600	ESTs, Highly similar to cis Golgi-locali	1.53	2.62
	457500	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	1.53	2.04
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	1.53	2.00
	439039	AI656707	Hs.48713	ESTs	1.53	2.38
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	1.52	2.65
10	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.52	2.06
	415198	AW009480	Hs.943	natural killer cell transcript 4	1.52	1.40
	431594	AI823999		ESTs	1.52	2.12
	432656	NM_000246	Hs.3076	MHC class II transactivator	1.52	2.20
	422426	W79117	Hs.58559	ESTs	1.52	2.22
15	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	1.51	2.80
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	1.50	1.67
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.49	3.12
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.49	1.78
	419166	AA234638	Hs.293584	ESTs	1.49	2.10
20	418323	NM_002118	Hs.1162	major histocompatibility complex, class	1.49	1.47
	435304	H10709	Hs.269524	ESTs	1.48	2.96
	452834	AI638627	Hs.105685	KIAA1688 protein	1.48	2.14
	446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.48	1.38
	429272	W25140	Hs.110667	ESTs	1.48	3.19
25	428379	X06026	Hs.2259	CD3G antigen, gamma polypeptide (Tit3 co	1.48	1.66
	433231	AB040926	Hs.143552	KIAA1493 protein	1.47	2.16
	408847	AW290997	Hs.30348	ESTs	1.46	2.08
	405441			Target Exon	1.46	2.99
30	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	1.45	1.56
	459644	AW197203		gb:xm38b01.x1 NCL_CGAP_GC6 Homo sapiens	1.45	2.44
	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	1.45	1.70
	422934	BE244189	Hs.122492	hypothetical protein	1.44	1.27
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	1.44	3.46
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.44	1.71
35	421407	T82331	Hs.182278	ESTs, Weakly similar to CGHU6C collagen	1.43	1.56
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	1.43	1.25
	400269			Eos Control	1.43	2.02
	420973	AA743415	Hs.291368	ESTs	1.42	2.06
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	1.42	2.20
40	430015	AW768399		ESTs	1.41	2.06
	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	1.41	1.31
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.40	1.72
	437479	R61866	Hs.101277	ESTs	1.40	2.52
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	1.40	2.17
45	416030	H15261	Hs.21948	ESTs	1.40	2.62
	419886	AA251562	Hs.146168	ESTs, Weakly similar to AF118023 1 SH3 d	1.40	1.68
	443951	F13272		ferritin, light polypeptide	1.40	1.64
	414875	H42679	Hs.77522	major histocompatibility complex, class	1.40	1.42
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platel	1.40	1.34
50	428782	X12830	Hs.193400	interleukin 6 receptor	1.40	2.30
	400680			NM_014207:Homo sapiens CD5 antigen (p56-	1.39	1.93
	428289	M26301	Hs.2253	complement component 2	1.39	1.39
	441410	AA932689	Hs.233304	ESTs, Weakly similar to I38022 hypothe	1.39	1.42
	406645	M57466	Hs.814	major histocompatibility complex, class	1.39	1.45
55	441379	AW175787	Hs.334841	selenium binding protein 1	1.38	1.32
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	1.38	2.04
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.38	1.35
	423526	AB011086	Hs.129739	KIAA0514 gene product	1.37	1.41
	424168	L29277	Hs.321677	signal transducer and activator of trans	1.37	1.33
60	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.37	1.74
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.35	1.38
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.35	1.54
	452353	C18825	Hs.29191	epithelial membrane protein 2	1.34	1.47
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	1.31	1.77
65	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	1.31	1.53
	444633	AF111713	Hs.286218	junctional adhesion molecule 1	1.30	1.37
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	1.29	1.49
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.28	1.36
	451864	N20370	Hs.69547	ESTs	1.28	1.42
70	421140	AA298741	Hs.102135	signal sequence receptor, delta (translo	1.28	1.31
	412790	NM_014767	Hs.74583	KIAA0275 gene product	1.28	1.63
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	1.28	1.38
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	1.28	1.36
	435822	T95594	Hs.187435	ESTs	1.27	1.82
75	455863	AA907305	Hs.36475	ESTs	1.27	1.36
	404277			NM_019111*:Homo sapiens major histocompa	1.27	1.52
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	1.27	1.54
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	1.27	1.53
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.26	1.27
80	434747	AA837085		ESTs	1.26	1.60
	425320	U29344	Hs.83190	fatty acid synthase	1.25	1.35
	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	1.25	1.41
	434644	H98071	Hs.4055	chromosome 21 open reading frame 50	1.25	1.30
	404854			Target Exon	1.25	1.57

5	406973	M34996	Hs.198253	major histocompatibility complex, class	1.25	1.57
	421071	AI311238	Hs.104476	ESTs, Weakly similar to CGHU1E collagen	1.24	1.26
	431779	AW971178	Hs.268571	apolipoprotein C-I	1.24	1.39
	416047	BE439894	Hs.78991	DNA segment, numerous copies, expressed	1.23	2.08
	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	1.23	1.20
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1.22	1.24
	415661	AF057307	Hs.78575	prosaposin (variant Gaucher disease and	1.22	1.16
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	1.22	1.17
10	420679	X57152	Hs.99853	fibrillarin	1.22	1.30
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	1.22	1.58
	418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfami	1.21	1.33
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	1.21	1.60
	406825	AI982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.20	1.20
15	436906	H95990	Hs.181244	major histocompatibility complex, class	1.19	1.27
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.19	1.62
	408279	AF216965	Hs.44095	Homo sapiens, clone MGC:12617, mRNA, com	1.18	1.25
	411372	AI147861	Hs.213289	low density lipoprotein receptor (famili	1.17	1.33
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.16	1.49
20	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.16	1.15
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	1.16	1.38
	432805	X94630	Hs.3107	CD97 antigen	1.16	1.22
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	1.16	1.41
	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group 1, m	1.16	1.36
25	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	1.15	1.27
	429832	AW293301	Hs.288472	ESTs, Weakly similar to UBPF_HUMAN UBIQU	1.15	1.72
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	1.15	1.21
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	1.14	1.21
	406782	AA430373		gb:zw20f11.s1 Soares ovary tumor NbHOT H	1.14	1.41
30	414662	AL036058	Hs.76807	major histocompatibility complex, class	1.12	1.25
	452547	AA335295	Hs.74120	adipose specific 2	1.11	1.39
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	1.11	1.22
	430280	AA361258	Hs.237868	interleukin 7 receptor	1.10	1.73
	441384	AA447849	Hs.288660	retinoic acid induced 3	1.09	1.22
35	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	1.09	1.14
	419200	AW966405		EST	1.08	1.64
	416511	NM_006762	Hs.79356	Lysosomal-associated multispinning membr	1.08	1.18
	409428	M33680	Hs.54457	CD81 antigen (target of antiproliferativ	1.07	1.12
	447023	AA356764	Hs.17109	integral membrane protein 2A	1.07	1.71
40	421481	AW391972	Hs.104696	KIAA1324 protein	1.07	1.58
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.07	1.23
	412819	T25829	Hs.24048	FK506 binding protein precursor	1.06	1.45
	418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	1.06	1.24
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.05	1.17
45	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.04	1.21
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.04	9.14
	418156	W17056	Hs.83623	nuclear receptor subfamily 1, group 1, m	1.03	6.65
	438089	W05391		nuclear receptor subfamily 1, group 1, m	1.03	8.00
	429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1	1.01	1.25
50	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.18
	438091	AW373062		nuclear receptor subfamily 1, group 1, m	0.99	12.84
	407018	U49869		NM_018955:Homo sapiens ubiquitin B (UBB)	0.99	1.07
	412896	AW804157	Hs.308026	major histocompatibility complex, class	0.98	1.57
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	0.97	1.40
55	426530	U24578	Hs.278625	complement component 4A	0.96	1.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	0.95	1.29
	407241	M34516		gb:Human omega light chain protein 14.1	0.94	1.11
	425371	D49441	Hs.155981	mesothelin	0.92	1.45
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	0.91	1.28

60

TABLE 35B:

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

65

Pkey CAT Number Accession

70

411089 5597\_6 BI009308 BI009893 BF9222023 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291  
AW905577 AW975593 AA713730 AW836781 AA666384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555 AA586369  
AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389  
AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680  
452194 90339\_1 AI694413 AW994700 AI912946 N73548 AI082035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043  
AI709339  
410910 1063929\_1 AW810196 AW810555 AW810507 AW810204 AW810619 AW810534  
412394 1174616\_1 AW947794 AW947793 AW947802 AW947798 AW947792 AW984150 AW984166 AW984167 AW984168 AW984179 AW984134 AW984160  
AW984180 AW984194 AW984202 AW984190  
413682 1527038\_1 BE156943 BE157375 BE156965 BE156949 BE156956  
441320 58978\_5 AI346734 AI377971 BG193341 BG548376 AA928353 AI768724 BG215700 AA449370 BI462157 BI060283 BG677508 AA318802 BG719160  
408544 683260\_1 AW293825 AW235391  
413454 1515217\_1 BE141291 BE141306 BE141288 BE141283 BE141162 BE141168 BE141290 BE141161 BE141165  
444404 16136\_1 BC013183 AW408658 NM\_002119 M31525 M26039 BM456399 BF732381 BM152457 AW407685 BM193161 AW407778 BI819141 AA702254  
BF855074 BI761232

80

436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593 AI147991 AI142274 AI198553 AA338252 AA338213 AW962691 AA333006 AA332289 D78831 C17898 D78863 BF330730 BF350539 BE153665 BE065062 BE064650 BE064863 BF330763 BE153820 BE064737 BE155079 BE064651 AW856751 AW856622 BE064691 BE153674 BE153698 BE064730 BE153536 BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW107777 AA586956 AL571889 AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 W79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586 AI000341 AI766341 AW873274 AI823999 AA970060 AA508176 AW972585 AI873427 AW972389 BI093452 AW970865 BG118285 AA569075 AA492132 AW753140 AA213770 AA143654 W03900 AW197203 AW753300 X65018 BC022318 NM_003019 BE465060 AI732255 BF446634 AI820677 AI002217 AI924488 BI821373 BI770406 BI823937 BI820265 BI489632 BG482911 AA617783 AI807697 AW205576 T94427 AA487101 T94513 BI819407 BI822450 BI820618 BI824619 BG542824 BG537862 BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H06534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF693929 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 AI334106 R63583 AI028079 AI140098 AI911625 AI890637 F34815 T65959 N40935 W52768 AA854747 AA861945 AA878472 AA778270 W32249 AA026061 W52662 W15352 W79670 W95384 T94283 AA002155 R82052 BE825493 BE825520 BE177661 H06215 BE144709 BE144829 AW976537 AI033582 AA837085 AA745261 AA648395 AA430373 AA968771 BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258 AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW747332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AI118798 BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 BI496876 AI264159 BM128481 AI624657 AI689301 AI969467 AA861685 AA251595 AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302 BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701 AK054860 AV652198 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
--------	--------	---

TABLE 35C:

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402550	7652009	Minus	80413-80673
403244	7637828	Plus	175792-176144
405452	7656638	Minus	93876-94275

5	401447	8574299	Minus	65053-65283
	405097	8072599	Plus	171191-171360
	400712	8118874	Plus	36087-36268
	403478	9958258	Plus	116458-116564
	405827	7109593	Plus	10279-10972
	405075	7770506	Minus	124680-125321
	406267	7528342	Minus	2570-2731
10	402240	7690131	Plus	104382-104527,106136-106372
	404811	3702428	Plus	26424-26596,28854-28987
	403589	8101229	Plus	5-330
	404088	9958257	Plus	184131-184295
	401897	8569218	Plus	604-767
15	405453	7656675	Minus	83710-83980
	402516	9798099	Minus	195342-195511
	406266	7528342	Minus	2365-2518
	404696	9800109	Minus	60037-60144,62675-63081
	403533	8076874	Plus	162922-163658
	406303	8575868	Plus	173622-173786
20	404240	5002624	Minus	116132-116407,116653-116922
	404056	3548785	Plus	75843-76980,77146-78263
	402736	9212044	Minus	66876-67010
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405441	7408124	Plus	100952-101283
25	400680	8118752	Plus	118343-118684,120720-121013
	404277	1834458	Minus	91665-91946
	404854	7143420	Plus	14260-14537

30 TABLE 36A: About 52 genes upregulated in non-specific interstitial pneumonitis relative to hypersensitivity pneumonitis or idiopathic pulmonary fibrosis

35 Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: 90th percentile of NSIP AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50.  
 R2: 90th percentile of NSIP AIs divided by 90th percentile of IPF AIs, where the minimum value for the numerator and denominator was set to 50.

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
40	435140	AA668123	Hs.134170	ESTs	2.76	2.76
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57	1.00
	435375	AI733610		ESTs	2.55	2.55
45	420813	X51501	Hs.99949	prolactin-induced protein	2.55	1.35
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.52	0.73
	421296	NM_002666	Hs.103253	perilipin	2.50	2.45
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	2.43	1.79
	408882	H12084	Hs.31110	ESTs, Weakly similar to MAGE-B4 [H.sapie	2.42	1.77
50	437318	AW362939	Hs.120721	ESTs	2.36	1.61
	421823	N40850	Hs.28625	ESTs	2.29	0.56
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.28	0.89
	430536	AI809163	Hs.9908	nitrogen fixation cluster-like	2.25	2.80
	414009	R67516		ESTs	2.19	1.86
55	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.19	0.33
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	2.18	1.24
	413722	BE247354	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.14	1.95
	433874	AW204429	Hs.155033	ESTs	2.13	1.72
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.12	0.91
60	414290	AI568801	Hs.71721	ESTs	2.11	0.81
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.11	1.01
	406785	AA588061		gb:nk10d03.s1 NCI_CGAP_Co2 Homo sapiens	2.10	1.61
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.08	0.85
	444179	W35132	Hs.267442	ESTs	2.08	1.13
65	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.05	0.80
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.04	0.79
	439134	AA830599		ESTs	2.04	1.89
	418512	AW498974		diacylglycerol kinase, zeta (104kD)	2.02	2.02
	457311	AI497811	Hs.172753	Homo sapiens chromosome 19, BAC 41195 (C	2.00	1.45
70	402274			C19000498*:gil4567179[gb]AAD23607.1[AC00	1.88	2.24
	453222	AA033929	Hs.19156	ESTs	1.77	2.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	1.73	2.02
	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	1.69	1.69
	406714	AI219304	Hs.266959	hemoglobin, gamma G	1.62	2.47
75	418333	W92113		gb:zh48e01.r1 Soares_fetal_liver_spleen_	1.59	2.04
	404090			Target Exon	1.48	2.03
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	1.39	2.06
	414386	X00442	Hs.75990	haptoglobin	1.09	1.44
	439372	AF088033	Hs.159225	ESTs	1.05	2.13
80	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.01	2.08
	412472	AW975398	Hs.293836	ESTs	1.00	2.26
	432894	AW167668	Hs.279772	brain specific protein	0.97	1.19
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.96	2.06
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	0.95	1.08

424310	AA338648	Hs.50334	testes development-related NYD-SP22	0.93	1.47
422109	S73265	Hs.1473	gastrin-releasing peptide	0.92	3.05
420440	NM_002407	Hs.97644	mammaglobin 2	0.91	2.11
418196	AI745649	Hs.26549	KIAA1708 protein	0.90	2.25
418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	0.89	1.11
419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	0.85	1.74
446608	N75217	Hs.257846	ESTs	0.82	2.10
418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	0.73	1.32
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	0.70	1.76

TABLE 36B:

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
435375	130020_1	AI733610 AI049989 AA678769
414009	438978_1	BE221268 R67515 AV730582 R67516
406785	Q_0	AA588061
439134	2581476_1	AA830599 AA970659 AA883802
418512	12225_6	BM046773 AA224297 T33786 T08951 T09274 T08592 T30936 AA350905
418333	73080_1	AF264624 AW668618 AV731446 R93353 AA584550 AV732728 BF802614 BF434359 AA077092 BI027317 AA199812 AW629027 AA831618 AI124782 AA765804 AA055698 AA677404 AA055366 AA89402 AA765530 BE503126 BE467367 AW139964 W81697 AI887846 W81696 AA447817 AA447667 F13631 BF055573 AW268271 AW088477 BF677839 AL601859 AW502118 AW502624 AA574189 BI020104

TABLE 36C:

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402274	2935596	Plus	5604-6527
404090	9967460	Minus	100815-100966

TABLE 37A: About 206 genes downregulated in lung fibrosis relative to normal lung

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UnigenelD: Unigene number  
Unigene Title: Unigene gene title  
R1: 90th percentile of normal lung AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.

Pkey	ExAccn	UnigenelD	Unigene Title	R1
454229	AW957744	Hs.278469	lacrimal proline rich protein	11.67
432128	AA127221	Hs.296502	ESTs	9.86
421218	NM_000499	Hs.72912	cytochrome P450, subfamily 1 (aromatic c	7.69
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	7.32
420958	AA309431	Hs.66	interleukin 1 receptor-like 1	7.13
402608			Homo sapiens defensin, alpha 1, myeloid-	6.67
406714	AI219304	Hs.266959	hemoglobin, gamma G	5.40
406673	M34996	Hs.198253	major histocompatibility complex, class	5.22
416539	Y07909	Hs.79368	epithelial membrane protein 1	5.04
418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horsfall gly	4.77
409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	4.74
450847	NM_003155	Hs.25590	stanniocalcin 1	4.46
404518			CD83 antigen (activated B lymphocytes, i	4.36
413951	AW051200	Hs.75640	natriuretic peptide precursor A	4.32
407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	4.25
456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.23
429509	AW614420	Hs.204354	ras homolog gene family, member B	4.14
445769	AI741471	Hs.23666	ESTs	4.10
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.06
425571	AJ007292	Hs.158306	ephrin-A2	3.92
423168	R34385	Hs.124940	GTP-binding protein	3.80
401234			mitogen-activated protein kinase 8 inter	3.78
402181			Target Exon	3.77
403479			NM_007064:Homo sapiens serine/threonine	3.68
435424	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL	3.68
402911			NM_021158*:Homo sapiens protein kinase d	3.66
442195	NM_001430		endothelial PAS domain protein 1	3.65
400089			Eos Control	3.60

	413948	C05145	Hs.75636	myosin light chain 2a	3.56
	438564	AA381553	Hs.198253	major histocompatibility complex, class	3.54
	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.54
	431319	AA873350	Hs.302232	ESTs	3.52
5	434292	AF124368	Hs.306551	Homo sapiens IMAGE Consortium ID 839832,	3.48
	401540			NM_002675:Homo sapiens promyelocytic leu	3.46
	426477	AA379464	Hs.154073	gb:EST92386 Skin tumor l Homo sapiens cD	3.43
	402328			Target Exon	3.42
10	401590			Target Exon	3.42
	403645			NM_024513*:Homo sapiens FYVE and coiled-	3.37
	403376			Target Exon	3.36
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.35
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.28
15	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.27
	401126			NM_006856*:Homo sapiens activating trans	3.27
	408243	Y00787	Hs.624	interleukin 8	3.23
	412429	AV650262	Hs.75765	GRO2 oncogene	3.22
	426420	BE383808	Hs.322430	NDRG family, member 4	3.21
20	449338	H73444	Hs.394	adrenomedullin	3.19
	401904			Target Exon	3.16
	401919			NM_012448*:Homo sapiens signal transduce	3.14
	406443			ENSP00000236574*:Hypothetical 21.8 kDa p	3.14
	458232	BE217872	Hs.279537	ESTs	3.12
25	406016			Target Exon	3.12
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	3.11
	451831	NM_001674	Hs.460	activating transcription factor 3	3.08
	450562	AW136468	Hs.202199	ESTs	3.07
	405838			Target Exon	3.04
30	451029	AA852097	Hs.25829	ras-related protein	3.02
	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	2.98
	439839	AA889354		ESTs	2.98
	439891	AL389940	Hs.109968	ESTs	2.96
	418935	T28499	Hs.89485	carbonic anhydrase IV	2.95
35	418853	NM_005236	Hs.89296	excision repair cross-complementing rode	2.95
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.94
	410326	AI368909	Hs.47650	ESTs	2.88
	407244	M10014		fibrinogen, gamma polypeptide	2.85
	459721	AI299050	Hs.143835	gb:gn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	2.84
40	416212	R40290	Hs.124685	ESTs	2.84
	428686	AA431801	Hs.98764	ESTs, Weakly similar to A29861 actin gam	2.83
	437508	AI204354	Hs.121347	ESTs	2.82
	437990	AI686579	Hs.121784	ESTs	2.82
	443709	AI082692	Hs.134662	ESTs	2.81
45	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	2.80
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	2.79
	404231			Target Exon	2.78
	434305	AI018280	Hs.130189	ESTs	2.77
	445493	AI915771		metallothionein 1E (functional)	2.76
50	418056	AA524886		gb:nh34f02.s1 NCI_CGAP_Pr3 Homo sapiens	2.76
	404102			Target Exon	2.75
	440206	AI762232	Hs.46794	ESTs	2.75
	403031			cathepsin D (lysosomal aspartyl protease	2.75
	413164	BE068494		gb:MR1-BT0371-050500-009-a12 BT0371 Homo	2.74
55	459330	C16931		gb:C16931 Clontech human aorta polyA mRNA	2.74
	456967	AW004056	Hs.168357	T-box 2	2.74
	427602	AI375258	Hs.98005	ESTs	2.74
	431367	Z20964	Hs.323817	DKFZP547E1010 protein	2.72
	406059			Target Exon	2.71
60	420575	BE263301	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	2.71
	457275	AA463422	Hs.209431	ESTs	2.71
	432559	AW452948	Hs.257631	ESTs	2.71
	402483			NM_020389:Homo sapiens putative capacita	2.70
	416069	R37101	Hs.20982	ESTs	2.70
65	445445	AF238870	Hs.275706	Homo sapiens clone GLSH-3 similar to gli	2.69
	436232	AA707006	Hs.187863	ESTs	2.68
	418773	T39748	Hs.325474	Target CAT	2.67
	434038	AA622104		ESTs	2.67
	405448			Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.66
70	404439			ENSP00000067222*:Mitochondrial 28S ribos	2.65
	435724	N39308	Hs.117898	ESTs	2.65
	404026			Target Exon	2.65
	400881			NM_025080:Homo sapiens hypothetical prot	2.64
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	2.62
75	405429			Target Exon	2.62
	402642			C1002296:gij6677817[ref NP_033126.1  rep	2.61
	438575	BE304709	Hs.146550	myosin, heavy polypeptide 9, non-muscle	2.61
	449293	AA001088	Hs.29739	ESTs, Weakly similar to C34323 GTP-bindi	2.61
	416157	NM_003243	Hs.342874	transforming growth factor, beta recepto	2.60
80	446122	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.59
	433291	AF007191		gb:Homo sapiens SIB 276 intestinal mucin	2.59
	426795	AI810474	Hs.196945	ESTs	2.58
	423503	M92843	Hs.343586	zinc finger protein homologous to Zfp-36	2.58
	430768	AB030207	Hs.247888	guanine nucleotide binding protein 13, g	2.58



	423387	AJ012074		vasoactive intestinal peptide receptor 1	2.57
	442681	AI809182	Hs.130907	ESTs	2.57
	408652	R43409	Hs.6829	Homo sapiens mRNA for KIAA1644 protein,	2.56
5	402217			C19001662*:gil6753872[ref]NP_034345.1 i	2.56
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.56
	455674	BE065941		gb:RC3-BT0319-100100-012-d12 BT0319 Homo	2.56
	457831	AA706937	Hs.120802	ESTs, Moderately similar to A26641 Na?ex	2.56
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.55
10	458648	AW444551	Hs.35380	x 001 protein	2.55
	456663	BE251104	Hs.113052	RNA cyclase homolog	2.54
	440178	AW502463	Hs.196521	ESTs	2.53
	457139	AI557280	Hs.184270	capping protein (actin filament) muscle	2.52
	405857			Target Exon	2.51
15	410204	AJ243425	Hs.326035	early growth response 1	2.50
	412851	AI826502	Hs.97269	ESTs	2.49
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	2.49
	409209	AA460160	Hs.73217	ESTs	2.49
	447173	AW449385	Hs.157294	ESTs	2.48
20	440034	AI908639	Hs.246781	ESTs	2.44
	418168	R85350	Hs.101368	ESTs	2.43
	417295	AW993524	Hs.43148	epithelial membrane protein 1	2.43
	405305			transcriptional adaptor 3 (ADA3, yeast h	2.42
	427886	AA417083	Hs.104789	ESTs	2.42
25	436409	AJ238982	Hs.183656	VNN3 protein	2.42
	413861	BE175424		gb:RC4-HT0578-170300-012-d01 HT0578 Homo	2.40
	403605			C3000142*:gil4503015[ref]NP_003900.1 co	2.37
	402594			C1002603*:gil9887091[gb]AAG01738.1 AF248	2.37
	402803			NM_001397:Homo sapiens endothelin conver	2.37
30	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.36
	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	2.36
	442630	AW572938	Hs.130580	ESTs	2.35
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	2.33
	405156			NM_003213*:Homo sapiens TEA domain famil	2.31
35	448162	AL039531	Hs.323363	hypothetical protein FLJ22169	2.31
	403591			Target Exon	2.31
	406193			Target Exon	2.30
	420813	X51501	Hs.99949	prolactin-induced protein	2.30
	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	2.28
40	400703			C11001794*:gil10946612[ref]NP_067286.1	2.27
	415026	AA159356	Hs.72308	ESTs	2.25
	400334	Y13187		Homo sapiens dmd gene, intron 11	2.18
	445878	AI262974	Hs.145587	ESTs	2.18
	404975			uncharacterized hypothalamus protein HT0	2.18
45	436370	R01220	Hs.185679	ESTs	2.17
	400513			Target Exon	2.16
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.15
	415405	R59141		gb:yg96d11.r1 Soares infant brain 1NIB H	2.15
	407612	U26403	Hs.37142	ephrin-A5	2.12
50	409837	AW501504		gb:UI-HF-BP0p-ajd-h-04-0-UI.r1 NIH_MGC_5	2.08
	458637	AE657446		gb:AV657446 GLC Homo sapiens cDNA clone	2.07
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	2.00
	418922	AW956580	Hs.42699	ESTs	1.98
	402404			NM_024967*:Homo sapiens hypothetical pro	1.98
55	421993	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	1.98
	413731	BE243845	Hs.75511	connective tissue growth factor	1.96
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	1.96
	428193	NM_004235		Kruppel-like factor 4 (gut)	1.93
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.92
60	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	1.92
	433883	AI925688	Hs.222312	ESTs	1.91
	406564			msh (Drosophila) homeo box homolog 2	1.91
	403581			Target Exon	1.90
	403716			Target Exon	1.90
	404758			Target Exon	1.90
65	439500	W73158	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	1.89
	448793	AI864581		ESTs	1.84
	435857	AF253468	Hs.3736	delta-like 4 homolog (Drosophila)	1.83
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.82
70	402051			Target Exon	1.81
	409859	AW501926		gb:UI-HF-BR0p-ajp-f-08-0-UI.r1 NIH_MGC_5	1.78
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	1.78
	405063			Target Exon	1.78
	405163			C5000561*:gil7513700[pir]T14151 Inv pro	1.75
75	402386			Target Exon	1.73
	406755	N80129	Hs.199263	metallothionein 1L	1.73
	409811	AW500896		gb:UI-HF-BP0p-air-a-03-0-UI.r1 NIH_MGC_5	1.70
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.70
	400489			Target Exon	1.70
80	428704	AA432007	Hs.192090	ESTs	1.69
	429307	AU076592	Hs.198951	jun B proto-oncogene	1.67
	400116			Eos Control	1.65
	404795			Target Exon	1.65
	408053	AW139474	Hs.246862	ESTs	1.65

414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	1.63
428800	M57627	Hs.193717	interleukin 10	1.63
451676	R84770	Hs.33538	ESTs, Weakly similar to oxygen-regulated	1.62
402394			Target Exon	1.61
404818			Target Exon	1.60
436364	X06096		gb:Human macrophage alpha1-antitrypsin c	1.55
420369	U96769	Hs.97220	chondroadherin	1.54
405590			CX001497*:gi 4557543 ref NP_001384.1  ex	1.54
402448			Target Exon	1.53
433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	1.51
409020	AA062549	Hs.21162	retbindin	1.51
405443			Target Exon	1.12

TABLE 37B:

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409385	110758_1	T65940 T64515 AA071267 AA071334
442195	15007_1	U81984 NM_001430 BE907085 B1333232 AI021986 AU138476 C18601 U51626 AU100517 BI054387 AU076970 BE786454 BG010080 AW377189 BF998789 AA368139 R11396 T83613 BG006324 BI012404 BG001643 BF757957 AL549361 AL544018 BE002870 BE929314 BE090199 AL046650 BI053717 BE929315 BI054967 BF960055 BF925432 R05421 BF922073 T70331 BI004403
439839	2594580_1	AI023587 AA889354 AA846791
445493	423456_1	AV711317 AI809938 AI808768 AI240593 AI915771
418056	286199_1	AW971347 AA524886 AA211537 BF903005 BF357120
413164	1492512_1	BE068758 BE068745 BE068689 BE068778 BE068529 BE068683 BE068445 BE068392 BE068719 BE068473 BE068521 BE068628 BE068422 BE068618 BE068354 BE068390 BE068414 BE068433 BE068369 BE068384 BE068661 BE068324 BE068301 BE068436 BE068754 BE068329 BE068672 BE068494 BE068596 BE068332 BE068347 BE068588 BE068328 BE068493 BE068740 BE068685 BE068759 BE068307 BE068429 BE068303 BE068693 BE068374 BE068295 BE068625 BE068302 BE068663 BE068675 BE068579 BE068311 BE068674 BE068547 BE068602 BE068605 BE068352 BE068306 BE068401 BE068537 BE068552 BE068450 BE068723 BE068393 BE068671 BE068748 BE068317 BE068447 BE068568 BE068632 BE068357 BE068330 BE068498 BE068631 BE068540 BE068410 BE068626 BE068591 BE068522 BE068676 BE068499 BE068361 BE068598 BE068350 BE068299 BE068580 BE068567 BE068692 BE068321 BE068327 BE068739 BE068526 BE068538 BE068765 BE068340 BE068733 BE068293 BE068565 BE068480 BE068476 BE068761 BE068712 BE068706 BE068549 BE068419 BE068383 BE068434 BE068418 BE068525 BE068543 BE068752 BE068550 BE068623 BE068470
459330	105725_1	BG563152 BF846777 BF849354 BF849359 BF846636 BF849201 BF849356 C16931 AA056717 AW864542 AW882724 AA056567
434038	630986_1	AI910738 AW139227 AA932891 AA622104
433291	73706_1	AF007191 AW820706 BG978594 BF872238
423387	2612_2	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138
455674	1490762_1	BE065941 BE065997 BE066003 BE066070 BE066098
413861	1561647_1	BF352282 BE175424 BE175418 BE175383
409368	110612_1	AA071059 AA085201 AA085020
415405	1872126_1	W18191 R59141 R54142 R12130 F11362 Z42794 F08242 F07925 H21084 R54090 R59142
409837	915621_1	AW501504 AW501656 AW503048 AW502449 AW502098
458637	395206_1	AV657752 AV657446
428193	430_1	AF105036 U70663 NM_004235 AF022184 AU141767 AU141110 AL040569 D44830 BI011351 AL575805 AI290876 AI014784 AI393429 AI266211 AW074303 AA620711 BF197792 AW008766 D25944 AI687397 AA621680 AV714408 BF446905 BM314505 BF514079 BM314197 AA845201 AW874084 BE720622 AI127241 AA236239 AI679709 AI679135 AI572470 AA573434 AI568487 BE049325 AA687950 BG925989 AI338031 AI365073 AI024576 AA298805 H04001 H45668 BG682146 AL552388 BI462361 BG547513 BG896863 BI256661
448793	3006936_1	A1936948 AI864581 AI570641
409859	916430_1	AW501926 AW502566 AW501927
409811	58948_2	AK057581 AW500962 AW500896 AW501105
400116	5269_1	D42041 NM_014610 AJ000332 BI758702 BG720650 AU141129 AU130711 AU141380 AU132402 BM048556 AU127520 BE259984 AU128952 BE614151 AL601516 BM146777 AU128103 BM194094 BE937951 BE696396 AK026997 AK026567 BF969293 BE798100 BI086881 BG166248 BE877845 BG385414 AW886747 BF093789 AW390159 BF820311 AA421676 AW880845 AW404827 BF726465 BE161190 BE254102 AW406002 BE161223 AI912055 BF930228 AW374357 AW794531 BE720524 BE933982 BE933658 BE933694 BE933978 BE933654 BE933583 BE166557 BE933874 BE933641 BE933859 BE933626 BE933866 BE933633 BE933864 BE933631 BE933867 BE933634 BE933857 BE933624 BE933883 BE933650 BE720491 AA420426 BE720410 BE720458 BE720444 BE720411 AW368748 BF874616 BE933498 BE835979 BF926667 AW849921 AW850026 AW850022 AW849977 AW849900 BG250251 W87689 AI192825 AI692824 AA426263 AI090315 AI309537 AA877437 AA478438 AI538868 AW276162 AI279916 AA600318 AI188836 AW662284 AI262619 AA293457 BF347442 AA421677 AA658063 AA565510 AA937060 AI142684 AA788940 AA827426 AU152614 AI342784 AU148738 AA219664 AA047835 H99450 AA018563 AI073634 BM475120 BG875251 BG248778 U46372 AA383858 AU140356 BG821891 BF935049 BI760656 BI054103 BF982309 BE872215 BI257291 AU158469 AU160599 AU152469 AU152375 AU152059 AU148575 N32267 AU149554 AI627459 AI719840 AW779017 AI291493 AW304181 AW470055 AI086491 AI311387 AI634232 AI151241 AI288848 AW050588 AW589580 AI241353 AI880219 AA039309 AA026517 AA016238 AA013444 H86822 R87530 AA058462 N27082 Z39679 BE544309 W52619 AA018076 AI813668 AW189907 AI418104 AU159878 AU150087 R21754 AA015932 H67274 AU153097 AI961344 AA018208 W32429 R45344 R77453 BM470129 AU130415 BI227374 BE298179 AW844963 AW844983 AI904066 AA379006 BF850571 AA355641 BG747156 AL547262 AW357941 BE560004 BI116061 BG899031 BE560318 BF174177 BI051456 BE001967 BE386446 BF969326 BF808765 BF684480 BG421617 AI940607 AW875483 BE789632 BF808711 BI192691 AW904249 BI911430 BE265407 BE730343 BE397808 BI226516
414580	623093_1	BG333973 BE385437 BE408833 BE387650
436364	1414_37	X05826 X06096 BG468890 AW951851 W23562 T28392 H56742 H58030 T69205

TABLE 37C:

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.

Nt\_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	402608	9910096	Plus	37495-37669
	404518	8151988	Plus	84494-84603
	401234	9929642	Plus	120173-120337
	402181	8575912	Plus	449746-450040
10	403479	7329292	Minus	148369-148533,150678-150809
	402911	7263904	Plus	142689-142979
	401540	8072433	Plus	106838-107310
	402328	4464283	Minus	13758-13922,14558-14752
	401590	9966320	Minus	33547-33649
	403645	8699714	Minus	4433-4582
15	403376	9369545	Minus	108698-108830
	401126	8699701	Minus	68290-68487
	401904	8671966	Plus	60959-61603,62670-62890,63778-63838
	401919	9502466	Plus	67536-67666
20	406443	9280765	Plus	85951-87327
	406016	8272661	Plus	41341-41940
	405938	6758795	Minus	166671-167411
	404231	8218035	Minus	61077-61322
	404102	7229900	Plus	97685-98018
25	403031	7768597	Minus	1308-1416
	406059	9103984	Minus	13856-14004
	402483	7574980	Minus	65578-66119
	405448	7582529	Plus	136347-136532
	404439	7139680	Plus	55316-55585
30	404026	7582549	Minus	79674-79968
	400881	2842777	Minus	91446-91603,92123-92265
	405429	7321905	Minus	51577-51723
	402642	9958129	Minus	125599-125756
	402217	9795981	Minus	21521-21757
35	405857	6758728	Plus	26564-26819
	406305	8575869	Plus	108239-108386,112216-112378,115388-11557
	403605	6862654	Plus	91614-91718
	402594	7705170	Plus	103082-103414
	402803	3287156	Minus	55923-56033
40	405156	9966228	Plus	146733-146860,147899-147961,153127-15325
	403591	8101229	Plus	4201-4833
	406193	7289992	Plus	30183-30662
	400703	8118859	Plus	63657-63857,64802-64905
	404975	3419864	Minus	86096-86605
45	400513	9796593	Plus	74613-74823
	402404	3970932	Plus	53154-53280
	406564	7711604	Minus	52788-53013
	403581	8101182	Plus	6794-7396
	403716	7239669	Plus	86899-87122
50	404758	7706327	Minus	130204-130806
	402051	8082020	Minus	19346-19480,20041-20119
	405063	7658414	Minus	111047-111666
	405163	9966267	Minus	161171-161299
	402386	9799769	Plus	22069-22303
55	400489	8954013	Plus	131475-131652
	404795	4826439	Plus	147501-147780
	402394	9929690	Plus	33308-33482
	404818	2769655	Plus	33671-33839
	405590	6960456	Plus	90492-90818
60	402448	9796640	Plus	112942-113069,114303-114521
	405443	7408143	Plus	90716-90887,101420-101577

65 TABLE 38A: About 207 genes upregulated in lung fibrosis relative to normal tissues

65 Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 70 Unigene Title: Unigene gene title  
 R1: 90th percentile of lung fibrosis AIs divided by 70th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
75	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.28
	407891	AA486620	Hs.41135	endomucin-2	4.14
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.07
	410219	T98226	Hs.171952	occludin	3.96
80	434666	AF151103	Hs.112259	T cell receptor gamma locus	3.88
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	3.87
	406617			Target Exon	3.76
	420568	F09247	Hs.247735	protocadherin alpha 10	3.70
	425873	NM_013390	Hs.160417	transmembrane protein 2	3.69

	438797	C16161	Hs.283040	hypothetical protein PRO2543	3.68
	410315	AI638871	Hs.152519	Homo sapiens cDNA: FLJ22524 fis, clone H	3.65
	446714	W73818	Hs.110028	ESTs	3.64
5	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.61
	430259	BE550182	Hs.127826	RaLGEF-like protein 3, mouse homolog	3.58
	412790	NM_014767	Hs.74583	KIAA0275 gene product	3.56
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	3.56
	412654	AI093480		hypothetical protein FLJ11896	3.56
10	414386	X00442	Hs.75990	haploglobin	3.54
	451035	AU076785	Hs.430	plastin 1 (I isoform)	3.52
	436473	AI193122	Hs.132275	ESTs	3.51
	406714	AI219304	Hs.266959	hemoglobin, gamma G	3.46
	414586	AA306160	Hs.16488	lymphocyte cytosolic protein 1 (L-plasti	3.45
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	3.45
15	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	3.39
	452813	U54727	Hs.191445	ESTs	3.36
	442831	AI798959	Hs.131686	ESTs	3.35
	427774	AA278583	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA	3.34
	445330	R52656	Hs.21691	ESTs	3.31
20	436001	AW903849	Hs.173840	HUEL (C4orf1)-interacting protein	3.31
	431681	AK000378	Hs.267566	hypothetical protein FLJ20371	3.29
	432314	AA533447	Hs.312989	ESTs	3.28
	435129	AI381659	Hs.267086	ESTs	3.28
25	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.24
	422607	Z45471	Hs.118684	stromal cell-derived factor 2	3.21
	421205	AL137540	Hs.102541	netrin 4	3.20
	428582	BE336699	Hs.185055	BENE protein	3.20
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.19
30	424880	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	3.17
	421233	AA209534	Hs.284243	tetraspan NET-6 protein	3.17
	429350	AI754634	Hs.131987	ESTs	3.16
	428727	AF078847	Hs.191356	general transcription factor IIH, polype	3.16
	434850	Z43161	Hs.283714	30 kDa protein	3.13
35	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	3.12
	446506	AI123118	Hs.15159	chemokine-like factor, alternatively spl	3.11
	416114	AI695549	Hs.183868	glucuronidase, beta	3.10
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	3.09
	444212	AW503976	Hs.10649	basement membrane-induced gene	3.08
40	422442	AA324998	Hs.147066	signal transducer and activator of trans	3.08
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	3.08
	424456	AA341017	Hs.25549	hypothetical protein FLJ20898	3.07
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.07
	445107	AI208121	Hs.147313	ESTs, Weakly similar to I38022 hypothe	3.06
45	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	3.04
	428106	BE620016	Hs.182470	PTD010 protein	3.04
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	3.04
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.03
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.02
50	423067	AA321355	Hs.285401	colony stimulating factor 2 receptor, be	3.01
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	2.96
	415000	AW025529	Hs.239812	Homo sapiens serologically defined treas	2.96
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	2.96
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	2.96
55	419660	BE280337	Hs.194693	solute carrier family 7 (cationic amino	2.96
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.95
	414493	AL133921	Hs.76272	retinoblastoma-binding protein 2	2.94
	416883	AW140128	Hs.184902	ESTs	2.92
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	2.92
60	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	2.92
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	2.92
	429640	U83508	Hs.2463	angiopoietin 1	2.91
	449843	R85337	Hs.24030	solute carrier family 31 (copper transpo	2.91
	401958			Target Exon	2.90
65	416926	H03109	Hs.263395	HT018 protein	2.90
	433691	AA605012		ESTs	2.88
	441892	AB028981	Hs.8021	KIAA1058 protein	2.87
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.87
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	2.87
70	414291	AI289619	Hs.13040	G protein-coupled receptor 86	2.87
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	2.87
	435913	W95006	Hs.269559	ESTs, Weakly similar to S65657 alpha-1C-	2.86
	422050	AA302741	Hs.25786	ESTs, Moderately similar to JC5238 galac	2.85
	451356	AA748418	Hs.164577	ESTs	2.85
	442085	AA975688	Hs.159955	ESTs	2.84
75	427704	AW971063	Hs.292882	ESTs	2.83
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	2.83
	441965	AA972712	Hs.269737	ESTs	2.82
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	2.82
80	450056	BE047394	Hs.8208	ESTs, Weakly similar to S71512 hypothe	2.80
	407245	X90568	Hs.172004	titin	2.80
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.80
	446601	AI312783	Hs.155772	Homo sapiens thymic stromal co-transport	2.80
	432195	AJ243669	Hs.8127	KIAA0144 gene product	2.80

	449088	AI654048	Hs.196556	ESTs	2.80
	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	2.80
	406648	AA563730	Hs.277477	major histocompatibility complex, class	2.79
5	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	2.78
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	2.78
	440255	AI932285	Hs.160569	ESTs	2.78
	410057	R66634	Hs.268107	multimerin	2.77
	417497	AW402482	Hs.82212	CD53 antigen	2.77
10	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.76
	431884	AA521246	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.75
	409669	AW514668	Hs.194258	ESTs, Moderately similar to ALU5_HUMAN A	2.75
	436729	BE621807		transmembrane 4 superfamily member 1	2.75
	431451	AA761378	Hs.192013	ESTs	2.74
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.74
15	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	2.74
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	2.74
	424673	AA345051	Hs.294092	ESTs, Weakly similar to I38022 hypotheti	2.74
	443194	AI954968		matrix Gla protein	2.71
20	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.71
	452870	AW502761	Hs.30909	KIAA0430 gene product	2.70
	430334	AI824719	Hs.143251	ESTs	2.70
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	2.70
	432279	N95104	Hs.274260	ATP-binding cassette, sub-family C (CFTR	2.70
25	413950	AA249096	Hs.32793	ESTs	2.70
	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus rec	2.70
	431710	AI735482		ESTs	2.70
	448749	AW859679	Hs.21902	Homo sapiens clone 25237 mRNA sequence	2.69
	451154	AA015879	Hs.33536	ESTs	2.69
30	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	2.69
	446899	NM_005397	Hs.16426	podocalyxin-like	2.68
	418031	AA648744	Hs.269493	ESTs	2.68
	453902	BE502341	Hs.3402	ESTs	2.68
	405121			mitogen-activated protein kinase 8 inter	2.68
35	410163	AF151977	Hs.59260	NTT5 protein	2.67
	429632	AW195336	Hs.148910	ESTs	2.67
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	2.67
	455004	AW850303		gb:IL3-CT0219-191199-030-F09 CT0219 Homo	2.67
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	2.67
40	401113			solute carrier family 22 (organic cation	2.66
	419462	AF071076	Hs.112255	nucleoporin 98kD	2.66
	407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-lin	2.66
	419175	AW270037		KIAA0779 protein	2.66
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	2.66
45	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	2.66
	430592	AJ224864	Hs.9688	leukocyte membrane antigen (IRC1)	2.65
	446830	BE179030		Human DNA sequence from clone RP5-1174N9	2.64
	433327	AI674779	Hs.126744	ESTs	2.64
	424868	AI568170	Hs.96886	ESTs	2.64
50	429854	R55508	Hs.99472	ESTs	2.63
	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.63
	456711	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	2.63
	419777	D60134	Hs.270975	ESTs	2.63
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	2.62
55	427596	AA449506	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.62
	452445	AB002438	Hs.29596	Homo sapiens mRNA from chromosome 5q21-2	2.62
	447482	AB033059	Hs.18705	KIAA1233 protein	2.62
	419110	AA234171	Hs.187626	ESTs	2.62
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	2.62
60	419828	T81422	Hs.14922	ESTs	2.62
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	2.62
	412491	W31589	Hs.73957	RAB5A, member RAS oncogene family	2.61
	436496	AA281959	Hs.5210	glia maturation factor, gamma	2.61
	435053	AW629386		ESTs	2.61
65	435029	AF167706	Hs.19280	cysteine-rich motor neuron 1	2.61
	425976	C75094	Hs.334514	NG22 protein	2.60
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	2.60
	430539	AK001489		ADP-ribosylation factor-like 1	2.60
	419825	AI754011	Hs.7326	ESTs	2.59
70	412577	Z22968	Hs.74076	CD163 antigen	2.58
	425894	AW954011	Hs.180711	ESTs	2.58
	410883	D43767	Hs.66742	CCL17 chemokine (TARC) (SCYA17)	2.58
	441028	AI333660	Hs.17558	Homo sapiens cDNA FLJ14446 fls, clone HE	2.58
	413949	AA316077	Hs.75639	Human TB1 gene mRNA, 3' end	2.58
75	434943	AI929819	Hs.92909	chromosome 21 open reading frame 50	2.58
	443605	H06865	Hs.134131	ESTs	2.57
	425017	AL119305	Hs.26409	ESTs	2.57
	440334	BE276112	Hs.7165	zinc finger protein 259	2.56
80	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.56
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.56
	407174	T79938	Hs.77062	leukocyte immunoglobulin-like receptor,	2.56
	443834	AI741510	Hs.173548	ESTs	2.55
	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	2.55
	420539	AA282735	Hs.44004	AD031 protein	2.55

421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	2.54
437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.54
422994	AW891802	Hs.296276	ESTs	2.54
411992	AW816214	Hs.143055	ESTs	2.54
451180	H61899	Hs.171937	steroid dehydrogenase-like	2.54
415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypothei	2.53
429752	H52348	Hs.36636	ESTs	2.53
414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.53
453329	T97205	Hs.193400	ESTs, Weakly similar to 2109260A B cell	2.53
436503	AJ277750	Hs.183924	ubiquitin associated and SH3 domain cont	2.52
445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	2.52
433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.52
435943	R60194	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.52
452253	AA928891	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H	2.52
442506	BE566411	Hs.41726	ESTs	2.52
419972	AL041465	Hs.182982	golgin-67	2.52
431074	BE072772	Hs.8997	ESTs, Moderately similar to A46010 X-lin	2.52
449129	AI631602	Hs.258949	ESTs	2.52
440524	R71264	Hs.16798	ESTs	2.51
419203	AA488719	Hs.190151	ESTs	2.51
404370			Target Exon	2.51
432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	2.51
439219	N33883	Hs.41322	ESTs	2.51
428044	AA093322	Hs.301404	RNA binding motif protein 3	2.50
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.50
437644	AA748575	Hs.136748	lectin-like NK cell receptor	2.50
442566	R37337	Hs.12111	ESTs	2.50
409317	U20165	Hs.53250	bone morphogenetic protein receptor, typ	2.50
450506	NM_004460	Hs.418	fibroblast activation protein, alpha	2.50
447484	AA464839	Hs.292566	hypothetical protein FLJ14697	2.50
415165	AW887604	Hs.78065	complement component 7	2.50
435284	AA879470	Hs.96849	Homo sapiens cDNA FLJ11492 fis, clone HE	2.50

TABLE 38B:

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
412654	1350_1	BG743181 AI830050 BE695688 AA126591 AI903503 R26045 N62894 N63950 AA131619 AI681480 N79626 AA461603 R78979 AW608865 N66622 BF448838 AA779000 AA460314 AI092721 AI870182 AI436284 AI494151 AI127704 AI127702 BE349350 AI093480 AA115264 AA131567 R26840 R78885
433691	2203511_1	AI223854 AI129852 AA605012
436729	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI242384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AI574095 AI576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AI556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 BW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI707221 BE910282 BG538748 AW960564 AV732879 DI16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 BI754027 BF696071 AI351939 BG151298 AI919334 AI401620 BI770165 W72057 T96158 T29478 AA181252 BG927793 AA714431 AA600749 AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832406 AA102441 BG928081 AA993445 AA916041 AA987847 AA983329 AA737219 AA916443 AW128994 AI492560 AI761847 BC005272 NM_000900 X53331 M58549 BI758966 AL598829 BI754530 BG699770 BE439699 BE440148 AV704365 AV733652 BG212015 BG184149 BG200180 BG212690 BI761222 BG182079 AW338822 AI925631 AI423041 AW071181 AI889836 AW129112 BG925339 AI017633 AA568864 BF725590 AI004210 AI809799 BE083097 BG896220 AW997681 BF668788 BE083134 AW631281 BG193052 BG183095 BE440088 BG185728 AI499579 AA188162 AA864282 BI493352 AA155854 AA836749 AA836844 AA985478 AW082299 AI816747 AA450221 AA971294 BE327509 AI719662 BG576659 AI479382 BF824747 AI741800 BG982962 AI088473 AA916151 AW473324 BG901177 BE439998 AW023269 BE813871 AW999947 BE839108 AV707983 AA369722 AW796627 AW890608 AI341771 AA302459 BI493353 AA366332 AA371104 AA367277 AL547972 BG928011 AI678903 AI699886 AI956165 AA484893 AA643953 AW591063 BG203275 BG211093 AI334791 AA916589 AW058266 AI362370 AI143352 AA508721 AI928079 D57214 BE045265 AA541785

BG219510 BG201686 BG195572 AW019904 AW089242 AA953322 AI686698 F27562 AA614749 D56645 F20774 F30660 F25646 AW023542  
 AA827300 AA582214 AI701289 AA228293 AI906950 AA230156 AA384572 AW438988 AA742516 BI490938 AA731082 BF665869 BG190518  
 AV704158 BE439643 AA910666 AA155913 AA923097 AA975721 AA985555 BG927032 AA948389 AA451625 AA916141 AL572719 AV707258  
 AW083733 AA128053 AI953789 AI911993 AA421798 BG429150 AI915306 Z30130 AA126929 BG926630 AA081013 AA553696 AA916094  
 BG924321 AI039722 AI954968 AI372839 AI401406 AI538215  
 AI422419 AA514370 AI741678 AI735482 AI735081 AI371436  
 AW850587 AW850589 AW850318 AW850303  
 AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331  
 AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA365626  
 Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618  
 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634  
 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572  
 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403  
 F02090 AI187299 AI609644 Z40516 AW952314  
 BC020595 BI488430 BG168023 BE179030 AW294203 BF849776 AA459064 AI917452 AW403072 W27419 BF914568 BF798468 AW370558  
 T35055 AW370623 AA399232 AA214221 AW802987 BF902228 AW370622 BF819597 AW370567 BF914313 AW954040 BF060706 AA194237  
 T25074 C01285 BI489433  
 AI332638 AA663215 AW629386  
 AK001489 AU129447 BF959274 BG565452 AI245327 AU116848 BF358559 BF358554 BF358570 BG678119 AI515852 AU154607 AI357567  
 AW874359 AI122554 AA406478 AI091013 AI866679 AI686163 AA662158 AA911580 D31095 AI302576 BF588761 AU151560 AU143828 AI291610  
 AW169600 D31161 AA905362 C21179 BE327258 D31474 AW439053 D31309 BF756901 BI838626 BF979839 AU149562 BM142116 AU156455  
 AA452028 AW473972 AW468490 AA410271 AI475944 BF821859 AA658188 AI360390 AA226320 F37355 F27660 F36093 AA152126 BF930021  
 BF375775 AW821784 AW975085 W16475 D31031 BG696392 AW860676 AW752864 BI013705 BF965715 BF326604 AW821786

TABLE 38C:

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406617	8439858	Plus	36430-36552
401958	3258613	Plus	108411-108629
405121	8102330	Minus	35816-36004,36587-36684
401113	9966541	Minus	19419-19959
404370	7631003	Plus	127868-128244

TABLE 40A: 656 genes upregulated in fibrosis relative to normal body tissues

Table 40A lists about 656 genes upregulated in fibrosis relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar accession number, GenBank accession number  
 UniGeneID: UniGene number  
 Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).  
 UniGene Title: UniGene gene title  
 R1 95th percentile of fibrosis AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prot.Domains; R1

442275; AW449467; Hs.54795; Homo sapiens secretoglobulin, family 3A, m; Uteroglobulin; TM=M; SS=Y; 39.47  
 428434; AW363590; Hs.65551; Homo sapiens, Similar to DNA segment, Ch; LBP\_BPL\_CETP\_C; TM=M; SS=Y; 32.35  
 439335; AA742697; Hs.62492; NM\_052863; Homo sapiens secretoglobulin, fa; none; 28.49  
 406964; M21305; ; FGENES predicted novel secreted protein; none, none; 27.90  
 425211; M18667; Hs.1867; progastricsin (pepsinogen C); asp; TM=M; SS=M; 27.90  
 441835; AB036432; Hs.184; advanced glycosylation end product-spec; homeobox, Acyltransferase, notch, EGF, ank, Acyltransferase; 27.23  
 446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL8; 24.97  
 428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase\_M10; 24.38  
 431723; AW058350; Hs.278966; Homo sapiens mRNA; cDNA DKFZp564B2062 (f; PMP22\_Claudin, none; 23.35  
 409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibrinogen\_C; 23.29  
 431089; BE041395; Hs.374629; ESTs, Weakly similar to unknown protein ; none, none; 18.23  
 425371; D49441; Hs.155981; mesothelin; none; TM=M; SS=M; 18.17  
 448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate\_rec, MIP; TM=M; SS=M; 17.64  
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phospho; Ribosomal\_L20, Na\_Pi\_cotrans; TM=Y; SS=N; 17.33  
 421798; N74880; Hs.355462; N-acylsphingosine amidohydrolase (acid c; SAPA, Surfactant\_B, none; 16.81  
 419556; U29615; Hs.91093; chitinase 1 (chitotriosidase); Glyco\_hydro\_18, CBM\_14; TM=M; SS=Y; 16.24  
 419092; J05581; Hs.89603; mucin 1, transmembrane; SEA; TM=Y; SS=M; 16.06  
 426174; AA547959; Hs.115838; Homo sapiens similar to Echinoidin (LOC1; none, none; 15.84  
 406672; M26041; Hs.198253; major histocompatibility complex, class ; ig, MHC\_II\_alpha; TM=M; SS=M; 15.42  
 421110; AJ250717; Hs.1355; cathepsin E; asp; 15.08  
 444342; NM\_014398; Hs.10887; similar to lysosome-associated membrane ; Lamp; TM=Y; SS=M; 14.94

- 406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 14.36  
 443709; AI082692; Hs.134662; ESTs; SNF,fn3,none; 14.05  
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm\_3;TM=Y;SS=M; 13.88  
 457200; U33749; Hs.197764; thyroid transcription factor 1; homeobox;TM=M;SS=N; 13.86  
 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUA S-100 pro; none,none; 13.82  
 422355; AW403724; Hs.300697; coagulation factor VII (serum prothrombin); none,ig; 13.62  
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 13.47  
 415457; AW081710; Hs.7369; Homo sapiens testes specific A2 homolog ; MORN,sugar\_lr;TM=Y;SS=M; 13.35  
 431164; AA493650; Hs.94367; thyroid transcription factor 1; none,homeobox; 13.32  
 414998; NM\_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin\_c;TM=Y;SS=M; 12.83  
 400269; ; Hs.253495; Eos Control; lectin\_c,Collagen,Xlink;; 12.30  
 424310; AA338648; Hs.50334; testes development-related NYD-SP22; none;TM=M;SS=N; 11.81  
 451558; NM\_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1; ABC\_tran,SRP54;TM=Y;SS=M; 11.79  
 452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine ; none,none; 11.68  
 445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM;; 11.56  
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr\_redox;TM=Y;SS=M; 11.41  
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 11.31  
 430832; AI073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior ; none,none; 11.25  
 407910; AA650274; Hs.41296; fibronectin leucine rich transmembrane p; fn3,LRR,LRRCT,LRRNT;TM=Y;SS=M; 11.15  
 451497; H83294; Hs.284122; Wnt inhibitory factor-1; EGF,WIF;; 11.07  
 430250; NM\_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;SS=N; 11.07  
 411020; NM\_006770; Hs.67726; macrophage receptor with collagenous str; SRCR,Collagen;TM=Y;SS=M; 11.05  
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin ; Osteopontin;; 11.01  
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone\_rec,zf-C4,none; 10.97  
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin\_c,Ricin\_B\_lectin,Xlink;TM=Y;SS=M; 10.93  
 432231; AA339977; Hs.274127; CLST 11240 protein; none;TM=M;SS=M; 10.81  
 416402; NM\_000715; Hs.1012; complement component 4-binding protein ; sushi;TM=M;SS=M; 10.77  
 418156; W17056; Hs.83623; nuclear receptor subfamily 1, group I, m; hormone\_rec,zf-C4,none; 10.63  
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 10.58  
 421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen ; none;TM=Y;SS=M; 10.57  
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (interstitial; hemopexin,Peptidase\_M10,Astacin,PG\_binding\_1;; 10.33  
 419086; NM\_000216; Hs.89591; Kallmann syndrome 1 sequence; fn3,wap;; 10.30  
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 10.28  
 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm\_3,none; 10.26  
 453914; NM\_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBPFase;TM=M;SS=N; 10.22  
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 10.09  
 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alph; vwa,CACHE;TM=M;SS=N; 10.03  
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 10.02  
 408562; AI436323; Hs.31141; roundabout (axon guidance receptor, Dros; ig,fn3;TM=M;SS=N; 10.02  
 448782; AL050295; Hs.362806; KIAA0758 protein; 7tm\_2,ig,GPS,SEA;TM=Y;SS=N; 9.86  
 419235; AW470411; Hs.288433; neurotrophin; none,none; 9.79  
 415992; C05837; Hs.145807; hypothetical protein FLJ13593; none;TM=Y;SS=M; 9.74  
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 9.70  
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.69  
 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; none;TM=M;SS=N; 9.68  
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 9.64  
 408380; AF123050; Hs.44532; diubiquitin; ubiquitin;TM=M;SS=N; 9.54  
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone\_rec,zf-C4,none; 9.52  
 449494; AW237014; Hs.315369; aquaporin 4; MIP,none; 9.51  
 456062; AI866286; Hs.71962; ESTs, Weakly similar to B36298 proline-r; none,none; 9.42  
 446428; AW082270; Hs.12496; ESTs, Weakly similar to ALU4\_HUMAN ALU S; none,none; 9.41  
 421952; AA300900; Hs.98849; dynein light chain 2B (DNLC2B); none,none; 9.19  
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell ; Ribosomal\_S14,ank,pkinase,death,none; 9.16  
 456034; AW405979; ; gb:U1-H-BI3-ala-a-12-0-UI.s1 NCL\_CGAP\_Su; none,none; 9.15  
 407788; BE514982; Hs.38991; S100 calcium-binding protein A2; ehand,S\_100,S\_100,ehand; 9.15  
 416965; N26223; Hs.160436; MDAC1; none;NA;NA; 9.03  
 443324; R44013; Hs.164225; ESTs; none,none; 9.03  
 435575; AF213457; Hs.44234; triggering receptor expressed on myeloid; ig;TM=Y;SS=M; 9.00  
 440273; AI805392; Hs.325335; Homo sapiens cDNA: FLJ23523 fis, clone L; none,none; 8.99  
 424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374 gene NF2 ; Zn\_carbOpept,none; 8.80  
 409203; AA780473; Hs.687; cytochrome P450, subfamily IVB, polypept; p450;TM=M;SS=Y; 8.76  
 423387; AJ012074; Hs.348500; vasoactive intestinal peptide receptor 1; 7tm\_2,HRM,CSD;TM=Y;SS=M; 8.74  
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 8.73  
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 8.68  
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; ig;TM=Y;SS=M; 8.56  
 421563; NM\_006433; Hs.105806; granulysin; none;; 8.55  
 450726; AW204600; Hs.355462; HUMPSBPA Human pulmonary surfactant-asso; SAPA,Surfactant\_B,none; 8.51  
 419693; AA133749; Hs.301350; FXID domain-containing ion transport reg; ATP1G1\_PLM\_MAT8;TM=Y;SS=M; 8.51  
 424450; AL137526; Hs.374425; dynein intermediate chain 2; WD40;; 8.42  
 402474; ; NM\_004079;Homo sapiens cathepsin S (CTSS; Peptidase\_C1;; 8.41  
 458079; AI796870; Hs.54277; Homo sapiens similar to RIKEN cDNA 28100; none;TM=M;SS=N; 8.40  
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 8.36  
 453310; X70697; Hs.553; solute carrier family 6 (neurotransmitter; SNF,5HT\_transporter;TM=Y;SS=N; 8.34  
 448140; AF146761; Hs.20450; BCM-like membrane protein precursor; ig;TM=Y;SS=N; 8.33  
 404240; ; NM\_018950;Homo sapiens major histocompat; ig,MHC\_I;TM=Y;SS=M; 8.28  
 459702; AI204995; ; gb:an03c03.x1 Stratagene schizo brain S1; none,none; 8.17  
 449523; NM\_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm\_1;TM=Y;SS=M; 8.17  
 442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal\_S14; 8.12  
 446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFZp564B2062 (f; PMP22\_Claudin,none; 8.07  
 420137; AA305478; Hs.95327; CD3D antigen, delta polypeptide (TIT3 co; ITAM;TM=Y;SS=M; 8.01  
 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; ig;TM=M;SS=M; 7.99  
 432441; AW292425; Hs.163484; intron of hepatocyte nuclear factor-3 al; Fork\_head,none; 7.99  
 409208; Y00093; Hs.172631; integrin, alpha X (antigen CD11C (p150)); vwa,FG-GAP,integrin\_A,vwa,integrin\_A,FG-GAP; 7.94



- 432606; NM\_002104; Hs.3066; granzyme K (serine protease, granzyme 3; trypsin; TM=Y; SS=M; 7.92  
 442832; AW206560; Hs.253569; ESTs; none, none; 7.90  
 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN cDNA 2210; none; TM=M; SS=N; 7.89  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 7.86  
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22, Claudin, none; 7.84  
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin\_B, EGF, PSI; TM=Y; SS=M; 7.79  
 447131; NM\_004585; Hs.17466; retinoic acid receptor responder (tazaro; none; TM=Y; SS=N; 7.78  
 423961; D13666; Hs.136348; periostin (OSF-2os); Fasciclin; TM=M; SS=M; 7.73  
 424917; AI636208; Hs.96901; hypothetical protein FLJ23049; none; TM=M; SS=N; 7.72  
 438564; AA381553; Hs.198253; major histocompatibility complex, class ; ig, MHC\_II\_alpha, none; 7.65  
 456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, com; none, PK, PK\_C, myosin\_head, RhoGAP; 7.64  
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily; SRP14, TNFR\_c6; 7.63  
 436954; AA740151; Hs.130425; ESTs; none, none; 7.58  
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 doma; SH2; 7.56  
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC; TM=Y; SS=M; 7.55  
 417105; X60992; Hs.81226; CD6 antigen; SRCR; TM=Y; SS=M; 7.51  
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 7.46  
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 7.40  
 432222; AI204995; gb:an03c03.x1 Stratagene schizo brain S1; none, none; 7.38  
 422667; H25642; Hs.132821; ESTs; FMO-like, FMO-like; 7.37  
 444527; NM\_005408; Hs.11383; small inducible cytokine subfamily A (Cy; IL8; 7.36  
 457411; AW085961; Hs.130093; iroquois-class homeobox protein IRX2; none, none; 7.32  
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep\_L\_domain, YLP, none; 7.32  
 419231; AL046294; Hs.136245; ESTs, Weakly similar to T17227 hypotheti; none, none; 7.30  
 438873; AI302471; Hs.124292; Homo sapiens cDNA: FLJ23123 fis, clone L; none, none; 7.27  
 424027; AW337575; Hs.201591; ESTs; 7tm\_2, HRM, none; 7.26  
 428927; AA441837; Hs.90250; Homo sapiens hypothetical protein FLJ231; none, none; 7.24  
 432435; BE218886; Hs.282070; ESTs; none, none; 7.22  
 428467; AK002121; Hs.184465; hypothetical protein FLJ11259; none; TM=Y; SS=M; 7.21  
 416030; H15261; Hs.21948; ESTs; none, none; 7.20  
 433293; AF007835; Hs.32417; hypothetical protein MGC2742; none; TM=M; SS=N; 7.18  
 418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosom; pkinase, Activin\_rec, pkinase, Activin\_rec; 7.16  
 420656; AA279098; Hs.187636; ESTs; none, none; 7.14  
 427698; AW972594; Hs.335499; ESTs; none, none; 7.11  
 432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate sy; APS\_kinase, ATP-sulfurylase; TM=M; SS=N; 7.06  
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM\_PNT, none; 7.04  
 430413; AW842182; Hs.241392; small inducible cytokine A5 (RANTES); IL8; TM=M; SS=Y; 7.04  
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement comp; C1q, Collagen; 7.03  
 421481; AW391972; Hs.104696; KIAA1324 protein; none; TM=M; SS=M; 7.01  
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase, PLAT; TM=M; SS=N; 6.97  
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb\_propeptide, TGF-beta, none; 6.96  
 458124; AW005548; Hs.124590; ESTs; none, none; 6.94  
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3, PX; TM=M; SS=N; 6.93  
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, ; inositol\_p, ig; TM=M; SS=N; 6.92  
 428820; AA436187; Hs.172631; integrin, alpha M (complement component ; vwa, integrin\_A, FG-GAP; TM=Y; SS=M; 6.90  
 423575; C18863; Hs.163443; intron of periostin (OSF-2os); Fasciclin, none; 6.89  
 419490; NM\_006144; Hs.90708; granzyme A (granzyme 1, cytotoxic T-lymp; trypsin; TM=M; SS=M; 6.89  
 450954; AI904740; Hs.25691; receptor (calcitonin) activity modifying; none; TM=Y; SS=M; 6.87  
 425976; C75094; Hs.334514; NG22 protein; voltage\_CLC; TM=Y; SS=M; 6.84  
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 fis, clone L; LRR; TM=M; SS=N; 6.81  
 414991; C17898; ; Homo sapiens up-regulated by BCG-CWS (LO; Zip, none; 6.80  
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM; TM=Y; SS=M; 6.80  
 422163; AF027208; Hs.112360; prominin (mouse)-like 1; none; TM=Y; SS=M; 6.79  
 445885; AI734009; Hs.127699; KIAA1603 protein; none, none; 6.77  
 436576; AI458213; Hs.77542; ESTs; 7tm\_1, DnaJ; 6.77  
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; 6.76  
 424711; NM\_005795; Hs.152175; calcitonin receptor-like; 7tm\_2, HRM; TM=Y; SS=M; 6.75  
 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3; TM=M; SS=N; 6.73  
 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54); ig, ICAM\_N; TM=M; SS=M; 6.71  
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; ig, abhydrolase; 6.70  
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none, lectin\_c; 6.70  
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 6.68  
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion\_trans, K\_tetra, asp; 6.65  
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH\_C, IMPDH\_N, CBS, integrin\_B, Ricin\_B\_lectin; 6.62  
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 6.60  
 453142; AA033648; Hs.7473; Homo sapiens gap junction protein, alpha; connexin; TM=Y; SS=M; 6.60  
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis, clone PL; none, none; 6.56  
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT\_bind, STAT\_prot; TM=M; SS=N; 6.54  
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2, SH3, pkinase; TM=M; SS=N; 6.51  
 446932; AA961459; Hs.125644; ESTs; none, LRR, LRRNT; 6.50  
 427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180); vwa, integrin\_A, FG-GAP; TM=Y; SS=M; 6.48  
 425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; ig, pkinase; TM=M; SS=M; 6.47  
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none; TM=M; SS=M; 6.46  
 431745; AW972448; Hs.163425; Novel FGENESH predicted cadherin repeat ; none, none; 6.43  
 417370; T28651; Hs.374466; tryptophanyl-tRNA synthetase; WHEP-TRS, tRNA-syntL\_1b; 6.41  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, fn3, Y\_phosphatase; TM=M; SS=N; 6.40  
 429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate lung and nas; none; 6.39  
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa\_permeases, pyridoxal\_deC, bromodomain, PHD, MBD, AT\_hook, DDT, PI3\_P14\_kinase, FAT, FATC, BclA, RUN; TM=M; SS=N; 6.37  
 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxygenase; IDO; TM=M; SS=N; 6.36  
 451820; AW058357; Hs.199248; ESTs; 7tm\_1; TM=Y; SS=M; 6.34  
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/pep; PTR2; TM=Y; SS=N; 6.32  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, ig, FAD\_Synth, ldh, ldh\_C, pkinase; 6.32

- 444090; S69115; Hs.10306; natural killer cell group 7 sequence; PMP22\_Claudin; TM=Y; SS=M; 6.31  
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase;; 6.30  
 421659; NM\_014459; Hs.106511; protocadherin 17; cadherin; TM=M; SS=M; 6.27  
 415198; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M; SS=N; 6.26  
 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip; TM=M; SS=Y; 6.24  
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; SS=N; 6.23  
 452194; A1694413; Hs.373599; olfactory receptor, family 2, subfamily ; none, none; 6.22  
 424144; AA454033; Hs.41644; AKAP-associated sperm protein; Rila; 6.21  
 414142; AW368397; Hs.334485; hemicentin (fibulin 6); EGF, ig, lsp\_1, hormone4, squash, TIL, Adeno\_E3\_CR1; TM=M; SS=M; 6.21  
 442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482 hypotheti; none, none; 6.20  
 420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin (vascula; cadherin, Cadherin\_C\_term; TM=Y; SS=M; 6.19  
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 6.17  
 440452; A1925136; Hs.55150; ESTs, Weakly similar to CAYP\_HUMAN CALCY; none; NA; NA; 6.17  
 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 6.16  
 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor t; Y\_phosphatase, none; 6.15  
 410361; BE391804; Hs.62661; guanylate binding protein 1, interferon-; GBP, GBP\_C; TM=Y; SS=M; 6.13  
 415765; NM\_005424; Hs.78824; tyrosine kinase with immunoglobulin and ; EGF, fn3, ig, pkinase, laminin\_EGF; TM=M; SS=Y; 6.12  
 430478; NM\_014349; Hs.241535; apolipoprotein L, 3; MotA\_ExbB; TM=Y; SS=M; 6.12  
 413869; NM\_000878; Hs.75596; interleukin 2 receptor, beta; none; TM=Y; SS=M; 6.09  
 446608; N75217; Hs.175622; ESTs; Armadillo\_seg, HEAT\_PBS; TM=M; SS=M; 6.08  
 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfami; IL2;; 6.08  
 426116; AA868729; Hs.144694; ESTs; none, none; 6.06  
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank;; 6.05  
 426721; AA383588; Hs.288545; ESTs, Weakly similar to T29012 hypotheti; zf-C2H2; TM=M; SS=N; 6.05  
 429228; A1553633; Hs.356828; ESTs; none, none; 6.05  
 421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase;; 6.04  
 437669; A1358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA; none, pkinase, pkinase\_C; 6.03  
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC\_tran, ABC\_membrane; TM=Y; SS=M; 6.02  
 428667; A1375550; Hs.346868; nucleolar protein p40; homolog of yeast ; none, none; 6.01  
 432731; R31178; Hs.287820; fibronectin 1; fn1, fn2, fn3, none; 5.95  
 446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.95  
 450656; AA010539; Hs.18912; unnamed protein product; zf-C2H2;; 5.94  
 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide (p32); ig; TM=Y; SS=M; 5.94  
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.94  
 408048; NM\_007203; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemmi; TM=M; SS=N; 5.94  
 438670; A1275803; Hs.123428; ESTs; none; NA; NA; 5.91  
 424238; AA337401; Hs.137635; ESTs; none; TM=M; SS=M; 5.90  
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2, none; 5.89  
 423690; AA329648; Hs.23804; ESTs, Weakly similar to PN0099 son3 prot; ion\_trans, IQ, none; 5.88  
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; SS=N; 5.81  
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, ; ig; TM=Y; SS=M; 5.81  
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none; TM=Y; SS=M; 5.80  
 420340; NM\_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TIT3 com; ITAM; TM=M; SS=M; 5.79  
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar\_tr; TM=Y; SS=N; 5.79  
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2, SH3; TM=M; SS=N; 5.79  
 443257; A1334040; Hs.11614; HSPC065 protein; trypsin; TM=M; SS=N; 5.76  
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; ig; TM=Y; SS=N; 5.70  
 435299; A1745458; Hs.343026; ESTs, Weakly similar to T20593 hypotheti; none; NA; NA; 5.69  
 415995; NM\_004573; Hs.355888; phospholipase C, beta 2; C2, PI-PLC-Y, PI-PLC-X; TM=M; SS=N; 5.67  
 436772; AW975688; Hs.348918; metallothionein 1E (functional); 7tm\_2, HRM, none; 5.67  
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A; none, none; 5.66  
 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA synthetas; WHEP-TRS, tRNA-synt\_1b, none; 5.66  
 421859; AA356620; Hs.108947; KIAA0050 gene product; ank, PH, ArfGap;; 5.64  
 407756; AA116021; Hs.38260; ubiquitin specific protease 18; UCH-1, UCH-2;; 5.63  
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm\_1; TM=Y; SS=M; 5.63  
 423533; NM\_014339; Hs.129751; interleukin 17 receptor; none; TM=Y; SS=M; 5.63  
 419577; L36531; Hs.91296; integrin, alpha 8; integrin\_A, FG-GAP; TM=Y; SS=N; 5.61  
 452561; A1692181; Hs.49169; KIAA1634 protein; TPR, PDZ, WW, Guanylate\_kin; TM=M; SS=N; 5.61  
 428677; A1657119; Hs.351582; troponin I, cardiac; none; TM=M; SS=N; 5.60  
 425509; AF079363; Hs.158213; sperm associated antigen 6; Armadillo\_seg, HEAT\_PBS; TM=M; SS=N; 5.58  
 453852; AW961818; Hs.211592; MUM2 protein; pkinase, DAG\_PE-bind, C2, pkinase\_C, none; 5.57  
 421924; BE514514; Hs.109606; coronin, actin-binding protein, 1A; WD40, Idh\_C; TM=M; SS=N; 5.57  
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.55  
 431630; NM\_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP, Rhabd\_glycop, integrin\_A; TM=Y; SS=M; 5.53  
 410257; BE244044; Hs.61489; hypothetical protein; none, none; 5.53  
 441965; AA92712; Hs.269737; ESTs; pkinase, Activin\_rec, TSPN, Collagen; 5.52  
 413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; integrin\_B, Glyco\_hydro\_56;; 5.52  
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2, STAT, STAT\_bind, STAT\_prot, none; 5.50  
 447357; A1375922; Hs.132821; ESTs; FMO-like, FMO-like; 5.46  
 422109; S73265; Hs.1473; gastrin-releasing peptide; Bombesin, Defensin\_propep; TM=M; SS=M; 5.46  
 447033; A1357412; Hs.157601; Predicted gene: Eos cloned; secreted w/V; none, none; 5.45  
 417412; X16896; Hs.82112; interleukin 1 receptor, type I; ig, TIR; TM=M; SS=M; 5.45  
 436057; AJ004832; Hs.5038; neuropathy target esterase; cNMP\_binding, ion\_trans, Patatin; TM=Y; SS=M; 5.41  
 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4; TM=Y; SS=M; 5.41  
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; ig, pkinase, LRR, LRRNT, LRRCT, none; 5.40  
 452698; NM\_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm\_1; TM=Y; SS=M; 5.40  
 443623; AA345519; Hs.9641; complement component 1, q subcomponent ; C1q, Collagen;; 5.40  
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3, HS1\_rep; TM=M; SS=N; 5.38  
 437275; AW976035; Hs.292396; ESTs, Weakly similar to A47582 B-cell gr; none, Frizzled, Fz; 5.37  
 419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino ; aa\_permeases; TM=Y; SS=M; 5.37  
 449853; AF006823; Hs.24040; potassium channel, subfamily K, member 3; ion\_trans; TM=Y; SS=M; 5.36  
 442434; AA995787; Hs.129583; ESTs; IRK, none; 5.36  
 428065; A1634046; Hs.157313; ESTs; ICE\_p20, DED, ICE\_p10, ICE\_p20, DED; 5.36

- 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras,arf,Tk; 5.33  
 425638; NM\_012337; Hs.158450; nasopharyngeal epithelium specific prote; none;TM=M;SS=N; 5.32  
 419034; NM\_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M;SS=N; 5.32  
 452416; AA026115; Hs.114777; ESTs; none,Porphobil\_deam; 5.29  
 425205; NM\_005854; Hs.155106; receptor (calcitonin) activity modifying; none;TM=Y;SS=N; 5.29  
 440475; AI807671; Hs.24040; potassium channel, subfamily K, member 3; ion\_trans,none; 5.28  
 417355; D13168; Hs.82002; endothelin receptor type B; 7tm\_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B\_box;TM=Y;SS=M; 5.28  
 436120; AI248193; Hs.119860; ESTs; heme\_1,none; 5.27  
 418307; U70867; Hs.83974; solute carrier family 21 (prostaglandin ; OATP\_N,OATP\_C;TM=Y;SS=M; 5.27  
 409745; AA077391; ; gb;B14E12 Chromosome 7 Fetal Brain cDNA; 7tm\_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B\_box;TM=Y;SS=M; 5.26  
 421554; AW137676; Hs.97775; ESTs; none,none; 5.23  
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none,none; 5.22  
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 5.21  
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2 ; 7tm\_1;TM=Y;SS=M; 5.19  
 400261; ; Hs.1802; Eos Control; ig,MHC\_II\_beta;TM=Y;SS=M; 5.19  
 436856; AI469355; Hs.127310; ESTs; pkinase,rm;TM=M;SS=N; 5.18  
 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not ava; 7tm\_1,none; 5.17  
 425023; AW956889; Hs.154210; EDG-1 (endothelial differentiation, sph; 7tm\_1;TM=Y;SS=M; 5.16  
 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC\_tran,ABC\_membrane,SRP54,Thymidylate\_kin;TM=Y;SS=M; 5.16  
 451220; AF124251; Hs.26054; novel SH2-containing protein 3; SH2;TM=M;SS=N; 5.15  
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 5.14  
 424925; NM\_002432; Hs.153837; myeloid cell nuclear differentiation ant; PAAD\_DAPIN,HIN;; 5.14  
 451099; R52795; Hs.25954; interleukin 13 receptor, alpha 2; fn3;TM=Y;SS=M; 5.13  
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm\_1;TM=Y;SS=M; 5.12  
 423196; AK001866; Hs.125139; hypothetical protein FLJ11004; none;TM=M;SS=N; 5.12  
 433671; AW138797; Hs.132906; 19A24 protein; ig;TM=M;SS=M; 5.11  
 426457; AW894667; Hs.380138; chimerin (chimaerin) 1; DAG\_PE-bind,RhoGAP,SH2;TM=M;SS=N; 5.06  
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,integrin\_A,FG-GAP;TM=Y;SS=M; 5.05  
 418185; AW958272; Hs.347326; intercellular adhesion molecule 2 (ICAM; none;TM=Y;SS=M; 5.05  
 437352; AL353957; Hs.284181; hypothetical protein DKFZp434P0531; DUF221;TM=Y;SS=M; 5.03  
 457918; AL359590; Hs.162604; hypothetical protein DKFZp762M186; PLDc;TM=M;SS=N; 5.02  
 452924; AW580939; Hs.97199; complement component C1q receptor; EGF,lectin\_c,Tissue\_fac,Xlink,TIL;TM=Y;SS=M; 5.02  
 426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR m; Kunitz\_BPTI,Kunitz\_BPTI,7tm\_2,HRM; 4.99  
 432805; X94630; Hs.3107; CD97 antigen; 7tm\_2,EGF,GPS,FecCD;TM=Y;SS=M; 4.95  
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,VVV,RhoGAP;; 4.95  
 414291; AI289619; Hs.13040; G protein-coupled receptor 86; 7tm\_1;TM=Y;SS=M; 4.94  
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2\_HUMAN ALU S; none,rm; 4.92  
 451154; AA015879; Hs.33536; ESTs; TIMP,none; 4.92  
 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase,TrkA-N,2-Hacid\_DH\_C;TM=M;SS=N; 4.90  
 413011; AW068115; Hs.821; biglycan; LRR,LRRNT;; 4.90  
 422732; AA577455; Hs.24937; transformer-2 alpha (htra-2 alpha); rm,ig; 4.89  
 417015; M83772; Hs.80876; flavin containing monooxygenase 3; FMO-like,pyr\_redox;TM=Y;SS=M; 4.88  
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L OR; PLDc;TM=M;SS=N; 4.88  
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7tm\_1,LRR;TM=Y;SS=N; 4.87  
 405102; ; C15001220; jil4469558[gb]AAD21311.1) (AF; DAG\_PE-bind,PH,RhoGEF,DC1;; 4.86  
 422795; AB033109; Hs.375610; KIAA1283 protein; 7tm\_1,kazal,A2M,A2M\_N;TM=Y;SS=M; 4.84  
 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 4.83  
 414936; C14774; ; gb:C14774 Clontech human aorta polyA mRNA; ank,pkinase,death,none; 4.82  
 430152; AB001325; Hs.234642; aquaporin 3; MiP;TM=Y;SS=M; 4.82  
 444838; AV651680; Hs.208558; ESTs; integrin\_A,FG-GAP,none; 4.81  
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-recept; SH2,Y\_phosphatase,DSPc;TM=M;SS=N; 4.81  
 453107; NM\_016113; Hs.279746; vanilloid receptor-like protein 1; ank,ion\_trans;TM=Y;SS=N; 4.80  
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE\_p10,ICE\_p20;; 4.80  
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar\_tr; 4.78  
 419542; AA366037; Hs.90911; solute carrier family 16 (monocarboxylic; none,none; 4.76  
 438899; AF085833; Hs.135624; ESTs; none,PI3\_P14\_kinase,PI3Ka,PI3K\_C2,PI3K\_rbd,PI3K\_p85B; 4.75  
 427418; AA402587; Hs.356667; LAT1-3TM protein; none,none; 4.75  
 431924; AK000850; Hs.272203; Homo sapiens cDNA FLJ20843 fis, clone AD; SH3,none; 4.73  
 424218; AF031824; Hs.143212; cystatin F (leukocystatin); cystatin;; 4.72  
 414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14\_17,none; 4.72  
 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none;TM=M;SS=N; 4.71  
 430037; BE409649; Hs.227789; mitogen-activated protein kinase-activat; pkinase;TM=M;SS=N; 4.71  
 451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none,none; 4.71  
 453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 fis, clone L; FG-GAP,integrin\_A,NIF; 4.71  
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm\_3,none; 4.70  
 438543; AA810141; Hs.192182; ESTs; SH2,pkinase,none; 4.70  
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal\_L24e,SRP54,dDENN,DENN,uDENN;TM=M;SS=N; 4.70  
 438113; AI467908; Hs.8882; ESTs; 7tm\_1,none; 4.70  
 422164; NM\_014312; Hs.112377; cortic al thymocyte receptor (X. laevis ; ig,Gemini\_mov;TM=Y;SS=M; 4.69  
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm\_1;TM=Y;SS=M; 4.69  
 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-; aldo\_ket\_red,none; 4.67  
 432314; AA533447; Hs.285173; ESTs; Xlink,none; 4.66  
 453518; AW503205; Hs.27268; gb:U1-HF-BN0-akt-g-03-0-U1.r1 NIH\_MGC\_50; SH3,PH,RhoGEF;TM=M;SS=N; 4.66  
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase ; pkinase,CNH;TM=M;SS=N; 4.66  
 446063; AI720140; Hs.151079; ESTs; ISK\_Channel,none; 4.65  
 454034; NM\_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh;; 4.65  
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 4.65  
 443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, ; none,PDZ,LIM,pkinase; 4.65  
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;SS=N; 4.64  
 427535; R29543; Hs.2164; pro-platelet basic protein (includes pla; IL8;TM=M;SS=M; 4.64  
 437119; AI379921; Hs.177043; XP\_171387 similar to rhotekin; none,none; 4.63  
 411779; AA292811; Hs.72050; non-metastatic cells 5, protein expresse; NDK;; 4.63  
 429784; M89796; Hs.30; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=N; 4.62

- 415934; NM\_000928; Hs.992; phospholipase A2, group IB (pancreas); phoslip; 4.61  
 408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delt; none, none; 4.61  
 426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase; TM=M; SS=N; 4.59  
 444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligas; WW,HECT,RNA\_pol\_A,none; 4.59  
 408000; L11690; Hs.198689; bulous pemphigoid antigen 1 (230/240kD); efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose\_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,ldh\_C,CH,AlP3; TM=M; SS=N; 4.59  
 431087; H12723; Hs.290791; ESTs; ion\_trans,none; 4.58  
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG\_PE-bind,pkinase\_C,OPR; TM=M; SS=N; 4.58  
 422427; AA310514; Hs.96692; ESTs; PH,Ets,CH,spectrin,Ca\_channel\_B,none; 4.57  
 441527; W19504; Hs.7884; solute carrier family 21 (organic anion ; OATP\_N,OATP\_C; TM=Y; SS=N; 4.56  
 416464; NM\_000132; Hs.79345; coagulation factor VIII, procoagulant co; Cu-oxidase,F5\_F8\_type\_C; 4.56  
 421233; AA209534; Hs.284243; tetraspan NET-6 protein; transmembrane4; TM=Y; SS=M; 4.56  
 422311; AF073515; Hs.114948; cytokine receptor-like factor 1; fn3; TM=M; SS=N; 4.55  
 444895; A1674383; Hs.22891; solute carrier family 7 (cationic amino ; ASC,death,TNFR\_c6; 4.55  
 428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled; Nramp; TM=Y; SS=N; 4.55  
 410290; AA402307; Hs.322844; hypothetical protein DKFp564A176; Sema,PSI,TIG,integrin\_B; TM=Y; SS=M; 4.54  
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo\_seg,UQ\_con,none; 4.54  
 450086; AW016343; Hs.233301; ESTs; ank,death,ZU5,NMU,none; 4.54  
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear trans; HLH,PAS,IL8; TM=M; SS=N; 4.54  
 414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase; TM=M; SS=N; 4.53  
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX; TM=M; SS=N; 4.53  
 427557; NM\_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR\_LY6,ET,PLA2\_inh; 4.53  
 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5\_F8\_type\_C,CUB,CUB,MAM,F5\_F8\_type\_C; 4.53  
 434158; T86534; Hs.14372; ESTs; adenylatekinase,none; 4.52  
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase,Furin-like,Recep\_L\_domain,none; 4.52  
 447341; AF106941; Hs.18142; arrestin, beta 2; arrestin,arrestin\_C,PX,PH,PLDc; 4.52  
 447656; NM\_003726; Hs.19126; src kinase-associated phosphoprotein of ; SH3,PH; TM=M; SS=N; 4.51  
 417018; M16038; Hs.80887; y-yes-1 Yamaguchi sarcoma viral related ; SH2,SH3,pkinase; TM=M; SS=N; 4.51  
 422893; X98411; Hs.380077; myosin IF; SH3,myosin\_head,IQ; TM=M; SS=N; 4.51  
 407202; N58172; Hs.109370; ESTs; F5\_F8\_type\_C,pkinase,Ets,none; 4.51  
 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.sa; zf-C2H2,zf-C3HC4,UIM; TM=M; SS=N; 4.51  
 450747; A1064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm,zf-RanBP,GAS2; 4.50  
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase; TM=Y; SS=M; 4.50  
 453856; AA804789; Hs.379109; PDZ-LIM protein mystique; LIM,PDZ; TM=M; SS=N; 4.49  
 432744; AA988835; Hs.38664; ESTs; none,none; 4.49  
 419032; W81330; Hs.99877; ESTs, Highly similar to JAK3B [H.sapiens; pkinase,SH2,Insulin,pkinase,SH2; 4.48  
 444009; A1380792; Hs.135104; ESTs; TNFR\_c6,TIL,none; 4.48  
 426416; AW612744; Hs.169824; killer cell lectin-like receptor subfami; lectin\_c; TM=Y; SS=M; 4.48  
 412802; U41518; Hs.74602; aquaporin 1 (channel-forming integral pr; MIP; TM=Y; SS=M; 4.48  
 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5\_F8\_type\_C; TM=M; SS=M; 4.47  
 408771; AW732573; Hs.47584; potassium voltage-gated channel, delayed; efhand,ion\_trans,K\_tetra,none; 4.47  
 435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none; TM=M; SS=N; 4.46  
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 4.45  
 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP; TM=M; SS=N; 4.45  
 434308; N51517; Hs.47282; ESTs; pkinase,pkinase\_C,none; 4.45  
 434448; W26667; Hs.184581; Homo sapiens cDNA FLJ14821 fis, clone OV; pkinase,pkinase\_C; 4.45  
 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin\_EGF,laminin\_Nterm,integrin\_B; 4.44  
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN\_MK; TM=M; SS=Y; 4.44  
 430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF; TM=M; SS=M; 4.44  
 436001; AW903849; Hs.173840; HUEL (C4orf1)-interacting protein; ig; TM=M; SS=M; 4.44  
 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm\_1,OATP\_C; TM=Y; SS=N; 4.43  
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory su; SH2,none; 4.43  
 410068; A1633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3; TM=M; SS=N; 4.43  
 449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep\_L\_domain,none; 4.42  
 451734; NM\_006176; Hs.26944; neurogranin (protein kinase C substrate.; IQ,7tm\_1; TM=M; SS=N; 4.42  
 410598; A1817130; Hs.9195; Homo sapiens cDNA FLJ13698 fis, clone PL; RasGEF,PRK; 4.42  
 439411; AA044876; Hs.58043; ESTs, Weakly similar to CYA2\_HUMAN ADENY; guanylate\_cyc; TM=Y; SS=M; 4.42  
 433179; AW362945; Hs.162459; ESTs; Armadillo\_seg,none; 4.42  
 414849; AW372721; Hs.291623; ESTs, Weakly similar to unnamed protein ; pkinase,none; 4.42  
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD,helicase\_C,CARD; TM=M; SS=N; 4.41  
 445903; A1347487; Hs.132781; class I cytokine receptor; fn3; TM=Y; SS=N; 4.41  
 438507; AA809052; Hs.356627; ESTs; none,none; 4.41  
 409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfami; TNF; TM=Y; SS=M; 4.40  
 453037; AA045175; Hs.17914; ESTs; none; TM=Y; SS=M; 4.40  
 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vi; sushi; TM=Y; SS=M; 4.40  
 451035; AU076785; Hs.430; plastin 1 (I isoform); efhand,CH,Adaptin\_N; 4.40  
 415149; X12451; Hs.78056; cathepsin L; Peptidase\_C1; 4.39  
 408105; AW152207; Hs.270977; ESTs, Weakly similar to I38022 hypothe; Y\_phosphatase,carb\_anhydrase,DSPc,none; 4.39  
 423099; NM\_002837; Hs.123641; protein tyrosine phosphatase, receptor t; fn3,Y\_phosphatase,DSPc,COX6C; TM=M; SS=M; 4.39  
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 4.39  
 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE\_p10,ICE\_p20; 4.39  
 429747; M87507; Hs.2490; caspase 1, apoptosis-related cysteine pr; CARD,ICE\_p10,ICE\_p20; 4.39  
 426410; BE298446; Hs.305890; BCL2-like 1; Bcl-2,BH4,none; 4.38  
 434511; R29882; Hs.18106; ESTs; pkinase,Glyco\_hydro\_39; 4.38  
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; SS=N; 4.37  
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; fn3,ig,Y\_phosphatase,MAM; TM=Y; SS=M; 4.36  
 432583; AW023624; Hs.162282; potassium channel TASK-4; potassium chan; ion\_trans,X; TM=Y; SS=M; 4.36  
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF; TM=Y; SS=M; 4.36  
 426828; NM\_000020; Hs.172670; activin A receptor type II-like 1; pkinase,Activin\_rec; TM=M; SS=M; 4.36  
 449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none; TM=Y; SS=M; 4.36  
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbon; HCO3\_cotransp; TM=Y; SS=N; 4.36  
 429670; L01087; Hs.211593; protein kinase C, theta; DAG\_PE-bind,pkinase,pkinase\_C,DNA\_pol\_viral\_N,PHD,DC1; TM=M; SS=N; 4.35  
 421195; BE464560; Hs.133017; ESTs; none,none; 4.35

- 415758; BE270465; Hs.78793; protein kinase C, zeta; pkinase,DAG\_PE-bind,pkinase\_C,OPR;; 4.35  
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone\_rec,zf-C4,Metallothio\_5;TM=M;SS=N; 4.34  
 419150; T29618; Hs.89640; TEK tyrosine kinase, endothelial (venous; EGF,fn3,pkinase,ig,laminin\_EGF,DSL;TM=Y;SS=M; 4.34  
 440675; AW005054; Hs.279788; ESTs, Weakly similar to KCC1\_HUMAN CALCI; pkinase,none; 4.34  
 429657; D13626; Hs.2465; KIAA0001 gene product; putative G-protei; 7tm\_1;TM=Y;SS=M; 4.34  
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4;TM=Y;SS=M; 4.34  
 425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinas; SH2,SH3,pkinase,PH,BTK;TM=M;SS=N; 4.34  
 452124; AA454220; Hs.61170; ESTs; pkinase,none; 4.33  
 407775; NM\_004914; Hs.38772; RAB36, member RAS oncogene family; ras,arf;TM=M;SS=N; 4.33  
 452688; AA721140; Hs.49930; ESTs, Weakly similar to putative p150 [H; SH3,none; 4.33  
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;SS=N; 4.32  
 445330; R52656; Hs.21691; ESTs; 7tm\_1,none; 4.32  
 437527; AI241019; Hs.145644; ESTs; PIP5K,none; 4.32  
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 ; TIMP,pkinase,DAG\_PE-bind,RBD; 4.31  
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated; ig,ITAM,Zn\_clus;TM=Y;SS=M; 4.31  
 416269; AA177138; Hs.161671; ESTs; pkinase,DAG\_PE-bind,RBD,none; 4.30  
 425458; H89317; Hs.182889; ESTs; ion\_trans,none; 4.30  
 424205; NM\_003734; Hs.198241; amine oxidase, copper containing 3 (vasc; Cu\_amine\_oxid,Cu\_amine\_oxidN2,Cu\_amine\_oxidN3;TM=M;SS=M; 4.29  
 451876; T63141; ; gb:yb99a12.s1 Stratagene lung (937210) H; SH3,none; 4.29  
 417801; AA417383; Hs.82582; integrin, beta-like 1 (with EGF-like rep; EGF;; 4.29  
 435240; AI025435; Hs.117532; ESTs; GHMP\_kinases,none; 4.27  
 444051; N48373; Hs.10247; activated leucocyte cell adhesion molecu; none,none; 4.26  
 423523; AW299828; Hs.193580; ESTs; none,none; 4.26  
 426274; D38122; Hs.2007; tumor necrosis factor (ligand) superfami; TNF;TM=Y;SS=N; 4.26  
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo\_endo\_phos,SH2;TM=M;SS=N; 4.26  
 448386; AB037750; Hs.21061; KIAA1329 protein; PKD,BNR;TM=Y;SS=M; 4.26  
 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 4.26  
 427274; NM\_005211; Hs.174142; colony stimulating factor 1 receptor, fo; ig,pkinase;TM=Y;SS=M; 4.26  
 416602; NM\_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF,vwc,TSPN;; 4.25  
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.25  
 436494; AA720997; Hs.128295; ESTs; none,CAP\_GLY,HCO3\_cotransp,Glyco\_hydro\_63,PH; 4.24  
 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm\_2,toxin\_2;TM=Y;SS=M; 4.24  
 418255; AW135405; Hs.37251; ESTs; pkinase,none; 4.24  
 400328; X87344; ; transporter 2, ATP-binding cassette, sub; none;TM=Y;SS=N; 4.24  
 405121; ; ; mitogen-activated protein kinase 8 inter; Cys\_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;; 4.24  
 425795; AJ000479; Hs.159543; EDG-6 (endothelial differentiation, G-p; 7tm\_1;TM=Y;SS=M; 4.23  
 405786; AW161678; Hs.111334; ferritin, light polypeptide; ferritin;TM=M;SS=N; 4.23  
 449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none;TM=Y;SS=M; 4.23  
 445657; AW612141; Hs.279575; Homo sapiens G-protein coupled receptor ; 7tm\_1;TM=Y;SS=M; 4.23  
 413795; AL040178; Hs.142003; ESTs; none,pkinase,LRR,LRRCT; 4.22  
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC\_tran,M,SMC\_N,SMC\_C,DUF164,none; 4.22  
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE\_p10,ICE\_p20,DED;TM=M;SS=N; 4.22  
 417318; AW953937; Hs.240845; ESTs; SH3,PH,RhoGEF;; 4.21  
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 4.21  
 408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, com; none,none; 4.20  
 432636; AA340864; Hs.278562; claudin 7; PMP22\_Claudin;TM=Y;SS=M; 4.20  
 424618; L29472; Hs.1802; major histocompatibility complex, class ; ig,MHC\_II\_beta;TM=Y;SS=M; 4.19  
 445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK,none; 4.19  
 432882; NM\_013257; Hs.279696; serum/glucocorticoid regulated kinase-II; pkinase,PX,pkinase\_C;; 4.19  
 425481; AW978162; Hs.372811; ESTs; none,Oxysterol\_BP; 4.19  
 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE\_p20,DED;TM=M;SS=N; 4.18  
 401083; ; NM\_016582; Homo sapiens peptide transpor; PTR2;TM=Y;SS=M; 4.18  
 420676; AI434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG\_PE-bind,none; 4.18  
 424377; AF081675; Hs.146322; killer cell lectin-like receptor subfami; lectin\_c;TM=Y;SS=M; 4.17  
 424148; BE242274; Hs.1741; integrin, beta 7; integrin\_B,EGF,metalthio,PSI;TM=Y;SS=M; 4.17  
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor tran; ig,none; 4.17  
 452100; AI668668; Hs.379032; inositol polyphosphate-5-phosphatase, 75; Exo\_endo\_phos,RhoGAP,none; 4.17  
 413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidylin; SH2,SH3,C2,PH,PI-PLC-Y,PI-PLC-X,PDGFG;; 4.17  
 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none,pkinase,fn3,ig; 4.17  
 444034; AL161957; Hs.10177; pleckstrin homology domain interacting p; E1-  
 E2\_ATPase,Cation\_ATPase\_C,Cation\_ATPase\_N,Hydrolase,Ribosomal\_S15,bromodomain,WD40;TM=M;SS=N; 4.16  
 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheti; ABC\_tran,ABC\_membrane,ig,MHC\_II\_beta,SRP54,proteasome,ABC\_membrane,ABC\_tran; 4.16  
 407245; X90568; Hs.172004; titin; fn3,ig,SGXXSG,pkinase;TM=M;SS=N; 4.16  
 418962; AA714835; Hs.271863; ESTs; RhoGAP,SH2,pkinase,POLO\_box,none; 4.15  
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 4.15  
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.15  
 446967; AI699629; Hs.156781; ESTs; none,none; 4.14  
 432176; AW090386; Hs.112278; arrestin, beta 1; arrestin,arrestin\_C,none; 4.14  
 452571; W31518; Hs.34665; ESTs; none;TM=M;SS=N; 4.14  
 425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar\_tr;TM=Y;SS=M; 4.14  
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl\_oxidase;; 4.14  
 417871; AA521368; Hs.24252; ESTs; IBB,Armaddillo\_seg,none; 4.13  
 429819; AL133011; Hs.253920; Homo sapiens mRNA; cDNA DKFZp434P201 (fr; none,none; 4.12  
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase\_C;; 4.12  
 429623; NM\_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase,RGS;TM=M;SS=N; 4.12  
 413019; BE281604; Hs.75140; low density lipoprotein-related protein-; none;TM=M;SS=Y; 4.12  
 434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M;SS=N; 4.11  
 434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK;TM=Y;SS=N; 4.11  
 449656; AA002008; Hs.188633; ESTs; PIP5K,none; 4.11  
 406403; ; NM\_002162; Homo sapiens intercellular ad; ig;TM=Y;SS=M; 4.10  
 427732; NM\_002980; Hs.2199; secretin receptor; 7tm\_2,HRM;TM=M;SS=M; 4.10  
 437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1\_HUMAN ALU S; pkinase,RIO1,none; 4.10  
 432885; AA595607; Hs.368129; ESTs, Weakly similar to ALU1\_HUMAN ALU S; pkinase,pkinase\_C,none; 4.10

- 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase, pkinase\_C, HR1; TM=M; SS=N; 4.10  
 418342; BE002723; Hs.334330; leptin receptor; ICE\_p20, DED, ICE\_p10, ICE\_p20, DED; 4.10  
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese;; 4.10  
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3, RhoGAP, FCH; TM=M; SS=N; 4.10  
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz, Frizzled, 7tm\_2; TM=Y; SS=M; 4.10  
 437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none; TM=Y; SS=M; 4.10  
 432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH, RhoGAP, SH3; TM=M; SS=N; 4.09  
 435140; AA668123; Hs.134170; ESTs; none, none; 4.09  
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC\_tran, ABC\_membrane, GTP\_EFTU; TM=M; SS=M; 4.08  
 428483; AI908539; Hs.184592; KIAA0344 gene product; none, none; 4.08  
 446232; AI281848; Hs.194691; retinoic acid induced 3; 7tm\_3, none; 4.07  
 431674; AA098901; Hs.301642; G-protein coupled receptor; none, GCV\_H; 4.07  
 409686; AK000002; Hs.55879; Homo sapiens mRNA; cDNA DKFZp434L0827 (f; ABC\_tran, ABC\_membrane; TM=M; SS=M; 4.07  
 441518; AW161697; Hs.294150; ESTs; Y\_phosphatase, DSPc, none; 4.07  
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3, ank; TM=M; SS=N; 4.06  
 436982; AB018305; Hs.5378; spondin 1, (f-spondin) extracellular mat; tsp\_1, Reeler;; 4.05  
 420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP, 7tm\_1; 4.05  
 439549; AW937885; Hs.137314; ESTs; SH2, none; 4.04  
 419981; AA897581; Hs.128773; ESTs; pkinase, DAG\_PE-bind, pkinase\_C, OPR, none; 4.04  
 418836; AI655499; Hs.161712; ESTs; pkinase, Activin\_rec, PDZ, ZU5, death; 4.04  
 408806; AW847814; Hs.75608; Homo sapiens cDNA: FLJ21532 fis, clone C; SH3, PDZ, Guanylate\_kin, none; 4.04  
 432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3, PDZ, Guanylate\_kin, none; 4.03  
 426086; T94907; Hs.188572; ESTs; PH, Ets, CH, spectrin, Ca\_channel\_B, none; 4.03  
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 4.03  
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha, arf; TM=M; SS=N; 4.03  
 416350; AF188625; Hs.189507; phospholipase A2, group IID; phospholip; TM=M; SS=Y; 4.02  
 434457; AF141332; Hs.200333; apolipoprotein B48 receptor; none; TM=M; SS=N; 4.02  
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain, PHD, PWWP, zf-MYND; TM=M; SS=N; 4.02  
 425694; U51333; Hs.159237; hexokinase 3 (white cell); hexokinase, hexokinase2; TM=M; SS=N; 4.02  
 449943; AF104266; Hs.24212; latrophilin; 7tm\_2, GPS, Gal\_Lectin, OLF, Latrophilin, HRM; TM=Y; SS=M; 4.01  
 408938; AA059013; Hs.22607; ESTs; fn3, Y\_phosphatase, carb\_anhydase, none; 4.01  
 426839; M74782; Hs.172689; interleukin 3 receptor, alpha (low affin; none; TM=M; SS=M; 4.00  
 422282; AF019225; Hs.114309; apolipoprotein L; MotA\_ExcB; TM=Y; SS=M; 4.00  
 410726; AI623859; Hs.15936; ESTs; pkinase, pro\_isomerase, none; 4.00  
 428318; BE300110; Hs.183842; ubiquitin B; lipocalin, aldedh, ubiquitin, IRK;; 4.00  
 440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK; TM=M; SS=N; 3.99  
 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase, ubiquitin, Enterotoxin\_A, PHO4, pkinase, ubiquitin; 3.99  
 414700; H63202; Hs.38163; ESTs; 7tm\_1; TM=Y; SS=M; 3.99  
 432269; NM\_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase, Sema, PSI, TIG, A4\_EXTRA; TM=M; SS=M; 3.99  
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M; SS=N; 3.98  
 427541; AI798983; Hs.375835; solute carrier family 35 (CMP-sialic aci; none, none; 3.98  
 440248; AA876138; Hs.369458; ESTs; SH2, none; 3.98  
 437400; AB011542; Hs.5599; EGF-like-domain, multiple 5; TNFR\_c6, laminin\_EGF; TM=Y; SS=N; 3.98  
 425262; D87119; Hs.155418; GS3955 protein; pkinase;; 3.98  
 420166; AW732276; Hs.95583; transmembrane 4 superfamily member (tetra; transmembrane4; TM=Y; SS=M; 3.98  
 437151; AA745618; Hs.380121; BANP homolog, SMAR1 homolog; none, none; 3.98  
 443574; U83993; Hs.321709; purinergic receptor P2X, ligand-gated io; P2X\_receptor; TM=Y; SS=M; 3.97  
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase\_M49, EGF, ig, Neuregulin; TM=M; SS=N; 3.97  
 411574; BE242842; Hs.6780; protein tyrosine kinase 9-like (A6-relat; LRR, LRRCT, TIR, cofilin\_ADF; TM=M; SS=N; 3.97  
 432639; AW973785;; gb:EST385886 MAGE resequences, MAGM Homo; none, IRK; 3.97  
 457675; AF119917; Hs.306574; Homo sapiens PRO3098 mRNA, complete cds; none;; 3.97  
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2, PH; TM=M; SS=N; 3.96  
 437157; BE048860; Hs.17287; ESTs; IRK, none; 3.96  
 453641; AA444140; Hs.90960; ESTs; Cbl\_N, Cbl\_N2, Cbl\_N3, UBA, zf-C3HC4, none; 3.96  
 446714; W73818; Hs.110028; ESTs; 7tm\_1, 7tm\_1; 3.96  
 427648; AI376722; Hs.180062; proteasome (prosome, macropain) subunit; proteasome;; 3.96  
 453686; AL110326; Hs.304679; ESTs, Moderately similar to Z195\_HUMAN Z; none, lectin\_c, lig\_chan; 3.96  
 457718; F18572; Hs.22978; ESTs, Weakly similar to ALU4\_HUMAN ALU S; pkinase, pkinase; 3.95  
 428727; AF078847; Hs.78452; general transcription factor IIH, polype; PHO4, LIM; TM=M; SS=N; 3.95  
 435411; AW444619; Hs.138211; ESTs; none, pkinase; 3.94  
 440209; H05049; Hs.247837; neurexin 3; laminin\_G, EGF, none; 3.94  
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none, none; 3.94  
 435272; AA906415; Hs.110041; ESTs; none, pkinase; 3.93  
 402550;; ; Target Exon; none, none; 3.93  
 425233; Z17861; Hs.155218; E1B-55kDa-associated protein 5; SPRY, SAP, pkinase, fn3, ig; 3.93  
 410073; AW408163; Hs.58488; catenin (cadherin-associated protein), a; Statmin, Vinculin;; 3.92  
 453548; AL079983; Hs.116774; integrin, alpha 1; none, vwa, FG-GAP, integrin\_A; 3.92  
 417226; AW505054; Hs.4283; ESTs; pkinase, RGS, PH, myosin\_head, Myosin\_tail; 3.92  
 446755; AW451473; Hs.16134; serine/threonine kinase 10; pkinase, TYA; TM=M; SS=N; 3.92  
 452344; AI264357; Hs.55405; hypothetical protein MGC16212; Sulfate\_transp, STAS;; 3.92  
 418516; NM\_006218; Hs.85701; phosphoinositide-3-kinase, catalytic, al; PI3\_P14\_kinase, PI3Ka, PI3K\_C2, PI3K\_rbd, PI3K\_p85B, none; 3.91  
 423069; W15613; Hs.1613; adenosine A2a receptor; 7tm\_1; TM=Y; SS=M; 3.91  
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor;; ig, pkinase; TM=Y; SS=N; 3.91  
 434392; AW983709; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone H; pkinase, none; 3.91  
 429615; AF258627; Hs.211562; ATP-binding cassette, sub-family A (ABC1; ABC\_tran; TM=Y; SS=M; 3.91  
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle, trypsin, plant\_thionins;; 3.91  
 442831; AI798959; Hs.131686; ESTs; ABC\_tran, PRK, ABC\_tran; 3.91  
 441657; BE314696; Hs.7936; BAI1-associated protein 2; SH3; TM=M; SS=N; 3.91  
 438698; AW297855; Hs.361171; ESTs, Weakly similar to I38022 hypotheti; lipoxigenase, PLAT, none; 3.90  
 447560; AF065214; Hs.18858; phospholipase A2, group IVC (cytosolic;; PLA2\_B; TM=M; SS=N; 3.90  
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC, none; 3.89  
 429379; NM\_014840; Hs.200598; KIAA0537 gene product; pkinase, RIO1; TM=M; SS=N; 3.89  
 410179; W27723; Hs.59498; cell division cycle 2-like 5 (cholineste; pkinase;; 3.89

428713; AA432067; Hs.268551; ESTs, Moderately similar to CYA4 RAT ADE; pkinase;; 3.89  
 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase\_c,zf-C2H2,PHD:none; 3.89  
 425190; AW028302; Hs.155079; protein phosphatase 2, regulatory subunit; B56;TM=M;SS=N; 3.89  
 426752; X69490; Hs.172004; titin; fn3,ig,pkinase,SGXXSG;TM=M;SS=N; 3.89  
 417767; BE242241; Hs.82542; acylxyacyl hydrolase (neutrophil); Lipase\_GDSL;TM=M;SS=M; 3.88  
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dep; Man-6-P\_recep;TM=M;SS=M; 3.88  
 416140; AI918035; Hs.301198; roundabout (axon guidance receptor, Dros; none:none; 3.88  
 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe co; fn3;TM=Y;SS=M; 3.88  
 410011; AB020641; Hs.57856; PFTAIRE protein kinase 1; pkinase;TM=M;SS=N; 3.87  
 406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gen; none:none; 3.87  
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD\_DAPIN,HIN;; 3.87  
 441859; AW194364; Hs.9877; interleukin-4 induced gene-1 protein (FI; Amino\_oxidase,FAD\_binding\_3,TBC;TM=M;SS=N; 3.87  
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p\_like;TM=M;SS=N; 3.87  
 415392; Z44067; Hs.10957; ESTs; PIP5K:none; 3.86  
 416033; NM\_012201; Hs.78979; Golgi apparatus protein 1; cys\_rich\_FGFR;TM=Y;SS=M; 3.86  
 414649; AI672727; Hs.76753; endoglin (CD105 antigen) (ENG); none;TM=Y;SS=M; 3.85  
 425729; L22647; Hs.159360; prostaglandin E receptor 1 (subtype EP1); 7tm\_1;TM=Y;SS=M; 3.85  
 414496; W73853; Hs.355424; ESTs; pkinase,F5\_F8\_type\_C,adh\_short:none; 3.84  
 412204; AI125507; Hs.24937; ESTs; ig,rrm:none; 3.84  
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS\_kinase,ATP-sulfurylase,PRK,Thymidylate\_kin;; 3.84  
 444981; AW855398; Hs.12210; hypothetical protein FLJ13732 similar to; SH2;TM=M;SS=N; 3.84  
 412309; M23892; Hs.73809; arachidonate 15-lipoxygenase; lipoxygenase,PLAT;; 3.84  
 405545; ; Target Exon; ABC\_tran,SRP54,ABC\_membrane;TM=Y;SS=M; 3.84  
 407143; C14076; Hs.332329; EST; none;TM=Y;SS=M; 3.84  
 420593; AA280356; Hs.187634; ESTs; B56:none; 3.84  
 413420; AW410235; Hs.75348; proteasome (prosome, macropain) activato; PA28\_alpha,PA28\_beta,bioplerin\_H;; 3.83  
 448253; H25899; Hs.201591; ESTs; 7tm\_2,HRM:none; 3.83  
 444042; NM\_004915; Hs.10237; ATP-binding cassette, sub-family G (WHIT; ABC\_tran,PRK,GBP;TM=Y;SS=N; 3.83  
 430397; AI924533; Hs.105607; bicarbonate transporter related protein ; HCO3\_cotransp;TM=Y;SS=N; 3.83  
 423067; AA321355; Hs.285401; colony stimulating factor 2 receptor, be; fn3;TM=Y;SS=M; 3.83  
 458188; AW297226; Hs.137840; ESTs, Moderately similar to SIX4\_HUMAN H; pkinase,WD40; 3.82  
 426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFZp586B0220 (f; pkinase:none; 3.82  
 428791; AA435661; Hs.264750; ESTs; zf-C3HC4:none; 3.82  
 438068; AI927209; Hs.306210; Homo sapiens cDNA: FLJ23133 fis, clone L; NusG;; 3.82  
 453370; AI470523; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC\_tran,ABC\_membrane;TM=Y;SS=N; 3.82  
 419250; AW770185; Hs.356066; U5 snRNP-specific protein, 116 kD; 7tm\_1,BAH,zf-CXXC,DNA\_methylase; 3.82  
 410017; AW952426; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none:none; 3.82  
 420679; X57152; Hs.165843; fibrillarin; CK\_IL\_beta,Fibrillarin,WD40;TM=M;SS=N; 3.82  
 417916; NM\_006416; Hs.82921; solute carrier family 35 (CMP-sialic aci; DUF6;TM=Y;SS=M; 3.81  
 425923; NM\_005025; Hs.162808; phosphoinositide-3-kinase, catalytic, de; none:none; 3.81  
 417365; D50683; Hs.82028; transforming growth factor, beta recepto; pkinase,WD40;TM=Y;SS=N; 3.64  
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 3.52  
 422398; AI476149; Hs.334489; hypothetical protein FLJ21992; SH2,SH3;; 3.51  
 418432; M14156; Hs.85112; insulin-like growth factor 1 (somatomedi; Insulin;; 3.50  
 459705; BE082764; Hs.270252; ESTs, Weakly similar to androgen recepto; none,C2,WW,HECT; 3.48  
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t; fn3,ig\_Y\_phosphatase,MAM;TM=Y;SS=M; 3.38  
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor t; fn3,Y\_phosphatase,carb\_anhydase;TM=Y;SS=M; 3.37  
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz,NTR;; 3.24  
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolo; EGF,cadherin,laminin\_G;TM=Y;SS=M; 3.11  
 419721; NM\_001650; Hs.315369; aquaporin 4; MIP:none; 2.99  
 433147; AF091434; Hs.43080; platelet derived growth factor C; PDGF,CUB;; 2.91  
 417976; BE565892; Hs.83077; interleukin 18 (interferon-gamma-inducin; none;TM=M;SS=N; 2.89  
 439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep\_L\_domain,Peptidase\_M24; 2.59  
 426158; NM\_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep\_L\_domain,Peptidase\_M24; 2.23  
 411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none:none; 2.07  
 428800; M57627; Hs.193717; interleukin 10; IL10;; 1.10

TABLE 40B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey CAT Number Accession

456034 685586\_1 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945  
 459702 539529\_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354  
 432222 539529\_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354  
 414991 1785136\_1 D78831 C17898 D78863  
 409745 MH1944\_5 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625  
 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377  
 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445  
 414936 1782849\_1 C14774 C17911 D79033  
 451876 2328579\_1 T63141 AI821021 BF370092 BF370127 BF370060 T62998  
 432639 1237887\_1 AW973785 H60163 AA557608

TABLE 40C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	404240	5002624	Minus	116132-116407,116653-116922
	405102	8076881	Minus	120922-121296
	405121	8102330	Minus	35816-36004,36587-36684
10	401083	3242744	Plus	33192-33360
	406403	9256305	Minus	151426-151680
	402550	7652009	Minus	80413-80673
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182

15

TABLE 41A: 556 GENES UP-REGULATED IN PANCREATIC TUMORS OR PANCREATITIS RELATIVE TO NORMAL TISSUES

20

Table 41A lists about 556 genes up-regulated in pancreatic tumors or pancreatitis relative to normal tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

25

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: 90th percentile of pancreatic cancer/median of normal pancreas

30

35

40

45

50

55

60

65

70

75

80

Pkey	ExAccn	UnigenelD	Unigene Title	R1
412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	7.25
431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.64
444995	AJ272265	Hs.12230	secreted phosphoprotein 2, 24kD	3.58
453863	X02544	Hs.572	orosomucoid 1	114.18
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	922.40
421344	AW631030	Hs.103665	villin-like	2.19
416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	61.10
438091	AW373062	Hs.83623	nuclear receptor subfamily 1, group 1, m	607.40
418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	228.20
418969	W33191	Hs.28907	hypothetical protein FLJ20258	4.97
443162	T49951	Hs.9029	DKFZP434G032 protein	38.01
423096	AA732684	Hs.278428	progesterone induced protein	189.60
413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	11.06
448243	AW369771	Hs.52620	integrin, beta 8	116.90
421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	21.52
407788	BE514982	Hs.38991	S100 calcium-binding protein A2	8.74
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (COM	3.11
432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	307.70
457059	BE561665	Hs.177677	exosome component Rrp40	33.60
451945	BE504055	Hs.211420	ESTs	7.31
453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE	133.70
443247	BE614387	Hs.333893	c-Myc target JPO1	349.10
410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	330.00
416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	3.78
413835	AI272727	Hs.249163	fatty acid hydroxylase	3.53
433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	73.90
414774	X02419	Hs.77274	plasminogen activator, urokinase	3.39
410639	BE269047	Hs.65234	hypothetical protein FLJ20596	1.72
410541	AA065003	Hs.64179	syntenin-2 protein	10.29
427722	AK000123	Hs.180479	hypothetical protein FLJ20116	6.79
429612	AF062649	Hs.252587	pituitary tumor-transforming 1	4.62
407604	AW191962	Hs.249239	collagen, type VIII, alpha 2	366.30
431193	AW749505	Hs.296770	KIAA1719 protein	6.99
442080	AW444761	Hs.44565	ESTs	118.00
427670	BE612888	Hs.180224	myosin regulatory light chain	2.73
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	647.30
419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	738.90
441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	68.43
407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.03
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	7.73
416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	227.30
418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	115.60
452355	N54926	Hs.29202	G protein-coupled receptor 34	192.20
419481	AI879195	Hs.90606	15 kDa selenoprotein	119.90
407230	AA157857	Hs.182265	keratin 19	12.11
418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	6.63
427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	592.10
411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	120.40
445517	AF208855	Hs.12830	hypothetical protein	117.40
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.25
428385	AF112213	Hs.184052	putative Rab5-interacting protein	3.12
448663	BE614599	Hs.106823	hypothetical protein MGC14797	135.20
406867	AA157857	Hs.182265	keratin 19	11.32
417426	NM_002291	Hs.82124	laminin, beta 1	406.20



	406366	AF026692	Hs.105700	secreted frizzled-related protein 4	0.62
	401201	#(NOCAT)		Target Exon	0.75
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	0.63
5	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.75
	442776	AW959498	Hs.8709	chymotrypsin C (caldecrin)	0.67
	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.83
	403207	#(NOCAT)		C2000960:gi 131432 sp P23132 LITH_BOVIN	0.80
	427858	NM_001971	Hs.21	elastase 1, pancreatic	0.98
10	426004	AW600300	Hs.124123	ESTs, Moderately similar to SYNLRAT SYN	0.88
	401541	NA		Target Exon	0.91
	429793	AI417638	Hs.114648	estrogen regulated gene 1	0.85
	423068	M25629	Hs.123107	kallikrein 1, renal/pancreas/salivary	0.81
	433110	D56494	Hs.3191	rat regenerating islet-derived-like, hum	0.72
15	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	0.95
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	0.87
	412470	M93283	Hs.73923	pancreatic lipase-related protein 1	0.89
	431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	0.97
	419219	AW583139	Hs.89717	carboxypeptidase A2 (pancreatic)	0.95
20	412688	AW583062	Hs.74502	chymotrypsinogen B1	0.95
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.07
	420937	AW966719	Hs.1340	colipase, pancreatic	0.99
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	1.02
	410839	NM_006849	Hs.66581	protein disulfide isomerase	1.00
25	437986	AA774575	Hs.121776	testis expressed sequence 11	1.02
	415934	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)	1.06
	427965	D00306	Hs.181289	elastase 3, pancreatic (protease E)	1.22
	406399	#(NOCAT)		NM_003122*:Homo sapiens serine protease	1.08
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.11
30	414061	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	1.22
	421243	AW873803	Hs.102876	pancreatic lipase	1.13
	419263	AW583874	Hs.89832	insulin	1.12
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.13
	408983	NM_000492	Hs.663	cystic fibrosis transmembrane conductanc	1.32
35	436217	T53925	Hs.107	fibrinogen-like 1	1.72
	435975	AL118990	Hs.41997	alpha-1-B glycoprotein	1.60
	431330	X69532	Hs.2777	inter-alpha (globulin) inhibitor, H1 pol	2.02
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	1.82
	415003	M11437	Hs.77741	kininogen	3.83
40	422281	M36803	Hs.1504	hemopexin	2.14
	414910	X12662	Hs.289057	arginase, liver	97.90
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	236.70
	400836	#(NOCAT)		Target Exon	2.47
	452983	L32140	Hs.531	afamin	117.10
45	419768	T72104	Hs.93194	apolipoprotein A-I	4.87
	413841	M34276	Hs.75576	plasminogen	374.00
	400560	#(NOCAT)		NM_030878*:Homo sapiens cytochrome P450,	144.50
	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	266.50
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	77.80
50	426205	D63521	Hs.167877	leukocyte cell-derived chemotaxin 2	169.80
	414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	3.60
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	400.40
	429023	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	4.72
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	5.26
55	425260	L47726	Hs.1870	phenylalanine hydroxylase	73.78
	443316	AI478463	Hs.18443	aldehyde dehydrogenase 8 family, member	182.20
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	335.00
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	173.40
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	565.30
60	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	86.20
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	477.20
	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	201.50
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	426.10
	425573	AB006423	Hs.158308	serine (or cysteine) proteinase inhibito	1.10
65	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H	0.62
	406672	M26041	Hs.198253	major histocompatibility complex, class	4.02
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	5.34
	421712	AK000140	Hs.107139	hypothetical protein	5.62
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	8.85
70	442896	R37725	Hs.261108	ESTs	157.70
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	137.70
	428486	AW583497	Hs.184604	pancreatic polypeptide	2.59
	457489	AI693815	Hs.127179	cryptic gene	3.23
	404866	NA		ENSP00000251112*:Sodium/potassium-transp	2.84
75	432874	W94322	Hs.279651	melanoma inhibitory activity	2.48
	445891	AW391342	Hs.199460	ESTs	70.38
	404682	NA		C9001188*:gi 12738842 ref NP_073725.1  p	1.38
	429547	AW009166	Hs.99376	ESTs	6.85
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	5.21
80	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	1.74
	446868	AV660737	Hs.135100	ESTs	102.10
	404287	NA		C6001909:gi 704441 dbj BAA18909.1  (D298	242.70
	443267	AW450630	Hs.133851	ESTs	98.90
	451635	AA018899	Hs.127179	cryptic gene	2.16

5	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	131.70
	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	128.70
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	92.90
	410309	BE043077	Hs.278153	ESTs	108.80
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	170.10
10	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	75.70
	449592	AI655494	Hs.195718	ESTs	4.58
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	188.50
	406685	M18728		gb:Human nonspecific crossreacting antig	1123.60
	411573	AB029000	Hs.70823	KIAA1077 protein	995.60
15	429201	X03178	Hs.198246	group-specific component (vitamin D bind	11.32
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	8.38
	428698	AA852773	Hs.334838	KIAA1866 protein	662.00
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	4.00
	432596	AJ224741	Hs.278461	matriin 3	283.50
20	428824	W23624	Hs.173059	ESTs	4.55
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.01
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.21
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	4.80
	448844	AI581519	Hs.177164	ESTs	362.80
25	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	133.90
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	128.20
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	13.83
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	316.00
	452571	W31518	Hs.34665	ESTs	245.50
30	443646	AI085198	Hs.164226	ESTs	189.40
	436032	AA150797	Hs.109276	latexin protein	291.10
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	252.20
	422109	S73265	Hs.1473	gastrin-releasing peptide	278.20
	430407	H23551	Hs.30974	ESTs	6.20
35	419235	AW470411	Hs.288433	neurotrimin	423.50
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.01
	444301	AK000136	Hs.10760	asporin (LRR class 1)	499.90
	427333	AF067797	Hs.176658	aquaporin 8	1.05
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	4.33
40	407777	AA161071	Hs.71465	squalene epoxidase	3.64
	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	1.47
	421341	AJ243212	Hs.279611	deleted in malignant brain tumors 1	3.98
	453935	AI633770	Hs.42572	ESTs	2.08
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	3.84
45	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	14.21
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	315.70
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.53
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	3.13
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	9.33
50	440484	BE328156	Hs.150356	ESTs	1.03
	447395	AI418412	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	1.09
	440099	AL080058	Hs.6909	DKFZP564G202 protein	14.74
	434665	AA642125		gb:nr60c01.s1 NCI_CGAP_Lym3 Homo sapiens	0.98
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	2.23
55	408915	NM_016651	Hs.48950	heptacell carcinoma novel gene-3 pro	329.40
	424411	NM_005209	Hs.146549	crystallin, beta A2	1.71
	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	2.69
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	1.70
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	3.19
60	429010	Y18198	Hs.194725	one cut domain, family member 2	1.96
	414420	AA043424	Hs.76095	immediate early response 3	2.54
	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	3.30
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	312.80
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	177.80
65	406173	\$(NOCAT)		ENSP00000250148*:Growth hormone variant	1.46
	403776	\$(NOCAT)		ENSP00000226542*:Small inducible cytokin	121.80
	403574	NA		Target Exon	16.12
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.94
	458449	HI04482	Hs.29019	ESTs	71.60
70	409958	NM_001523	Hs.57697	hyaluronan synthase 1	1.77
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	3.13
	451181	AI796330	Hs.207461	ESTs	68.00
	440508	BE267911	Hs.196970	ESTs	38.00
	429636	AA455692	Hs.163232	ESTs	30.70
75	419570	W68738		gb:zd37g06.s1 Soares_fetal_heart_NbHH19W	1.02
	431779	AW971178	Hs.268571	apolipoprotein C-I	3.36
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.20
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (MMP7; uterin	3.94
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fasciclin	1171.10
80	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	809.50
	440482	AA886658	Hs.50873	ESTs	9.95
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	30.70
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	82.90
	452239	AW379378	Hs.170121	protein tyrosine phosphatase, receptor t	26.01
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	5.38
	409335	NM_001502	Hs.53985	glycoprotein 2 (zymogen granule membrane	0.54
	420876	AA918425	Hs.177744	ESTs	0.89

	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	0.94
	401732	#(NOCAT)		NM_001176*:Homo sapiens Rho GDP dissocia	1.13
	404142	NA		Target Exon	1.33
5	424165	AW582904	Hs.142255	islet amyloid polypeptide	2.95
	413880	AI660842	Hs.110915	interleukin 22 receptor	1.34
	407007	U22961		gb:Human mRNA clone with similarity to L	1.57
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.48
	432855	AF017988	Hs.279565	secreted frizzled-related protein 5	1.28
10	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.31
	445730	AI624342	Hs.170042	ESTs	2.14
	406666	V00495	Hs.184411	albumin	2.95
	435849	BE305242	Hs.16098	claudin 2	1.96
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	2.49
	430272	X04898	Hs.237658	apolipoprotein A-II	3.29
15	412374	X01388	Hs.73849	apolipoprotein C-III	2.42
	419276	BE165909	Hs.306881	MSTP043 protein	83.40
	415448	T68645	Hs.952	solute carrier family 10 (sodium/bile ac	3.52
	423541	AA296922	Hs.129778	gastrointestinal peptide	3.16
20	428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	6.24
	425551	AA359252	Hs.126485	hypothetical protein FLJ12604; KIAA1692	14.67
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	4.30
	428786	Y16577	Hs.2314	mannose-binding lectin (protein C) 2, so	92.10
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	203.30
25	451253	H48299	Hs.26126	claudin 10	1.37
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	3.38
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibito	7.04
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.84
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.65
30	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	9.28
	422237	M13149	Hs.1498	histidine-rich glycoprotein	34.26
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	1.92
	414386	X00442	Hs.75990	haptoglobin	8.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stro	1.74
35	452689	F33868	Hs.284176	transferrin	6.51
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	35.08
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	170.30
	428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis t	2.34
	405849	#(NOCAT)		Target Exon	103.10
40	405281	#(NOCAT)		NM_002864:Homo sapiens pregnancy-zone pr	31.20
	419078	M93119	Hs.89584	insulinoma-associated 1	6.28
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.89
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.80
45	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.82
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	13.15
	450400	AI694722	Hs.279744	ESTs	5.22
	413916	N49813	Hs.75615	apolipoprotein C-II	8.60
	444632	AI184027	Hs.146986	ESTs, Weakly similar to FATH_HUMAN CADHE	71.30
	415906	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.70
50	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.65
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	3.01
	436961	AW375974	Hs.156704	ESTs	164.60
	446319	AW207590	Hs.160711	ESTs	1.88
	427899	AA829286	Hs.332053	serum amyloid A1	6.98
55	419092	J05581	Hs.89603	mucin 1, transmembrane	2.12
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	132.20
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.23
	406319	NA		CX000780:gi 6679197 ref NP_032800.1  pol	51.50
	404286	NA		C6001909:gi 704441 dbj BAA18909.1  (D298	1.75
60	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	52.90
	406293	NA		Target Exon	68.30
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	102.43
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	206.30
	425200	BE255203	Hs.155101	ATP synthase, H transporting, mitochondr	5.76
65	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	200.10
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	97.70
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.96
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	30.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.66
70	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	193.80
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.05
	420001	J05064	Hs.1282	complement component 6	159.00
	449038	AL133084	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f	39.10
	423184	NM_004428	Hs.1624	ephrin-A1	2.39
75	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	327.90
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	90.50
	445593	AW203963	Hs.150896	ESTs	49.20
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	3.12
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.93
80	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	39.90
	417940	R28205	Hs.24230	ESTs	57.20
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	2.51
	439920	H05430	Hs.288433	neurotrimin	1.91
	432542	AW083920	Hs.16098	claudin 2	3.47

	410418	D31382	Hs.63325	transmembrane protease, serine 4	3.82
	415989	AI267700	Hs.317584	ESTs	182.50
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.84
	400024			AFFX control - HUMRGE/M10098_5	4.82
5	418067	AI127958	Hs.83393	cystatin E/M	4.19
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.92
	405909	NA		Target Exon	71.80
	448811	AI590371	Hs.174759	ESTs	6.74
	430044	AA464510	Hs.152812	ESTs	14.91
10	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	757.80
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	1.65
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapi	104.70
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	143.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	311.80
15	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	63.00
	422330	D30783	Hs.115263	epiregulin	141.70
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	2.59
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	181.90
	430691	C14187	Hs.103538	ESTs	95.80
20	401682	NA		Target Exon	6.17
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	318.60
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.51
	442560	AA365042	Hs.228598	ESTs, Weakly similar to 2004399A chromos	3.90
25	414812	X72755	Hs.77367	monokine induced by gamma interferon	434.60
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	6.58
	421430	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	35.10
	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	2.45
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	8.56
	448437	AW470125		gb:wx60c04.x1 NCL_CGAP_Pan1 Homo sapiens	79.80
30	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	147.30
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	30.07
	424586	NM_003401	Hs.150930	X-ray repair complementing defective rep	55.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (CX	405.20
35	438746	AI885815	Hs.184727	ESTs	3.57
	456032	AW957446	Hs.301711	ESTs	136.80
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	36.10
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	9.93
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	146.40
40	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	20.60
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.58
	437157	BE048860	Hs.120655	ESTs	91.80
	404285	NA		C6001909:gil704441 dbj BAA18909.1  (D298	123.80
	424036	AA770688	Hs.28777	H2A histone family, member L	5.26
45	422026	U80736	Hs.110826	trinucleotide repeat containing 9	130.40
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	48.80
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	3.15
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	253.20
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	80.00
50	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	3.05
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.66
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	23.02
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	78.10
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	1.74
55	421298	AW172431	Hs.13012	ESTs	133.10
	422424	AI186431	Hs.296638	prostate differentiation factor	2.65
	421582	AI910275	Hs.1406	trefol factor 1 (pS2)	5.17
	401480	NA		Target Exon	73.70
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	137.70
60	409757	NM_001898	Hs.123114	cystatin SN	9.36
	449722	BE280074	Hs.23960	cyclin B1	162.70
	452240	AI591147	Hs.61232	ESTs	151.90
	415165	AW887604	Hs.78065	complement component 7	2.85
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	290.30
65	428450	NM_014791	Hs.184339	KIAA0175 gene product	6.89
	409041	AB033025	Hs.50081	KIAA1199 protein	334.10
	453331	AI240665	Hs.8895	ESTs	12.85
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	12.42
	453160	AI263307	Hs.239884	H2B histone family, member L	156.40
70	444015	AI472865	Hs.135534	ESTs	14.60
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	87.20
	448045	AJ297436	Hs.20166	prostate stem cell antigen	526.20
	422426	W79117	Hs.58559	ESTs	58.30
	450737	AW007152	Hs.203330	ESTs	281.00
75	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	31.25
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	78.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	212.10
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	3.40
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	3.48
80	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	281.50
	431753	X76029	Hs.2841	neuromedin U	60.50
	428651	AF196478	Hs.188401	annexin A10	508.30
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	85.80
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	55.30

	435039	AW043921	Hs.130526	ESTs	64.00
	447033	AI357412	Hs.157601	ESTs	123.20
	433578	BE336886	Hs.3416	adipose differentiation-related protein	9.22
5	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	525.70
	411274	NM_002776	Hs.69423	kalikrein 10 (KLK10) (PRSSL1) (nes1)	44.36
	452705	H49805	Hs.246005	ESTs	120.10
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	92.30
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	29.37
10	422562	AI962060	Hs.118397	AE-binding protein 1	3.84
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	27.80
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	4.09
	440868	R79707	Hs.263339	ESTs, Moderately similar to I38022 hypot	76.30
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.37
15	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fis, clone H	3.44
	426320	W47595	Hs.169300	transforming growth factor, beta 2	138.10
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	3.45
	459309	AA040620	Hs.5672	hypothetical protein AF140225	127.80
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	361.20
20	422553	AI697720	Hs.171455	ESTs, Weakly similar to T31613 hypothei	136.60
	423275	BE536069	Hs.2962	S100 calcium-binding protein P	6.87
	400534	#(NOCAT)		C22000015:gil12741327[ref]XP_008833.2] z	89.00
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.78
25	423739	AA398155	Hs.97600	ESTs	135.60
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	148.50
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	87.70
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, partial cds	76.80
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	110.60
	419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (	234.60
30	428471	X57348	Hs.184510	stratifin	3.72
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	437.90
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothei	219.20
	419842	AA765489	Hs.104350	ESTs	3.80
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (MMP1; inters	606.80
35	444207	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl protease	2.62
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	258.70
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	304.80
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	8.78
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	10.95
40	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	199.70
	438199	AW016531	Hs.122147	ESTs	67.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	107.20
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.59
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	3.45
45	421937	AI878857	Hs.109706	hematological and neurological expressed	3.17
	427961	AW293165	Hs.143134	ESTs	109.30
	422043	AL133649	Hs.110953	retinoic acid induced 1	2.98
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	276.50
50	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	5.28
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	27.85
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	342.30
	424086	AI351010	Hs.102267	lysyl oxidase	213.50
	432731	R31178	Hs.287820	fibronectin 1	185.10
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	106.10
55	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	2.27
	417308	H60720	Hs.81892	KIAA0101 gene product	405.30
	438146	Z36842	Hs.57548	ESTs	8.38
	424800	AL035588	Hs.153203	MyoD family inhibitor	172.10
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	45.70
60	408380	AF123050	Hs.44532	diubiquitin	11.18
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	149.10
	422963	M79141	Hs.13234	ESTs	33.60
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	6.73
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	8.96
65	424897	D63216	Hs.153684	frizzled-related protein	312.40
	421110	AJ250717	Hs.1355	cathepsin E	790.80
	411789	AF245505	Hs.72157	DKFZP564I1922 protein	3.17
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	8.52
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	558.00
70	406837	R70292	Hs.156110	immunoglobulin kappa constant	4.36
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.83
	421470	R27496	Hs.1378	annexin A3	242.90
	407242	M18728		gb:Human nonspecific crossreacting antig	36.91
	432101	AI918950	Hs.123642	EphA3	221.60
75	406687	M31126	Hs.272620	matrix metalloproteinase 11 (MMP11; stro	5.34
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	292.00
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	184.90
	435202	AI971313	Hs.170204	KIAA0551 protein	64.80
	407216	N91773	Hs.102267	lysyl oxidase	73.70
80	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	3.20
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	288.70
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	502.60
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	6.13
	441020	W79283	Hs.35962	ESTs	178.90

	453857	AL080235	Hs.35861	DKFZP586E1621 protein	504.30
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	242.10
	413435	X51405	Hs.75360	carboxypeptidase E	7.30
5	436476	AA326108	Hs.33829	bHLH protein DEC2	247.20
	406747	AI925153	Hs.217493	annexin A2	110.00
	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	112.10
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	583.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	6.56
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	460.90
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	204.40
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	7.75
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	14.61
	424560	AA158727	Hs.150555	protein predicted by clone 23733	99.80
15	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	242.20
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	17.88
	410668	BE379794	Hs.65403	hypothetical protein	4.18
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	116.40
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	60.30
20	442577	AA292998	Hs.163900	ESTs	4.18
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	334.20
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	8.16
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	375.30
	445133	AW157646	Hs.153506	ESTs	292.40
25	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	4.38
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	89.00
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	322.10
	410687	U24389	Hs.65436	lysyl oxidase-like 1	9.10
	417409	BE272506	Hs.82109	syndecan 1	4.05
30	426471	M22440	Hs.170009	transforming growth factor, alpha	138.60
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	250.50
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.89
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	11.76
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.79
35	408491	AI088063	Hs.7882	ESTs	8.25
	437802	AI475995	Hs.122910	ESTs	4.54
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	175.10
	421155	H87879	Hs.102267	lysyl oxidase	170.10
	451310	AW250651	Hs.26213	Human DNA sequence from clone RP3-447F3	2.91
40	439867	AA847510	Hs.161292	ESTs	261.60
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	723.00
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	251.70
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	155.50
	457180	R26022	Hs.194662	calponin 3, acidic	68.00
45	424408	AI754813	Hs.146428	collagen, type V, alpha 1	17.19
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	5.32
	425139	AW630488	Hs.325820	protease, serine, 23	371.90
	432978	AF126743	Hs.279884	DNAJ domain-containing	7.27
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	19.30
50	421991	NM_014918	Hs.110488	KIAA0990 protein	190.50
	421814	L12350	Hs.108623	thrombospondin 2	15.02
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	28.57
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	519.20
	413048	M93221	Hs.75182	mannose receptor, C type 1	240.60
55	404210	#(NOCAT)		NM_005936:Homo sapiens myeloid/lymphoid	404.60
	452862	AW378065	Hs.8687	ESTs	364.20
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	226.20
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	4.31
	427390	AI432163	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L	10.41
60	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	22.46
	451295	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene	23.74
	448569	BE382657	Hs.21486	signal transducer and activator of trans	5.68
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	190.80
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	230.50
65	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	361.90
	422545	X02761	Hs.287820	fibronectin 1	8.81
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	7.30
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	267.20
	422110	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	5.07
70	431512	BE270734	Hs.2795	lactate dehydrogenase A	270.10
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	504.60
	426369	AF134157	Hs.169487	Kreisler (mouse) maf-related leucine zip	10.62
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.80
	417944	AJ077196	Hs.82985	collagen, type V, alpha 2	14.01
	428797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f	9.15
75	434423	NM_006769	Hs.3844	LIM domain only 4	297.30
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	486.20
	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	9.73
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	762.90
80	424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	7.81
	400133	NA		Eos Control	357.00
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1150.30
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.50
	446019	AI362520	Hs.279789	histone deacetylase 3	11.26

426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	459.50
422687	AW068823	Hs.119206	insulin-like growth factor binding prote	2.68
432401	NM_013330	Hs.274479	NME7	4.99
437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	7.65

Table 41B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
419570	1860604_1	W68738 W68831
423733	231476_1	AA330281 OAA330232 AW962521
434665	390530_1	AA642125 AA654516
448437	763310_1	AW470125 AI734872 AI749559 AW856504 AI583942 AW779036 AW843429 AW844876 AI520713 AW847236

Table 41C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400534	6981826	Minus	278637-279292
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400836	8954179	Plus	677-1188
401201	9743387	Minus	138534-138629,139234-139294,140121-140335,142033-142479
401480	7321503	Plus	166120-166347,166451-166557,169651-169832
401541	8072607	Minus	50018-50158
401682	4755167	Plus	13022-13473
401732	1200312	Plus	19346-19525,19625-19708,19897-19973,20067-20130,20215-20414
403207	7630829	Plus	89914-90033,90729-90855,91131-91198
403574	8101156	Plus	5542-6176
403776	7770611	Minus	1414-1513,1624-1756
404142	9856692	Minus	80316-80459
404210	5006246	Plus	169926-170121
404285	2326514	Plus	32282-32416
404286	2326514	Plus	51086-51301
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404866	9366919	Minus	11743-11929
405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
405849	7651817	Minus	17705-18287
405909	7705180	Minus	86985-87233
406173	7230224	Plus	12925-13213
406293	5686274	Minus	17646-17953
406319	9211730	Minus	82320-82561
406399	9256288	Minus	63448-63554

TABLE 42A: 574 genes upregulated in pancreatic cancer relative to normal body tissues

Table 42A lists about 574 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar accession number, GenBank accession number  
 UniGeneID: UniGene number  
 Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).  
 UniGene Title: UniGene gene title  
 R1 90th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs  
 R2 90th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prot.Domains; R1; R2

426230; AA367019; Hs.241395; protease, serine, 1 (trypsin 1); trypsin,toxin\_4;SS=M; 107.29; 1.07  
 415934; NM\_000928; Hs.992; phospholipase A2, group IB (pancreas); phoslip;SS=M; 83.67; 1.06  
 421996; AW583807; Hs.1460; glucagon; hormone2;SS=M; 59.35; 1.61  
 406399; ; NM\_003122; Homo sapiens serine protease ; kazal;SS=M; 55.49; 1.08  
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 53.65; 43.61

- 406685; M18728; ; gb:Human nonspecific crossreacting antigen; ig; TM=M; SS=M; 52.73; 22.83  
 428698; AA852773; Hs.334838; KIAA1866 protein; none; NA; NA; 32.44; 13.11  
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbonate; HCO<sub>3</sub> cotransp; TM=Y; 29.80; 1.46  
 428874; W32133; Hs.194366; transthyretin (prealbumin, amyloidosis t; Transthyretin; SS=M; 29.42; 1.94  
 444754; T83911; Hs.374341; transmembrane 4 superfamily member 4; none; TM=Y; SS=M; 28.78; 3.13  
 418068; AW971155; Hs.293902; ESTs, Weakly similar to ISHUS protein d; none; TM=M; SS=M; 28.61; 0.98  
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone\_rec, zfc4, none; 25.38; 3.63  
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; SS=M; 24.64; 7.21  
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarot; none, none; 23.77; 6.74  
 414998; NM\_002543; Hs.77729; oxidized low density lipoprotein (lectin; lectin\_c; TM=Y; SS=M; 22.96; 4.57  
 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4; TM=Y; SS=M; 22.31; 5.42  
 425573; AB006423; Hs.158308; serine (or cysteine) proteinase inhibitor; serpin, GCV\_H; TM=M; SS=M; 21.91; 1.03  
 433110; D56494; Hs.3191; rat regenerating islet-derived-like, hum; lectin\_c; TM=M; SS=M; 21.90; 0.60  
 426490; NM\_001621; Hs.170087; aryl hydrocarbon receptor; PAC, PAS; TM=M; 21.41; 19.89  
 453863; X02544; Hs.572; orosomucoid 1; lipocalin, aldehyd, ubiquitin, IRK; SS=M; 20.80; 8.12  
 421126; M74587; Hs.102122; insulin-like growth factor binding prote; thyroglobulin\_1, IGFBP; SS=Y; 20.60; 8.48  
 451035; AU076785; Hs.430; plasmin 1 (I isoform); efhand, CH, Adaptin\_N; SS=M; 19.25; 3.53  
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM\_PNT, none; 18.38; 2.53  
 420332; NM\_001756; Hs.1305; serine (or cysteine) proteinase inhibitor; serpin; TM=M; SS=M; 18.19; 2.29  
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone\_rec, zfc4, none; 17.67; 4.80  
 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin\_EGF, laminin\_Nterm, integrin\_B; SS=M; 17.08; 6.37  
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm\_1; TM=Y; SS=M; 16.89; 7.15  
 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen\_C, G-alpha, arf; TM=M; SS=M; 16.59; 7.74  
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 16.28; 9.22  
 431183; NM\_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER\_lumen\_recept; TM=M; SS=M; 15.96; 2.38  
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodi; Somatomedin\_B, Endonuclease, Phosphodiect; TM=Y; SS=M; 15.65; 1.33  
 408243; Y00787; Hs.624; interleukin 8; HLH, PAS, IL8; TM=M; 15.53; 4.34  
 419355; AA428520; Hs.90061; progesterone binding protein; heme\_1; TM=Y; SS=M; 15.45; 10.50  
 426006; R49031; Hs.22627; ESTs; pkinase, TBC; 15.17; 0.58  
 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD, ICE\_p10, ICE\_p20; SS=M; 14.84; 3.04  
 422260; AA315993; Hs.105484; regenerating gene type IV; lectin\_c; SS=M; 14.71; 2.89  
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3, none; 14.28; 11.47  
 408983; NM\_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC\_tran, ABC\_membrane, PRK, Bac\_export\_3; TM=Y; 13.98; 1.18  
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 13.81; 7.69  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese, DSPC, Y\_phosphatase, Ribosomal\_S3\_N; TM=M; 13.59; 2.24  
 425988; BE045897; Hs.53985; ESTs, Weakly similar to 138022 hypotheti; none, none; 13.54; 0.95  
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase\_C, CARD; TM=M; 13.48; 3.59  
 429556; AW139399; Hs.98988; ESTs; none; TM=M; 13.20; 1.16  
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; SS=M; 12.83; 7.72  
 427286; AW732802; Hs.2132; epidermal growth factor receptor pathway; SH3, TonB\_boxC; TM=M; 12.72; 9.01  
 431912; A1660552; Hs.356183; ESTs, Weakly similar to A56154 Abl subst; none, Acyl-CoA\_dh, Acyl-CoA\_dh\_M, Acyl-CoA\_dh\_N; 12.72; 6.72  
 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7tm\_1; TM=Y; SS=M; 12.71; 12.56  
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA\_gyraseB, DNA\_topoisolv, HATPase\_c; SS=M; 12.52; 4.92  
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC\_tran, M\_SMC\_N, SMC\_C, DUF164, none; 12.38; 7.59  
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase, hexokinase2, none; 12.34; 11.53  
 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip; TM=M; SS=Y; 12.32; 3.02  
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 12.29; 2.21  
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3, TPR; TM=M; 12.16; 4.14  
 427283; AL119796; Hs.174185; ectonucleotide pyrophosphatase/phosphodi; Sulfatase, Somatomedin\_B, Phosphodiect, Endonuclease; TM=M; SS=Y; 11.97; 5.93  
 434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK; TM=Y; 11.76; 1.58  
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm\_1; TM=Y; SS=M; 11.75; 3.56  
 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vi; sushi; TM=Y; SS=M; 11.67; 3.77  
 450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin, Idl\_recept\_La, none; 11.65; 4.52  
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH\_C, IMPDH\_N, CBS, integrin\_B, Ricin\_B\_lectin; 11.56; 5.46  
 431512; BE270734; Hs.2795; lactate dehydrogenase A; Idh, Idh\_C, SH3, pkinase, UBA; TM=M; 11.55; 5.11  
 429638; A1916662; Hs.211577; kinesin 1 (kinesin receptor); bZIP, Tropomyosin, spectrin, LBP, BPI, CETP, B56, M; TM=Y; SS=M; 11.47; 4.65  
 445133; AW157646; Hs.198689; ESTs; efhand, spectrin, GAS2, SH3, Plectin, RA, Xylose\_isom, FliD, bZIP, Tropomyosin, Myc-LZ, M, Idh\_C, CH, AIP3; TM=M; 11.41; 12.62  
 411352; NM\_002890; Hs.758; RAS p21 protein activator (GTPase activa; SH2, SH3, C2, PH, RasGAP; TM=M; SS=M; 11.24; 9.95  
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none, none; 11.19; 4.16  
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS, AIRS\_C; TM=M; 11.17; 5.98  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, fn3\_Y\_phosphatase; TM=M; 11.14; 9.09  
 440594; AW445167; Hs.126036; ESTs; none, none; 11.05; 16.45  
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD, DAPIN, HIN; SS=M; 11.05; 10.38  
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese, DSPC; TM=M; 11.05; 4.70  
 448811; A1590371; Hs.199460; ESTs; none; TM=Y; 10.85; 9.69  
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2, SH3, pkinase; TM=M; 10.72; 8.65  
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; 10.51; 12.97  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, ig, FAD\_Synth, Idh, Idh\_C, pkinase; SS=M; 10.37; 6.35  
 436856; A1469355; Hs.127310; ESTs; pkinase, rrm; TM=M; 10.36; 2.74  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 10.34; 3.14  
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related; SH2, SH3, pkinase; TM=M; 10.34; 4.47  
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin\_B, EGF, PSI; TM=Y; SS=M; 10.21; 4.58  
 451820; AW058357; Hs.199248; ESTs; 7tm\_1; TM=Y; SS=M; 10.18; 2.67  
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2, lectin\_c, Ricin\_B\_lectin, Xlink; TM=Y; SS=M; 10.17; 8.35  
 429752; H52348; Hs.36636; ESTs; pkinase, pkinase; 10.13; 12.35  
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-pho; MORN, sugar\_tr; TM=Y; SS=M; 10.08; 8.74  
 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 10.05; 6.06  
 452698; NM\_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm\_1; TM=Y; SS=M; 9.98; 3.16  
 416389; AA180072; Hs.149846; integrin, beta 5; integrin\_B, none; 9.85; 9.59  
 421044; AF051871; Hs.101302; Human DNA sequence from clone RP1-238D15; fn3, vwa, Collagen, TSPN; TM=M; SS=M; 9.78; 5.96  
 446620; AA128808; Hs.179902; transporter-like protein; none; TM=Y; SS=M; 9.75; 2.64  
 405102; ; C15001220; gij4469558[gijAAD21311.1] (AF; DAG, PE-bind, PH, RhoGEF, DC1; SS=M; 9.74; 1.88  
 418693; A1750878; Hs.87409; thrombospondin 1; EGF, tsp\_1, vwc, TSPN, tsp\_3; SS=M; 9.72; 6.94



- 426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR m; Kunitz\_BPTI,Kunitz\_BPTI,7tm\_2,HRM; 9.68; 10.58  
 448105; AW591433; Hs.298241; Transmembrane protease, serine 3; Idl\_receptL\_a,trypsin;TM=Y;SS=M; 9.67; 4.06  
 456266; L29073; Hs.198726; cold shock domain protein A; 7tm\_2,HRM,CSD;TM=Y;SS=M; 9.62; 2.36  
 410240; AL157424; Hs.61289; synaptotagmin 2; Exo\_endo\_phos,Syja\_N,rrm,Gram-ve\_porins;TM=M; 9.62; 3.77  
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone\_rec,zf-C4,Metallothio\_5;TM=M; 9.60; 8.05  
 456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A; none;TM=Y; 9.57; 3.77  
 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3;TM=M; 9.56; 10.50  
 437158; AW090198; Hs.348709; KIAA1150 protein; none;NA;NA; 9.55; 8.87  
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M; 9.47; 5.67  
 403344; ; NM\_000341;Homo sapiens solute carrier fa; alpha-amylase;TM=Y; 9.47; 1.42  
 449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K\_tetra,ion\_trans,none; 9.46; 3.12  
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M; 9.42; 4.01  
 444838; AV651680; Hs.208558; ESTs; integrin\_A,FG-GAP,none; 9.42; 1.87  
 439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none,none; 9.41; 5.55  
 428505; AL035461; Hs.2281; chromogranin B (secretogranin 1); Granin;SS=M; 9.40; 3.46  
 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5\_F8\_type\_C,CUB,CUB,MAM,F5\_F8\_type\_C; 9.38; 6.32  
 432810; AA863400; Hs.374489; ESTs; none,Skp1,AAA; 9.38; 4.36  
 427581; NM\_014788; Hs.179703; KIAA0129 gene product; SPRY,zf-B\_box;TM=M; 9.34; 8.26  
 413109; AW389845; Hs.110855; ESTs, similar to leukemia virus receptor; PHO4,none; 9.34; 4.67  
 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M; 9.31; 4.24  
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm\_3,none; 9.24; 7.12  
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.23; 6.03  
 437672; AW748265; Hs.5741; flavohemoprotein b57; heme\_1,NAD\_binding,lipoxygenase,FAD\_binding\_6;TM=M; 9.22; 10.72  
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion\_trans;TM=Y;SS=M; 9.20; 4.46  
 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta,TGFb\_propeptide,Tub;SS=M; 9.19; 16.46  
 413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-rel; none,START; 9.15; 2.18  
 418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodi; Phosphodiester;TM=Y;SS=M; 9.14; 3.03  
 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor t; Y\_phosphatase,none; 9.14; 11.75  
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; coflin\_ADF;SS=M; 9.11; 4.29  
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M; 9.06; 9.68  
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit,; proteasome;TM=M; 9.05; 5.61  
 413367; NM\_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar\_tr;TM=Y; 9.04; 5.79  
 437296; AA350994; Hs.20281; KIAA1700; Rhodanese,DSPC;TM=M; 9.02; 5.75  
 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestin; cadherin;TM=Y;SS=M; 8.94; 5.01  
 446406; AI553681; Hs.348490; Arg/Abl-interacting protein ArgBP2; Sorb,none; 8.91; 1.77  
 428820; AA436187; Hs.172631; integrin, alpha M (complement component ; vwa,integrin\_A,FG-GAP;TM=Y;SS=M; 8.85; 4.74  
 434398; AA121098; Hs.3838; serum-inducible kinase (SNK); pkinase,POLO\_box;TM=M; 8.78; 4.54  
 453902; BE502341; Hs.3402; ESTs; none,none; 8.72; 3.71  
 433334; AI927208; Hs.231958; matrix metalloproteinase 28; Peptidase\_M10,none; 8.71; 4.28  
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;SS=M; 8.70; 3.71  
 450247; AF123303; Hs.24713; hypothetical protein; ehand,mito\_carr;TM=Y;SS=M; 8.68; 3.40  
 432101; AI918950; Hs.123642; EphA3; fn3,pkinase,SAM,EPH\_1bd;TM=Y;SS=M; 8.62; 5.62  
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; none,none; 8.61; 13.53  
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm\_2;TM=Y;SS=M; 8.55; 4.82  
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG\_PE-bind,pkinase\_C,OPR;TM=M; 8.50; 3.18  
 419111; AA234172; Hs.137418; ESTs; none,IRK; 8.47; 7.51  
 430024; AI808780; Hs.227730; integrin, alpha 6; integrin\_A,FG-GAP;TM=Y;SS=M; 8.45; 3.46  
 447574; AF162666; Hs.18895; tousled-like kinase 1; pkinase;TM=M; 8.45; 5.30  
 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5\_F8\_type\_C;TM=M;SS=M; 8.44; 6.30  
 419034; NM\_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M; 8.43; 4.87  
 405555; ; homeodomain-interacting protein kinase 3; trypsin;TM=M; 8.39; 0.68  
 417412; X16896; Hs.82112; interleukin 1 receptor, type I; ig,TIR;TM=M;SS=M; 8.35; 4.74  
 405556; ; homeodomain-interacting protein kinase 3; trypsin;TM=M; 8.31; 0.87  
 407687; AK002011; Hs.37558; hypothetical protein FLJ11149; lys,ig,FAD\_Synth,ldh\_C,pkinase;SS=M; 8.28; 3.12  
 408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 8.27; 5.65  
 449523; NM\_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm\_1;TM=Y;SS=M; 8.26; 5.49  
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 doma; SH2;SS=M; 8.24; 8.91  
 405204; ; NM\_002086;Homo sapiens growth factor re; SH2,SH3;TM=M; 8.23; 6.43  
 426806; T19228; Hs.172572; hypothetical protein FLJ20093; ank,pkinase,UPF0073;SS=M; 8.20; 6.11  
 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xe; pkinase;TM=M; 8.18; 8.37  
 450375; AA009647; Hs.352537; a disintegrin and metalloproteinase doma; Reprolysin,Pep\_M12B\_propep,disintegrin,Reprolysin,Pep\_M12B\_propep,disintegrin; 8.17; 12.24  
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE\_p10,ICE\_p20;TM=M;SS=M; 8.15; 4.61  
 413132; NM\_006823; Hs.75209; protein kinase (cAMP-dependent, catalyti; PKI;SS=M; 8.15; 11.12  
 428513; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI,none; 8.13; 13.28  
 429345; R11141; Hs.199695; hypothetical protein; K\_tetra,SAM; 8.13; 1.15  
 425838; NM\_014071; Hs.159613; nuclear receptor coactivator RAP250; per; none;TM=M; 8.12; 4.54  
 425836; AW955696; Hs.90960; ESTs; Cbl\_N,Cbl\_N2,Cbl\_N3,UBA,zf-C3HC4,none; 8.11; 7.47  
 406366; ; secreted frizzled-related protein 4; trypsin;SS=M; 8.05; 0.69  
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic; C2,PLA2\_B;TM=M; 8.04; 5.20  
 458946; AA009716; Hs.42311; ESTs; none,DSPc,Y\_phosphatase; 8.02; 1.93  
 425280; U31519; Hs.1872; phosphoenolpyruvate carboxykinase 1 (sol; PEPCCK;TM=M; 7.97; 19.33  
 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, ty; none,none; 7.90; 11.44  
 449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.89; 7.00  
 426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo\_seg,HEAT\_PBS; 7.83; 11.16  
 400408; S75765; ; Homo sapiens delta CCK-B gene, partial c; 7tm\_1,none; 7.81; 0.78  
 448362; AA641767; Hs.21015; hypothetical protein DKFZp564L0864 simil; sugar\_tr;TM=Y;SS=M; 7.78; 7.02  
 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substra; SH3;TM=M; 7.75; 2.63  
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M; 7.72; 2.68  
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE\_p10,ICE\_p20,DED;TM=M; 7.68; 2.40  
 421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo\_seg;SS=M; 7.49; 6.57  
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside\_tra2,none; 7.47; 2.53  
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin\_c,sushi;TM=M;SS=M; 7.38; 5.60  
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 7.29; 5.78

428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm\_3; TM=Y; SS=M; 7.26; 11.00  
 426761; AI015709; Hs.172089; PORIMIN Pro-oncrosis receptor inducing me; none; TM=Y; SS=M; 7.25; 7.22  
 413880; AI660842; Hs.110915; interleukin 22 receptor; Tissue\_fac; TM=Y; SS=M; 7.24; 0.98  
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase, PLAT; TM=M; 7.22; 6.45  
 413441; AI929374; Hs.75367; Src-like-adaptor; SH2, SH3; TM=M; 7.20; 5.72  
 426158; NM\_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep\_L\_domain, Furin-like, pkinase, Recep\_L\_domain, Peptidase\_M24; 7.13; 3.97  
 428474; AB023182; Hs.184523; KIAA0965 protein; pkinase; TM=M; 7.13; 5.43  
 421582; AI910275; Hs.350470; trefoil factor 1 (breast cancer, estroge; trefoil, Gastrin; SS=M; 7.08; 21.61  
 449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none; TM=Y; SS=M; 7.07; 6.18  
 452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PL; pkinase, Activin\_rec, none; 6.94; 4.82  
 451295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene; pkinase, DAG\_PE-bind, pkinase\_C, OPR, none; 6.92; 15.34  
 430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7\_HUMAN ALU S; Y\_phosphatase, Adaptin\_N\_Y\_phosphatase; 6.88; 1.94  
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIG; 7tm\_1, Idl\_recept\_a, LRR; SS=M; 6.86; 0.97  
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl\_oxidase; SS=M; 6.83; 7.24  
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t; fn3, ig\_Y\_phosphatase, MAM; TM=Y; SS=M; 6.83; 11.43  
 400539; ; Target Exon; none; TM=M; 6.70; 1.19  
 431113; AK000673; Hs.274337; hypothetical protein FLJ20666; pkinase; TM=M; 6.65; 2.21  
 445280; AW055063; Hs.343220; v-ckr avian sarcoma virus CT10 oncogene; SH2, SH3, none; 6.61; 10.66  
 425834; NM\_001639; Hs.1957; amyloid P component, serum; pentaxin; TM=M; SS=M; 6.57; 2.20  
 435706; W31254; Hs.7045; GL004 protein; PDEase, GAF, none; 6.55; 11.44  
 415906; AI751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fis, clone H; Ephrin, none; 6.45; 5.25  
 408308; AI033377; Hs.44197; hypothetical protein DKFZp564D0462; none, none; 6.42; 9.14  
 432336; NM\_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm, pkinase; TM=M; 6.42; 4.12  
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y\_phosphatase; TM=Y; 6.42; 2.26  
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm\_1; TM=Y; SS=M; 6.41; 4.54  
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; Idl\_recept\_a, PKD, MHC\_I; TM=M; SS=Y; 6.38; 3.55  
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese, DSPc; SS=M; 6.35; 4.95  
 422583; AA410506; Hs.27973; KIAA0874 protein; ank, G-alpha; TM=M; 6.35; 3.56  
 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm\_1, OATP\_C; TM=Y; 6.32; 11.02  
 422282; AF019225; Hs.114309; apolipoprotein L; MotA, ExbB; TM=Y; SS=M; 6.32; 5.15  
 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, y; none, Ribosomal\_S13, Galactosyl\_T, Zip, adh\_short, zf-C3HC4; 6.30; 8.35  
 428486; AW583497; Hs.184604; pancreatic polypeptide; hormone3; TM=M; SS=Y; 6.29; 3.51  
 408847; AW290997; Hs.30348; ESTs; pkinase, ig, none; 6.28; 3.63  
 428179; AI127772; Hs.279696; serum/glucocorticoid regulated kinase-II; pkinase, PX, pkinase\_C; SS=M; 6.28; 3.50  
 443614; AV655386; Hs.7645; fibrinogen, B beta polypeptide; none, none; 6.26; 7.48  
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm\_1; TM=Y; SS=M; 6.25; 3.98  
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 6.21; 4.10  
 428180; AI129767; Hs.182874; guanine nucleotide binding protein (G pr; G-alpha, ar; TM=M; 6.18; 4.62  
 409245; AA361037; Hs.356436; tRNA isopentenylpyrophosphate transferas; Armadillo\_seg; TM=M; 6.17; 11.15  
 417952; AI192838; Hs.372643; dual-specificity tyrosine-(Y)-phosphoryl; pkinase, none; 6.17; 3.05  
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2, PH; TM=M; 6.16; 11.90  
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none; TM=M; 6.10; 2.96  
 426797; AW936258; Hs.342849; ADP-ribosylation factor-like 5; arf, Ca\_channel\_B, SH3; 6.03; 3.17  
 408331; NM\_007240; Hs.44229; dual specificity phosphatase 12; DSPc; TM=M; 5.99; 2.55  
 441384; AA447849; Hs.288660; Homo sapiens cDNA: FLJ22182 fis, clone H; 7tm\_3, none; 5.97; 13.12  
 414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none; NA; NA; 5.92; 6.47  
 418506; AA084248; Hs.85339; Unknown protein for MGC:29643; none, none; 5.91; 1.94  
 436345; AA873008; Hs.121572; ESTs; CARD, BIR, zf-C3HC4, CARD, BIR, zf-C3HC4; 5.90; 1.40  
 414087; W19712; ; gb:zb36d03.r1 Soares\_parathyroid\_tumor\_N; pkinase, none; 5.85; 0.90  
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank, death, ZU5, EGF, kringle, trypsin, Nebulin, LIM; SS=M; 5.77; 1.24  
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A; none, none; 5.71; 4.00  
 427557; NM\_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR\_LY6, ET, PLA2\_inh; SS=M; 5.71; 3.83  
 414171; AA360328; Hs.865; RAP1A, member of RAS oncogene family; pkinase, DAG\_PE-bind, RBD, ras, DC1, GFP; TM=M; 5.69; 3.07  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm\_1, 7tm\_2; TM=Y; SS=M; 5.68; 12.92  
 425317; AW205118; Hs.210546; interleukin 21 receptor; none; TM=Y; SS=M; 5.60; 5.45  
 417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase; TM=M; 5.59; 4.19  
 400151; ; Eos Control; AT\_hook, DNA\_mis\_repair, HATPase\_c, UQ\_con; TM=M; 5.53; 8.13  
 450139; AK001838; Hs.355608; serum/glucocorticoid regulated kinase; none, none; 5.52; 8.61  
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 5.52; 10.04  
 433556; W56321; Hs.111460; calcium/calmodulin-dependent protein kin; pkinase, none; 5.51; 6.75  
 424701; NM\_005923; Hs.151988; mitogen-activated protein kinase kinase; pkinase; TM=M; 5.47; 4.58  
 415875; AA894876; Hs.5687; protein phosphatase 1B (formerly 2C), ma; PP2C; TM=M; 5.43; 5.30  
 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not ava; 7tm\_1, none; 5.42; 2.59  
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4, LIM; TM=M; 5.37; 8.69  
 444184; T87841; Hs.282990; Human DNA sequence from clone RP1-28H20; pkinase, RIO1, APH, KOW; TM=M; 5.36; 3.32  
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR, LRRCT, TIR; TM=M; SS=M; 5.36; 3.94  
 429023; NM\_000312; Hs.2351; protein C (inactivator of coagulation fa; EGF, trypsin, gla; SS=M; 5.31; 4.30  
 421559; NM\_014720; Hs.105751; Ste20-related serine/threonine kinase; pkinase, UVR; TM=M; 5.31; 3.26  
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker\_histone; TM=M; 5.27; 3.12  
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin, bZIP; TM=M; 5.26; 4.82  
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A recepto; Neur\_chan\_LBD, Neur\_chan\_memb; TM=Y; SS=M; 5.25; 11.26  
 428234; U93553; Hs.183123; nuclear receptor subfamily 5, group A, m; hormone\_rec, zf-C4; SS=M; 5.20; 1.11  
 408683; R58665; Hs.46847; TRAF and TNF receptor-associated protein; Exo\_endo\_phos; TM=M; 5.19; 6.25  
 408657; AA782601; Hs.173328; ESTs; B56, none; 5.18; 5.47  
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin, Guanylate\_kin, PDZ, SH3; 5.17; 4.02  
 438698; AW297855; Hs.361171; ESTs, Weakly similar to I38022 hypotheti; lipoxygenase, PLAT, none; 5.16; 2.91  
 442200; AW590572; Hs.235768; ESTs; none, none; 5.11; 4.22  
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 5.08; 2.71  
 419088; AI538323; Hs.367688; integrin, beta 8; Integrin\_B, none; 5.07; 3.53  
 414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets, ; phoslip; TM=M; SS=Y; 5.05; 3.42  
 408414; AI114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell ; fn3, ig; TM=Y; SS=M; 5.05; 3.41  
 430407; H23551; Hs.30974; ESTs; pkinase, PBD, none; 5.03; 1.63  
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C, none; 5.00; 5.14

- 452194; A1694413; Hs.373599; Ubiquitin-like protein FAT107?? - diubiq; none,none; 4.98; 2.65  
 410073; AW408163; Hs.58488; catenin (cadherin-associated protein),  $\alpha$ ; Stathmin,Vinculin;SS=M; 4.97; 10.60  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 4.96; 2.87  
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept; Y\_phosphatase;SS=M; 4.88; 21.69  
 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.88; 4.60  
 418529; AW005695; Hs.250897; TRK-fused gene; Band\_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 4.79; 5.47  
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand,kazal,arf,ras,7tm\_1;TM=M;; 4.75; 5.41  
 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y\_phosphatase;TM=M;; 4.74; 9.76  
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 4.73; 4.68  
 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M;; 4.66; 5.61  
 452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none,none; 4.63; 6.62  
 427333; AF067797; Hs.176658; aquaporin 8; MIP;TM=Y;SS=M; 4.63; 0.80  
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit); vwa,integrin\_A,FG-GAP;TM=Y;SS=M; 4.58; 11.38  
 428065; A1634046; Hs.157313; ESTs; ICE\_p20,DED,ICE\_p10,ICE\_p20,DED; 4.55; 4.51  
 428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 4.54; 8.76  
 416224; NM\_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand;SS=M; 4.54; 19.57  
 450056; BE047394; Hs.8208; ESTs, Weakly similar to S71512 hypothet; ABC\_tran,ABC\_membrane,ig,MHC\_II\_beta,SRP54,proteasome,ABC\_membrane,ABC\_tran; 4.49; 10.47  
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;; 4.41; 7.27  
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 4.41; 10.25  
 433208; AW002834; Hs.24095; ESTs; arf,Ca\_channel\_B,SH3; 4.39; 12.14  
 403208; ; ; Target Exon; lecln\_c,none; 4.37; 0.76  
 440486; BE243513; Hs.7212; hypothetical protein PP1044; LRR,PAAD\_DAPIN,AAA,CARD,NB-ARC;NA;NA; 4.36; 10.34  
 414278; AA330116; Hs.355877; Human glucose transporter pseudogene; none,none; 4.35; 7.95  
 424833; NM\_003894; Hs.153405; period (Drosophila) homolog 2; PAS;SS=M; 4.34; 6.23  
 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin receptor; FG-GAP,integrin\_A,none; 4.32; 5.85  
 418721; NM\_002731; Hs.87773; protein kinase, cAMP-dependent, catalyti; pkinase,pkinase\_C;SS=M; 4.31; 3.09  
 412330; NM\_005100; Hs.788; A kinase (PRKA) anchor protein (gravin); none;TM=M;; 4.25; 12.74  
 421939; BE169531; Hs.109727; TAK1-binding protein 2; KIAA0733 protein; zf-RanBP,CUE;TM=M;; 4.25; 12.54  
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant\_thionins;SS=M; 4.24; 6.91  
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 4.22; 5.27  
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; ig;TM=Y;; 4.16; 7.22  
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin\_G,CorA;SS=M; 4.16; 9.27  
 445496; AB007860; Hs.12802; development and differentiation enhancin; SH3,ank,PH,ArfGap;TM=M;; 4.15; 23.43  
 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 4.14; 3.76  
 414462; BE622743; Hs.301064; arfaptin 1; none,none; 4.08; 13.43  
 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase,TrkA-N,2-Hacid\_DH\_C;TM=M;; 4.06; 9.12  
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar\_lr;TM=Y;; 4.04; 10.05  
 429379; NM\_014840; Hs.200598; KIAA0537 gene product; pkinase,RIO1;TM=M;; 4.00; 6.35  
 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE\_p20,DED;TM=M;; 3.98; 5.66  
 405203; ; ; NM\_002086; Homo sapiens growth factor re; SH2,SH3;TM=M;; 3.95; 17.71  
 409335; NM\_001502; Hs.53985; glycoprotein 2 (zymogen granule membrane; zona\_pellucida;TM=M;SS=M; 3.94; 0.58  
 446006; NM\_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 3.89; 7.59  
 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3,PDZ,Guanylate\_kin;TM=M;; 3.84; 8.89  
 438000; A1825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M;; 3.83; 4.22  
 418054; NM\_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl\_oxidase;TM=M;SS=M; 3.81; 6.45  
 450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M;; 3.78; 8.49  
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone\_rec,zf-C4;SS=M; 3.77; 4.22  
 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M;; 3.68; 4.92  
 438113; A1467908; Hs.8882; ESTs; 7tm\_1,none; 3.59; 12.12  
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 3.58; 10.93  
 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin\_A,PHO4,pkinase,ubiquitin; 3.57; 5.10  
 415088; A1077288; Hs.374374; serum/glucocorticoid regulated kinase; none,none; 3.56; 4.60  
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 3.55; 4.52  
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT\_bind,STAT\_prot;TM=M;; 3.54; 8.19  
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 3.52; 9.70  
 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor; integrin\_A,FG-GAP;TM=Y;; 3.45; 6.44  
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase\_2;TM=M;; 3.41; 6.03  
 418255; AW135405; Hs.37251; ESTs; pkinase,none; 3.41; 13.97  
 408822; AW500715; Hs.57079; Homo sapiens cDNA FLJ13267 fis, clone OV; PIP5K,none; 3.40; 8.97  
 426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase;TM=M;; 3.39; 11.24  
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none;TM=M;SS=Y; 3.39; 5.10  
 414291; A1289619; Hs.13040; G protein-coupled receptor 86; 7tm\_1;TM=Y;SS=M; 3.38; 10.25  
 457329; A1634860; Hs.247043; type 1 tumor necrosis factor receptor sh; Peptidase\_M1;SS=M; 3.38; 13.78  
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 3.36; 4.17  
 443710; A1928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha,none; 3.32; 20.33  
 454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M;; 3.31; 6.94  
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo\_seg;TM=M;SS=M; 3.29; 3.07  
 426728; NM\_007118; Hs.367689; triple functional domain (PTPRF interact; SH3,ig,pkinase,PH,spectrin,RhoGEF;TM=M;; 3.27; 14.90  
 427202; BE272922; Hs.173936; interleukin 10 receptor, beta; Tissue\_fac;TM=Y;SS=M; 3.24; 4.49  
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M;; 3.24; 12.27  
 425976; C75094; Hs.334514; NG22 protein; voltage\_CLC;TM=Y;SS=M; 3.23; 13.40  
 417534; NM\_004998; Hs.82251; myosin IE; SH3,myosin\_head,IQ;TM=M;; 3.21; 15.21  
 458097; AW341135; Hs.58104; ESTs; none,SH3,PID; 3.21; 7.34  
 437928; NM\_005476; Hs.5920; UDP-N-acetylglucosamine-2-epimerase/N-ac; hexokinase,FGGY,ROK,Epimerase\_2;SS=M; 3.20; 8.38  
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 3.19; 5.09  
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none,none; 3.18; 4.17  
 453489; AA300067; Hs.102000; hypothetical protein DKFZp434N185; F5\_F8\_type\_C,pkinase,Ets,F5\_F8\_type\_C,pkinase,Ets; 3.17; 7.88  
 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3\_PI4\_kinase;TM=M;; 3.16; 4.71  
 412767; AA233808; Hs.286241; protein kinase, cAMP-dependent, regulator; SH3,7tm\_2,cadherin,GPS,laminin\_G,EGF,laminin\_EGF,Sulfate\_transp,STAS,cNMP\_binding,R11a; 3.16; 7.19  
 415662; AW972481; Hs.170610; ESTs, Highly similar to G01887 MEK kinas; pkinase,none; 3.16; 7.21  
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 3.15; 22.66

- 437175; AW968078; Hs.87773; protein kinase, cAMP-dependent, catalytic; pkinase, pkinase\_C; none; 3.14; 11.72  
 409270; BE090051; Hs.23120; PIST1; fn3, pkinase, PDZ, DUF139; TM=Y; SS=M; 3.09; 7.81  
 419591; AF090900; Hs.91393; Homo sapiens cDNA: FLJ21887 fis, clone H; PDZ, L27; TM=M; 3.06; 5.46  
 447225; R62676; Hs.17820; Rho-associated, coiled-coil containing p; PH, pkinase, HR1; none; 3.04; 13.05  
 412692; AF044288; Hs.74515; aryl hydrocarbon receptor nuclear trans; HLH, PAS, PAC; TM=M; 2.95; 12.28  
 409274; NM\_003930; Hs.52644; SKAP55 homologue; SH3, PH; SS=M; 2.90; 14.62  
 417707; AL035786; Hs.82425; actin related protein 2/3 complex, subunit; none; TM=M; 2.90; 11.00  
 427045; H86504; Hs.173328; protein phosphatase 2, regulatory subunit; B56; TM=M; 2.89; 6.12  
 431177; NM\_003304; Hs.250687; transient receptor potential channel 1; ion\_trans, ank; TM=Y; 2.89; 6.53  
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none; TM=M; 2.87; 9.18  
 418546; AA224827; gb:nc32g04.s1 NCL\_CGAP\_Pr2 Homo sapiens; vwa, integrin\_A, FG-GAP; none; 2.86; 9.94  
 446668; W58353; Hs.285123; Homo sapiens mRNA full length insert cDN; NDK, PH, Oxysterol\_BP; SS=M; 2.85; 14.25  
 454080; AI199711; Hs.576; fucosidase, alpha-L-1, tissue; Alpha\_L\_fucos; TM=M; SS=M; 2.81; 28.84  
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3; TM=M; SS=Y; 2.80; 10.53  
 433000; U26710; Hs.3144; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4, UBA, Cbl\_N, Cbl\_N3; 2.77; 10.93  
 444488; AW192879; Hs.355660; ancient conserved domain protein 4; none, none; 2.77; 12.58  
 417904; AI750762; Hs.82911; protein tyrosine phosphatase type IVA, m; Y\_phosphatase, DSPc; TM=M; 2.76; 12.78  
 425204; NM\_002436; Hs.1861; membrane protein, palmitoylated 1 (55kD); SH3, PDZ, Guanylate\_kin; SS=M; 2.74; 5.71  
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS, zf-C2H2, SET; 2.73; 12.50  
 410793; AW581906; Hs.66392; intersectin 1 (SH3 domain protein); SH3, ehfand, C2, PH, RhoGEF, M; SS=M; 2.73; 9.84  
 446081; AA972412; Hs.13755; f-box and WD-40 domain protein 2; WD40, F-box, Ribosomal\_L14; TM=M; 2.71; 12.29  
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor; ig, pkinase; TM=Y; 2.71; 10.53  
 452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox; none; 2.69; 12.53  
 423533; NM\_014339; Hs.129751; interleukin 17 receptor; none; TM=Y; SS=M; 2.67; 8.59  
 426272; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC\_tran, ABC\_membrane, GTP\_EFTU; TM=M; SS=M; 2.67; 12.22  
 453915; AA588721; Hs.12284; ribosomal protein L44; none, T-box; 2.65; 6.38  
 416810; AF035606; Hs.80019; programmed cell death 6; ehfand; TM=M; 2.61; 13.89  
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none; TM=M; SS=M; 2.58; 10.19  
 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3; none; 2.56; 19.04  
 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS; SS=M; 2.55; 14.99  
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep\_L\_domain, YLP; none; 2.52; 14.71  
 409098; AA132672; Hs.7984; pleckstrin homology, Sec7 and coiled/coi; PH, Sec7; TM=M; 2.51; 14.51  
 413040; AA193338; Hs.12321; sodium calcium exchanger; Na\_Ca\_Ex; TM=Y; SS=M; 2.49; 9.28  
 422070; AF149785; Hs.111126; pituitary tumor-transforming 1 interact; TCTP; TM=M; SS=Y; 2.45; 12.49  
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase; pkinase; TM=M; 2.44; 6.68  
 427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none; TM=M; 2.43; 7.97  
 446287; BE247683; Hs.14611; dual specificity phosphatase 11 (RNA/RNP); DSPc; SS=M; 2.41; 9.51  
 410017; AW952426; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none, none; 2.41; 14.01  
 424756; AW504657; Hs.152931; lamin B receptor; ERG4, ERG24, FKBP; TM=Y; 2.40; 5.98  
 447580; AI953360; Hs.88201; ESTs; none, none; 2.36; 11.63  
 426276; AW881411; Hs.169078; hypothetical protein FLJ23018; hormone\_rec, zf-C4; TM=M; 2.34; 13.34  
 424441; X14850; Hs.147097; H2A histone family, member X; histone, CBFD\_NFYB\_HMF; 2.33; 12.17  
 429623; NM\_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase, RGS; TM=M; 2.32; 15.80  
 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm, NTF2; TM=M; 2.32; 12.48  
 453648; W21493; Hs.28329; hypothetical protein FLJ14005; none, none; 2.31; 13.19  
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22, Claudin; none; 2.31; 8.51  
 453327; AW500180; Hs.356109; tryptophanyl-tRNA synthetase; rrm, vwa, FG-GAP; 2.30; 13.02  
 439256; AA322302; Hs.183302; PCTAIRE protein kinase 2; none, none; 2.26; 10.36  
 424467; AI929392; Hs.350026; DnaJ (Hsp40) homolog, subfamily B, member; DnaJ, pkinase, UBA, pkinase\_C; SS=M; 2.26; 11.82  
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar\_tr; TM=Y; SS=M; 2.26; 12.54  
 456607; AI660190; Hs.106070; cyclin-dependent kinase inhibitor 1C (p5; CDI; TM=M; 2.25; 13.11  
 423960; AA164516; Hs.136309; SH3-containing protein SH3GLB1; SH3; none; 2.20; 20.05  
 424058; AL121516; Hs.138617; thyroid hormone receptor interactor 12; HECT, WWE; TM=M; 2.20; 13.38  
 446644; NM\_003272; Hs.15791; transmembrane 7 superfamily member 1 (up; none; TM=Y; SS=M; 2.18; 15.68  
 411218; H46440; Hs.180528; dynamin 1-like; dynamin\_2, dynamin, GED; none; 2.18; 13.83  
 414721; X90392; Hs.77091; ribosomal protein L10; Exo\_endo\_phos, Ribosomal\_L10e, Acyltransferase, SCP; TM=M; SS=M; 2.14; 11.24  
 421759; AA027968; Hs.107979; small membrane protein 1; none; TM=Y; SS=M; 2.14; 14.03  
 416240; NM\_001981; Hs.79095; epidermal growth factor receptor pathway; ehfand, DUF164; TM=M; 2.13; 12.86  
 435521; W23814; Hs.6361; mitogen-activated protein kinase kinase; none, none; 2.12; 11.08  
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa\_permeases, pyridoxal\_deC, bromodomain, PHD, MBD, AT\_hook, DDT, PI3\_Pi4\_kinase, FAT, FATC, BclA, RUN; TM=M; 2.12; 14.05  
 453064; R40334; Hs.89463; potassium large conductance calcium-acti; none, none; 2.12; 8.96  
 409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory su; SH2, SH3, RhoGAP; none; 2.08; 11.60  
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm\_1; TM=Y; SS=M; 2.06; 14.23  
 414496; W73853; Hs.355424; ESTs; pkinase, F5\_F8\_type\_C, adh\_short; none; 2.05; 13.45  
 450455; AL117424; Hs.25035; chloride intracellular channel 4; none, TNF; 2.05; 19.04  
 449906; NM\_005638; Hs.24167; synaptobrevin-like 1; synaptobrevin, NTF2; TM=Y; 2.04; 13.34  
 422112; BE540240; Hs.111783; Lsm1 protein; Sm, BAG; SS=M; 2.03; 12.60  
 434935; BE561824; Hs.273369; uncharacterized hematopoietic stem/proge; none; TM=M; 2.02; 10.52  
 433427; AI816449; Hs.171889; cholinephosphotransferase 1; SH2, CDP-OH\_P\_transf; TM=M; 2.02; 16.87  
 410850; AW362867; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate\_transp, STAS, HMG\_box; 2.02; 9.37  
 440481; AA182907; Hs.7200; Homo sapiens, clone MGC:16714, mRNA, com; pkinase, RCC1; TM=M; 2.02; 12.31  
 434645; AF255303; Hs.112227; membrane-associated nucleic acid binding; zf-CCH1, gpdh, Adeno\_E1B\_55K, zf-C3HC4; TM=M; 2.00; 9.15  
 410113; AW996564; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone H; pkinase; none; 1.99; 10.64  
 414636; AL120259; Hs.76691; stannin; none; TM=M; SS=Y; 1.95; 7.72  
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylate kinase; none; 1.95; 14.95  
 422690; AU077275; Hs.119222; suppression of tumorigenicity 13 (colon); TPR; TM=M; 1.94; 10.91  
 427881; BE538296; Hs.323834; cytochrome c oxidase subunit Va; none, GKAP; 1.93; 20.57  
 433387; L76528; Hs.3260; presenilin 1 (Alzheimer disease 3); Presenilin, 7tm\_3, oxidored\_q5\_N; TM=Y; 1.92; 12.58  
 453938; AF082569; Hs.36794; D-type cyclin-interacting protein 1; B56; TM=M; 1.90; 12.74  
 433592; NM\_004642; Hs.3436; deleted in oral cancer (mouse, homolog); none; TM=M; 1.89; 23.27  
 447791; BE241859; Hs.19575; CGI-11 protein; V-ATPase\_H, Armadillo\_seg; TM=M; 1.88; 12.82  
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone H; adenylate kinase; none; 1.88; 14.95

- 432650; D00860; Hs.56; phosphoribosyl pyrophosphate synthetase ; none,none; 1.88; 12.70  
 424250; AF073310; Hs.143648; insulin receptor substrate 2; PH,IRS;TM=M;; 1.86; 19.50  
 424482; BE268621; Hs.149155; voltage-dependent anion channel 1; Euk\_porin;SS=M; 1.85; 11.29  
 425335; BE394327; Hs.296267; follistatin-like 1; efhand,kazal,arf,ras,7tm\_1;TM=M;; 1.85; 13.62  
 426122; NM\_006925; Hs.166975; splicing factor, arginine/serine-rich 5; rrm;SS=M; 1.83; 10.88  
 451579; AW607731; Hs.26670; Human PAC clone RP3-515N1 from 22q11.2-q; kringle;TM=Y;SS=M; 1.83; 20.35  
 428901; AI929568; Hs.146668; KIAA1253 protein; 7tm\_2,UPF0073,TMS\_TDE;TM=Y;SS=M; 1.83; 19.00  
 453963; AA040311; Hs.28959; ESTs; pkinase,Activin\_recpt,none; 1.82; 15.25  
 417414; AA434589; Hs.367676; dUTP pyrophosphatase; dUTPase,KRAB;; 1.81; 14.20  
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 1.81; 22.29  
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo\_endo\_phos,SH2;TM=M;; 1.80; 18.30  
 417733; AL048678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown prot; none;NA;NA; 1.80; 6.28  
 424805; AF230904; Hs.153260; c-Cbl-interacting protein; SH3;TM=M;; 1.80; 11.99  
 420747; BE294407; Hs.99910; phosphofructokinase, platelet; PFK;TM=M;; 1.79; 25.25  
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase;SS=M; 1.78; 15.25  
 437708; AB033020; Hs.5801; KIAA1194 protein; LRR,Exo\_endo\_phos;TM=M;; 1.77; 11.11  
 439877; H39685; Hs.258730; tryptase beta 1; pkinase;SS=M; 1.77; 21.91  
 440256; U23841; Hs.18851; hypothetical protein FLJ10875; none,UBA,UBX; 1.76; 12.95  
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 1.76; 21.01  
 414703; BE243877; Hs.374366; ATPase, Na<sup>+</sup> transporting, beta 3 polypep; Na\_K-ATPase;TM=Y;SS=M; 1.75; 20.03  
 443693; AI344782; Hs.349261; DnaJ (Hsp40) homolog, subfamily C, membe; rrm,DnaJ,TPR;TM=M;; 1.75; 13.29  
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC\_tran,GTP\_EFTU,ABC\_membrane,none; 1.75; 8.75  
 413796; AW408094; Hs.75545; interleukin 4 receptor; fn3,granulin;TM=M;SS=M; 1.74; 14.73  
 438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyrosine kinas; pkinase,SH2,adenylatekinase,none; 1.73; 24.10  
 429655; U48959; Hs.211582; myosin, light polypeptide kinase; pkinase,fn3,lg,none; 1.73; 31.59  
 421456; AW579842; Hs.104557; hypothetical protein FLJ10697; zf-C2H2,DUF18,efhand,C2,PI-PLC-Y,PI-PLC-X;TM=M;; 1.73; 16.87  
 444252; R21135; Hs.54985; ESTs; none,none; 1.71; 10.40  
 442819; BE622721; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; none,pkinase,PBD; 1.69; 14.02  
 447918; AI129320; Hs.115175; ESTs, Highly similar to JC5818 gamma-act; pkinase,SAM,none; 1.69; 17.14  
 429279; AB018271; Hs.198689; KIAA0728 protein; Myosin\_tail,efhand,spectrin,GAS2,Myosin\_tail; 1.68; 14.21  
 450440; AB024334; Hs.25001; tyrosine 3-monooxygenase/tryptophan 5-mo; 14-3-3;TM=M;; 1.67; 24.67  
 413423; AU076684; Hs.75350; vinculin; Vinculin,none; 1.65; 29.28  
 420972; AW814616; Hs.31431; hypothetical protein FLJ12171; Fructosamin\_kin;SS=M; 1.65; 10.75  
 416884; M60484; Hs.80350; protein phosphatase 2 (formerly 2A), cat; Metallophos;SS=M; 1.63; 24.55  
 436719; Y11192; Hs.5299; aldehyde dehydrogenase 5 family, member ; lipocalin,aldehyd,ubiquitin,IRK;SS=M; 1.61; 11.20  
 419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4;TM=Y;SS=M; 1.61; 14.93  
 414176; BE140638; Hs.75794; EDG-2 (endothelial differentiation, lys; 7tm\_1,CRCB;TM=Y;; 1.61; 8.03  
 431476; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT;SS=M; 1.60; 24.37  
 412347; AW970026; Hs.73818; ubiquinol-cytochrome c reductase hinge p; UCR\_hinge,G-alpha,arf;TM=M;; 1.59; 18.09  
 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;; 1.59; 10.99  
 426552; BE297660; Hs.170328; moesin; Band\_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 1.58; 25.97  
 428216; M18468; Hs.183037; protein kinase, cAMP-dependent, regulato; cNMP\_binding,Rlla;SS=M; 1.56; 10.58  
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ;SS=M; 1.56; 13.51  
 448581; NM\_002709; Hs.21537; protein phosphatase 1, catalytic subunit; none,none; 1.55; 12.33  
 417098; AB017365; Hs.173859; frizzled (Drosophila) homolog 7; Frizzled,Fz,7tm\_2,toxin\_2;TM=Y;SS=M; 1.55; 13.77  
 437076; AA961260; Hs.5443; BCL2-associated athanogene 5; BAG,Hanta\_nucleocap;TM=M;; 1.54; 10.93  
 426653; AA530892; Hs.171695; dual specificity phosphatase 1; Rhodanese,DSPc,Y\_phosphatase;TM=M;; 1.54; 11.88  
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing le; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 1.53; 23.05  
 414457; AW514320; Hs.76159; ATPase, H transporting, lysosomal (vacuo; pkinase,ATP-synl\_C,none; 1.53; 32.59  
 414382; AW380339; Hs.8068; hematopoietic PBX-interacting protein; M;TM=M;; 1.52; 8.66  
 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; rrm;TM=M;; 1.52; 11.74  
 402705; ; ; activator of S phase kinase; AhpC-TSA;TM=M;SS=M; 1.51; 26.85  
 426268; AF083420; Hs.168913; serine/threonine kinase 24 (Ste20, yeast; pkinase;SS=M; 1.50; 24.04  
 414604; AU076649; Hs.76556; growth arrest and DNA-damage-inducible 3; none;TM=M;; 1.50; 14.35  
 445584; AF217518; Hs.8360; PTD012 protein; none;SS=M; 1.49; 12.00  
 407232; X04526; ; gb:Human liver mRNA for beta-subunit sig; WD40;TM=M;; 1.49; 19.32  
 424206; NM\_003734; Hs.198241; amine oxidase, copper containing 3 (vasc; Cu\_amine\_oxid,Cu\_amine\_oxidN2,Cu\_amine\_oxidN3;TM=M;SS=M; 1.48; 13.21  
 458761; AF090922; Hs.152738; mitochondrial ribosomal protein L11; ER\_lumen\_recept,Ribosomal\_L11,Ribosomal\_L11\_N;TM=Y;SS=M; 1.48; 12.50  
 426340; Z97989; Hs.169370; FYN oncogene related to SRC, FGR, YES; BNR,SH2,SH3,pkinase;TM=Y;SS=M; 1.48; 17.75  
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase\_C,rrm,Ndr,Cys\_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPc,isp\_1,Ribosomal\_S21,rvp;TM=M;; 1.46; 20.47  
 452516; AA058630; Hs.29759; RNA POLYMERASE I AND TRANSCRIPT RELEASE ; none;SS=M; 1.46; 12.72  
 414240; AL046742; Hs.75842; dual-specificity tyrosine-(Y)-phosphoryl; pkinase;SS=M; 1.45; 14.38  
 420532; AA248016; Hs.194110; hypothetical protein PRO2730; pkinase,WD40;SS=M; 1.43; 13.92  
 402575; ; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.43; 13.71  
 414765; X07854; Hs.77269; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M;; 1.41; 24.62  
 448423; BE390905; Hs.21198; translocase of outer mitochondrial membr; TPR;TM=M;SS=M; 1.41; 10.70  
 422587; AI879352; Hs.118625; hexokinase 1; hexokinase,hexokinase2;TM=M;; 1.41; 19.31  
 415995; NM\_004573; Hs.355888; phospholipase C, beta 2; C2,PI-PLC-Y,PI-PLC-X;TM=M;; 1.40; 11.21  
 446108; AL036596; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemmn;TM=M;; 1.40; 13.98  
 427721; AI582843; Hs.180455; RAD23 (S. cerevisiae) homolog A; ubiquitin,UBA,integrin\_B;SS=M; 1.39; 15.01  
 417891; W79410; Hs.82887; protein phosphatase 1, regulatory (inhib; none;TM=M;; 1.39; 15.97  
 427373; AB007972; Hs.130760; myosin phosphatase, target subunit 2; ank;TM=M;; 1.39; 14.49  
 446334; U52427; Hs.14839; polymerase (RNA) II (DNA directed) polyp; COX8,SHMT,MIF,GST\_C,EF1G\_domain,GST\_N,S1,Fz,Frizzled,calreticulin,7tm\_2,rrm,PAP\_assoc;TM=Y;SS=M; 1.38; 12.58  
 447042; AB035863; Hs.182217; succinate-CoA ligase, ADP-forming, beta ; ligase-CoA,ATP-grasp,Zip,CPSase\_L\_D2,GARS\_B;TM=Y;SS=M; 1.37; 11.37  
 427705; AI870421; Hs.180394; signal recognition particle 14kD (homolo; SRP14,TNFR\_c6;SS=M; 1.37; 22.05  
 425969; AW576265; Hs.301763; KIAA0554 protein; SH3,FCH,HR1;TM=M;; 1.37; 13.68  
 433572; AL046859; Hs.3407; protein kinase (cAMP-dependent, catalyti; PKI;SS=M; 1.35; 12.43  
 410597; W16518; Hs.279518; amyloid beta (A4) precursor-like protein; Kunitz\_BPTI,A4\_EXTRA,Coprogen\_oxidas;TM=Y;SS=M; 1.35; 22.54  
 418424; Y13622; Hs.85087; latent transforming growth factor beta b; EGF,TB,spidertoxin,granulin,ANF\_receptor;SS=M; 1.34; 12.09  
 442603; AL035719; Hs.303091; pleckstrin homology, Sec7 and coiled/coi; PH,Sec7;TM=M;; 1.34; 11.40  
 418043; AW377752; Hs.83341; AXL receptor tyrosine kinase; fn3,lg,pkinase;TM=Y;SS=M; 1.31; 10.79

439278; AF077046; Hs.6518; ganglioside expression factor 2; MAP1\_LC3,aminotran\_3;TM=M; 1.31; 15.89  
 425875; AU077333; Hs.160483; erythrocyte membrane protein band 7.2 (s; PBP,Band\_7;TM=M; 1.31; 17.93  
 407744; AB020629; Hs.38095; ATP-binding cassette, sub-family A (ABC1; ABC\_tran,PRK;TM=Y;SS=M; 1.29; 10.95  
 420679; X57152; Hs.99853; fibrillarin; CK\_II\_beta,Fibrillarin,WD40;TM=M; 1.29; 18.69  
 427397; AI929885; Hs.177656; calmodulin 1 (phosphorylase kinase, delt; efhand,RmaAD;SS=M; 1.29; 15.68  
 424661; M29551; Hs.151531; protein phosphatase 3 (formerly 2B), cat; Metallophos;TM=M; 1.28; 13.39  
 428950; BE311879; Hs.194673; phosphoprotein enriched in astrocytes 15; DED;TM=M; 1.27; 11.15  
 440820; AL031846; Hs.356416; plakophilin 4; none,none; 1.26; 10.65  
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevi; NusG;SS=M; 1.25; 12.07  
 447386; NM\_006289; Hs.375001; KIAA1027 protein; Band\_41,L\_LWEQ,Apolipoprotein,IRS;SS=M; 1.22; 10.65  
 433053; BE301909; Hs.279952; glutathione S-transferase subunit 13 hom; HCCA\_isomerase;TM=M; 1.20; 15.78  
 440708; AF038962; Hs.7381; voltage-dependent anion channel 3; Euk\_porin,Enterotoxin\_A,PHO4,none; 1.20; 14.06  
 417069; AA442192; Hs.374980; cytochrome c oxidase subunit VIII; COX8,SHMT,MIF,GST\_C,EF1G\_domain,GST\_N,S1,Fz,Frizzled,calreticulin,7tm\_2,rrm,PAP\_assoc;TM=Y;SS=M; 1.18; 16.91  
 402559; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.16; 15.49  
 426636; BE242634; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; ThiF,UBACT;TM=M; 1.14; 10.99  
 428773; BE256238; Hs.193163; bridging integrator 1; BAR,SH3;SS=M; 1.14; 11.38  
 406906; Z25424; ; gb:H.sapiens protein-serine/threonine ki; none,none; 1.13; 12.97  
 443932; AW888222; Hs.9973; tensin; SH2,WW,PID,none; 1.07; 15.41  
 421996; AW583807; Hs.1460; glucagon; hormone2;SS=M; 59.35; 1.61  
 414998; NM\_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin\_c;TM=Y;SS=M; 22.96; 4.57  
 442573; H93366; Hs.7567; branched chain aminotransferase 1, cytos; aminotran\_4,none; 21.41; 1.15  
 451035; AU076785; Hs.430; plastin 1 (i isoform); efhand,CH,Adaptin\_N;SS=M; 19.25; 3.53  
 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M; 15.53; 4.34  
 421340; F07783; Hs.1369; decay accelerating factor for complement; sushi;SS=M; 14.84; 19.59  
 422260; AA315993; Hs.105484; regenerating gene type IV; lectin\_c;SS=M; 14.71; 2.89  
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 14.28; 11.47  
 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7tm\_1;TM=Y;SS=M; 12.71; 12.56  
 451820; AW058357; Hs.199248; ESTs; 7tm\_1;TM=Y;SS=M; 10.18; 2.67  
 418693; AI750878; Hs.87409; thrombospondin 1; EGF,tsp\_1,vwc,TSPN,tsp\_3;SS=M; 9.72; 6.94  
 448105; AW591433; Hs.298241; Transmembrane protease, serine 3; ldl\_recept\_a,trypsin;TM=Y;SS=M; 9.67; 4.06  
 456266; L29073; Hs.198726; cold shock domain protein A; 7tm\_2,HRM,CSD;TM=Y;SS=M; 9.62; 2.36  
 413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-rel; none,START; 9.15; 2.18  
 417933; X02308; Hs.82962; thymidylate synthetase; thymidylat\_synt,MR\_MLE,MR\_MLE\_N;SS=M; 8.97; 5.01  
 433334; AI927208; Hs.231958; matrix metalloproteinase 28; Peptidase\_M10,none; 8.71; 4.28  
 418030; BE207573; Hs.83321; neuromedin B; Bombesin;TM=M;SS=Y; 8.38; 1.55  
 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE\_p10,ICE\_p20;SS=M; 8.31; 4.23  
 449523; NM\_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm\_1;TM=Y;SS=M; 8.26; 5.49  
 428513; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI,none; 8.13; 13.28  
 449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.89; 7.00  
 453459; BE047032; Hs.257789; ESTs; none,none; 7.40; 0.60  
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 7.29; 5.78  
 426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 7.25; 7.22  
 426158; NM\_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep\_L\_domain,Furin-like,pkinase,Recep\_L\_domain,Peptidase\_M24; 7.13; 3.97  
 419968; X04430; Hs.93913; interleukin 6 (interferon, beta 2); IL6;SS=Y; 6.93; 3.43  
 457133; M54968; Hs.351221; v-Ki-ras2 Kirsten rat sarcoma 2 viral on; ras,ldh;SS=M; 6.90; 2.85  
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf\_5;TM=Y;SS=M; 6.88; 3.10  
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y\_phosphatase;TM=Y; 6.42; 2.26  
 427969; NM\_001963; Hs.82226; epidermal growth factor (beta-urogastron; EGF,ldl\_recept\_b,EB;TM=M;SS=M; 6.37; 1.07  
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 5.77; 1.24  
 427557; NM\_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR\_LY6,ET,PLA2\_inh;SS=M; 5.71; 3.83  
 418283; S79895; Hs.83942; cathepsin K (pseudosynostosis); Peptidase\_C1;SS=M; 5.59; 38.68  
 458471; AV648609; Hs.194240; ESTs; none,none; 5.23; 1.05  
 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.88; 4.60  
 433293; AF007835; Hs.32417; hypothetical protein MGC4309; none;TM=M; 4.56; 4.96  
 410867; X63556; Hs.750; fibrillin 1 (Marfan syndrome); EGF,TB,wnt,EB,TIL;SS=M; 4.32; 26.87  
 417512; X76534; Hs.82226; glycoprotein (transmembrane) nmb; PKD;TM=Y;SS=M; 4.26; 9.04  
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian ; Furin-like,pkinase,Recep\_L\_domain;TM=M;SS=M; 3.94; 1.16  
 439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep\_L\_domain,Furin-like,pkinase,Recep\_L\_domain,Peptidase\_M24; 3.76; 2.21  
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC\_tran,ABC\_membrane;TM=Y;SS=M; 3.47; 2.24  
 419749; X73608; Hs.93029; sparco/osteonection, cwcv and kazal-like d; kazal,thyroglobulin\_1;SS=M; 3.37; 7.10  
 436576; AI458213; Hs.77542; ESTs; 7tm\_1,DnaJ; 3.15; 3.27  
 428093; AW594506; Hs.104830; ESTs; none,none; 2.81; 3.40  
 459683; AI674906; Hs.199460; gb:wc73f02.x1 NCL\_CGAP\_Pan1 Homo sapiens; none;TM=Y; 2.77; 1.36  
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor.; ig,pkinase;TM=Y; 2.71; 10.53  
 430451; AA836472; Hs.297939; cathepsin B; Peptidase\_C1,pro\_isomerase;SS=M; 2.28; 14.59  
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfam; 60s\_ribosomal,Ribosomal\_L10,TNFR\_c6,DEAD; 2.21; 6.33  
 435496; AW840171; Hs.265398; PAR-6 beta; none,none; 2.17; 2.00  
 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin,Repolyisin,Pep\_M12B\_propep,EGF;TM=Y;SS=M; 1.91; 13.06  
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigeni; DAN;TM=M;SS=M; 1.81; 22.29  
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 1.52; 8.40  
 452795; AW392555; Hs.18878; hypothetical protein FLJ21620; 2OG-Fell\_Oxy;TM=M; 1.49; 3.29  
 432199; AI693815; Hs.127179; cryptic gene; none;TM=M;SS=M; 1.23; 1.60  
 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin,ldl\_recept\_a,none; 1.00; 3.92  
 445418; AW139377; Hs.127179; cryptic gene; none,none; 1.00; 2.45  
 451106; BE382701; Hs.25960; N-MYC oncogene; HLH,Myc\_N\_term;TM=M; 1.00; 1.87  
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00; 1.30

TABLE 42B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
5	406685	0_0 M18728
	414087	1632850_1 W19712 BE247277
	400151	9575_21 BC006850 U07418 NM_000249 U07343 AL574783 BI090482 BG684481 AA385302 BG196167 BI091720 BG195132 AI680106 AI457552 AA402478
		BG249688 AA347119 BG755996 BG822578
	418546	242836_1 T59708 AA224827 T59843 BE156903

TABLE 42C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
20	406399	9256288	Minus 63448-63554
	405102	8076881	Minus 120922-121296
	403344	8569726	Plus 70823-70990
	405555	1552511	Plus 153405-153564,154623-154876,155272-15540
25	405556	1552511	Plus 163497-163623,164715-164968,165369-16550
	405204	7230116	Plus 126569-126754
	406366	9256126	Minus 10639-10800,10890-11023,11113-11293
	400539	7574902	Plus 8559-8721
	403208	7630829	Minus 147706-147903,148667-148804
30	405203	7230116	Plus 125295-125463
	402705	8782736	Plus 89961-90114,90773-90895,91131-91261
	402575	9884830	Minus 109742-109883
	402559	9864273	Plus 33539-33715

TABLE 43A: 43 genes upregulated in pancreatic cancer relative to normal body tissues

Table 43A lists about 43 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins particularly useful for diagnostic or prognostic applications. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar accession number, GenBank accession number  
 UniGeneID: UniGene number  
 Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).  
 UniGene Title: UniGene gene title  
 R1 90th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs  
 R2 90th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prod.Domains; R1; R2

446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin;SS=M; 44.95; 2.17  
 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;SS=M; 35.40; 29.13  
 411274; NM\_002776; Hs.69423; kallikrein 10; trypsin;TM=M; 30.10; 13.59  
 446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL8;SS=Y; 29.33; 16.08  
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8;SS=M; 24.64; 7.21  
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGF-beta\_propeptide,TGF-beta,none; 23.81; 10.74  
 407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagon; TGF-beta,DAN;SS=Y; 22.33; 10.20  
 404682; ; C9001188\*gi12738842[ref]NP\_073725.1| p; none;TM=M; 17.72; 1.40  
 413554; AA319146; Hs.75426; secretogranin II (chromogranin C); Granin;TM=M;SS=Y; 17.36; 2.01  
 428392; H10233; Hs.2265; secretory granule, neuroendocrine protei; none;TM=M;SS=M; 16.82; 1.70  
 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M; 15.53; 4.34  
 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8;SS=M; 15.40; 3.70  
 428242; H55709; Hs.2250; leukemia inhibitory factor (cholinergic ; LIF\_OSM;SS=M; 14.85; 6.58  
 421340; F07783; Hs.1369; decay accelerating factor for complement; sushi;SS=M; 14.84; 19.59  
 409757; NM\_001898; Hs.123114; cystatin SN; cystatin;SS=M; 14.61; 12.75  
 425071; NM\_013989; Hs.154424; deiodinase, iodothyronine, type II; T4\_deiodinase;TM=M;SS=Y; 14.35; 17.22  
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 13.81; 7.69  
 409420; Z15008; Hs.54451; laminin, gamma 2 (nicein (100kD), kalini; laminin\_B,laminin\_EGF;SS=M; 13.05; 7.72  
 432596; AJ224741; Hs.278461; matrilin 3; EGF,ywa;SS=M; 12.80; 9.91  
 422109; S73265; Hs.1473; gastrin-releasing peptide; Bombesin,Defensin\_propep;TM=M;SS=M; 12.79; 4.69  
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 11.36; 2.22  
 429547; AW009166; Hs.99376; FGENESH predicted novel secreted protein; none,none; 10.25; 5.62  
 422424; A1186431; Hs.296638; prostate differentiation factor; TGF-beta;SS=M; 9.96; 1.88  
 428505; AL035461; Hs.2281; chromogranin B (secretogranin 1); Granin;SS=M; 9.40; 3.46  
 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB A; TGF-beta,TGFb\_propeptide,Tub;SS=M; 9.19; 16.46  
 418030; BE207573; Hs.83321; neuromedin B; Bombesin;TM=M;SS=Y; 8.38; 1.55  
 452401; NM\_007115; Hs.29352; tumor necrosis factor, alpha-induced pro; Xlink,CUB;SS=M; 7.46; 4.96

421582; AI910275; Hs.350470; trefoil factor 1 (breast cancer, estroge; trefoil,Gastrin;SS=M; 7.08; 21.61  
 423634; AW959908; Hs.1690; heparin-binding growth factor binding pr; none;TM=M;SS=M; 6.78; 12.19  
 428486; AW583497; Hs.184604; pancreatic polypeptide; hormone3;TM=M;SS=Y; 6.29; 3.51  
 443646; AI085198; Hs.164226; ESTs; EGF,tsp\_1,vwc,TSPN,tsp\_3,none; 6.17; 4.25  
 457489; AI693815; Hs.127179; cryptic gene; none;TM=M;SS=M; 5.19; 2.79  
 450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; none;SS=M; 5.01; 7.43  
 422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; tsp\_3,EGF;SS=M; 4.87; 9.40  
 426322; J05068; Hs.2012; transcobalamin I (vitamin B12 binding pr; Cobalamin\_bind;SS=M; 4.71; 11.74  
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant\_thionins;SS=M; 4.24; 6.91  
 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA;TM=Y;; 3.52; 8.43  
 422048; NM\_012445; Hs.288126; spondin 2, extracellular matrix protein; tsp\_1;TM=M;SS=M; 3.45; 7.69  
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2,hemoexin,Peptidase\_M10;SS=M; 3.43; 10.37  
 417931; W95642; Hs.82961; trefoil factor 3 (intestinal); trefoil;SS=M; 2.98; 9.65  
 445417; AK001058; Hs.12680; Homo sapiens cDNA FLJ10196 fis, clone HE; tsp\_1,Repolyisin,Pep\_M12B\_propep,none; 2.97; 5.74  
 432874; W94322; Hs.279551; melanoma inhibitory activity; SH3;TM=M;SS=Y; 2.80; 10.53  
 431462; AW583672; Hs.256311; granin-like neuroendocrine peptide precu; none,none; 2.70; 1.99

TABLE 43C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404682	9797231	Minus	40977-41150

TABLE 44A: 754 GENES UP-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

Table 44A lists about 754 genes up-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title

Pkey	ExAccn	UnigenelD	Unigene Title
100042	M10098		AFFX control - HUMRGE/M10098_3
101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h
103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa
104743	AA021157	Hs.33619	Homo sapiens cDNA FLJ20096 fis, clone CO
104996	AA112307	Hs.105894	hypothetical protein FLJ21919
105437	AA252191	Hs.25199	hypothetical protein
108258	AA063269		gb:zm02a09.s1 Stralagene corneal stroma
109086	AA166695	Hs.270737	tumor necrosis factor (ligand) superfamI
109279	AA196625	Hs.86080	ESTs
109779	F10527	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur
111794	R32647	Hs.23545	ESTs
112531	R69798	Hs.29036	ESTs
112784	R96306	Hs.191290	ESTs
113293	T67026	Hs.187403	ESTs
115416	AA283893	Hs.337079	ESTs
116548	D20433		gb:HUMGS01407 Human promyelocyte Homo sa
116565	D45533	Hs.129691	hypothetical protein FLJ21603
118104	N55332	Hs.39785	ESTs
119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa
119336	T55340	Hs.208238	ESTs
120101	W95414	Hs.55497	EST
120715	AA292700		gb:zs59a06.s1 NCL_CGAP_GCB1 Homo sapiens
120872	AA357993	Hs.96996	ESTs
121010	AA398355	Hs.97330	ESTs
121509	AA412092	Hs.97888	ESTs
121722	AA419482	Hs.98874	similar to proline-rich protein 48
122265	AA436838	Hs.98906	EST
123206	AA489681	Hs.102248	Homo sapiens cDNA: FLJ22105 fis, clone H
123490	AA599723		gb:ag11c07.s1 Gessler Wilms tumor Homo s
124198	H53099	Hs.198271	NADH dehydrogenase (ubiquinone) 1 alpha
124294	H90573	Hs.102298	EST
125067	T86429	Hs.111725	ESTs
125153	W38294		
125330	AA401804	Hs.114574	ESTs
125335	T86620	Hs.16230	hypothetical protein FLJ20619
125361	T90348	Hs.183404	ESTs
125439	AA826305		gb:PM0-LT0017-031299-001-c07 LT0017 Homo
125535	R17430	Hs.22215	secretogranin III
125583	R22272	Hs.86022	ESTs
125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,
125742	H81181	Hs.261023	hypothetical protein FLJ20958



5	125795	T98190	Hs.7756	proteasome (prosome, macropain) 26S subu
	125858	H11549	Hs.31066	ESTs
	125865	H12876	Hs.283078	hOAT4
	126039	AA160575	Hs.181102	p30 DBC protein
	126143	N29315	Hs.266331	hypothetical protein MGC4595
10	126177	H93164	Hs.129750	hypothetical protein FLJ10546
	126219	N36368	Hs.293483	ESTs, Weakly similar to similar to C. el
	126221	AI248169	Hs.172965	ESTs
	126262	C75147	Hs.143764	ESTs, Weakly similar to unknown [H.sapi
	126277	N39132	Hs.15441	Crm (Cramped Drosophila)-like
15	126292	AA491328		gb:aa65d09.r1 NCI_CGAP_GCB1 Homo sapiens
	126293	Z18870	Hs.248121	G protein-coupled receptor 22
	126353	AI243114	Hs.94031	ESTs
	126556	AA491325	Hs.112227	membrane-associated nucleic acid binding
	126559	R15866	Hs.170263	tumor protein p53-binding protein, 1
20	126609	W87435	Hs.186802	ESTs
	126616	AA348581	Hs.134605	ESTs
	126628	AI357886	Hs.170994	hypothetical protein MGC10946
	126636	AA001527		gb:zf56g09.r1 Soares retina N2b4HR Homo
	126861	AA742428	Hs.144432	ESTs
25	126990	AA215510	Hs.191650	ESTs
	127017	AA740146	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I
	127049	AA235966	Hs.291811	ESTs
	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil
	127331	F20186		gb:HSPD05873 HM3 Homo sapiens cDNA clone
30	127357	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
	127368	AA434362	Hs.193326	fibroblast growth factor receptor-like 1
	127374	AA448728	Hs.312110	ESTs, Weakly similar to I38022 hypothet
	127429	AA961490	Hs.293751	ESTs, Moderately similar to TPTE_HUMAN P
	127490	W52891	Hs.7278	cryptochrome 2 (photolyase-like)
35	127502	AA614422	Hs.183502	ESTs
	127647	AI087279	Hs.148410	ESTs
	127650	AA873776	Hs.261957	ESTs
	127676	D31237	Hs.279938	HSPC067 protein
	127746	AI239495	Hs.120189	ESTs
40	127812	AA749094	Hs.291434	ESTs
	127824	AI208365	Hs.127811	ESTs
	127933	AA811102	Hs.303581	ESTs, Moderately similar to ALU1_HUMAN A
	128006	AA058693	Hs.129908	KIAA0591 protein
	128011	AI347067	Hs.124636	ESTs
45	128038	AA868782	Hs.137024	ESTs
	128058	AI126617	Hs.132449	ESTs
	128199	AI073548	Hs.164597	ESTs
	128308	AI079496	Hs.134169	ESTs
	128389	AI142639	Hs.146662	ESTs
50	128410	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
	129199	H90914	Hs.200332	hypothetical protein FLJ20651
	130998	C00810	Hs.293981	guanine nucleotide binding protein (G pr
	134409	AA281600	Hs.164915	small nuclear RNA activating complex, p
	134578	AA194724	Hs.224137	hypothetical protein
55	134644	S83308	Hs.87224	SRY (sex determining region Y)-box 5
	100262	D38500	Hs.278468	postmeiotic segregation increased 2-like
	100676	HG3044-HT3742	Hs.287820	fibronectin 1
	100704	HG3242-HT3419	Hs.166110	calcium channel, voltage-dependent, alph
	100787	HG3872-HT4142	Hs.302063	immunoglobulin heavy constant mu
60	100873	HG4333-HT4603	Hs.17364	zinc finger protein 79 (pT7)
	100943	HG880-HT880		gb:PM0-SN0019-280300-001-D11 SN0019 Homo
	100996	J03909	Hs.14623	interferon, gamma-inducible protein 30
	101046	K01160		
	101371	M13232	Hs.36989	coagulation factor VII (serum prothrombi
65	101461	M22430	Hs.76422	phospholipase A2, group IIA (platelets,
	101697	M64358		gb:Human rhom-3 gene, exon.
	101909	S69265		
	102199	U21128	Hs.79914	lumican
	102275	U30998	Hs.17752	phosphatidylserine-specific phospholipas
70	102295	U32581	Hs.168052	KIAA0421 protein
	102319	U34587	Hs.66578	corticotropin releasing hormone receptor
	102383	U40622	Hs.150930	X-ray repair complementing defective rep
	102470	U49835	Hs.154138	chitinase 3-like 2
	102544	U57721	Hs.169139	kynureninase (L-kynurenine hydrolase)
75	102649	U68133		gb:U68133 Human cell line PCI-O6A Homo s
	102798	U88898		gb:Human endogenous retrovirus H proteas
	102804	U89942	Hs.83354	lysyl oxidase-like 2
	102851	V00532	Hs.93907	interferon, alpha 14
	102852	V00571	Hs.75294	corticotropin releasing hormone
80	102860	X00368		gb:Human prolactin gene 5' region.
	103262	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)
	103484	Y08374	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	103559	Z19585	Hs.75774	thrombospondin 4
	103658	Z74615	Hs.172928	collagen, type I, alpha 1
	103719	AA054109	Hs.4273	hypothetical protein FLJ13159
	103876	AA226865	Hs.8203	endomembrane protein emp70 precursor iso
	103897	AA248870	Hs.55058	EH-domain containing 4

	103906	AA249437	Hs.317403	hypothetical protein MGC2744
	103985	AA313880	Hs.99872	fetal Alzheimer antigen
	104056	AA397529	Hs.58297	CLLL8 protein
5	104209	AB000221	Hs.16530	small inducible cytokine subfamily A (Cy
	104386	H41895	Hs.144164	ESTs, Moderately similar to ALU8_HUMAN A
	104398	H53555	Hs.36790	ESTs, Weakly similar to putative p150 [H
	104422	H86858	Hs.132909	ESTs
	104561	R60100	Hs.323817	DKFZP547E1010 protein
10	104593	R81267	Hs.98640	hypothetical protein FLJ21069
	104643	AA004701	Hs.18978	Homo sapiens cDNA: FLJ22822 fis, clone K
	104673	AA007633	Hs.20010	ESTs
	104681	AA009832	Hs.34500	ESTs
	104711	AA017254	Hs.32794	ESTs
	104812	AA034111	Hs.124187	ESTs
15	104877	AA047437	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se
	104886	AA053348	Hs.339699	growth differentiation factor 11
	104924	AA058532	Hs.28774	ESTs, Weakly similar to I38022 hypotheti
	105071	AA136532	Hs.29475	ESTs
20	105105	AA151872	Hs.87016	hypothetical protein FLJ22938
	105203	AA195660	Hs.7882	ESTs
	105317	AA233926	Hs.52620	integrin, beta 8
	105617	AA280687	Hs.4069	glucocorticoid modulatory element bindin
	105707	AA291012	Hs.37617	ESTs, Weakly similar to A53933 myosin I
25	105754	AA302657	Hs.192028	ESTs
	105770	AA347964	Hs.269873	Homo sapiens clone IMAGE:297403, mRNA se
	105882	AA400292	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	105883	AA400490	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com
	105890	AA400766	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,
30	106080	AA418046	Hs.35124	ESTs
	106090	AA418909	Hs.169333	hypothetical protein DKFZp761E2110
	106096	AA419609	Hs.170121	protein tyrosine phosphatase, receptor t
	106124	AA423987	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H
	106308	AA436186	Hs.30662	ESTs
35	106438	AA449199	Hs.21342	ESTs
	106660	AA460936	Hs.27056	KIAA1284 protein
	106731	AA465657	Hs.29205	alpha integrin binding protein 63
	106880	AA488889	Hs.32425	ESTs
	107055	AA600152	Hs.29419	ESTs
40	107151	AA621169	Hs.8687	ESTs
	107183	C20974	Hs.12114	vanin 1
	107231	D59299	Hs.34727	ESTs, Moderately similar to I38759 zinc
	107490	W74158	Hs.103189	lipopolysaccharide specific response-68
	107572	AA001903	Hs.59962	ESTs
45	107620	AA005039	Hs.60171	ESTs
	107801	AA019433	Hs.285803	Homo sapiens cDNA FLJ10674 fis, clone NT
	107817	AA020781	Hs.60847	ESTs
	107823	AA021057	Hs.60836	ESTs
	107857	AA024687	Hs.61208	ESTs
50	107882	AA025630	Hs.231967	ALL1 fused gene from 5q31
	108005	AA037769	Hs.194293	ESTs, Weakly similar to I54374 gene NF2
	108092	AA045961	Hs.184029	hypothetical protein DKFZp761A052
	108115	AA047291	Hs.165216	ESTs
	108214	AA058661	Hs.60764	ESTs
55	108382	AA074885	Hs.67726	macrophage receptor with collagenous str
	108409	AA075578		gb:zm88h03.r1 Stratagene ovarian cancer
	108436	AA078801		gb:zm94a09.s1 Stratagene colon HT29 (937
	108625	AA101983	Hs.283022	triggering receptor expressed on myeloid
	108631	AA102553	Hs.334337	ESTs
60	108763	AA127539	Hs.281397	hypothetical protein AD034
	108852	AA133131		gb:zm25d03.s1 Stratagene pancreas (93720
	108931	AA147186		gb:zo38d01.s1 Stratagene endothelial cel
	108976	AA151480	Hs.91202	ESTs
	109026	AA157811		gb:zo35d07.s1 Stratagene colon (937204)
65	109170	AA180352	Hs.191472	ESTs, Weakly similar to ALU1_HUMAN ALU
	109303	AA206126	Hs.269291	ESTs
	109326	AA210719		gb:zr88e04.s1 NCI_CGAP_GCB1 Homo sapiens
	109345	AA213774	Hs.203396	ESTs
	109404	AA224594	Hs.86941	ESTs
70	109473	AA233151	Hs.81796	ESTs
	109725	F10003	Hs.79658	casein kinase 1, epsilon
	109794	F10684	Hs.23687	ESTs
	109835	H00615	Hs.170044	ESTs
	109896	H04794	Hs.30489	ESTs
75	109918	H05641	Hs.216701	Homo sapiens mRNA; cDNA DKFZp564I0816 (f
	109950	H08200	Hs.268770	ESTs, Weakly similar to 2004399A chromos
	110078	H15054	Hs.318773	KIAA1836 protein
	110182	H20402	Hs.31746	hypothetical protein DKFZp547F072
	110213	H23216	Hs.86905	ATPase, H+ transporting, lysosomal (vacu
80	110310	H38209	Hs.32728	EST
	110354	H41280	Hs.22586	ESTs
	110413	H48124	Hs.279454	ESTs
	110422	H48467	Hs.36094	EST
	110433	H49425	Hs.301062	UDP-N-acetyl-alpha-D-galactosamine:polyp

	110434	H49446	Hs.26299	ESTs
	110553	H58934	Hs.124990	ESTs
	110750	N20522	Hs.30981	ESTs
5	110827	N30077	Hs.14855	ESTs
	110829	N30198	Hs.28625	ESTs
	110917	N46363	Hs.5170	ESTs
	111100	N62522	Hs.20450	BCM-like membrane protein precursor
	111112	N63281	Hs.35452	ESTs
10	111179	N67239	Hs.10760	asporin (LRR class 1)
	111185	N67551	Hs.12844	EGF-like-domain, multiple 6
	111223	N68921	Hs.334838	KIAA1866 protein
	111275	N70970	Hs.35006	ESTs
	111443	R01901		gb:Homo sapiens endogenous retrovirus W
15	111573	R10305	Hs.185683	ESTs
	111590	R11157	Hs.75425	ubiquitin associated protein
	111671	R19368	Hs.229084	Homo sapiens cDNA FLJ11666 fis, clone H
	111732	R25153	Hs.163813	ESTs
	111809	R33616	Hs.24688	EST
20	111829	R36070		gb:Homo sapiens full length insert cDNA
	111944	R40606	Hs.21263	suppressor of potassium transport defect
	112015	R42836	Hs.23198	ESTs
	112023	R43020	Hs.236223	EST
	112055	R43621	Hs.26139	ESTs
25	112334	R56239	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S
	112340	R56602	Hs.8904	Ig superfamily protein
	112353	R58986	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (f
	112467	R65706		gb:yi16g12.s1 Soares placenta Nb2HP Homo
	112478	R66067	Hs.28664	ESTs
30	112533	R69886		gb:yi47f03.s1 Soares placenta Nb2HP Homo
	112588	R77302		gb:yi75h08.s1 Soares placenta Nb2HP Homo
	112595	R77783	Hs.22404	protease, serine, 12 (neurotrypsin, moto
	112676	R86976	Hs.34060	ESTs
	112744	R93206	Hs.293762	ESTs, Weakly similar to I38022 hypotheti
35	112777	R95869	Hs.35467	EST
	112817	R98491	Hs.14584	ESTs
	112902	T09262	Hs.129190	Human DNA sequence from clone RP5-1046G1
	113009	T23699	Hs.7246	ESTs
	113151	T51620	Hs.9326	EST
40	113297	T67161	Hs.13059	ESTs
	113398	T82280	Hs.87016	hypothetical protein FLJ22938
	113484	T87795	Hs.187543	ESTs
	113769	U55966	Hs.22985	alpha2,8-sialyltransferase
	113794	W37382	Hs.11090	membrane-spanning 4-domains, subfamily A
45	113971	W86760	Hs.269172	ESTs
	114066	Z38152	Hs.26920	ESTs
	114178	Z39063	Hs.17930	chromosome 6 open reading frame 11
	114206	Z39294	Hs.27339	EST
	114371	Z41835	Hs.27810	ESTs
50	114428	AA017130	Hs.84790	KIAA0225 protein
	114466	AA026970	Hs.135150	lung type-I cell membrane-associated gly
	114625	AA084362		gb:zn05b10.r1 Stratagene hNT neuron (937
	114862	AA235174	Hs.106432	Homo sapiens cDNA FLJ13410 fis, clone PL
	114908	AA236545	Hs.54973	cadherin-like protein VR20
55	114973	AA250845	Hs.87762	ESTs
	115009	AA251561	Hs.48689	ESTs
	115055	AA253005	Hs.61753	ESTs
	115098	AA256161	Hs.161729	ESTs
	115321	AA280805	Hs.191540	ESTs
60	115385	AA282540	Hs.109694	KIAA1451 protein
	115466	AA287008	Hs.285655	ESTs
	115479	AA287596	Hs.278188	ESTs, Moderately similar to I54374 gene
	115663	AA405838	Hs.40507	ESTs
	115689	AA410645	Hs.199014	ESTs, Moderately similar to ALU7_HUMAN A
65	115748	AA418835	Hs.90286	ESTs
	115810	AA426026	Hs.187615	ESTs
	115827	AA427890	Hs.83583	actin related protein 2/3 complex, subun
	115881	AA435577	Hs.184942	G protein-coupled receptor 64
	116148	AA460708	Hs.62905	hypothetical protein FLJ14834
70	116257	AA481493	Hs.88537	ESTs
	116365	AA521080	Hs.46765	ESTs
	116941	H77395	Hs.39749	ESTs
	116982	H81933	Hs.312582	ESTs
	116995	H83928		gb:ys64b03.s1 Soares retina N2b4HR Homo
75	116997	H84214	Hs.40594	ESTs
	117016	H87171	Hs.52170	ESTs
	117097	H93608	Hs.41919	EST
	117101	H94043	Hs.24341	transcriptional co-activator with PDZ-bi
	117238	N20815	Hs.173337	ESTs
80	117303	N22776	Hs.264079	ESTs
	117399	N26480	Hs.43805	lipoma HMGIC fusion partner-like 3
	117503	N31963	Hs.44286	ESTs
	117544	N33222	Hs.44451	ESTs
	117594	N34929	Hs.171984	ESTs

5	117627	N36113	Hs.44789	ESTs, Weakly similar to B34087 hypothet
	117653	N38970	Hs.194214	ESTs
	117695	N40953	Hs.45093	EST
	117697	N40976		gb:yy80b06.s1 Soares_multiple_sclerosis_
	117766	N47807	Hs.46767	EST
10	117807	N48701	Hs.46523	EST
	117816	N48872		gb:yy77a05.s1 Soares_multiple_sclerosis_
	117882	N50101	Hs.301406	hypothetical protein PP3501
	117987	N51935	Hs.47374	Homo sapiens cDNA FLJ13561 fis, clone PL
	118074	N54188	Hs.130323	Homo sapiens, clone IMAGE:3960432, mRNA
15	118114	N56875	Hs.143212	cystatin F (leukocystatin)
	118151	N58276	Hs.229119	EST
	118270	N62868	Hs.48653	ESTs
	118291	N63076	Hs.138746	EST
	118358	N64017	Hs.144633	hypothetical protein DKFZp434F2322
20	118383	N64529	Hs.49001	EST
	118412	N64856	Hs.97437	centrosomal protein 1
	118433	N66248	Hs.141609	EST
	118600	N69222	Hs.238936	ESTs, Weakly similar to (define not av
	118641	N70298	Hs.49829	ESTs
25	118643	N70324	Hs.49840	ESTs
	118695	N71781	Hs.50081	KIAA1199 protein
	118915	N91481	Hs.54713	ESTs
	119041	R02591	Hs.284294	Breakpoint cluster region protein, uteri
	119069	R27619	Hs.231046	EST
30	119105	R42357	Hs.91453	ESTs
	119154	R61293		gb:yh07a05.s1 Soares infant brain 1NIB H
	119241	T12559		gb:CHR90079 Chromosome 9 exon II Homo sa
	119269	T16367	Hs.65327	EST
	119310	T40427		gb:ya01a06.s2 Stratagene lung (937210) H
35	119345	T63474	Hs.90696	EST
	119353	T66867	Hs.187402	ESTs
	119390	T89122	Hs.249712	ESTs, Weakly similar to ALU1_HUMAN ALU
	119423	T99544	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU
	119428	W02129	Hs.55242	EST
40	119529	W38053		
	119795	W73370	Hs.339722	ESTs, Highly similar to S03917 fibronec
	119817	W74257	Hs.159690	ESTs
	119831	W78050	Hs.58419	DKFZP586L2024 protein
	119930	W86471	Hs.151624	hypocretin (orexin) receptor 2
45	120039	W92548	Hs.94985	ESTs
	120256	AA169801	Hs.98710	hypothetical protein
	120284	AA182626		gb:zp54e11.s1 Stratagene NT2 neuronal pr
	120350	AA211300	Hs.108614	KIAA0627 protein; Drosophila multiple as
	120379	AA227849		gb:DKFZp434B1822_r1 434 (synonym: hles3)
50	120383	AA228030	Hs.123122	FSH primary response (LRPR1, rat) homolo
	120420	AA236031	Hs.112885	spinal cord-derived growth factor-B
	120437	AA243427	Hs.104311	novel protein with MAM domain
	120461	AA251301	Hs.293369	ESTs
	120594	AA282054	Hs.5094	ring finger protein 10
55	120611	AA284178	Hs.110637	homeo box A10
	120626	AA285064	Hs.104485	EST
	120696	AA291503	Hs.97249	ESTs
	120747	AA302976	Hs.96672	ESTs
	120749	AA303235		gb:EST14544 Testis tumor Homo sapiens cD
60	120752	AA311972	Hs.22895	hypothetical protein FLJ23548
	120851	AA349662	Hs.174248	ESTs
	120866	AA350718	Hs.291272	ESTs
	120949	AA397830	Hs.98347	ESTs, Weakly similar to JC5308 testis-sp
	120996	AA398281	Hs.308114	ESTs
65	121038	AA398536	Hs.97365	ESTs
	121065	AA398658	Hs.97300	ESTs
	121067	AA398662	Hs.97302	ESTs
	121071	AA398678	Hs.139355	ESTs
	121082	AA398722		gb:zl75h07.s1 Soares_testis_NHT Homo sap
70	121172	AA400013	Hs.97750	EST, Weakly similar to MPL3 RAT MICROTUB
	121191	AA400205	Hs.104447	ESTs
	121354	AA405384	Hs.193737	ESTs
	121393	AA405981	Hs.262643	ESTs
	121399	AA406059	Hs.332700	EST
75	121479	AA411911	Hs.98110	ESTs
	121498	AA412033	Hs.178045	ESTs
	121704	AA418743	Hs.98306	KIAA1862 protein
	121736	AA421131	Hs.148515	Human clone 23564 mRNA sequence
	122198	AA435892	Hs.97541	ESTs
80	122220	AA436011	Hs.98187	ESTs
	122250	AA436692	Hs.98892	EST
	122279	AA437209	Hs.234016	ESTs
	122286	AA437259	Hs.104944	ESTs
	122330	AA442870	Hs.98628	Homo sapiens, clone IMAGE:4214491, mRNA,
	122338	AA443311	Hs.98998	ESTs
	122355	AA443789	Hs.19978	CGI-30 protein
	122590	AA453264	Hs.99310	ESTs

	122746	AA458791		gb:aa88c02.s1 Stratagene fetal retina 93
	122805	AA460702	Hs.82772	collagen, type XI, alpha 1
	122841	AA461536	Hs.288908	WASP protein family, member 2
5	122899	AA469960	Hs.178420	ESTs, Highly similar to WASP interacting
	122933	AA476728	Hs.107537	chromosome 7 open reading frame 2
	123005	AA479726	Hs.52620	integrin, beta 8
	123142	AA487504	Hs.105718	EST
	123153	AA488349	Hs.334808	hypothetical protein MGC4189
10	123168	AA488881	Hs.105218	EST
	123188	AA489092	Hs.177726	ESTs
	123276	AA491270	Hs.187946	ESTs
	123305	AA496133		gb:zv51e12.s1 Soares_testis_NHT Homo sap
	123328	AA496968		gb:aa42g03.s1 Soares_NhHMPu_S1 Homo sapi
15	123450	AA598913	Hs.111207	ESTs
	123464	AA599014	Hs.153321	Homo sapiens cDNA FLJ10577 fis, clone NT
	123650	AA609332	Hs.180696	ESTs
	123700	AA609606	Hs.191956	ESTs
	123858	AA620821	Hs.112911	EST
20	123863	AA620873	Hs.112916	ESTs
	124046	F10243		gb:HSC3CC122 normalized infant brain cDN
	124059	F13673	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	124196	H52617	Hs.144167	ESTs
	124197	H52921		gb:yq76c09.s1 Soares fetal liver spleen
25	124229	H62793	Hs.268945	ESTs
	124230	H63111	Hs.6655	Homo sapiens EST from clone 208499, full
	124241	H65947	Hs.165355	ESTs, Moderately similar to ZN91_HUMAN Z
	124251	H68286	Hs.107924	ESTs
	124400	N30597	Hs.179152	toll-like receptor 7
30	124416	N34042	Hs.271674	ESTs
	124570	N67117	Hs.102808	ESTs
	124575	N68168		gb:za11c01.s1 Soares fetal liver spleen
	124588	N69197	Hs.191361	ESTs, Weakly similar to I38022 hypotheti
35	124598	N70294	Hs.269137	ESTs, Weakly similar to A56194 thromboxa
	124655	N93176	Hs.102914	ESTs
	124706	R07499	Hs.193612	ESTs, Weakly similar to ALU8_HUMAN ALU
	124848	R60135	Hs.203498	EST
	124882	R74041	Hs.101539	ESTs
	124898	R82846	Hs.273789	ESTs
40	125086	T91161	Hs.173880	interleukin 1 receptor accessory protein
	125145	W38001		
	125216	W73409	Hs.103185	ESTs
	125342	AI055916	Hs.133552	ESTs
45	125351	T96520	Hs.324746	alpha-2-HS-glycoprotein
	125419	AI076822	Hs.134544	ESTs
	125424	T99667	Hs.18564	ESTs
	125526	R14487	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f
	125539	R17870	Hs.248120	G protein-coupled receptor 21
	125633	AA908225	Hs.15463	Homo sapiens, clone IMAGE:2959994, mRNA
50	125689	R48940	Hs.108043	Friend leukemia virus integration 1
	125707	C14616	Hs.284122	Wnt inhibitory factor-1
	125790	AA868325	Hs.99962	proteoglycan 2, bone marrow (natural kil
	125876	AA324967	Hs.7298	biphenyl hydrolase-like (serine hydrolas
	125969	R94247	Hs.88414	BTB and CNC homology 1, basic leucine zi
55	125970	AI400964	Hs.177516	high density lipoprotein binding protein
	125975	AA495891	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv
	125985	H54857	Hs.35981	ESTs
	126018	H54866	Hs.167583	ESTs
60	126032	H59735	Hs.269065	ESTs, Highly similar to KIAA0349 [H.sapi
	126059	H66582	Hs.308486	ESTs
	126107	H79155	Hs.93361	ESTs
	126154	AI004105	Hs.190488	Homo sapiens, Similar to nuclear localiz
	126199	AI000492	Hs.125829	ESTs
	126207	W77936	Hs.83583	actin related protein 2/3 complex, subun
65	126227	N27236	Hs.269034	ESTs
	126269	AA830432	Hs.44701	ESTs
	126373	F11606	Hs.6079	B cell RAG associated protein
	126378	AA347842		gb:yy62a11.s1 Soares_multiple_sclerosis_
70	126383	AA885594	Hs.6298	KIAA1151 protein
	126403	N73388	Hs.125976	ESTs, Weakly similar to S71949 metallopr
	126525	AA884833	Hs.166432	ESTs
	126527	AA548559	Hs.103853	hypothetical protein FLJ20043
	126566	W67245	Hs.103142	ESTs
	126583	W92895	Hs.279746	vanilloid receptor-like protein 1
75	126610	AA460338	Hs.191391	ESTs
	126622	AA699443	Hs.193213	ESTs
	126633	AA206993	Hs.315367	Homo sapiens, Similar to hypothetical pr
	126727	AA037230	Hs.135084	cystatin C (amyloid angiopathy and cereb
	126762	AA064671		gb:zm13b04.s1 Stratagene pancreas (93720
80	126775	S86382	Hs.957	putative opioid receptor, neuromedin K (
	126783	AA126047		gb:zn09d10.s1 Stratagene hNT neuron (937
	126882	AA761143	Hs.250581	SWI/SNF related, matrix associated, acti
	126945	R51877	Hs.25845	ESTs
	126968	AI311457	Hs.99472	ESTs

5	127070	AA641812	Hs.190037	ESTs
	127087	AA380418	Hs.88012	SHP2 interacting transmembrane adaptor
	127187	AA297138	Hs.207422	ESTs, Weakly similar to S71949 metallopro
	127215	AI246377	Hs.127675	ceroid-lipofuscinosis, neuronal 8 (epile
	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of
10	127278	AA342715		gb:EST48309 Fetal spleen Homo sapiens cD
	127299	AA360710	Hs.158480	ESTs
	127325	AA393073	Hs.126099	ESTs
	127347	AA428350	Hs.58389	hypothetical protein MGC4090
	127401	AA921944	Hs.127639	ESTs
15	127420	AA699582	Hs.82171	Homo sapiens clone 191B7 placenta expres
	127438	AI224421	Hs.77100	general transcription factor IIe, polype
	127441	AA835684	Hs.287601	Homo sapiens cDNA FLJ13830 fis, clone TH
	127449	AI421866	Hs.75722	ribophorin II
	127493	AA808081	Hs.291701	ESTs
20	127505	AA594244	Hs.292245	ESTs, Weakly similar to ALU1_HUMAN ALU S
	127620	AI025699	Hs.116200	ESTs
	127623	AA773234	Hs.271877	angiopoietin-like 2
	127633	AI339609	Hs.268538	potassium voltage-gated channel, Isk-rel
	127701	AA935466		gb:zf84c06.s1 Soares_pineal_gland_N3HPG
25	127713	AA688322	Hs.150683	ESTs
	127722	AA700444	Hs.189186	ESTs, Weakly similar to ALUD_HUMAN !!!!
	127733	AA704680	Hs.189005	ESTs
	127816	AA743646	Hs.120604	ESTs, Weakly similar to YA02_HUMAN HYPOT
	127966	AI493406	Hs.292514	ESTs
30	127973	AI336794	Hs.129117	ESTs
	127989	AA909267	Hs.132413	ESTs
	127997	AI281549	Hs.311054	Homo sapiens mRNA full length insert cDN
	128016	N92597	Hs.82689	tumor rejection antigen (gp96) 1
	128037	AA868394	Hs.181129	ESTs, Weakly similar to S18968 cyritesti
35	128053	T65605	Hs.65377	ESTs, Moderately similar to KIAA1399 pro
	128066	AA884838	Hs.189171	ESTs
	128071	AA889398	Hs.189241	ESTs
	128091	AA904559	Hs.129329	ESTs
	128113	AI341423	Hs.288433	neurotrimin
40	128145	AI498467	Hs.166669	solute carrier family 4, sodium bicarbon
	128167	AA932961	Hs.85752	uncharacterized hematopoietic stem/proge
	128195	AI143866	Hs.127778	ESTs
	128265	T95851	Hs.17691	ESTs
	128283	AI076570	Hs.134053	ESTs
45	128309	AI457235	Hs.166479	ESTs
	128313	AI051250	Hs.157775	ESTs
	128346	AI088907	Hs.160189	ESTs
	128359	AI096526	Hs.270244	ESTs, Weakly similar to I38022 hypotheti
	128369	F12681	Hs.30445	Homo sapiens cDNA FLJ14687 fis, clone NT
50	128371	H12876	Hs.283078	hOAT4
	128421	T77876	Hs.268589	ESTs
	128453	X02761	Hs.287820	fibronectin 1
	128496	T83496	Hs.32944	inositol polyphosphate-4-phosphatase, ty
	128514	H84261	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA,
55	128551	H09058	Hs.278398	KIAA1117 protein
	128683	AA316862	Hs.9605	cleavage and polyadenylation specific fa
	128731	AF005271	Hs.104555	neuropeptide FF-amide peptide precursor
	128843	AA234141	Hs.275675	katanin p80 (WD40-containing) subunit B
	128988	AA411040	Hs.294140	ESTs
60	129016	W84524	Hs.184194	transmembrane 4 superfamily member 5
	129021	AA426406	Hs.173081	KIAA0530 protein
	129095	L12350	Hs.108623	thrombospondin 2
	129171	AA234048	Hs.7753	calumenin
	129188	M30257	Hs.109225	vascular cell adhesion molecule 1
65	129410	U25987	Hs.272620	pregnancy specific beta-1-glycoprotein 9
	129467	AA410311	Hs.44208	hypothetical protein FLJ23153
	129518	AA369807	Hs.112238	ESTs
	129534	R73640	Hs.11260	hypothetical protein FLJ11264
	129632	L27213	Hs.11176	solute carrier family 4, anion exchanger
70	129691	X06700	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl
	129881	AA458952	Hs.181406	hypothetical protein FLJ22301
	129930	N30316		gb:yw75b05.s1 Soares_placenta_8to9weeks_
	130049	V01515	Hs.1460	glucagon
	130171	AA454177	Hs.245257	ESTs, Weakly similar to A46010 X-linked
75	130411	AA505009	Hs.169910	KIAA0173 gene product
	130479	R44163	Hs.12457	hypothetical protein FLJ10814
	130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
	130521	U92971	Hs.194351	coagulation factor II (thrombin) recepto
	130645	AA020942	Hs.17200	STAM-like protein containing SH3 and ITA
80	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)
	130656	Z20481	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro
	130889	D57622	Hs.20985	sin3-associated polypeptide, 30kD
	131064	AA598441	Hs.22583	DKFZP434K2235 protein
	131070	F13694	Hs.22607	ESTs
	131189	L16782	Hs.240	M-phase phosphoprotein 1
	131318	X51699	Hs.2558	bone gamma-carboxyglutamate (gla) protei
	131506	W47579	Hs.5801	KIAA1194 protein

	131551	AA127867	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H
	131563	C20547	Hs.302810	Novel human gene mapping to chromosome 20
	131830	U33054	Hs.32959	G protein-coupled receptor kinase 2 (Dro
5	131879	AA017161	Hs.33792	ESTs
	132017	W67251	Hs.267659	vav 3 oncogene
	132025	U58516	Hs.3745	milk fat globule-EGF factor 8 protein
	132096	AA131410	Hs.3964	Homo sapiens clone 24877 mRNA sequence
10	132159	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi
	132164	U84573	Hs.41270	procollagen-llysine, 2-oxoglutarate 5-dio
	132180	AA405569	Hs.418	fibroblast activation protein, alpha
	132223	R77451	Hs.4245	chromosome 11 hypothetical protein ORF3
	132238	AA453446	Hs.42673	ESTs
	132406	F09979	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f
15	132945	N40559	Hs.6129	ATP-binding cassette, sub-family B (MDR/
	133185	AA481404	Hs.6686	hypothetical protein DKFZp564O1664
	133193	C14015	Hs.303075	EST
	133370	AA156897	Hs.72157	DKFZP564I1922 protein
	133406	U22172	Hs.179697	Human DNA damage repair and recombatio
20	133409	U65918	Hs.73078	deleted in azoospermia-like
	133591	T82292	Hs.75111	protease, serine, 11 (IGF binding)
	133899	X00588	Hs.77432	epidermal growth factor receptor (avian
	134137	F10045	Hs.79347	KIAA0211 gene product
	134339	AA478971	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
25	134421	AA122386	Hs.82985	collagen, type V, alpha 2
	134462	U11037	Hs.181300	sel-1 (suppressor of lin-12, C.elegans)-
	134515	C20737	Hs.84469	ESTs
	134527	T40835	Hs.322978	EST
	134711	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro
30	134824	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor
	134854	J03464	Hs.179573	collagen, type I, alpha 2
	134921	W60186	Hs.125511	Homo sapiens mRNA; cDNA DKFZp434P1530 (f
	135003	H42527	Hs.26102	trichorhinophalangeal syndrome 1
	135210	W90522	Hs.93589	hypothetical protein DKFZp564B1162
35	135348	AA442054	Hs.268177	phospholipase C, gamma 1 (formerly subty
	100547	HG2149-HT2219		gb:Homo sapiens mucin (mucin) mRNA, part
	100572	HG2271-HT2367	Hs.73995	filaggrin
	100687	HG3115-HT3291		gb:Human Golli-mbp gene, exon 2.
	100695	HG315-HT315	Hs.272620	pregnancy specific beta-1-glycoprotein 9
40	101447	M21305		gb:Human alpha satellite and satellite 3
	102329	U35407	Hs.158084	peroxisome receptor 1
	102892	X05232	Hs.83326	matrix metalloproteinase 3 (stromelysin
	103036	X54925	Hs.83169	matrix metalloproteinase 1 (interstitial
	103206	X72755	Hs.77367	monokine induced by gamma interferon
45	103260	X78416	Hs.3155	casein, alpha
	103751	AA082824		gb:zo08b08.s1 Stratagene neuroepithelium
	104113	AA427510	Hs.181202	hypothetical protein FLJ10038
	104316	D61871	Hs.330821	EST
	104453	M19169	Hs.123114	cystatin SN
50	104668	AA007312		gb:EST376458 MAGE resequences, MAGH Homo
	104916	AA056588	Hs.155489	NS1-associated protein 1
	106151	AA424958	Hs.294132	ESTs
	106899	AA490107	Hs.21753	JM5 protein
	107379	U93868	Hs.333861	polymerase (RNA) III (DNA directed) (32k
55	107412	W26105	Hs.287797	integrin, beta 1 (fibronectin receptor,
	107652	AA010195	Hs.52642	ESTs, Weakly similar to ALUF_HUMAN !!!!
	107754	AA017462	Hs.269244	ESTs
	107897	AA026240		gb:nc077a05.s1 NCI_CGAP_AA1 Homo sapiens
	108238	AA059473	Hs.66783	EST
60	108497	AA083070		gb:zm85a05.r1 Stratagene ovarian cancer
	108710	AA121960		gb:zm24g09.r1 Stratagene pancreas (93720
	109012	AA156576	Hs.5947	mel transforming oncogene (derived from
	109043	AA159605	Hs.72580	ESTs
	109560	F01778	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H
65	110572	H60523	Hs.37844	EST
	110687	H93005	Hs.177311	ESTs
	111418	R01084	Hs.19081	ESTs
	111507	R07728	Hs.268668	ESTs
	111644	R16539	Hs.223649	EST, Moderately similar to Cd-7 Metallo
	111919	R39926	Hs.21031	ESTs, Weakly similar to I78885 serine/th
70	112102	R44840	Hs.326475	ESTs
	112229	R50938	Hs.24949	ESTs
	112309	R55021		gb:yj76d05.s1 Soares breast 2NbHBst Homo
	112368	R59371	Hs.26653	ESTs
75	112397	R60822	Hs.26805	ESTs, Weakly similar to putative p150 [
	112532	R69824	Hs.28313	ESTs
	112858	T02963	Hs.4454	ESTs
	113170	T54342	Hs.270373	ESTs, Weakly similar to S65657 alpha-1C
	113321	T70580	Hs.13759	RAB3A interacting protein (rabin3)-like
80	113404	T82323	Hs.70337	immunoglobulin superfamily, member 4
	113420	T83964	Hs.15400	ESTs, Weakly similar to S65824 reverse
	113613	T93337	Hs.17167	ESTs, Highly similar to LRR FLI-I intera
	113663	T95909		gb:ye47g07.s1 Soares fetal liver spleen
	113790	W33178	Hs.26912	ESTs

	113889	W72720		gb:zd61c03.s1 Soares_fetal_heart_NbHH19W
	114016	W90671	Hs.11087	ESTs
	114251	Z39898	Hs.21948	ESTs
5	115187	AA261805	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,
	115722	AA417297	Hs.59609	ESTs
	115775	AA424030	Hs.46627	ESTs
	116380	AA598455	Hs.66817	ESTs
	116551	D20458	Hs.229071	EST
10	117009	H85422	Hs.108556	ESTs
	117329	N23680	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone H
	117523	N32626	Hs.145532	ESTs, Weakly similar to FV1 MOUSE FRIEND
	118387	N64579		gb:yz51d11.s1 Morton Fetal Cochlea Homo
	118456	N66580		gb:yy69f01.s1 Soares_multiple_sclerosis_
15	118741	N74042	Hs.50421	KIAA0203 gene product
	118771	N74690	Hs.50547	ESTs
	119075	R36451	Hs.287820	fibronectin 1
	119217	R95778	Hs.237309	EST
	119306	T26914	Hs.132785	EAP30 subunit of ELL complex
20	119347	T64349		gb:yc10d08.s1 Stratagene lung (937210) H
	120006	W90108	Hs.10848	KIAA0187 gene product
	120441	AA243588	Hs.190035	ESTs
	120651	AA287286	Hs.99657	ESTs
	120811	AA346854	Hs.52788	fragile X mental retardation, autosomal
25	121186	AA400156	Hs.339808	hypothetical protein FLJ10120
	121599	AA416770	Hs.98255	EST
	122146	AA435584	Hs.250173	hypothetical protein FLJ13158
	122261	AA436830	Hs.98902	ESTs
	122352	AA443725	Hs.159677	ESTs
30	122433	AA447417	Hs.285491	ESTs
	122489	AA448342	Hs.178551	ribosomal protein L8
	122554	AA451886	Hs.154654	cytochrome P450, subfamily I (dioxin-ind
	122857	AA463879	Hs.99606	EST, Weakly similar to STK2_HUMAN SERIN
	122889	AA465704	Hs.287687	Homo sapiens cDNA: FLJ21960 fis, clone H
35	123399	AA521274	Hs.105516	EST
	123662	AA609385	Hs.112703	ESTs, Moderately similar to AF171102 1 r
	123762	AA610013		gb:af18d04.s1 Soares_testis_NHT Homo sap
	123792	AA620333	Hs.112857	ESTs
	123900	AA621223	Hs.112953	EST
40	123981	C20797	Hs.95481	ESTs
	124126	H18517	Hs.164568	fibroblast growth factor 7 (keratinocyte
	124404	N31998	Hs.164256	hypothetical protein FLJ20657
	124557	N66025	Hs.141604	ESTs, Moderately similar to ALU1_HUMAN A
	124703	R07294	Hs.300076	solute carrier family 22 (organic cation
45	124867	R68971	Hs.168500	ESTs
	125092	T92544	Hs.137548	CD84 antigen (leukocyte antigen)
	125111	T96240	Hs.178658	RAD23 (S. cerevisiae) homolog B
	125331	AI422996	Hs.161378	ESTs
	125349	T87826	Hs.164480	ESTs, Weakly similar to T50609 hypotheti
50	125426	R43963	Hs.184029	hypothetical protein DKFZp761A052
	125436	R64472	Hs.16131	hypothetical protein FLJ12876
	125465	AI375276	Hs.158732	ESTs
	125515	R13353		gb:yf76c04.r1 Soares infant brain 1N1B H
	125626	AI038854	Hs.180789	S164 protein
55	125656	AA040118	Hs.78687	neutral sphingomyelinase (N-SMase) activ
	125743	H17151		gb:ym37a05.r1 Soares infant brain 1N1B H
	125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass
	125760	W03020	Hs.40300	calpain 3, (p94)
	125804	R79519	Hs.16899	ESTs
60	125967	AI341206	Hs.173770	ESTs
	126068	AI190171	Hs.144413	ESTs
	126081	AI346024	Hs.227835	KIAA1049 protein
	126150	AA018427	Hs.64616	chromosome 12 open reading frame 3
	126171	AA704771	Hs.191942	ESTs
65	126198	AI69355	Hs.127310	ESTs
	126224	AI097280	Hs.44493	Human DNA sequence from clone 462023 on
	126289	AA194603	Hs.73451	ESTs, Weakly similar to S55024 nebulin,
	126343	AA628890	Hs.158701	ESTs
	126406	AA034096		gb:yy41h02.r1 Soares fetal liver spleen
70	126419	AA451775	Hs.129064	Homo sapiens chromosome 19, cosmid F2216
	126479	T78141	Hs.12285	ESTs, Weakly similar to I55214 salivary
	126500	AA885306	Hs.184376	synaptosomal-associated protein, 23kD
	126520	AA292988	Hs.72071	hypothetical protein FLJ20038
	126701	AA515212	Hs.339670	ESTs, Weakly similar to AF147790 1 trans
75	126718	AA322718	Hs.309435	ESTs, Weakly similar to KIAA0927 protein
	126739	AI160709	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE
	126745	AA057506		gb:zf49g04.r1 Soares retina N2b4HR Homo
	126846	AA663527	Hs.116910	ESTs
	126872	AA136653		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su
80	126952	AA195575	Hs.85962	hyaluronan synthase 3
	127036	AI468598	Hs.276916	nuclear receptor subfamily 1, group D, m
	127039	AA233366	Hs.168103	prp28, U5 snRNP 100 kd protein
	127067	F06732		gb:HSC1JA051 normalized infant brain cDN
	127083	Z44079	Hs.91608	otoferlin



5	127116	AA278492	Hs.288304	Homo sapiens cDNA FLJ11529 fis, clone HE
	127282	AA347547	Hs.185780	ESTs
	127349	AA412108	Hs.269350	ESTs
	127352	AA416577	Hs.189105	ESTs, Weakly similar to NBR13 [H.sapiens
	127482	AI337294	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I
	127543	AI364367	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO
	127553	AA282433		gb:aa63g02.r1 NCL_CGAP_GCB1 Homo sapiens
10	127556	AA679831	Hs.190228	ESTs
	127859	AA806837	Hs.291559	ESTs
	127993	AA847856	Hs.124565	ESTs
	128277	AI018275	Hs.269791	ESTs
	128285	AA634569	Hs.13351	LanC (bacterial lantibiotic synthetase c
	128317	AI051960	Hs.303754	ESTs
15	128334	AI080130	Hs.134207	ESTs
	128428	AI185718	Hs.143900	ESTs
	128582	U22963	Hs.101840	major histocompatibility complex, class
	128592	AA470056	Hs.113994	Homo sapiens cDNA FLJ20796 fis, clone CO
	128751	AA442274	Hs.183176	ESTs
20	129105	AA224351	Hs.108681	Homo sapiens brain tumor associated prot
	129161	N27334	Hs.181780	hypothetical protein FLJ20241
	129246	N99174	Hs.206063	ESTs
	129361	X64229	Hs.110713	DEK oncogene (DNA binding)
	129577	AA424952	Hs.82906	CDC20 (cell division cycle 20, S. cerevi
25	129600	N78980	Hs.271599	hypothetical protein MGC10500
	129989	AF005887	Hs.247433	activating transcription factor 6
	130024	U15197	Hs.113271	ABO blood group (transferase A, alpha 1-
	130292	U70136	Hs.218791	proteoglycan 4, (megakaryocyte stimulat
	130589	AA234308	Hs.16441	DKFZP434H204 protein
30	130736	T99385		gb:ow89g07.s1 Soares_fetal_liver_spleen_
	131238	R82327	Hs.24625	ESTs
	131378	AA463886	Hs.203910	small glutamine-rich tetrairicopeptide r
	131601	M31165	Hs.29352	tumor necrosis factor, alpha-induced pro
	131605	AA256220	Hs.29383	Homo sapiens mRNA; cDNA DKFZp434E2321 (f
35	131676	C20785	Hs.30514	ESTs
	131861	D11925	Hs.184245	KIAA0929 protein Msx2 interacting nuclea
	131873	H39997	Hs.166852	KIAA1683 protein
	132023	F01927	Hs.3743	matrix metalloproteinase 24 (membrane-in
	132273	AA489716	Hs.43658	DKFZP586L151 protein
40	132770	AA425647	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL
	132859	D20925	Hs.69235	transportin-SR
	133052	R40166	Hs.106826	KIAA1696 protein
	133373	S72487	Hs.73946	endothelial cell growth factor 1 (platelet
	133446	M25322	Hs.73800	selectin P (granule membrane protein 140
45	134693	N70361	Hs.8854	Human transcription unit PVT gene, exons
	134733	U03644	Hs.89421	CBF1 interacting corepressor
	134965	J05480	Hs.272458	protein phosphatase 3 (formerly 2B), cat
	135327	AA477989	Hs.98800	ESTs
	135377	C21382	Hs.99766	Homo sapiens mRNA; cDNA DKFZp564J0323 (f
50	135398	AA194075	Hs.287270	ret proto-oncogene (multiple endocrine

TABLE 44B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

60	Pkey	CAT number	Accessions
65	108497	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204 AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070 AA102076 AA115163 AA074198 AA134725 AA113689 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209 AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053 AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA065051 AA079143 AA071110 AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200 AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929
70	107897	91776_1	AA604872 AA026240
	130736	611414_1	AI168326 T99385
	108710	133560_1	AA121959 AA121960
	100943	45976_1	AW864944 L07517 AW869606
75	124575	1666649_1	N68168 N69188 N90450
	125439	465590_1	AW835829 AA826305 R01759
	117697	499877_1	N40976 AA902795
	125515	181_2	R13353 R13890 H11359
	118387	65081_5	N64579
80	126292	327512_1	AA491328 N42312
	102798	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
	126378	244444_1	N58924 AA347842
	125743	5025_5	H17151 H11956
	126406	95703_1	N76683 AA034096 AA034082

5	127067	1534978_1	F06732 Z43705
	119243	1774795_1	T12603 T12604
	111443	31528_18	AF072503 AF208161 AA613238 H12439 N76991 D78692 BE019603 AA776439 R37932 T93615 AF072508 R00744 R01948 R68685
			AI128496 AA865193 AI797629 H13302 AF072506 NM_014590 AF072505 R00743 T93661 T39519 R68740 H13097 N58614 N77302
			H01372 N41878 H04136 AA426511 AW971553 AW900030 R76136 T52094 AI598135 AA781423 R76086 R77278 AI393478 AA837267
			AI570707 R01901 R27412 N53177 AI379210 AI128526 AA250958 R79323 R27389 H01325 N55091 T69704 AA868777 T47345 R27591
			AA860368 AA729556 H04137 T87297 C17420 AA293243 AA419144
	127278	240640_1	AA342715 AA367634
10	103751	118557_1	AA131367 AA082824
	126636	80804_1	AA057531 AA001527
	127331	379388_1	F20186 AA622352
	127357	288073_1	AA424107 AA452788
	126745	104479_1	AA047854 AA057506 AA053841
	126762	110350_1	AA064613 AA064671
15	126783	113388_1	AA083531 AA126047 AA074915 AA148649
	112309	1576900_1	R55021 H26613
	126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363
20	120284	158963_1	AA179656 AA182626 AA182603
	111829	46636_1	AF074991 R36070
	104668	82752_1	AW964385 AA007312 AI081711 AA318253 AW891655 T99192
	127553	202308_2	AA505046 AW969109 AA505047
	120379	34624_3	AL042725 BE063316 AW975610 AA457591 BE062092 AI655202 AA714296 AI267264 AI075321 AA223286 AA071122 AA227849
25			AA216700 AI696002 AA101867 AA099426 AA135997 AL041698 T02815 T51824 AA207189 T59230 T51868 AA663341 BE165757
			AW818104 AW392886 AA584918 AA099408 AW856396 AW861859 AA053045
	127701	405284_1	AA679064 AA935466
	128410	288073_1	AA424107 AA452788
	114625	111686_1	AA081507 AA070071 AA070840 AA084362
	109026	150431_1	AA157811 AA836869
30	108409	113869_1	AA075631 AA075578
	100687	tigr_HT3291	L18862
	109326	genbank_AA210719	AA210719
	123762	genbank_AA610013	AA610013
35	116548	genbank_D20433	D20433
	125145	entrez_W38001	W38001
	125153	entrez_W38294	W38294
	116995	genbank_H83928	H83928
	102649	genbank_U68133	U68133
40	118456	genbank_N66580	N66580
	102860	entrez_X00368	X00368
	120715	genbank_AA292700	AA292700
	120749	genbank_AA303235	AA303235
	113663	genbank_T95909	T95909
45	113889	genbank_W72720	W72720
	108258	genbank_AA063269	AA063269
	101046	entrez_K01160	K01160
	129990	genbank_N30316	N30316
	122746	genbank_AA458791	AA458791
50	124046	genbank_F10243	F10243
	108436	genbank_AA078801	AA078801
	124197	genbank_H52921	H52921
	101447	entrez_M21305	M21305
	108852	genbank_AA133131	AA133131
	101697	entrez_M64358	M64358
55	108931	genbank_AA147186	AA147186
	101909	entrez_S69265	S69265
	117816	genbank_N48872	N48872
	119154	genbank_R61293	R61293
60	119241	genbank_T12559	T12559
	119310	genbank_T40427	T40427
	119347	genbank_T64349	T64349
	119529	entrez_W38053	W38053
	112467	genbank_R65706	R65706
65	112533	genbank_R69886	R69886
	112588	genbank_R77302	R77302
	121082	genbank_AA398722	AA398722
	123305	genbank_AA496133	AA496133
	123328	genbank_AA496968	AA496968
70	100547	tigr_HT2219	M57417
	123490	genbank_AA599723	AA599723

75 TABLE 45A: 90 GENES DOWN-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

Table 45A lists about 90 genes down-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip.

80 Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title

	Pkey	ExAccn	UnigenelD	Unigene Title
5	100137	D13627	Hs.15071	chaperonin containing TCP1, subunit 8 (t
	100240	D31767	Hs.75416	DAZ associated protein 2
	100289	D45248	Hs.179774	proteasome (prosome, macropain) activato
	100658	HG2855-HT2995	Hs.75452	heat shock 70kD protein 2
	100763	HG3597-HT3800		gb:Human major histocompatibility comple
10	100779	HG3731-HT4001	Hs.302063	immunoglobulin heavy constant mu
	101091	L06132	Hs.149155	voltage-dependent anion channel 1
	101155	L13972	Hs.301698	sialyltransferase 4A (beta-galactosidase
	102223	U24685		gb:Homo sapiens immunoglobulin heavy cha
	102282	U31383	Hs.79126	guanine nucleotide binding protein 10
15	102378	U40369	Hs.28491	spermidine/spermine N1-acetyltransferase
	102386	U40998	Hs.81728	unc119 (C.elegans) homolog
	102389	U41371	Hs.75916	splicing factor 3b, subunit 2, 145kD
	102480	U50327	Hs.1432	protein kinase C substrate 80K-H
	102566	U59752	Hs.303091	pleckstrin homology, Sec7 and coiled/coi
20	102605	U64444	Hs.181369	ubiquitin fusion degradation 1-like
	102693	U73824	Hs.183684	eukaryotic translation initiation factor
	102710	U77827	Hs.113207	G protein-coupled receptor 30
	102920	X12451	Hs.78056	cathepsin L
	102929	X13238	Hs.74649	cytochrome c oxidase subunit VIc
25	103166	X67951	Hs.180909	peroxiredoxin 1
	103283	X80199	Hs.83422	MLN51 protein
	103463	Y00281	Hs.2280	ribophorin I
	103835	AA172215	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT
	104796	AA029368	Hs.33026	hypothetical protein PP2447
30	105714	AA291429	Hs.12211	GDP-fucose transporter 1
	105927	AA402968	Hs.332040	hypothetical protein MGC13010
	105945	AA404512	Hs.14453	interferon consensus sequence binding pr
	106001	AA410986	Hs.8963	Homo sapiens mRNA full length insert cDN
	106027	AA412119	Hs.234799	breakpoint cluster region
35	106227	AA429262	Hs.19613	ESTs
	106295	AA435664	Hs.8583	similar to APOBEC1
	106417	AA448008	Hs.261828	G protein-coupled receptor kinase 7
	107391	W02877	Hs.284294	Breakpoint cluster region protein, uteri
	109107	AA169180	Hs.269280	ESTs
40	109885	F09325	Hs.28102	ESTs
	110021	H11252	Hs.31037	ESTs
	110738	H99370	Hs.139648	kinesin family member 1C
	112746	R93237	Hs.74170	metallothionein 1E (functional)
	113059	T26925	Hs.172684	vesicle-associated membrane protein 8 (e
45	113822	W47350	Hs.17466	retinoic acid receptor responder (tazaro
	113859	W67225	Hs.13273	KIAA0592 protein
	113909	W78127	Hs.9956	hypothetical protein FLJ20259
	114693	AA122158	Hs.300683	Homo sapiens cDNA FLJ12825 fis, clone NT
	115399	AA283182	Hs.92023	core histone macroH2A2.2
50	116606	D80217	Hs.259842	protein kinase, AMP-activated, gamma 2 n
	116633	F02702	Hs.268726	ESTs, Highly similar to ZN91_HUMAN ZINC
	119254	T15837	Hs.279009	matrix Gla protein
	119493	W35384	Hs.50477	RAB27A, member RAS oncogene family
	120108	W95696	Hs.16803	LUC7 (S. cerevisiae)-like
55	120886	AA365566	Hs.301342	hypothetical protein MGC4342
	120953	AA397911	Hs.97499	ESTs, Weakly similar to unknown [H.sapie
	121303	AA402441	Hs.303197	B-cell CLL/lymphoma 7C
	121547	AA412448	Hs.104777	ESTs
	123495	AA599850	Hs.106747	serine carboxypeptidase 1 precursor prot
60	123608	AA609144	Hs.112851	ESTs
	123749	AA609949	Hs.112790	EST
	124763	R39610	Hs.76288	calpain 2, (mII) large subunit
	125366	H60192	Hs.76853	Homo sapiens mRNA; cDNA DKFZp434N1728 (f
	125657	AA481719	Hs.150540	Homo sapiens, clone IMAGE:3954961, mRNA,
65	125670	AI432621	Hs.82685	CD47 antigen (Rh-related antigen, integr
	125882	H45538	Hs.101448	metastasis associated 1
	126541	AA204913	Hs.7854	zinc/iron regulated transporter-like
	126715	R70160	Hs.241552	KIAA0268 protein
	126817	AA478642	Hs.291623	ESTs, Weakly similar to unnamed protein
70	127112	AI143906	Hs.125103	ESTs
	127273	AA335263	Hs.144950	ESTs
	127615	AA718919		gb:zv88a04.s1 Soares_NhHMPu_S1 Homo sapi
	127635	AA766903	Hs.116346	ESTs, Highly similar to A46297 beta-1,6-
	128528	R39234	Hs.251699	ESTs, Weakly similar to IDN4-GGTR14 [H.s
75	129398	AA437374	Hs.234573	Homo sapiens mRNA for TL132
	129621	AA489459	Hs.301005	purine-rich element binding protein B
	131037	AA256171	Hs.22391	chromosome 20open reading frame 3
	131328	V01512	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131631	AA486868	Hs.29802	slit (Drosophila) homolog 2
80	132079	H67964	Hs.38694	ESTs
	132455	T15774	Hs.4892	Homo sapiens clone 24841 mRNA sequence
	132582	AA318547	Hs.278712	eukaryotic translation initiation factor
	132610	AA443114	Hs.5326	amino acid system N transporter 2; porcu
	132755	AA609201	Hs.182635	ESTs
	133192	AA393804	Hs.67052	vacuolar protein sorting 26 (yeast homol

133437	R57419	Hs.7370	phosphatidylinositol transfer protein, b
133449	AA094989	Hs.7381	voltage-dependent anion channel 3
133649	AA479139	Hs.75393	acid phosphatase 1, soluble
133814	M33882	Hs.76391	myxovirus (influenza) resistance 1, homo
134378	AF006088	Hs.82425	actin related protein 2/3 complex, subun
134419	L08044	Hs.82961	trefoil factor 3 (intestinal)
134548	U41515	Hs.333495	Deleted in split-hand/split-foot 1 regio
134776	J05582	Hs.89603	mucin 1, transmembrane
135032	AA243497	Hs.173685	hypothetical protein FLJ12619

TABLE 45B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT number	Accessions
127615	380951_1	AA626215 AA718919
100763	tigr_HT3800	X12432 Y08693
102223	221_265	AF013616 AA300945 X65907 AF062264 AF062250 Z47228 Z75389 Z75374 AF062152 AF062146 Z75398 X64153 AF062101 AF062218 S59161 Z75392 AF062196 AF062192 X65904 U24685 AF062181 Z47241 Z75376 AF062217 Z47234 X64152 AF062187 AF062173 AF062158 Z47229 M74018 M74021 X54441 M84512 L29115 M84508 Z75384 AJ244983 AJ245240 AJ245030 AJ245042 M26998 L03635 S64473 AJ244997 AJ245013 AJ279535 U89766 AF174049 AF174085 AF174086 U97246 AJ245011 AJ245017 AJ245028 AJ245041 AJ245051 AJ245065 AJ245236 U22391 Z49143 Z74665 AF087428 S66098 Z70650 AJ244929 AF006528 AF022004 AF021983 U00556 AJ245035 Z70617 Z70605 AJ245052 AJ245046 AF087424 AF174054 S67110 U21257 U21267 U21268 Z35492 U71103 AF021991 L23518 Z70644 AJ245036 Z49141 AF089001 Z74695 Z46304 AF021957 AF021990 AF022005 AF052527 AF021947 Z70604 Z70610 AF062104 Z49135 X64235 Z46341 Z46305 Z46307 Z49136 AJ244996 Z46342 AJ244931 AJ244935 AJ244937 AJ244938 L12192 AJ244939 AJ244940 AJ244941 Z46308 AJ244962 AF062234 AJ244973 AJ244984 AJ244985 AF174088 AJ279519 AJ279521 AJ279526 AJ245009 AJ279531 AJ245008 AJ244994 AJ244991 AJ244990 AJ244988 AJ244987 X87440 AJ245238 Z70625 Z70626 Z70641 Z70640 Z70643 AJ244975 Z70616 Z70637 AJ244982 AJ244967 AJ239377 AJ245057 AF021948 AF107239 AJ245040 L34163 AF062231 Z70627 AF062113 AF006527 AF174041 AJ279537 Z70642 U00497 Z70639 AJ245054 AJ244960 AJ279524 AJ244943 AJ249631 AF035041 AJ245039 AJ245050 AF107233 AJ239362 AJ244969 Z46278 Z46290 Z46274 Z46281 AJ239351 L25293 AJ244944 AJ244951 Z46280 Z46270 AJ245043 Z46276 AF107241 Z46271 Z46277 AJ245034 Z46273 AJ244992 Z46282 Z70638 Z46275 AJ244972 Z46272 Z46279 Z46269 AF087422 M74469 X64159 AF103243 X64156 AJ244942 Z46316 AJ222547 Z46322 Z46324 Z46326 Z46327 AJ222556 Z46329 Z46330 Z46302 AJ222561 AJ222549 AJ222568 AJ222570 AJ222571 Z49139 AJ222578 AJ222562 AJ222577 Z46323 AJ222576 AJ222566 Z46315 AJ222557 AJ222564 AJ222559 AJ222573 AJ222575 Z46318 AJ222548 Z46319 AJ222552 AJ222550 AJ222567 AJ222558 AJ222563 Z46317 X87438 AJ222555 AJ240581 AF103161 AJ240580 AJ240594 Y17929 AJ240553 AJ240573 AJ240558 AJ240555 Y17927 Y17949 AJ240561 Y17948 Y17933 Y17947 Y17944 Y17928 Y17931 Y17934 AJ240595 Y17943 Y17932 Y17930 AJ240590 AJ240560 Y17945 AJ240556 S79918 AF103278 AW364256 AF103299 AF103122 X75022 AF004937 Z30557 Z30677 Z30573 Z30576 Z30561 Z30674 Z30562 Z30675 AW403129 AI203192 AW404253 AW237246 AI654630 H61354

Table 46A lists about 714 genes upregulated in esophageal cancer relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 47A lists about 113 genes upregulated in esophageal tumors relative to normal esophagus. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 48A lists about 162 genes downregulated in esophageal tumors relative to normal esophagus. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

TABLE 46A:

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UnigenelD: Unigene number  
Unigene Title: Unigene gene title  
R1: 90th percentile of esophageal tumor AIs divided by the 70th percentile of normal tissue AIs, where the 15th percentile of the normal tissue AIs was subtracted from both the numerator and denominator.

Pkey	ExAccn	UnigenelD	Unigene Title	R1
413808	J00287		Homo sapiens mRNA for caldesmon, 3' UTR	31.57
411243	AB039886	Hs.69319	CA11	26.06
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	25.65
401781			Target Exon	23.23
424098	AF077374	Hs.139322	small proline-rich protein 3	21.35
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	20.37
417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	20.33
401780			NM_005557*:Homo sapiens keratin 16 (foca	18.94
421948	L42583	Hs.334309	keratin 6A	18.13
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	18.01
429538	BE182592	Hs.11261	small proline-rich protein 2A	17.31
400666			NM_002425:Homo sapiens matrix metallopro	17.28
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	16.96

	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	16.35
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	16.22
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	15.64
5	421582	AI910275		trefoil factor 1 (breast cancer, estroge	14.86
	425679	X05997	Hs.159177	lipase, gastric	14.53
	421773	W69233	Hs.112457	ESTs	14.26
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	14.26
10	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	13.93
	444325	AW152618	Hs.16757	ESTs	13.24
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	13.19
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	11.98
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.99
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	10.77
15	422239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	10.31
	446292	AF081497	Hs.279682	Rh type C glycoprotein	9.69
	421978	AJ243662	Hs.110196	NICE-1 protein	9.68
	448811	AI590371	Hs.199460	ESTs	9.38
	453331	AI240665		ESTs	9.37
20	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	9.28
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	9.18
	406687	M31126		matrix metalloproteinase 11 (stromelysin	9.13
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	9.04
	450701	H39960	Hs.288467	hypothetical protein XP_098151	8.77
25	418686	Z36830	Hs.87268	annexin A8	8.76
	421110	AJ250717	Hs.1355	cathepsin E	8.42
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	8.42
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.38
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	8.18
30	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	8.11
	450375	AA009647		a disintegrin and metalloproteinase doma	8.03
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	7.97
	445891	AW391342	Hs.199460	DPCR1 protein	7.95
	437053	AJ077018	Hs.3235	keratin 4	7.93
35	423271	W47225	Hs.126256	interleukin 1, beta	7.80
	409757	NM_001898	Hs.123114	cystatin SN	7.74
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	7.64
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.58
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	7.55
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.26
	448045	AJ297436	Hs.20166	prostate stem cell antigen	7.14
	408243	Y00787	Hs.624	interleukin 8	7.13
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	7.08
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	7.04
45	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	7.04
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.98
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	6.89
	414774	X02419	Hs.77274	plasminogen activator, urokinase	6.85
	439926	AW014875	Hs.137007	ESTs	6.84
50	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.82
	429259	AA420450	Hs.292911	Plakophilin	6.77
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	6.71
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	6.67
	429228	AI553633	Hs.326447	ESTs	6.61
55	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	6.60
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.58
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.55
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	6.54
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.53
60	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.51
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.49
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	6.48
	428471	X57348	Hs.184510	stratifin	6.46
	422511	AJ076442	Hs.117938	collagen, type XVII, alpha 1	6.45
65	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.44
	401747			Homo sapiens keratin 17 (KRT17)	6.42
	421508	NM_004833	Hs.105115	absent in melanoma 2	6.42
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	6.42
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	6.41
70	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	6.38
	422596	AF063611	Hs.118633	2'-5'-oligoadenylate synthetase-like	6.38
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	6.36
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	6.35
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	6.33
75	425415	M13903	Hs.157091	involucrin	6.32
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.30
	415989	AI267700		ESTs	6.23
	406673	M34996	Hs.198253	major histocompatibility complex, class	6.21
	449228	AJ403107	Hs.148590	protein related with psoriasis	6.21
80	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	6.18
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	6.06
	418663	AK001100	Hs.41690	desmocollin 3	6.04
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.98
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	5.96

5	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	5.93
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	5.92
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	5.92
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum corn	5.84
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.76
10	400665			NM_002425:Homo sapiens matrix metallopro	5.75
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.72
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	5.72
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	5.71
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	5.70
15	439606	W79123	Hs.58561	G protein-coupled receptor 87	5.70
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	5.68
	433447	U29195	Hs.3281	neuronal pentraxin II	5.67
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.64
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	5.62
20	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PL	5.60
	428450	NM_014791	Hs.184339	KIAA0175 gene product	5.53
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.50
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	5.48
	447164	AF026941	Hs.17518	Homo sapiens cig 5 mRNA, partial sequence	5.47
25	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	5.44
	439223	AW238299	Hs.250618	UL16 binding protein 2	5.44
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	5.42
	402994			NM_002463*:Homo sapiens myxovirus (infl	5.40
	447333	BE090580	Hs.70704	hypothetical protein dJ616B8.3	5.40
30	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	5.36
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	5.33
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	5.32
	449722	BE280074	Hs.23960	cyclin B1	5.31
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.30
35	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	5.29
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	5.29
	417720	AA205625	Hs.208067	ESTs	5.29
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.28
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	5.27
40	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	5.26
	430280	AA361258	Hs.237868	interleukin 7 receptor	5.25
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	5.24
	402075			ENSP00000251056*:Plasma membrane calcium	5.24
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	5.24
45	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	5.22
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.22
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death domai	5.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	5.20
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epider	5.20
50	406663	U24683	Hs.293441	immunoglobulin heavy constant mu	5.19
	409178	BE393948	Hs.50915	kallikrein 5	5.15
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	5.14
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	5.10
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	5.09
55	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.09
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platel	5.08
	411274	NM_002776	Hs.69423	kallikrein 10	5.07
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	5.03
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	5.03
60	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	5.02
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	5.02
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.02
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	5.00
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	5.00
65	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.97
	405770			NM_002362:Homo sapiens melanoma antigen,	4.96
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.94
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.94
	426866	U02330	Hs.172816	neuregulin 1	4.93
70	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	4.92
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	4.91
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	4.90
	427786	BE407863	Hs.256871	ESTs	4.87
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	4.86
75	444371	BE540274	Hs.239	forkhead box M1	4.86
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	4.85
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	4.84
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	4.83
	409402	AF208234	Hs.695	cystatin B (stefin B)	4.81
80	408202	AA227710	Hs.43658	DKFZP586L151 protein	4.79
	401994			Target Exon	4.77
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.74
	421574	AJ000152	Hs.105924	defensin, beta 2	4.69
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.69
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.68
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.68
	407944	R34008	Hs.239727	desmocollin 2	4.67

	411296	BE207307	Hs.10114	growth suppressor 1	4.65
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	4.65
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.61
5	421335	X99977	Hs.103505	ARS component B	4.60
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.59
	453779	N35187	Hs.43388	28kD interferon responsive protein	4.59
	423575	C18863	Hs.163443	perioestin (OSF-2os)	4.59
	417308	H60720	Hs.81892	KIAA0101 gene product	4.58
10	428651	AF196478	Hs.188401	annexin A10	4.58
	424354	NM_014314	Hs.145612	RNA helicase	4.58
	404996			Target Exon	4.56
	404240			NM_018950:Homo sapiens major histocompat	4.56
	453095	AW295660	Hs.252756	ESTs	4.55
15	410407	X66839	Hs.63287	carbonic anhydrase IX	4.55
	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	4.55
	450685	L15533	Hs.423	pancreatitis-associated protein	4.54
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	4.53
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.52
20	408380	AF123050	Hs.44532	diubiquitin	4.47
	443859	NM_013409	Hs.9914	folistatin	4.46
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	4.44
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakbines	4.44
	421777	BE562088	Hs.108196	HSPC037 protein	4.44
25	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.43
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	4.42
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	4.42
	400419	AF084545		Target	4.42
	452571	W31518	Hs.34665	ESTs	4.41
30	430044	AA464510	Hs.152812	ESTs	4.41
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	4.39
	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	4.39
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	4.39
	453884	AA355925	Hs.36232	KIAA0186 gene product	4.38
35	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	4.37
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	4.37
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	4.37
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	4.36
	448357	N20169	Hs.108923	RAB38, member RAS oncogene family	4.36
40	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.34
	439999	AA115811	Hs.6838	ras homolog gene family, member E	4.34
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.34
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	4.32
	402447			C1000201:gil204416[gb]AA02627.1] (L0519	4.31
45	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	4.28
	432731	R31178	Hs.287820	fibronectin 1	4.27
	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	4.27
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	4.25
	425580	L11144	Hs.1907	galanin	4.25
50	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	4.23
	409433	AA074382	Hs.135255	ESTs	4.23
	430630	AW269920	Hs.2621	cystatin A (stefin A)	4.22
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	4.21
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	4.20
55	432375	BE536069	Hs.2962	S100 calcium-binding protein P	4.20
	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.19
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	4.19
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	4.18
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	4.17
60	410286	AI739159	Hs.61898	DKFZP586N2124 protein	4.16
	448844	AI581519	Hs.177164	ESTs	4.16
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	4.16
	417599	AA204688	Hs.62954	ESTs	4.16
	402992			Target Exon	4.15
65	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoactin)	4.14
	422100	AI096988	Hs.111554	ADP-ribosylation factor-like 7	4.13
	409512	AW979187	Hs.293591	melanoma differentiation associated prot	4.12
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.11
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.10
70	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	4.10
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.10
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	4.09
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.08
	417933	X02308	Hs.82962	thymidylate synthetase	4.08
75	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	4.06
	417678	X06560	Hs.82396	2',5'-oligoadenylate synthetase 1 (40-46	4.06
	451541	BE279383	Hs.26557	plakophilin 3	4.06
	433848	AF095719	Hs.93764	carboxypeptidase A4	4.06
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.04
80	429599	AA806106	Hs.123664	ESTs	4.03
	450823	T81223	Hs.22011	complement-c1q tumor necrosis factor-rel	4.02
	423787	AJ295745	Hs.236204	nuclear pore complex protein	4.00
	431250	BE264649	Hs.251377	taxol resistance associated gene 3	4.00
	416091	AF295370	Hs.283082	defensin, beta 3	3.97

	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	3.97
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.97
	402408			NM_030920*:Homo sapiens hypothetical pro	3.97
5	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.95
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	3.95
	452888	AW955454	Hs.30942	ephrin-B2	3.95
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.95
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.94
10	419693	AA133749	Hs.301350	FXFD domain-containing ion transport reg	3.94
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.94
	422094	AF129535	Hs.272027	F-box only protein 5	3.94
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	3.93
	404286			C6001909:gil704441 dbj BAA18909.1  (D298	3.93
15	423961	D13666	Hs.136348	periostin (OSF-2os)	3.92
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	3.91
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	3.91
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	3.91
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	3.91
20	421904	BE143533	Hs.109309	hypothetical protein FLJ20035	3.90
	441553	AA281219	Hs.121296	ESTs	3.90
	428093	AW594506	Hs.104830	ESTs	3.90
	441020	W79283	Hs.35962	ESTs	3.89
	447078	AW885727	Hs.9914	ESTs	3.89
25	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	3.89
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	3.87
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	3.87
	426059	BE292842	Hs.166120	interferon regulatory factor 7	3.86
	419833	AA251131	Hs.220697	ESTs	3.85
30	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	3.85
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.83
	452203	X57522		transporter 1, ATP-binding cassette, sub	3.83
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	3.83
	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	3.83
35	442599	AF078037	Hs.324051	RelA-associated inhibitor	3.82
	405387			NM_022170*:Homo sapiens Williams-Beuren	3.82
	449539	W80363	Hs.58446	ESTs	3.82
	419079	AW014836	Hs.18844	ESTs	3.81
	410434	AF051152	Hs.63668	toll-like receptor 2	3.81
40	408660	AA525775		ESTs, Moderately similar to PC4259 ferri	3.80
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.80
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.80
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.79
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp58612022 (f	3.79
45	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.78
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.78
	414561	AI064813	Hs.195155	Homo sapiens amino acid transport system	3.78
	411789	AF245505	Hs.72157	Adican	3.77
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	3.77
50	449378	AW664026	Hs.59892	ESTs	3.76
	449961	AW265634	Hs.133100	ESTs	3.76
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.75
	407242	M18728		gb:Human nonspecific crossreacting anti	3.75
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	3.75
55	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	3.75
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	3.74
	422699	BE410590	Hs.119257	ems1 sequence (mammary tumor and squamou	3.74
	441954	AI744935	Hs.8047	Fanconi anemia, complementation group G	3.74
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	3.73
60	422648	D86983	Hs.118893	Melanoma associated gene	3.72
	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam	3.71
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	3.71
	428728	NM_016625	Hs.191381	hypothetical protein	3.71
	400245			Eos Control	3.71
65	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.70
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.70
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	3.70
	440659	AF134160	Hs.7327	claudin 1	3.69
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.67
70	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.67
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	3.66
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	3.65
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	3.63
	414883	AA926960		CDC28 protein kinase 1	3.63
75	428398	AI249368	Hs.98558	ESTs	3.63
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	3.63
	408482	NM_000676	Hs.45743	adenosine A2b receptor	3.63
	404287			C6001909:gil704441 dbj BAA18909.1  (D298	3.63
80	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.61
	414110	BE251752		gb:60112444F1 NIH_MGC_16 Homo sapiens c	3.61
	427857	AL133017	Hs.2210	hypothetical protein FLJ22865	3.61
	419968	X04430	Hs.93913	interleukin 6 (Interferon, beta 2)	3.61
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.60
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	3.60



	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.60
	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, com	3.60
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.59
5	437340	AL353935	Hs.135917	hypothetical protein DKFZp761D1823	3.59
	435793	AB037734	Hs.4993	KIAA1313 protein	3.59
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	3.59
	420247	AA256930	Hs.44680	hypothetical protein FLJ20979	3.58
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	3.57
10	422282	AF019225	Hs.114309	apolipoprotein L	3.57
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.57
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.57
	408015	AW136771	Hs.244349	epidermal differentiation complex protei	3.56
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	3.56
15	449039	AI962602	Hs.74284	hypothetical protein MGC2714	3.56
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.55
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	3.55
	428977	AK001404	Hs.194698	cyclin B2	3.55
	402995			NM_002463*:Homo sapiens myxovirus (infl	3.55
20	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.54
	432917	NM_014125	Hs.241517	PRO0327 protein	3.54
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	3.53
	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	3.52
	438113	AI467908	Hs.8882	ESTs	3.52
25	414420	AA043424	Hs.76095	immediate early response 3	3.51
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.50
	447208	BE315291	Hs.237971	hypothetical protein MGC5627	3.50
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	3.49
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	3.49
30	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	3.49
	429249	X81479	Hs.2375	egf-like module containing, mucin-like,	3.48
	413900	AW409747	Hs.75612	stress-induced-phosphoprotein 1 (Hsp70/H	3.48
	424242	AA337476	Hs.347408	hypothetical protein MGC13102	3.48
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.47
35	446480	NM_014578	Hs.15114	ras homolog gene family, member	3.46
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.46
	428865	BE544095	Hs.164960	BarH-like homeobox 1	3.46
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.46
	450506	NM_004460		fibroblast activation protein, alpha	3.46
40	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	3.45
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.45
	405545			Target Exon	3.45
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.44
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.44
45	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.44
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	3.44
	431228	AB006746	Hs.198282	phospholipid scramblase 1	3.44
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.43
	440502	AI824113	Hs.78281	regulator of G-protein signalling 12	3.43
50	448741	BE614567	Hs.19574	hypothetical protein MGC5469	3.43
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.43
	406646	M33600	Hs.308026	major histocompatibility complex, class	3.42
	413281	AA861271	Hs.222024	transcription factor BMAL2	3.42
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.42
55	430890	X54232	Hs.2699	glypican 1	3.41
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.41
	412429	AV650262	Hs.75765	GRO2 oncogene	3.41
	443211	AI128388	Hs.143655	ESTs	3.41
	422209	AF005210	Hs.113222	chemokine (C-C motif) receptor 8	3.40
60	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	3.39
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	3.39
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.39
	422101	AW404176	Hs.111611	ribosomal protein L27	3.39
	457670	AF119666	Hs.23449	insulin receptor tyrosine kinase substra	3.38
65	437033	AW248364	Hs.5409	RNA polymerase I subunit	3.37
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.37
	417059	AL037672	Hs.81071	extracellular matrix protein 1	3.37
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	3.36
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.36
70	436748	BE159107	Hs.159263	collagen, type VI, alpha 2	3.36
	401797			Target Exon	3.36
	428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	3.35
	421563	NM_006433	Hs.105806	granulysin	3.35
	402294			Target Exon	3.34
75	414024	AA134712	Hs.22410	gb:zm79g08.r1 Stratagene neuroepithelium	3.34
	401961			NM_021626:Homo sapiens serine carboxypep	3.33
	418462	BE001596	Hs.85266	integrin, beta 4	3.33
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	3.33
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.33
80	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.33
	404440			NM_021048:Homo sapiens melanoma antigen,	3.33
	432398	AA307808	Hs.2979	trefoil factor 2 (spasmolytic protein 1)	3.33
	421677	H64092	Hs.38282	ESTs	3.33
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.32

	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.32
	417197	AW994561	Hs.151777	eukaryotic translation initiation factor	3.32
	429669	BE185499	Hs.2471	KIAA0020 gene product	3.32
5	409636	AA305729	Hs.18272	amino acid transporter system A1	3.32
	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3.32
	405386			Target Exon	3.32
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.31
	448275	BE514434	Hs.20830	kinesin-like 2	3.31
10	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.31
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.31
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.31
	422575	AK000546	Hs.118552	hypothetical protein FLJ20539	3.31
	404171			NM_000636*:Homo sapiens superoxide dismu	3.31
	418464	R87580	Hs.144531	gb:ym89h07.r1 Soares adult brain N2b4HB5	3.31
15	425566	AW162943	Hs.250618	UL16 binding protein 2	3.31
	410226	AI831958	Hs.61053	hypothetical protein	3.30
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.30
	443247	BE614387	Hs.333893	c-Myc target JPO1	3.30
20	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	3.30
	428336	AA503115	Hs.183752	microseminoprotein, beta-	3.29
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	3.29
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.28
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.28
25	405778			NM_005361:Homo sapiens melanoma antigen,	3.28
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.27
	421150	AI913562	Hs.189902	ESTs	3.27
	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	3.27
	455813	BE141577		gb:QV2-HT0083-071299-018-a11 HT0083 Homo	3.27
30	426064	BE387014	Hs.166146	Homer, neuronal immediate early gene, 3	3.27
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.27
	458791	BE615453	Hs.346509	dedicator of cyto-kinesis 1	3.27
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	3.26
	429002	AW248439	Hs.2340	junction plakoglobin	3.26
35	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	3.25
	407777	AA161071	Hs.71465	squalene epoxidase	3.25
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	3.25
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	3.24
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	3.24
40	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	3.24
	447519	U46258	Hs.339665	ESTs	3.24
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	3.24
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.24
	423198	M81933	Hs.1634	cell division cycle 25A	3.23
45	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.23
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.22
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.22
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	3.22
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	3.22
50	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.22
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.21
	409197	N54706	Hs.303025	chromosome 11 open reading frame 24	3.21
	412641	M16660	Hs.74335	heat shock 90kD protein 1, beta	3.21
	413436	AF238083	Hs.68061	sphingosine kinase 1	3.21
55	408636	BE294925	Hs.46680	CGI-12 protein	3.21
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	3.21
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.21
	411573	AB029000	Hs.70823	KIAA1077 protein	3.20
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.19
60	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	3.19
	435014	BE560898	Hs.10026	mitochondrial ribosomal protein L17	3.18
	401176			Target Exon	3.18
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.17
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.16
65	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	3.16
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	3.16
	452012	AA307703	Hs.279766	kinesin family member 4A	3.16
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.15
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	3.15
70	433020	AI375726	Hs.279918	hypothetical protein	3.14
	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	3.14
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.14
	420005	AW271106	Hs.133294	ESTs	3.14
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.13
75	412270	AC005262	Hs.73797	guanine nucleotide binding protein (G pr	3.13
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	3.13
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.12
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.11
	431722	AF161528	Hs.268049	hypothetical protein	3.11
80	427239	BE270447	Hs.174070	ubiquitin carrier protein	3.11
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	3.10
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.10
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1	3.10
	418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfam	3.10

	439755	AW748482	Hs.77873	B7 homolog 3	3.10
	404170			NM_000636*:Homo sapiens superoxide dismu	3.09
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	3.09
5	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.09
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	3.08
	421155	H87879	Hs.102267	lysyl oxidase	3.08
	441224	AU076964	Hs.7753	calumenin	3.08
	424326	NM_014479	Hs.145296	disintegrin protease	3.08
10	429413	NM_014058	Hs.201877	DESC1 protein	3.08
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	3.08
	446510	H58306	Hs.15165	retinoic acid induced 14	3.08
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668 protein,	3.07
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	3.07
15	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	3.07
	448853	NM_012204	Hs.22302	general transcription factor IIIc, polyp	3.07
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.07
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	3.06
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	3.06
20	412577	Z22968	Hs.74076	CD163 antigen	3.06
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.06
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	3.05
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	3.05
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	3.04
25	451578	NM_016323	Hs.26663	cyclin-E binding protein 1	3.04
	444726	NM_006147	Hs.84981	interferon regulatory factor 6	3.04
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	3.04
	437741	BE561610	Hs.5809	putative transmembrane protein; homolog	3.04
	442643	U82756	Hs.3991	PRP4/STKWD splicing factor	3.04
30	429358	AB037825	Hs.200317	KIAA1404 protein	3.03
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	3.03
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orolat	3.03
	409154	U72882	Hs.50842	interferon-induced protein 35	3.02
	442173	N76101	Hs.8127	KIAA0144 gene product	3.02
35	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	3.01
	450962	BE535647	Hs.25723	Sjogren's syndrome/scleroderma autoantig	3.01
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	3.01
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	3.01
40	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	3.01
	459107	AA811881	Hs.28505	ubiquitin-conjugating enzyme E2H (homolo	3.00
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.00
	416110	Z42262	Hs.322844	hypothetical protein DKFZp564A176	3.00
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	3.00
	448569	BE382657	Hs.21486	signal transducer and activator of trans	3.00
45	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.00
	400200			NM_002788*:Homo sapiens proteasome (pros	3.00
	403330			Target Exon	2.99
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.99
	403416	AI744626		KIAA0564 protein	2.97
50	403438			NM_031419*:Homo sapiens molecule possess	2.96
	447942	F12628	Hs.155470	hypothetical protein MGC16040	2.96
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.95
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	2.94
	440086	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom	2.94
55	429547	AW009166	Hs.99376	ESTs	2.93
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	2.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.89
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2.89
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.86
60	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	2.86
	423425	AA375756	Hs.14449	KIAA1609 protein	2.86
	412851	AI826502	Hs.106149	ESTs	2.86
	400664			NM_002425:Homo sapiens matrix metallopro	2.86
	454140	AB040888	Hs.41793	hypothetical protein FLJ10474	2.85
65	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.85
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	2.84
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.83
	423767	H18283	Hs.132753	F-box only protein 2	2.82
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	2.82
70	441801	AW242799	Hs.86366	ESTs	2.80
	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	2.80
	416539	Y07909	Hs.79368	epithelial membrane protein 1	2.79
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	2.79
	422947	AA306782	Hs.122552	G-2 and S-phase expressed 1	2.75
75	417849	AW291587	Hs.82733	nidogen 2	2.74
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.73
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.72
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	2.71
	424874	AA347951	Hs.326413	Homo sapiens cDNA FLJ20812 fis, clone AD	2.71
80	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.71
	447854	AW138454	Hs.11594	ESTs	2.71
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.70
	412636	NM_004415		desmoplakin (DPI, DPII)	2.69
	420576	AA297634	Hs.54925	KIAA1858 protein	2.68

	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	2.68
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.68
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.66
5	428698	AA852773	Hs.334838	KIAA1866 protein	2.64
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	2.64
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro	2.64
	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.63
	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.63
10	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.62
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	2.59
	452620	AA436504	Hs.119286	ESTs	2.59
	420552	AK000492	Hs.98806	hypothetical protein	2.59
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.56
15	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.56
	448454	NM_005879	Hs.21254	TRAF interacting protein	2.55
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	2.55
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.54
	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like doma	2.54
20	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.54
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.53
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	2.53
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	2.51
	411908	L27943	Hs.72924	cytidine deaminase	2.49
25	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.48
	430024	AI808780	Hs.227730	integrin, alpha 6	2.47
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.46
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.45
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	2.45
30	407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	2.45
	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.44
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.42
	413048	M93221	Hs.75182	mannose receptor, C type 1	2.40
	403851			C5002154*:gi 7299015 gb AAF54217.1  (AE0	2.39
35	433745	AF075320	Hs.28980	hypothetical protein FLJ14540	2.37
	423903	M57765	Hs.1721	interleukin 11	2.37
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.36
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	2.32
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	2.31
40	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	2.31
	406974	M57293		gb:Human parathyroid hormone-related pep	2.31
	401924			ENSP00000246632*:CDNA FLJ20261 fis, clon	2.30
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	2.29
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	2.29
45	436608	AA628980		down syndrome critical region protein DS	2.28
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	2.27
	434398	AA121098	Hs.3838	serum-inducible kinase	2.27
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	2.26
	418030	BE207573	Hs.83321	neuromedin B	2.25
50	404927			Target Exon	2.25
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	2.24
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.23
	411388	X72925	Hs.69752	desmocollin 1	2.21
	445757	AW449065	Hs.13264	KIAA0856 protein	2.18
55	405069			NM_006212*:Homo sapiens 6-phosphofructo-	2.17
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.16
	443168	AI038653	Hs.50500	ESTs	2.15
	444301	AK000136	Hs.10760	asporin (LRR class 1)	2.13
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.11
60	426471	M22440	Hs.170009	transforming growth factor, alpha	2.10
	445019	AI205540	Hs.281295	ESTs	2.08
	402021			NM_031891:Homo sapiens cadherin 20, type	2.07
	431866	NM_012098	Hs.8025	angiopoietin-like 2	2.05
65	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.04
	409571	AA504249	Hs.187585	ESTs	2.03
	450831	R37974	Hs.25255	ESTs	1.99
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.99
	445960	AI268399	Hs.140489	ESTs, Weakly similar to LIN1_HUMAN LINE-	1.98
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	1.97
70	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	1.91
	426850	BE247670	Hs.172766	MAP/microtubule affinity-regulating kina	1.90
	427335	AA448542	Hs.251677	G antigen 7B	1.90
	450649	NM_001429	Hs.25272	E1A binding protein p300	1.88
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	1.88
75	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	1.88
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	1.86
	433226	AW503733	Hs.9414	KIAA1488 protein	1.86
	413129	AF292100	Hs.104613	RP42 homolog	1.85
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.85
80	446620	AA128808	Hs.179902	transporter-like protein	1.81
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	1.79
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	1.78
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	1.77
	423482	BE280172	Hs.129228	galactokinase 2	1.77

5	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	1.76
	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.75
	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	1.74
	405102			C15001220*:gij4469558[gblAAD21311.1](AF	1.74
	433201	AB040896	Hs.21104	KIAA1463 protein	1.73
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	1.65
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.62
	414961	U27266	Hs.927	myosin-binding protein H	1.61
10	428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha p	1.61
	422170	AI791949	Hs.112432	anti-Mullerian hormone	1.61
	431846	BE019924	Hs.271580	uroplakin 1B	1.58
	404468			C3000442*:gij11120696[ref]NP_068518.1] c	1.57
	405779			NM_005367:Homo sapiens melanoma antigen,	1.55
15	441129	AA074904	Hs.296420	ESTs, Weakly similar to T18651 hypotheti	1.55
	427244	AA042400	Hs.178045	ESTs	1.52
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	1.52
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	1.51
	418367	AA326035	Hs.59236	hypothetical protein DKFZp434L0718	1.51
20	440340	AW895503	Hs.125276	ESTs	1.48
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	1.47
	424750	D29956	Hs.152818	ubiquitin specific protease 8	1.46
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	1.44
	406374			C16001364:gij11067373[ref]NP_067689.1] C	1.43
25	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	1.40
	404405			Target Exon	1.39
	401258			NM_030932*:Homo sapiens diaphanous (Dros	1.38
	433323	AA805132	Hs.159142	ESTs	1.36
	427441	AA412605	Hs.343879	SPANX family, member C	1.33
30	444707	AI188613	Hs.41690	desmocollin 3	1.31
	409103	AF251237	Hs.112208	XAGE-1 protein	1.27
	451106	BE382701	Hs.25960	N-MYC oncogene	1.27
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	1.23
	430686	NM_001942	Hs.2633	desmoglein 1	1.21
35	429325	AW088739	Hs.243770	ESTs	1.19
	406703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	1.03
	418827	BE327311	Hs.47166	HT021	1.01
	404104			C6001378*:gij1171748[sp]P46530[NOTC_BRAR	1.00

TABLE 46B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

45	Pkey	CAT Number	Accession
	413808	2905_1	AI570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188 AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204 BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155 AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841728 BI335729 BE841739 BE841663 AW863104 AA335201 AA335143 BF906965 AW867493 BE841505 BF374250 BE841766 BF373837 AW863191 BE841705 AW863154 AW868673 AW867311 AA335896 BE841753 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI801799 AI610344 AI452852 AW131174 AI581069 AI225028 AI446689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354652 AI470250 AI536872 AI891151 AW868019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681 AA335141 AW008176 AA335223 AI888837 AW868622 AI803901 AW005718 AI538062 AI282258 AI580678 AI445803 AI445394 AI868168 AA335144 AI926349 AA335210 AA334919 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109 AI453488 AI678606 AW869289 AW869211 BE841580 AI679368 AI888882 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584 AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404 AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154 AW868815 BF373812 BE841657 BE841780 AI440394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236 AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048 AW029395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012 AA335227 AW869307 AW869350 AW868709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607 AW008153 AI520957 AI610620 AI679828 AI868151 AI537839 AI679547 T28354 AI282567 AA335207 R36555 BF906963 AW131160 AI925626 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246 AW868723 BE937150 AA955002 AW863338 BE841767 421582 13358_1 X00474 NM_003225 X52003 M12075 BI765761 AW950155 AI571948 BI760569 AA308400 AA568312 BI761955 AA507595 AA614579 AA614409 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA582876 BM142503 AW050700 AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418 BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 AI61014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035 75 406687 0_0 M31126 450375 16559_3 BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758 415989 10194_1 BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236 80 426991 29771_1 AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF685525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635 454241 685806_1 BE184942 BE184946 AW238414 BE144666

452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 B1823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AI577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586 AW975281 AA664986 AA525775 AA056342 AI538978 X79449 BC017853 AL121035 BF196384 AW119044 AI028023 AW451110 AI971911 AW015069 AI079170 AI376367 AI264113 AA829646 AA737579 AA449679 AA740864 NM_001111 U18121 AL567297 BG773801 BF973874 AV687104 AA527579 AA843525 BE706355 AI074589 AI523475 BE890249 AW406263 BE074258 AV729485 BF809610 BG058619 AA677244 BE179838 AA622264 AI460106 AA740411 AI499168 AI078223 AI682923 BE696559 AW375385 AA788739 BG984978 Z40874 T17054 F09669 AW844043 U10439 BI711870 AW245957 AU158657 AA679305 AA679316 W72510 AI346029 BG059762 AW251062 AA132373 AI925621 AI860230 AI340172 AW192891 AI079890 AI094937 AI042115 AI200901 BE328452 AA644678 AA551209 BE351065 AA970761 N68609 AW002028 AA160826 AI422774 AW873114 AW073597 AW664483 AI218710 AW020550 AW190607 AI984545 AI871921 AI333970 AI452887 AI818335 AA398655 AI554424 AI274187 BE465703 AW512940 AW241366 AI923954 AA576649 AW168294 AA813181 AA912168 AI049738 AW514073 AA548255 AI569630 BE710031 AA244182 AI341697 AA563904 AI537990 AW517908 AW172943 Z39498 AI750294 AW150414 AI253293 BE825720 T31860 AW150775 D20310 AA150892 AU133933 BE781148 AL038957 BF910979 AA352297 BG988142 AW372175 BF229106 AW866705 BE093482 BG990396 AI499917 AA054452 H05484 AI828502 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418 BF998473 T92021 BI021048 BM049873 AW501366 AW501342 AW501549 BE939021 BE707147 BE160974 BE305207 N49011 AA947119 AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 BI919250 BI253018 AW130996 BE074249 BE895428 BI034862 BE083277 BF952166 AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363 BE253764 BE250764 BE255757 BE251752 BE251925 U09278 NM_004460 U76833 AF007822 AL550894 BG203919 AL575714 AI478772 AW022667 AW613820 AI435793 AI051768 AI200109 AA436611 BG208151 AI446661 BG215551 BM449645 AW630055 BG620125 AL550932 AW471133 AU136648 BE925603 BF828688 BE141577 BE141585 BE141587 AL109688 R23665 R26578 BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA448162 AA129977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI250053 AI870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 AI077043 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA337549 AI248473 M77830 NM_004415 AF139065 BG681115 BG740377 BI122964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW959615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA126330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI668869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW995245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 BC015981 AJ301615 AA628980 AI126603 BF184719
--------	--------	---

TABLE 46C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423

5	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
	400666	8118496	Plus	17982-18115,20297-20456
	401785	7249190	Minus	165776-165996,166189-166314,166408-16656
	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	400665	8118496	Plus	16879-17023
	402994	2996643	Minus	4727-4969
	402075	8117407	Plus	121907-122035,122804-122921,124019-12416
	405770	2735037	Plus	61057-62075
10	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	404240	5002624	Minus	116132-116407,116653-116922
	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
	402992	7767907	Minus	42137-42515
15	402408	9796239	Minus	110326-110491
	404286	2326514	Plus	51086-51301
	405387	6587915	Minus	3769-3833,5708-5895
	404287	2326514	Plus	53134-53281
	402995	2996643	Minus	5962-6216
20	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	401797	6730720	Plus	6973-7118
	402294	2282012	Minus	2575-3000
	401961	4581193	Minus	124054-124209
	404440	7528051	Plus	80430-81581
25	405386	6579238	Minus	40959-41297
	404171	9930793	Plus	173667-173783,176876-177055
	405778	7280331	Plus	18748-19757
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
	401176	9438469	Minus	20475-20734
30	404170	9930793	Plus	168836-169248

TABLE 47A:

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Maximum of esophageal tumor Als divided by the 98th percentile of the normal esophagus Als

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	31.70
	411243	AB039886	Hs.69319	CA11	30.12
45	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	18.46
	444325	AW152618	Hs.16757	ESTs	18.22
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	17.52
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	16.28
50	400666			NM_002425:Homo sapiens matrix metallopro	15.59
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	15.22
	425679	X05997	Hs.159177	lipase, gastric	14.60
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	13.14
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	12.60
55	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.00
	453331	AI240665		ESTs	11.20
	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	10.77
	408380	AF123050	Hs.44532	diubiquitin	10.32
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.32
60	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	10.22
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	10.18
	408243	Y00787	Hs.624	interleukin 8	9.80
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	9.75
	450375	AA009647		a disintegrin and metalloproteinase doma	9.12
65	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	8.88
	433447	U29195	Hs.3281	neuronal pentraxin II	8.64
	421508	NM_004833	Hs.105115	absent in melanoma 2	8.46
	452862	AW378065	Hs.8687	ESTs	8.34
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	7.92
70	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	7.86
	409757	NM_001898	Hs.123114	cystatin SN	7.62
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.60
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	7.58
	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	7.46
75	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	7.44
	406687	M31126		matrix metalloproteinase 11 (stromelysin	7.24
	430280	AA361258	Hs.237868	interleukin 7 receptor	7.18
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	7.13
80	429228	AI553633	Hs.326447	ESTs	7.04
	421110	AJ250717	Hs.1355	calthepsin E	6.98
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	6.88
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	6.88
	406673	M34996	Hs.198253	major histocompatibility complex, class	6.72
	421582	AI910275		trefoil factor 1 (breast cancer, estroge	6.52

5	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	6.40
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	6.32
	439926	AW014875	Hs.137007	ESTs	6.32
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.12
	411296	BE207307	Hs.10114	growth suppressor 1	6.03
	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	5.86
	413441	AI929374	Hs.75367	Src-like-adaptor	5.86
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	5.81
10	417715	AW969587	Hs.86366	ESTs	5.76
	413808	J00287		Homo sapiens mRNA for caldesmon, 3' UTR	5.63
	400665			NM_002425:Homo sapiens matrix metallopro	5.60
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.53
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	5.44
15	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.42
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.40
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	5.38
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	5.08
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	5.08
20	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	5.04
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	4.92
	436856	AI469355	Hs.127310	ESTs	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.60
	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	4.53
25	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.48
	404240			NM_018950:Homo sapiens major histocompat	4.36
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	4.34
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.29
	425139	AW630488	Hs.25338	protease, serine, 23	4.24
30	415989	AI267700		ESTs	4.20
	408202	AA227710	Hs.43658	DKFZP586L151 protein	4.11
	450701	H39960	Hs.288467	hypothetical protein XP_098151	4.06
	423271	W47225	Hs.126256	interleukin 1, beta	4.02
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.96
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	3.90
35	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.86
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.86
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	3.76
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	3.49
40	408049	AW076098	Hs.345588	desmoplakin (DPI, DPII)	3.44
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	3.37
	435370	AI964074	Hs.225838	ESTs	3.29
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.19
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.18
45	409154	U72882	Hs.50842	interferon-induced protein 35	3.13
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	3.12
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.00
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.76
	402992			Target Exon	2.57
50	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.54
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	2.52
	413945	NM_000591	Hs.75627	CD14 antigen	2.51
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	2.50
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	2.48
55	415149	X12451	Hs.78056	calhepsin L	2.47
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	2.46
	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	2.45
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.45
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.39
60	422562	AI962060	Hs.118397	AE-binding protein 1	2.35
	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	2.28
	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	2.19
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	2.19
	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	2.03
65	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.03
	428981	BE313077	Hs.93135	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.83
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	1.79
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (fr	1.70
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	1.69
70	412773	H15785	Hs.74573	similar to vaccinia virus HindIII K4L OR	1.66
	414024	AA134712	Hs.22410	gb:zm79g08.r1 Stratagene neuroepithelium	1.65
	426530	U24578	Hs.278625	complement component 4A	1.58
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.52

TABLE 47B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993



H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620  
AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665  
BF989591 BI056086 BG001590 BF107035  
450375 16559\_3 BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410  
5 452410 59661\_1 H59605 BE157601 AA113758  
AL133619 AI435410 AA622747 AW272464 AI215594 AI673758 AI476447 AI804128 AI581345 AI026826 AI300820 AW513621 AA256162 AI559724  
AI493388 AA614641 AI125754 AI214351 AI567080 AI200813 AI476629 AI685732 AA602400 AA730140 AI565082 AI269603 AI807095 AA905453  
AA505909 AI204595 AI582930 AI686077 AA757863 AA730154 AA664048 BI831663 AI734138 AI734130 AI732734 AW043563 AI741241 AI732741  
10 406687 0\_0 BF111446 BE677727 AA437369 AA426284 AA433997 AA425820  
421582 13358\_1 M31126  
X00474 NM\_003225 X52003 M12075 BI765761 AW950155 AI571948 BI760569 AA308400 AA568312 BI761955 AA507595 AA614579 AA614409  
BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA858276 BM142503 AW050700  
AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418  
15 413808 2905\_1 AI570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188  
AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204  
BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155  
AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841728 BI335729 BE841739 BE841663 AW863104 AA335201  
AA335143 BF906965 AW867493 BE841505 BF374250 BE841766 BF373837 AW863191 BE841705 AW863154 AW868673 AW867311 AA335896  
BE841753 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230  
20 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI801799 AI610344 AI452852  
AW131174 AI581069 AI225028 AI446689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354652 AI470250  
AI536872 AI891151 AW868019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681  
AA335141 AW008176 AA335223 AI888837 AW868622 AI803901 AW005718 AI538062 AI282258 AI580678 AI445803 AI445394 AI868168  
25 AA335144 AI926349 AA335210 AA334919 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109  
AI453488 AI678606 AW869289 AW869211 BE841580 AI679368 AI888882 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584  
AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532  
30 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404  
AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154  
AW868815 BF373812 BE841657 BE841780 AI440394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236  
AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048  
AW029395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012  
AA335227 AW869307 AW869350 AW868709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607  
AW008153 AI520957 AI610620 AI679828 AI868151 AI537839 AI679547 T28354 AI282567 AA335207 R83655 BF906963 AW131160 AI925626  
35 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246  
AW868723 BE937150 AA955002 AW863338 BE841767  
415989 10194\_1 BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153  
BG285837 AI720344 BF541715 AA355086 AA172236

TABLE 47C

Pkey:	Unique number corresponding to an Eos probeset		
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.		
Strand:	Indicates DNA strand from which exons were predicted.		
Nt_position:	Indicates nucleotide positions of predicted exons.		
Pkey	Ref	Strand	Nt_position
400666	8118496	Plus	17982-18115,20297-20456
400665	8118496	Plus	16879-17023
404240	5002624	Minus	116132-116407,116653-116922
402992	7767907	Minus	42137-42515

TABLE 48A:

Pkey:	Unique Eos probeset identifier number		
ExAccn:	Exemplar Accession number, Genbank accession number		
UnigenelD:	Unigene number		
Unigene Title:	Unigene gene title		
R1:	90th percentile of normal esophagus AIs divided by the 90th percentile of esophageal tumor AIs		

Pkey	ExAccn	UnigenelD	Unigene Title	R1
407245	X90568	Hs.172004	titin	37.43
426752	X69490	Hs.172004	titin	30.23
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	23.69
407013	U35637		gb:Human nebulin mRNA, partial cds	17.09
400440	X83957	Hs.83870	nebulin	15.56
406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	14.21
428087	AA100573	Hs.182421	troponin C2, fast	13.03
417070	Z19077	Hs.172004	titin	13.02
406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	12.61
405001	U58196		interleukin enhancer binding factor 1	12.53
418391	NM_003281	Hs.84673	troponin I, skeletal, slow	12.46
418205	L21715	Hs.83760	troponin I, skeletal, fast	12.40
422633	X56832	Hs.118804	enolase 3, (beta, muscle)	12.21
400499			C10001858.gij6679124[ref]NP_032759.1] ne	11.99
418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	10.53
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	10.21
417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	10.14
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	10.13
408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	10.00
416373	AA195845	Hs.73680	ESTs, Weakly similar to S12658 cysteine-	9.65
415672	N53097	Hs.193579	ESTs	9.57
409096	AA194412	Hs.50550	sarcomeric muscle protein	9.48

	431360	NM_000427	Hs.251680	loricrin	9.42
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	9.20
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	9.15
5	422069	AJ010063	Hs.343603	titin-cap (telethonin)	8.96
	409028	AB014513	Hs.49998	Z-band alternatively spliced PDZ-motif	8.64
	437206	AW975934	Hs.283382	ESTs, Weakly similar to I38344 titin, ca	8.48
	421296	NM_002666	Hs.103253	perilipin	8.47
	412129	M21984	Hs.73454	troponin T3, skeletal, fast	8.39
10	434352	AF129505	Hs.86492	small muscle protein, X-linked	8.28
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	7.93
	408591	AF015224	Hs.46452	mammaglobin 1	7.88
	435124	AA725362	Hs.120456	ESTs	7.76
	430681	AW969675	Hs.291232	ESTs	7.70
	454229	AW957744	Hs.278469	lacrimal proline rich protein	7.68
15	424734	AI217685	Hs.96844	ESTs	7.59
	428221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	7.57
	431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	7.41
	443727	Z25389	Hs.18459	ESTs	7.21
20	408753	AI337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	7.04
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	6.98
	424485	AI685069	Hs.272556	peptidylarginine deiminase type I	6.93
	403805			Target Exon	6.87
	429997	NM_006789	Hs.227457	apolipoprotein B mRNA editing enzyme, ca	6.72
25	418532	F00797	Hs.85844	neurotrophic tyrosine kinase, receptor,	6.70
	419711	C02621	Hs.159282	ESTs	6.70
	422640	M37984	Hs.118845	troponin C, slow	6.68
	433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.55
	406703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	6.34
30	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.27
	446962	AI351421	Hs.279709	muscle specific ring finger protein 1	6.20
	411102	AA401295	Hs.23926	triadin	6.17
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	6.15
	454059	NM_003154	Hs.37048	statherin	5.95
35	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	5.85
	434360	AW015415	Hs.127780	ESTs	5.57
	420813	X51501	Hs.99949	prolactin-induced protein	5.52
	417376	AA253314	Hs.154103	LIM protein (similar to rat protein kina	5.46
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	5.42
40	446523	NM_003063	Hs.334629	sarcolipin	5.41
	402270			Target Exon	5.25
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	5.24
	424982	U94777		phosphorylase, glycogen; muscle (McArdle	5.17
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	5.14
45	410621	AA194329	Hs.172004	titin	5.10
	429134	AA446953	Hs.99004	ESTs	5.06
	436519	AJ278124	Hs.238756	myozenin	5.04
	447023	AA356764	Hs.17109	integral membrane protein 2A	5.03
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	5.02
50	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	5.00
	433635	AI074502	Hs.134292	hypothetical protein MGC12921	4.98
	429892	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	4.96
	411021	F00055	Hs.172004	titin	4.95
	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	4.93
55	424897	D63216	Hs.153684	frizzled-related protein	4.92
	406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	4.92
	428824	W23624	Hs.173059	ESTs	4.78
	418692	AK000268	Hs.87383	hypothetical protein	4.74
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	4.73
60	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.66
	424049	AB014524	Hs.138380	KIAA0624 protein	4.65
	439609	AW971945	Hs.293236	ESTs	4.65
	433122	AB019391	Hs.58049	ESTs	4.62
	415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	4.59
65	415655	W05433		ESTs	4.59
	442376	W95588	Hs.129982	Homo sapiens cDNA FLJ12228 fis, clone MA	4.58
	452308	AI167560	Hs.61297	ESTs	4.57
	418072	F35210	Hs.86507	Human DNA sequence from clone RP3-353C17	4.56
	429413	NM_014058	Hs.201877	DESC1 protein	4.53
70	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.53
	438704	AI435060	Hs.32825	ESTs	4.50
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	4.49
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	4.48
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	4.46
75	422313	AF045941	Hs.115166	sclellin	4.43
	417045	F01180	Hs.332030	Homo sapiens ORF1	4.41
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	4.39
	435101	AI743156	Hs.131064	ESTs	4.37
	432408	N39127		ESTs, Weakly similar to A46010 X-linked	4.35
80	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	4.35
	429930	AI580809	Hs.99569	ESTs	4.30
	429624	AA458648	Hs.99476	ESTs, Weakly similar to 1313184B alpha1	4.26
	429454	AL039940	Hs.202949	KIAA1102 protein	4.20
	411000	N40449	Hs.201619	ESTs, Weakly similar to S38383 SEB4B pro	4.11

5	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	3.99
	428560	AI243209	Hs.98669	ESTs, Weakly similar to B47411 ADPribosy	3.95
	438328	AI492261	Hs.32450	ESTs	3.84
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.84
	453876	AW021748	Hs.110406	ESTs, Weakly similar to I38022 hypotheti	3.83
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	3.82
	430171	AF086289	Hs.234766	skin-specific protein	3.80
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	3.75
10	446082	AI274139	Hs.156452	ESTs	3.74
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.70
	431205	AA194560	Hs.250763	tropomodulin 4 (muscle)	3.68
	443265	AI916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	3.68
	424747	AA346241	Hs.231887	EST	3.67
	410223	S73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	3.63
15	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.62
	453817	AW755253	Hs.61920	ESTs	3.57
	416431	AW384459	Hs.172004	titin	3.52
	425971	AF135024	Hs.165296	kallikrein 13	3.49
	412452	AA215731	Hs.79265	suppression of tumorigenicity 5	3.48
20	421512	AB007923	Hs.265848	myomegalin	3.41
	413922	AI535895	Hs.221024	ESTs	3.37
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.36
	418067	AI127958	Hs.83393	cystatin E/M	3.32
25	428666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	3.29
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	3.26
	420197	AW139647	Hs.88134	ESTs, Weakly similar to A57291 cytokine	3.23
	425869	AA524547	Hs.160318	FXFD domain-containing ion transport reg	3.21
	404270			NM_006061:Homo sapiens specific granule	3.21
30	409169	F00991	Hs.50889	(clone PWHL2-24) myosin light chain 2	3.17
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	3.13
	452023	AB032999	Hs.27566	KIAA1173 protein	3.08
	417713	D42047	Hs.82432	KIAA0089 protein	2.99
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	2.97
	450300	AL041440	Hs.58210	ESTs, Highly similar to ITH4_HUMAN INTER	2.97
35	451814	AA847992	Hs.137003	ESTs	2.83
	452360	AI742082	Hs.98539	ESTs	2.67
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	2.57
	408104	AW972927	Hs.293968	ESTs	2.57
40	444329	W73753	Hs.209637	hypothetical protein FLJ12921	2.54
	439652	W67826	Hs.55412	ESTs, Weakly similar to K1CJ_HUMAN KERAT	2.50
	432191	AA043193	Hs.273186	hypothetical protein, clone Telethon(Ita	2.33
	425855	AF135025	Hs.159679	kallikrein 12	2.32
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	2.28
45	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.25
	411388	X72925	Hs.69752	desmocollin 1	2.25
	425721	AC002115	Hs.159309	uroplakin 1A	2.12
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	2.10
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	2.02
50	417405	W28657	Hs.5307	ESTs	2.01
	434560	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence	1.95
	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	1.79
	430513	AJ012008	Hs.241586	G6C protein	1.68
	454478	AW805749	Hs.138885	superoxide dismutase 2, mitochondrial	1.68
55	416559	AI039195	Hs.128060	ESTs	1.66
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasm	1.64
	415780	U75898	Hs.78846	heat shock 27kD protein 2	1.55
	409702	AI752244		eukaryotic translation elongation factor	1.50

60

TABLE 48B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

65

Pkey	CAT Number	Accession
------	------------	-----------

70

407013	2073_7	U35637 AA192323 AA194508 BG011583 F25712 AL596820 BE185376
424982	25362_1	AK057547 BG181248 AA883756 F25670 AA778128 F27657 F18914 F25171 AA178844 F21556 F25872 F20457 F27617 F36059 F34817 F26967 F25922 F31278 F34666 F01176 F36333 F01226 F27406 F27130 F28742 F24126 F29891 AA195955 AA086351 W69291 F25880 F32791 F31311 F32380 F25216 F19679 F18656 F29700 F24954 F32741 F30404 F35470 F33989 F33141 F36382 F34118 F17714 AA176345 F24700 AA550940 F18617 F16859 F15633 F34675 F16528 F17281 AA086388 F30859 F21852 C02644 F29425 F25286 C03553 F35259 W80691 F16457 F24094 F16783 AA180319 F28443 F17763 F17448 F00542 AA197179 AA193012
415655	15499_1	AJ276240 N70563 F37502 F29200 F27903 F18577 F19683 F20867 Z28857 F30994 F31752 F17375 F15601 F17543 F17411
432408	2061_18	AV724258 AA247153 BF736219 BF513744 AW058048 AI082691 AA865520 N39127 AV724549 F20776 AA249747 AW970392 AA535433 F36964 F33894
409702	38388_1	AK056951 AK026458 BI439120 BM021106 F30243 BM055214 BM054962 BM069667 F37401 AA563621 AI752243 AI720773 AI933014 F18964 F35317 F35258 F27772 H39537 AW445222 F19408 H28557 F30608 F31797 F30960 BF837737 BF837688 AL551046 BI758668 BI765038 BI837440 BE392882 BI438801 AI093511 AI752244 AI784111 BG490221 BF338840 BF338974 BG896472 AL576843 AW966769 F25388 F37436 H28558 AI025548 AA782333 F30929 F36002 F21229 AI720539 AA719449 F21231 F18924 AA626886 F30774 F27704 F31411 F31127 F33381 F36153 F31793 F31138 F31966 F33901 AA298244 BI757347 AI810201 AI692843 F29441 H51409 F21804 AW973249 F18440 F17572 F32499 AA327152 AA534140 AI188088 F18893 F23362 AA010888 F18143 Z28500 H27651 AI720790 F22425 H13178 H28677 F21098 F37777 F21466 F16598 F23420 AL574723 R75610 F34035 F17845 F18560 F25902 R79117 F35534 F15713 AI612800 F16563 F15645 F33609 F29995 BG939623 F17385 F17384 F18660 F17922 F15523 AI093253 F18359 F31452 F00232 AI583430 BM021353 AA284108 H27650 H29935 BE708208 AA010737 H51451

80

Z19399 AI678418 AI952535 F17265 F17826 F37939 F35639 F17367 W75962 R70189 Z28755 R72106 AA335915 R75700 R79116 W72887  
AI581552 R71403 F23388 C03913 B1756149 B116109 BF790727 AL553994 R82966 W47487 AA456066 AW984608 BE708220 BG490537 W47419

## TABLE 48C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405001	6015406	Minus	104646-104819
400499	9796071	Minus	148495-148806
403805	8140491	Minus	51483-51742,53429-53511
402270	3108020	Plus	117656-117822
404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965

Table 49A. 1562 genes upregulated in lung cancer relative to normal body tissues

Table 49A shows 1562 genes upregulated in lung cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar accession number, GenBank accession number  
UniGeneID: UniGene number  
Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).  
UniGene Title: UniGene gene title  
R1 90th percentile of lung tumor AIs divided by the 50th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from the numerator and denominator.

Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prod.Domains; R1

421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphate), member 2; Ribosomal\_L20,Na\_Pi\_cotrans;TM=Y;; 24.06  
439335; AA742697; Hs.62492; ESTs, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus]; none;SS=M; 21.70  
406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;; 19.36  
421341; AJ243212; Hs.279611; deleted in malignant brain tumors 1; zona\_pellucida,CUB,SRCR;SS=M; 16.99  
452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine proteinase [H.sapiens]; none,none; 16.67  
429259; AA420450; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none,none; 16.50  
454034; NM\_000691; Hs.575; aldehyde dehydrogenase 3 family, member A1; aldedh; 16.24  
408000; L11690; Hs.620; bulous pemphigoid antigen 1 (230/240kD); ehand,spectrin,GAS2,SH3,Plectin,RA,Xylose\_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,ldh\_C,CH,AIP3;TM=M;; 14.75  
421798; N74880; Hs.29877; N-acylsphingosine amidohydrolase (acid ceramidase)-like; SAPA,Surfactant\_B,none; 14.18  
439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1\_HUMAN DEATH-ASSOCIATED PROTEIN 1 [H.sapiens]; none,none; 13.94  
431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 13.54  
417079; U65590; Hs.81134; Interleukin 1 receptor antagonist; IL1;SS=M; 12.97  
444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypothetical protein YGL050w - yeast (Saccharomyces cerevisiae) [S.cerevisiae]; Collagen;TM=M;SS=M; 12.92  
408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M;; 12.76  
448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate\_rec,MIP;TM=M;SS=M; 12.50  
414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y;; 12.12  
436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;; 12.00  
418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none,none; 11.99  
419693; AA133749; Hs.301350; FXFD domain-containing ion transport regulator 3; ATP1G1\_PLM\_MAT8;TM=Y;SS=M; 11.88  
417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin\_G,CorA;SS=M; 11.38  
414998; NM\_002543; Hs.77729; oxidised low density lipoprotein (lectin-like) receptor 1; lectin\_c;TM=Y;SS=M; 11.21  
428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm\_3;TM=Y;SS=M; 11.08  
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member B2; aldedh;TM=M;SS=M; 11.01  
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA\_gyraseB,DNA\_topoisolV,HATPase\_c;SS=M; 10.69  
418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4); ank; 10.65  
439223; AW238299; Hs.250618; UL16 binding protein 2; ldl\_recept\_a,PKD,MHC\_L;TM=M;SS=Y; 10.52  
441835; AB036432; Hs.184; advanced glycosylation end product-specific receptor; homeobox,Acyltransferase,notch,EGF,ank,Acyltransferase; 10.47  
451558; NM\_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ABC\_tran,SRP54;TM=Y;SS=M; 10.33  
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;; 10.21  
452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhbd\_glycop;TM=Y;SS=M; 10.14  
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor 2); PTN\_MK;TM=M;SS=Y; 10.13  
433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR\_LY6,toxin,Activin\_rec;TM=M;SS=Y; 10.12  
454098; W27953; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none,none; 10.05  
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 9.98  
430832; A073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]; none,none; 9.79  
422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; none,kinase,fn3,ig; 9.60  
414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;; 9.54  
439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC\_tran,CoaE;TM=M;; 9.52  
430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 9.48

- 423217; NM\_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); Kunitz\_BPT1,fn3,vwa,Collagen,beta-lactamase;TM=M;SS=M; 9.44
- 418882; NM\_004996; Hs.89433; ATP-binding cassette, sub-family C (CFTR/MRP), member 1; ABC\_membrane,ABC\_tran;TM=Y;SS=M; 9.32
- 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid cells 1; ig;TM=M;SS=M; 9.26
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-macroglobulin receptor precursor [H.sapiens]; none,none; 9.18
- 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR/MRP), member 3; ABC\_tran,ABC\_membrane;TM=Y;SS=M; 9.06
- 441384; AA447849; Hs.288660; Homo sapiens cDNA: FLJ22182 fis, clone HRC00953; 7tm\_3,none; 8.98
- 446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium\_transp,FecCD;TM=Y;SS=M; 8.74
- 436972; AA284679; Hs.25640; claudin 3; PMP22\_Claudin;TM=Y;SS=M; 8.71
- 421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; Fasciclin,ABC\_tran,ABC\_membrane,GTP\_EFTU;TM=M;SS=M; 8.71
- 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; vwa,Cache;TM=M; 8.66
- 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm\_1;TM=Y;SS=M; 8.63
- 438091; AW373062; ; nuclear receptor subfamily 1, group I, member 3; hormone\_rec,zf-C4,none; 8.60
- 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M; 8.57
- 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin;SS=M; 8.56
- 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;SS=M; 8.52
- 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant\_thionins;SS=M; 8.49
- 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M; 8.42
- 413011; AW068115; Hs.821; biglycan; LRR,LRRNT;SS=M; 8.40
- 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 8.39
- 411089; AA456454; ; cell division cycle 2-like 1 (PITSLRE proteins); none,none; 8.37
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); BIR;TM=M; 8.34
- 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; none;SS=M; 8.25
- 449019; AI949095; Hs.67776; ESTs, Weakly similar to T22341 hypothetical protein F47B8.5 - Caenorhabditis elegans [C.elegans]; none,none; 8.24
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M; 8.22
- 416819; U77735; Hs.80205; pim-2 oncogene; pkinase;SS=M; 8.19
- 451541; BE279383; Hs.26557; plakophilin 3; Armadillo\_seg;TM=M; 8.16
- 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; ABC\_tran,M,SMC\_N,SMC\_C,DUF164,none; 8.16
- 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo\_seg;TM=M; 8.14
- 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.14
- 421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase;SS=Y; 8.10
- 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); ig;TM=Y;SS=M; 8.03
- 439285; AL133916; ; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 7.97
- 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B; Sema,PSI,integrin\_B;TM=Y; 7.86
- 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2; pkinase;TM=M; 7.85
- 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 7.85
- 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa\_permeases,pyridoxal\_deC,bromodomain,PHD,MBD,AT\_hook,DDT,PI3\_P14\_kinase,FAT,FATC,BolA,RUN;TM=M; 7.84
- 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); SH3,TPR;TM=M; 7.73
- 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); ig;TM=Y;SS=M; 7.72
- 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfamily, member 17; IL2;SS=M; 7.71
- 451253; H48299; Hs.26126; claudin 10; PMP22\_Claudin,Peptidase\_M1,K\_tetra;TM=Y;SS=M; 7.70
- 435575; AF213457; Hs.44234; triggering receptor expressed on myeloid cells 2; ig;TM=Y;SS=M; 7.70
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M; 7.70
- 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; ig,ICAM\_N;TM=M;SS=M; 7.67
- 422282; AF019225; Hs.114309; apolipoprotein L; MolA\_ExcB;TM=Y;SS=M; 7.64
- 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; SAM\_PNT,none; 7.54
- 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding protein; 7tm\_1;TM=Y;SS=M; 7.52
- 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); Y\_phosphatase,DSPC;TM=M; 7.46
- 421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen alpha 1(XI) chain precursor [H.sapiens]; none;TM=Y;SS=M; 7.40
- 421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 7.39
- 438089; W05391; ; nuclear receptor subfamily 1, group I, member 3; hormone\_rec,zf-C4,none; 7.38
- 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; aa\_permeases,pyridoxal\_deC,bromodomain,PHD,MBD,AT\_hook,DDT,PI3\_P14\_kinase,FAT,FATC,BolA,RUN;TM=M; 7.36
- 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor, epsilon; Neur\_chan\_LBD,Neur\_chan\_memb;TM=Y;SS=M; 7.36
- 416178; AI808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; none;TM=M; 7.31
- 418506; AA084248; Hs.85339; G protein-coupled receptor 39; none,none; 7.25
- 441553; AA281219; Hs.121296; ESTs; none,FG-GAP,integrin\_A; 7.25
- 422311; AF073515; Hs.114948; cytokine receptor-like factor 1; fn3;TM=M; 7.21
- 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-type, Z polypeptide 1; fn3,Y\_phosphatase,carb\_anhydrase;TM=Y;SS=M; 7.20
- 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; transferrin,Guanylate\_kin,PDZ,SH3; 7.20
- 412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M; 7.14
- 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 7.14
- 428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 7.12
- 418462; BE001596; Hs.85266; integrin, beta 4; fn3,integrin\_B,Calx-beta,EGF;TM=M;SS=M; 7.08
- 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf\_5;TM=Y;SS=M; 7.02
- 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M; 7.00
- 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; ig,isodh,Ribosomal\_L6,F-box;TM=Y;SS=M; 6.98
- 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; Furin-like,pkinase,Recep\_L\_domain,YLP,none; 6.97
- 421508; NM\_004833; Hs.105115; absent in melanoma 2; PAAD\_DAPIN,HIN;TM=M; 6.96
- 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; ITAM;TM=Y;SS=M; 6.93
- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; pkinase,ICE\_p10,ICE\_p20;TM=M;SS=M; 6.93
- 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo\_seg,HEAT;TM=M; 6.91
- 451035; AU076785; Hs.430; plastin 1 (I isoform); ehand,CH,Adaptin\_N;SS=M; 6.86
- 432407; AA221036; ; gb:z03f12.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL\_BAEVM P10272 POL POLYPROTEIN ;, mRNA sequence; DEAD,helicase\_C,rm,Ndr,Cys\_knot,TIL,vwa,vwc,vwd,IQ,Rila,abhydrolase,TGF-beta,DUF139,TPR,DSPC,isp\_1,Ribosomal\_S21,rvp;TM=M; 6.84
- 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M; 6.77
- 448243; AW369771; Hs.52620; integrin, beta 8; integrin\_B,none; 6.76
- 427557; NM\_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR\_LY6,ET,PLA2\_inh;SS=M; 6.75
- 418054; NM\_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl\_oxidase;TM=M;SS=M; 6.74
- 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; sugar\_tr;TM=Y;SS=M; 6.73

- 430397; AI924533; Hs.105607; bicarbonate transporter related protein 1; HCO3\_cotransp;TM=Y;; 6.71  
 449523; NM\_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm\_1;TM=Y;SS=M; 6.71  
 431630; NM\_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor); FG-GAP,Rhbd\_glycop,integrin\_A;TM=Y;SS=M; 6.70  
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR;TM=M;SS=M; 6.69  
 424925; NM\_002432; Hs.153837; myeloid cell nuclear differentiation antigen; PAAD\_DAPIN,HIN;; 6.69  
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor); vwa,integrin\_A,FG-GAP;TM=Y;SS=M; 6.65  
 428157; AI738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 6.64  
 430770; AA765694; Hs.123296; ESTs; none,none; 6.63  
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G protein), alpha 15 (Gq class); G-alpha,arf;TM=M;; 6.59  
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005735; IMPDH\_C,IMPDH\_N,CBS,integrin\_B,Ricin\_B\_lectin; 6.59  
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPc;TM=M;; 6.59  
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin\_c,Ricin\_B\_lectin,Xlink;TM=Y;SS=M; 6.58  
 429345; R11141; Hs.199695; hypothetical protein; K\_tetra,SAM; 6.58  
 416110; Z42262; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin\_B;TM=Y;SS=M; 6.58  
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 6.57  
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); Pribosyltran,OMPdecase;TM=M;; 6.57  
 402260; ; NM\_001436; Homo sapiens fibrillarin (FBL), mRNA. transcript (F8A), mRNA.; pkinase,Fibrillarin,none; 6.56  
 456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide); none;TM=Y;; 6.53  
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ldl\_recept\_a,PKD,MHC\_1;TM=M;SS=Y; 6.53  
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; inositol\_P,ig;TM=M;; 6.52  
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none;TM=Y;SS=M; 6.52  
 432920; U37689; Hs.3128; polymerase (RNA) II (DNA directed) polypeptide H; none;TM=M;; 6.48  
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; PLDC;TM=M;; 6.48  
 409208; Y00093; Hs.51077; integrin, alpha X (antigen CD11C (p150), alpha polypeptide); vwa,FG-GAP,integrin\_A,vwa,integrin\_A,FG-GAP; 6.43  
 424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD\_NFYB\_HMF;; 6.43  
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; ig;TM=Y;SS=M; 6.41  
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PLACE2000103; HLH,death,TNFR\_c6,Acyl-CoA\_hydro; 6.41  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y\_phosphatase,Ribosomal\_S3\_N;TM=M;; 6.39  
 453914; NM\_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBpase;TM=M;; 6.37  
 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip;TM=M;SS=Y; 6.37  
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;SS=M; 6.36  
 432636; AA340864; Hs.278562; claudin 7; PMP22\_Claudin;TM=Y;SS=M; 6.34  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.34  
 451734; NM\_006176; Hs.26944; neurogranin (protein kinase C substrate, RC3); IQ,7tm\_1;TM=M;; 6.34  
 443907; AU076484; Hs.8963; TYRO protein tyrosine kinase binding protein; none;TM=M;SS=Y; 6.34  
 401027; ; Target Exon; none,none; 6.26  
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin\_B,EGF,PSI;TM=Y;SS=M; 6.22  
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); SH2;SS=M; 6.21  
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone ADKA02377; 7tm\_3,none; 6.20  
 408771; AW732573; Hs.47584; potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3; efnad,ion\_trans,K\_tetra,none; 6.19  
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudogene; LIM,PDZ,pkinase;SS=M; 6.18  
 408482; NM\_000676; Hs.45743; adenosine A2b receptor; 7tm\_1;TM=Y;SS=M; 6.17  
 426427; M86699; Hs.169840; TTK protein kinase; pkinase;; 6.17  
 445019; AI205540; Hs.281295; ESTs; none,none; 6.16  
 438552; AJ245820; Hs.6314; type I transmembrane receptor (seizure-related protein); none,none; 6.16  
 414907; X90725; Hs.77697; polo (Drosophila)-like kinase; Ribosomal\_L37ae,pkinase,POLO\_box,tRNA-synt\_1b,dynamin,dynamin\_2,GED,bZIP,M; 6.14  
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; PI3\_P14\_kinase,FAT,FATC;TM=M;; 6.13  
 417421; AL138201; Hs.82120; nuclear receptor subfamily 4, group A, member 2; hormone\_rec,zf-C4;SS=M; 6.13  
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm\_2,HRM;TM=Y;SS=M; 6.12  
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm\_2;TM=Y;SS=M; 6.12  
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M;; 6.12  
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion\_trans,K\_tetra,asp; 6.11  
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 thromboxane A-2 receptor, endothelial [H.sapiens]; Bcl-2,none; 6.10  
 423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC\_tran;TM=Y;; 6.10  
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa\_trans;TM=Y;; 6.09  
 411020; NM\_006770; Hs.67726; macrophage receptor with collagenous structure; SRCR,Collagen;TM=Y;SS=M; 6.09  
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm\_1;TM=Y;SS=M; 6.08  
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); PAF-AH\_Ib,Lipase\_GDSL;TM=M;; 6.07  
 421753; BE314828; Hs.107911; ATP-binding cassette, sub-family B (MDR/TAP), member 6; ABC\_tran,ABC\_membrane;TM=Y;SS=M; 6.07  
 406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gene, complete CDS.; none,none; 6.07  
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated kinase; pkinase,pkinase\_C;TM=M;SS=M; 6.06  
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; C1q,Collagen;SS=M; 6.05  
 414883; AA926960; ; CDC28 protein kinase 1; CKS;; 6.05  
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase\_C,rm,Ndr,Cys\_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPc,isp\_1,Ribosomal\_S21,rvp;TM=M;; 6.03  
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 6.03  
 448782; AL050295; Hs.22039; KIAA0758 protein; 7tm\_2,ig,GPS,SEA;TM=Y;; 6.03  
 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm\_1;TM=Y;SS=M; 6.01  
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none;; 6.00  
 424381; AA285249; Hs.146329; protein kinase Chk2; pkinase,FHA,DnaI;TM=M;; 6.00  
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase;TM=M;; 5.99  
 439310; AF086120; Hs.102793; ESTs; casein\_kappa,pkinase,ig,none; 5.97  
 414972; BE263782; Hs.77695; KIAA0008 gene product; GKAP;TM=M;; 5.97  
 425976; C75094; Hs.334514; NG22 protein; voltage\_CLC;TM=Y;SS=M; 5.94  
 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase\_2;TM=Y;SS=M; 5.93  
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin;TM=M;; 5.93  
 421462; AF016495; Hs.104624; aquaporin 9; MIP;TM=Y;SS=M; 5.92  
 426761; AI015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586I2022 (from clone DKFZp586I2022); none;TM=Y;SS=M; 5.92  
 407792; AI077715; Hs.39384; putative secreted ligand homologous to fxi1; none;TM=M;SS=Y; 5.91  
 428771; AB028992; Hs.193143; KIAA1069 protein; C2,PI-PLC-Y,PI-PLC-X;TM=M;; 5.91  
 438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; ig,MHC\_II\_alpha,none; 5.91

- 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD\_DAPIN;NA;NA; 5.90  
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase\_M49,EGF,ig,Neuregulin;TM=M;; 5.90  
 408790; AW580227; Hs.47860; neurotrophic tyrosine kinase, receptor, type 2; ig,pkinase,LRR,LRRNT,LRRCT;TM=Y;SS=M; 5.89  
 413186; AU077141; Hs.75231; solute carrier family 16 (monocarboxylic acid transporters), member 1; sugar\_tr;TM=Y;SS=M; 5.89  
 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 5.88  
 422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR,SH2,SH3,pkinase;TM=Y;SS=M; 5.88  
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; none;TM=M;SS=Y; 5.88  
 429619; AL120751; Hs.211568; eukaryotic translation initiation factor 4 gamma, 1; none,none; 5.86  
 437429; H79981; Hs.5613; Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DKFZp564E2222); SH2,SH3,BTB; 5.86  
 436576; AI458213; Hs.77542; ESTs; 7tm\_1,DnaJ; 5.85  
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, calcium-dependent); C2,PLA2\_B;TM=M;; 5.85  
 419981; AA897581; Hs.128773; ESTs; pkinase,DAG\_PE-bind,pkinase\_C,OPR,none; 5.83  
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily, member 6b, decoy; 60s\_ribosomal,Ribosomal\_L10,TNFR\_c6,DEAD;; 5.83  
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 5.82  
 451320; AW118072; diacylglycerol kinase, zeta (104kD); none;TM=M;; 5.82  
 400991; ; Target Exon; Armadillo\_seg,lectin\_c,none; 5.81  
 456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral transforming sequence c; zfc3HC4,Cbl\_N,Cbl\_N2,Cbl\_N3;TM=M;; 5.81  
 434263; N34895; Hs.44648; ESTs; ig,none; 5.81  
 428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino acid transporter), member 5; elF6,SDF;TM=M;; 5.78  
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; p450;TM=Y;SS=M; 5.78  
 449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep\_L\_domain,none; 5.77  
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 5.77  
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); MIF,sugar\_tr,none; 5.75  
 409533; AW969543; Hs.21291; mitogen-activated protein kinase kinase kinase 13; Peptidase\_C48,none; 5.73  
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) receptor; hormone\_rec,zf-C4,Metallothio\_5;TM=M;; 5.73  
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kinase); none,none; 5.72  
 448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; SH2,STAT,STAT\_bind,STAT\_prot;TM=M;; 5.72  
 452295; BE379936; Hs.28866; programmed cell death 10; serpin,none; 5.72  
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; NUDIX;TM=M;SS=M; 5.72  
 448733; NM\_005629; Hs.187958; solute carrier family 6 (neurotransmitter transporter, creatine), member 8; SNF;TM=Y;; 5.71  
 417015; M83772; Hs.80876; flavin containing monooxygenase 3; FMO-like,pyr\_redox;TM=Y;SS=M; 5.69  
 453323; AF034102; Hs.32951; solute carrier family 29 (nucleoside transporters), member 2; Nucleoside\_tran;TM=Y;SS=M; 5.69  
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,Integrin\_B;TM=Y;SS=M; 5.69  
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 46kD; rrm,hormone\_rec,zf-C4,sugar\_tr;; 5.69  
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; none;TM=Y;SS=M; 5.66  
 447250; AI878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; PP2C;TM=M;; 5.65  
 438113; AI467908; Hs.8882; ESTs; 7tm\_1,none; 5.65  
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; ig,none; 5.64  
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; Sm,pkinase;; 5.64  
 406137; ; NM\_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA. VERSION NM\_000178.1 GI; MutS\_C,PWWP,MutS\_N;TM=M;; 5.63  
 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3\_P4\_kinase,PI3Ka;TM=M;; 5.62  
 445873; AA2050970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-like; PABP,rrm,pkinase,14-3-3; 5.62  
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; SH3,PH,RhoGEF;TM=M;; 5.61  
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein coupled, 6; 7tm\_1;TM=Y;SS=M; 5.59  
 433662; W07162; Hs.150826; CATX-8 protein; ras,ABC\_tran,arf;TM=M;SS=M; 5.59  
 449029; N28989; Hs.22891; solute carrier family 7 (cationic amino acid transporter, y system), member 8; aa\_permeases;TM=Y;SS=M; 5.58  
 431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 5.57  
 430508; AI015435; Hs.104637; ESTs; SDF;TM=Y;SS=M; 5.56  
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; 7tm\_1;TM=Y;SS=M; 5.55  
 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo\_seg,IBB; 5.54  
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;; 5.54  
 429563; BE619413; Hs.2437; eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD); hexapep,W2,hormone2,DUF29;TM=M;; 5.52  
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subunit, non-ATPase, 2; PC\_rep;TM=M;; 5.51  
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; pkinase;TM=M;; 5.51  
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (from clone DKFZp547C136); ABC\_tran,GTP\_EFTU,ABC\_membrane,none; 5.50  
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr\_redox;TM=Y;SS=M; 5.48  
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); SH3,PX;TM=M;; 5.48  
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304; Nucleoside\_tra2,none; 5.48  
 426691; NM\_006201; Hs.171834; PCTAIRE protein kinase 1; pkinase;TM=M;; 5.48  
 453905; NM\_002314; Hs.36566; LIM domain kinase 1; pkinase,LIM,PDZ,zf-PARP;TM=M;; 5.48  
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor 1 gamma; none,none; 5.44  
 430486; BE062109; Hs.241551; chloride channel, calcium activated, family member 2; none;TM=Y;SS=M; 5.43  
 430066; AI929659; Hs.237825; signal recognition particle 72kD; TPR,AIRC,SAICAR\_synt; 5.40  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; kinesin,fn3,Y\_phosphatase;TM=M;; 5.40  
 411825; AK000334; Hs.72289; hypothetical protein FLJ20327; SNF,Zip;TM=Y;; 5.36  
 400205; ; NM\_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA.(APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA.; DUF173;SS=M; 5.35  
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl\_oxidase;SS=M; 5.34  
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 5.34  
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase; myb\_DNA-binding,THF\_DHG\_CYH,THF\_DHG\_CYH\_C,CAP\_GLY,AAA,LON,Peptidase\_C9,bZIP,M,xan\_ur\_permease,HCO3\_cotransp;TM=M;; 5.32  
 400210; ; Eos Control; Adap\_comp\_sub,Clat\_adaptor\_s;TM=M;; 5.32  
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog); Furin-like,pkinase,Recep\_L\_domain;TM=M;SS=M; 5.31  
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2; serpin;SS=M; 5.30  
 416000; R82342; Hs.79856; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; none,sugar\_tr; 5.30  
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 5.29  
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; SH2,SH3,pkinase;TM=M;; 5.29  
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; none,none; 5.29  
 456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, complete cds; none,PK,PK\_C,myosin\_head,RhoGAP; 5.28  
 410068; AI633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3;TM=M;; 5.28  
 456629; AW891965; Hs.279789; histone deacetylase 3; HSP90,HATPase\_c,zf-C2H2,PHD,none; 5.27  
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); pkinase,Sema,PSI,TIG,Integrin\_B;TM=Y;SS=M; 5.26  
 444051; N48373; Hs.10247; activated leucocyte cell adhesion molecule; none,none; 5.26

- 404083; ; C6002159\*gi|628027|pir||A53593 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor ty; none;SS=M; 5.26  
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1; mito\_carr;TM=M;; 5.26  
 419034; NM\_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M;; 5.26  
 427732; NM\_002980; Hs.2199; secretin receptor; 7tm\_2,HRM;TM=M;SS=M; 5.25  
 425921; NM\_007231; Hs.162211; solute carrier family 6 (neurotransmitter transporter), member 14; SNF;TM=Y;SS=M; 5.25  
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A, member 4A; none;TM=Y;SS=M; 5.24  
 441607; NM\_005010; Hs.7912; neuronal cell adhesion molecule; WD40,fn3,ig;TM=M;; 5.23  
 446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 5.23  
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS\_C;TM=M;; 5.23  
 447131; NM\_004585; Hs.17466; retinoic acid receptor responder (tazarotene induced) 3; none;TM=Y;; 5.21  
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; SH3,HS1\_rep;TM=M;; 5.20  
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;; 5.19  
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; Troponin,Exo\_endo\_phos,IQ;TM=M;; 5.19  
 446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonine kinase 21); CNH,DAG\_PE-bind,PH,Involucrin,M;TM=M;; 5.19  
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 5.19  
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, subfamily J, member 15; IRK;TM=Y;; 5.19  
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; Ribosomal\_S14,ank,pkinase,death,none; 5.18  
 442200; AW590572; Hs.235768; ESTs; none,none; 5.18  
 446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A, member 6A; none;TM=Y;SS=M; 5.18  
 452690; AI536070; Hs.15085; ESTs; pou,homeobox,lig\_chan,ANF\_receptor; 5.18  
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); Ion\_trans,SPRY,RYDR,ITPR,RyR,MIR;TM=Y;; 5.17  
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;; 5.16  
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M;; 5.16  
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta (Liddle syndrome); ASC;TM=Y;SS=M; 5.15  
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cytotactin); EGF,fn3,fibrinogen\_C,toxin\_2,Keratin\_B2;TM=M;SS=Y; 5.15  
 411984; NM\_005419; Hs.72988; signal transducer and activator of transcription 2, 113kD; SH2,STAT,STAT\_bind,STAT\_prot;TM=M;; 5.15  
 433470; AW960564; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 5.14  
 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M;; 5.14  
 453102; NM\_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm\_2;TM=Y;SS=M; 5.14  
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; SRP14,TNFR\_c6;SS=M; 5.14  
 430563; AA481269; ; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; ABC\_tran,GTP\_EFTU,ABC\_membrane,none; 5.13  
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar\_tr;TM=Y;; 5.12  
 431183; NM\_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3; ER\_lumen\_recept;TM=M;SS=M; 5.12  
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarotene induced) 1; none,none; 5.11  
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase kinase kinase 1; pkinase,CNH;TM=M;; 5.11  
 409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfamily, member 13; TNF;TM=Y;SS=M; 5.11  
 436856; AI469355; Hs.127310; ESTs; pkinase,rm;TM=M;; 5.09  
 411296; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell\_Oxy;TM=M;SS=M; 5.09  
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; rm;TM=M;; 5.09  
 404440; ; NM\_021048;Homo sapiens melanoma antigen, family A, 10 (MAGEA10), mRNA. VERSION NM\_021049.1 GI; MAGE;TM=M;; 5.08  
 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; none,none; 5.08  
 422100; AI096988; Hs.111554; ADP-ribosylation factor-like 7; arf,ras;TM=M;; 5.07  
 452222; AW806287; Hs.21432; SEX gene; Sema,TIG,PSI,GDI; 5.07  
 430300; U60805; Hs.238648; oncostatin M receptor; fn3;TM=Y;SS=M; 5.07  
 408369; R38438; Hs.182575; solute carrier family 15 (H??? transporter), member 2; PTR2;TM=Y;; 5.07  
 422112; BE540240; Hs.111783; Lsm1 protein; Sm,BAG;SS=M; 5.06  
 449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep\_L\_domain,none; 5.06  
 430024; AI808780; Hs.227730; integrin, alpha 6; integrin\_A,FG-GAP;TM=Y;SS=M; 5.06  
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; HSP90,HATPase\_c;TM=M;; 5.05  
 437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; pkinase,RIO1,none; 5.05  
 400296; AA305627; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC\_tran,ABC\_membrane;TM=Y;; 5.04  
 446232; AI281848; Hs.194691; retinoic acid induced 3; 7tm\_3,none; 5.04  
 425262; D87119; Hs.155418; GS3955 protein; pkinase;SS=M; 5.04  
 414703; BE243877; Hs.76941; ATPase, Na? transporting, beta 3 polypeptide; Na\_K-ATPase;TM=Y;SS=M; 5.03  
 434808; AF155108; Hs.256150; Homo sapiens, Similar to RIKEN cDNA 2810027O19 gene, clone MGC:14827, mRNA, complete cds; none;TM=M;; 5.03  
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member 21; death,TNFR\_c6;TM=Y;SS=M; 5.03  
 449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; none,none; 5.03  
 448913; AA194422; Hs.22564; myosin VI; rm,zf-RanBP,pkinase,GST\_C,Ets,SAM\_PNT,ABC2\_membrane,myosin\_head,IQ,Myosin\_N,bZIP,zf-C2H2,PHD,BTB,TFILS,AT\_hook,SAM;TM=M;; 5.02  
 413441; AI929374; Hs.75367; Src-like-adaptor; SH2,SH3;TM=M;; 5.02  
 427618; NM\_000760; Hs.2175; colony stimulating factor 3 receptor (granulocyte); fn3;TM=M;SS=M; 5.02  
 417666; AI345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4;TM=M;; 5.02  
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); CDK5\_activator,none; 5.01  
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; ras,arf,TK;SS=M; 5.01  
 426285; U20620; Hs.343581; karyopherin alpha 1 (importin alpha 5); Armadillo\_seg,IBB;TM=M;; 5.01  
 421233; AA209534; Hs.284243; tetraspan NET-6 protein; transmembrane4;TM=Y;SS=M; 5.01  
 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; SH2,STAT,STAT\_bind,STAT\_prot,none; 5.00  
 425345; AU077297; Hs.155894; protein tyrosine phosphatase, non-receptor type 1; Y\_phosphatase,DSPc;TM=M;SS=M; 5.00  
 446946; AI878932; Hs.317; topoisomerase (DNA) I; Topoisomerase\_I,Tpoisomer\_I\_N,RnaAD,Hanta\_nucleocap;TM=M;; 4.99  
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); TPR,PDZ,WW,Guanylate\_kin;TM=M;; 4.98  
 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor); 7tm\_1;TM=Y;SS=M; 4.98  
 400792; AA635062; ; Homo sapiens mRNA; cDNA DKFZp434O0515 (from clone DKFZp434O0515); zf-C3HC4,CARD,BIR;TM=M;; 4.98  
 417018; M16038; Hs.80887; y-yes-1 Yamaguchi sarcoma viral related oncogene homolog; SH2,SH3,pkinase;TM=M;; 4.98  
 427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); vwa,integrin\_A,FG-GAP;TM=Y;SS=M; 4.98  
 442080; AW444761; Hs.44565; ESTs; ank; 4.97  
 454042; H22570; ; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT,none; 4.97  
 452698; NM\_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm\_1;TM=Y;SS=M; 4.96  
 416276; U41060; Hs.79136; LIV-1 protein, estrogen regulated; Peptidase\_C4,Osteopontin,Zip;TM=Y;SS=M; 4.96  
 408847; AW290997; Hs.30348; ESTs; pkinase,ig,none; 4.96  
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 4.95  
 450737; AW007152; Hs.203330; ESTs; trypsin,ldl\_recept\_a,none; 4.95  
 443354; AW970672; Hs.9247; protein kinase, AMP-activated, alpha 1 catalytic subunit; pkinase,RIO1;TM=M;; 4.94



- 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y\_phosphatase;TM=M;; 4.94  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,ig,FAD\_Synth,ldh\_C,phkinase;SS=M; 4.94  
 434206; AW136973; Hs.180479; ESTs, Weakly similar to S69890 mitogen inducible gene mig-2 [H.sapiens]; PH;TM=M;; 4.93  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); 7tm\_1,7tm\_2;TM=Y;SS=M; 4.93  
 5 408716; A1567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein, partial cds; UvrD-helicase,RNB,Run;TM=M;; 4.93  
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo\_seg,UQ\_con;none; 4.92  
 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; Ets,SAM\_PNT;TM=M;; 4.92  
 414570; Y00285; Hs.76473; insulin-like growth factor 2 receptor; fn2,CIMR;TM=M;SS=M; 4.92  
 10 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; ig;TM=Y;SS=M; 4.92  
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; DEAD,helicase\_C,CARD;TM=M;; 4.91  
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); ig,ITAM,Zn\_clus;TM=Y;SS=M; 4.91  
 404289; ; NM\_002944; Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA; fn3,phkinase,DUF139;TM=Y;SS=M; 4.90  
 428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1; Nramp;TM=Y;; 4.90  
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none;TM=M;SS=Y; 4.89  
 15 432179; X75208; Hs.2913; EphB3; EPH\_lbd,fn3,phkinase,SAM;TM=Y;SS=M; 4.89  
 401083; ; NM\_016582; Homo sapiens peptide transporter 3 (LOC51296), mRNA. VERSION NM\_016579.1 GI; PTR2;TM=Y;SS=M; 4.89  
 402211; AA811738; ; KIAA0430 gene product; ion\_trans,K\_tetra;TM=Y;; 4.88  
 421541; NM\_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polypeptide 4; phkinase,phkinase\_C;TM=M;; 4.87  
 20 431810; X67155; Hs.270845; kinesin-like 5 (mitotic kinesin-like protein 1); kinesin;TM=M;; 4.86  
 425295; AA431366; Hs.37251; ESTs; phkinase;none; 4.86  
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; DNA\_ligase;; 4.86  
 419168; A1336132; Hs.33718; Homo sapiens cDNA FLJ12641 fis, clone NT2RM4001953; none;none; 4.86  
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequence; K\_tetra,DUF51;none; 4.86  
 25 425465; L18964; Hs.1904; protein kinase C, iota; phkinase,DAG\_PE-bind,phkinase\_C,OPR;TM=M;; 4.86  
 410293; AK000047; Hs.61960; hypothetical protein; K\_tetra;TM=M;; 4.86  
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; C1q,Collagen;SS=M; 4.85  
 445903; A1347487; Hs.132781; class I cytokine receptor; fn3;TM=Y;; 4.85  
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a ligand); 7tm\_1;TM=Y;SS=M; 4.85  
 30 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); vva,integrin\_A,Fc-GAP;TM=Y;SS=M; 4.84  
 445143; U29171; Hs.75852; casein kinase 1, delta; zf-C3HC4,Filamin,zf-B\_box,NHL,phkinase,zf-MIZ;TM=M;; 4.82  
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;; 4.81  
 427857; AL133017; Hs.2210; hypothetical protein FLJ22865; myosin\_head,IQ,zf-MYND;TM=M;SS=M; 4.81  
 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); aldedh,aakinase;TM=M;; 4.81  
 35 414280; BE410768; Hs.75873; zyxin; LIM,ig,phkinase;TM=M;SS=M; 4.81  
 424570; AA343306; Hs.133511; ESTs; SH3,ank;none; 4.80  
 451144; AW956103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase\_c;none; 4.80  
 402705; AA214618; ; activator of S phase kinase; AhpC-TSA;TM=M;SS=M; 4.80  
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3;TM=M;; 4.80  
 40 419972; AL041465; Hs.182982; golgin-67; none;none; 4.80  
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C;none; 4.80  
 413476; U25849; Hs.75393; acid phosphatase 1, soluble; LMWPc;TM=M;SS=M; 4.80  
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, receptor for (CD32); ig;TM=Y;; 4.79  
 402233; ; NM\_030760; Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 8 (EDG8), mRNA; 7tm\_1;TM=Y;SS=M; 4.79  
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; NusG;SS=M; 4.79  
 407722; BE252241; Hs.38041; pyridoxine (pyridoxine, vitamin B6) kinase; phkB;TM=M;; 4.79  
 405370; ; NM\_005569; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA; phkinase,LIM,PDZ;SS=M; 4.79  
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1 (TWIK-1); ion\_trans;TM=Y;SS=M; 4.78  
 429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin\_G,CorA;SS=M; 4.78  
 50 424415; NM\_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase;TM=M;; 4.78  
 433133; AB027249; Hs.104741; PDZ-binding kinase; T-cell originated protein kinase; phkinase;TM=M;; 4.78  
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); none;TM=M;SS=Y; 4.78  
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; ig,abhydrolase; 4.78  
 55 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2;TM=Y;SS=M; 4.78  
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; phkinase;SS=M; 4.77  
 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (from clone DKFZp586P2321); none;NA;NA; 4.77  
 446196; A1744888; Hs.149470; ESTs; zf-C3HC4,Sulfate\_transp,STAS; 4.77  
 429305; AF095727; Hs.287832; myelin protein zero-like 1; ig,transmembrane4;TM=Y;SS=M; 4.77  
 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chloride transporters), member 7; none;TM=Y;; 4.77  
 60 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); Armadillo\_seg,IBB,DEAD,helicase\_C,Sec63,DDT,PHD,bromodomain;TM=M;; 4.77  
 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; DSPc;TM=M;; 4.77  
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702; GDI,7tm\_1;none; 4.76  
 447207; AA442233; Hs.17731; hypothetical protein FLJ12892; none;TM=M;; 4.76  
 400846; ; sortilin-related receptor, L(DLR class) A repeats-containing (SORL1); EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 4.76  
 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm\_1,OATP\_C;TM=Y;; 4.75  
 406809; AF000574; Hs.22405; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2; ig,Gemini\_mov;TM=M;SS=M; 4.75  
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE;TM=M;; 4.75  
 444042; NM\_004915; Hs.10237; ATP-binding cassette, sub-family G (WHITE), member 1; ABC\_tran,PRK,GBP;TM=Y;; 4.74  
 70 410406; A1969703; Hs.1466; glycerol kinase; FGGY,FGGY\_C;TM=M;; 4.73  
 411653; AF070578; Hs.71168; Homo sapiens clone 24674 mRNA sequence; none;NA;NA; 4.73  
 437667; BE616412; Hs.286218; junctional adhesion molecule 1; none;HLH; 4.73  
 417781; BE279380; Hs.82563; KIAA0153 protein; TTL,AcyL\_transf; 4.73  
 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin,ldl\_recept\_a;none; 4.73  
 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr virus) receptor 2; sushi;TM=Y;SS=M; 4.73  
 75 418255; AW135405; Hs.37251; ESTs; phkinase;none; 4.73  
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; SDF;TM=Y;SS=M; 4.73  
 406906; Z25424; ; gb;H.sapiens protein-serine/threonine kinase gene, complete CDS; none;none; 4.73  
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; Metallophos;TM=M;; 4.72  
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese;SS=M; 4.72  
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; NDK,PH,Oxysterol\_BP;SS=M; 4.71  
 426136; AW997239; ; gb;EST369309 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence; PP2C;none; 4.71  
 446203; Z47553; Hs.14286; flavin containing monooxygenase 5; FMO-like,pyr\_redox;TM=Y;SS=M; 4.71  
 451295; A1557212; Hs.17132; ESTs, Moderately similar to 154374 gene NF2 protein [H.sapiens]; phkinase,DAG\_PE-bind,phkinase\_C,OPR;none; 4.71

- 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC\_tran,ABC\_membrane;TM=Y;; 4.70
- 424959; NM\_005781; Hs.153937; activated p21cdc42Hs kinase; ldn,ldh\_C,SH3,pkinase,UBA;TM=M;; 4.70
- 427206; NM\_004586; Hs.173965; ribosomal protein S6 kinase, 90kD, polypeptide 3; none,none; 4.70
- 421662; NM\_014141; Hs.106552; cell recognition molecule Caspr2; EGF,F5\_F8\_type\_C,laminin\_G,Sulfate\_transp,STAS,7tm\_3,xan\_ur\_permease;TM=Y;SS=M; 4.70
- 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); UQ\_con;TM=M;; 4.70
- 405484; ; C3002124; gjl12737280[ref]XP\_006682.2| keratin 18 [Homo sapiens]||6633; none;SS=M; 4.70
- 401345; M83738; ; protein tyrosine phosphatase, non-receptor type 9; none;TM=M;; 4.70
- 416602; NM\_006159; Hs.79389; nel (chicken)-like 2; EGF,ywc,TSPN;SS=Y; 4.69
- 412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH\_lbd;TM=Y;SS=M; 4.69
- 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC;none; 4.69
- 432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M;; 4.69
- 400843; ; NM\_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 4.68
- 433409; AI278802; Hs.25661; ESTs; pkinase,pkinase; 4.68
- 413869; NM\_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 4.68
- 430259; BE550182; Hs.127826; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 4.68
- 425761; AW664214; Hs.196729; ESTs; SH3,Ribosomal\_S3Ae; 4.68
- 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone COL04544; pkinase,Furin-like,Recep\_L\_domain;none; 4.68
- 419493; AF001212; Hs.90744; proteasome (prosome, macropain) 26S subunit, non-ATPase, 11; CDK5\_activator,PCI;none; 4.67
- 425966; NM\_001761; Hs.1973; cyclin F; cyclin F-box,cyclin\_C;TM=M;; 4.67
- 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 4.67
- 453476; AI640500; Hs.24633; SAM domain, SH3 domain and nuclear localisation signals, 1; SH3,SAM;SS=M; 4.67
- 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; MARCKS;SS=M; 4.67
- 424635; AA406887; Hs.115455; Homo sapiens cDNA FLJ14259 fis, clone PLACE1001076; pkinase,Furin-like,Recep\_L\_domain;none; 4.66
- 446051; BE048061; Hs.37054; ephrin-A3; Ephrin,A\_deamin,dsm,z-alpha; 4.66
- 436729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.66
- 408204; AA454501; Hs.43666; protein tyrosine phosphatase type IVA, member 3; Y\_phosphatase;TM=M;; 4.66
- 435542; AA687376; ; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF;none; 4.66
- 429682; NM\_006306; Hs.211602; SMC1 (structural maintenance of chromosomes 1, yeast)-like 1; ABC\_tran,SMC\_N,SMC\_C,KID;TM=M;; 4.66
- 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4;TM=Y;SS=M; 4.66
- 418736; T18979; Hs.87908; Snf2-related CBP activator protein; helicase\_C,AT\_hook,SNF2\_N;TM=M;; 4.65
- 415117; AF120499; Hs.78016; polynucleotide kinase 3'-phosphatase; Viral\_helicase1;TM=M;; 4.65
- 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA;SS=M; 4.65
- 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;; 4.64
- 429263; AA019004; Hs.198396; ATP-binding cassette, sub-family A (ABC1), member 4; ABC\_tran,SRP54;TM=Y;SS=M; 4.64
- 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M;; 4.63
- 435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none;TM=M;; 4.63
- 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor); TIMP,pkinase,DAG\_PE-bind,RBD; 4.63
- 413436; AF238083; Hs.68061; sphingosine kinase 1; DAGKc;TM=M;; 4.63
- 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; ehfand,ldl\_recept\_a;SS=M; 4.62
- 442590; AI002686; Hs.130313; ESTs; none,Y\_phosphatase,Band\_41,connexin; 4.62
- 416224; NM\_002902; Hs.79088; reticulocalbin 2, EF-hand calcium binding domain; ehfand;SS=M; 4.62
- 423740; Y07701; Hs.293007; aminopeptidase puromycin sensitive; Peptidase\_M1,Armado\_seg; 4.61
- 429300; AB011108; Hs.198891; serine/threonine-protein kinase PRP4 homolog; pkinase;TM=M;; 4.60
- 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 4.60
- 412942; AL120344; Hs.75074; mitogen-activated protein kinase-activated protein kinase 2; pkinase;TM=M;; 4.60
- 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPc;; 4.59
- 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); EGF,lectin\_c,sushi;TM=M;SS=M; 4.59
- 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 4.59
- 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,WW,RhoGAP;SS=M; 4.58
- 447312; AI434345; Hs.36908; activating transcription factor 1; rrm,zf-RanBP,pkinase,GST\_C,Ets,SAM\_PNT,ABC2\_membrane,myosin\_head,IQ,Myosin\_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT\_hook,SAM;TM=M;; 4.58
- 435254; AW194689; Hs.30778; ESTs; pkinase,Bacterial\_PQQ;none; 4.58
- 426925; NM\_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fis, clone HRC06741; Esterase,enolase,Peptidase\_S9;TM=M;; 4.58
- 421685; AF189723; Hs.106778; ATPase, Ca transporting, type 2C, member 1; Cation\_ATPase\_C,Cation\_ATPase\_N,E1-E2\_ATPase,Hydrolase,XPG\_N;TM=Y;; 4.58
- 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; fn3,ig\_Y\_phosphatase,MAM;TM=Y;SS=M; 4.58
- 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST\_C,EF1G\_domain,GST\_N,S1,Fz,Frizzled,calreticulin,7tm\_2,rrm,PAP\_assoc;TM=Y;SS=M; 4.57
- 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT2RM4000200; none,none; 4.57
- 409581; U66243; Hs.55039; mitogen-activated protein kinase 12; pkinase;SS=M; 4.57
- 423184; NM\_004428; Hs.1624; ephrin-A1; Ephrin;TM=M;SS=M; 4.56
- 443920; AL037764; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; none,FMO-like; 4.56
- 422627; BE336857; Hs.118787; transforming growth factor, beta-induced, 68kD; Fasciclin,ABC\_tran,ABC\_membrane,GTP\_EFTU;TM=M;SS=M; 4.56
- 418869; AW516565; ; gb:xq01d05.x1 Soares\_NHCCc\_cervical\_tumor Homo sapiens cDNA clone 3' similar to contains Alu repetitive element;contains element MER11 repetitive element ;, mRNA sequence; none,RasGAP,WW,IQ; 4.56
- 430016; NM\_004736; Hs.227656; xenotropic and polytropic retrovirus receptor; SPX,EXS;TM=Y;; 4.56
- 437157; BE048860; Hs.120655; ESTs; IRK;none; 4.55
- 422769; AA938905; Hs.120017; olfactory receptor, family 7, subfamily E, member 38 pseudogene; none,none; 4.55
- 457918; AL359590; Hs.162604; hypothetical protein DKFZp762M186; PLDC;TM=M;; 4.55
- 434467; BE552368; Hs.231853; Homo sapiens cDNA FLJ13445 fis, clone PLACE1002962; 7tm\_1,none; 4.55
- 421140; AA298741; Hs.102135; signal sequence receptor, delta (translocon-associated protein delta); none;TM=Y;SS=M; 4.55
- 406364; ; Target Exon; hexapep;TM=M;; 4.55
- 434682; AA827165; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; ig;none; 4.54
- 438939; H21012; Hs.287657; Homo sapiens cDNA: FLJ21291 fis, clone COL01963; F5\_F8\_type\_C,pkinase,Ets;none; 4.54
- 433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; EF\_TS,UBA;; 4.54
- 411165; NM\_000169; Hs.69089; galactosidase, alpha; Melibiase;SS=M; 4.54
- 408956; AK001868; Hs.49344; hypothetical protein FLJ11006; ion\_trans;TM=Y;; 4.54
- 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related); SH3;TM=M;; 4.53
- 410226; AI831958; Hs.61053; hypothetical protein; SH3,TPR;TM=M;; 4.53
- 422753; AI928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); Sm;SS=M; 4.52
- 418355; L42563; Hs.1165; ATPase, H7 transporting, nongastric, alpha polypeptide; E1-E2\_ATPase,Cation\_ATPase\_C,Cation\_ATPase\_N,Hydrolase;TM=Y;; 4.52
- 400261; ; Eos Control; ig,MHC\_IL\_beta;TM=Y;SS=M; 4.52
- 444633; AF111713; Hs.286218; junctional adhesion molecule 1; ig;TM=Y;SS=M; 4.52
- 422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo sapiens cDNA, mRNA sequence; Sec7,PH,ANF\_receptor,lig\_chan,WD40,IRK; 4.52

- 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none,none; 4.51  
 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase,DAG\_PE-bind,kinase\_C,OPR;TM=M;; 4.51  
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin;TM=M;; 4.51  
 457906; AW975939; Hs.153290; Homo sapiens cDNA FLJ14318 fis, clone PLACE3000402; none,kinase; 4.51  
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 4.51  
 429690; AW956329; Hs.23721; ESTs; none,sugar\_tr,Ribosomal\_S25; 4.50  
 424618; L29472; Hs.1802; major histocompatibility complex, class II, DO beta; ig,MHC\_II\_beta;TM=Y;SS=M; 4.50  
 444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 4.50  
 405490; ; NM\_031414;Homo sapiens serine/threonine kinase 31 (STK31), transcript variant 1, mRNA.; pkinase,TUDOR;TM=M;; 4.50  
 424494; U78575; Hs.149255; phosphatidylinositol-4-phosphate 5-kinase, type I, alpha; PIP5K;SS=M; 4.50  
 441031; A1110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen\_C,G-alpha,arf;TM=M;SS=M; 4.50  
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22\_Claudin,none; 4.50  
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; SH2,Y\_phosphatase,DSPc;TM=M;; 4.50  
 429556; AW139399; Hs.98988; ESTs; none;TM=M;; 4.50  
 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y;; 4.49  
 425209; AL049761; Hs.155140; casein kinase 2, alpha 1 polypeptide; pkinase,ABC1;TM=M;; 4.49  
 425695; NM\_005401; Hs.159238; protein tyrosine phosphatase, non-receptor type 14; Y\_phosphatase,Band\_41,DSPc;TM=M;; 4.49  
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal\_L24e,SRP54,dDENN,DENN,uDENN;TM=M;; 4.49  
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPc;SS=M; 4.48  
 400755; AA635062; ; Homo sapiens mRNA; cDNA DKFZp43400515 (from clone DKFZp43400515); zf-C3HC4,CARD,BIR;TM=M;; 4.48  
 425566; AW162943; Hs.250618; UL16 binding protein 2; ldl\_recept\_a,PKD,MHC\_I;TM=M;SS=Y; 4.48  
 410151; X15723; Hs.59242; paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein); Peptidase\_S8,P;TM=Y;SS=M; 4.48  
 423536; L22075; Hs.1666; guanine nucleotide binding protein (G protein), alpha 13; UCR\_hinge,G-alpha,arf;TM=M;; 4.48  
 424711; NM\_005795; Hs.152175; calcitonin receptor-like; 7tm\_2,HRM;TM=Y;SS=M; 4.48  
 427878; C05766; Hs.181022; CGI-07 protein; none,zf-C2H2; 4.48  
 443991; NM\_002250; Hs.10082; potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4; CaMBD,SK\_channel,ion\_trans;TM=Y;SS=M; 4.48  
 422605; H16646; Hs.118666; hypothetical protein PP591; PAPS\_reduct,MoCF\_biosynth;; 4.47  
 410583; AW770280; Hs.36258; ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]; SH3,PDZ,Guanylate\_kin,none; 4.47  
 434419; AL046060; Hs.296938; dual specificity phosphatase 7; DSPc;TM=M;; 4.47  
 410032; BE065985; ; gb:RC3-BT0319-120200-014-a09 BT0319 Homo sapiens cDNA, mRNA sequence; abhydrolase\_2,none; 4.46  
 423078; M35198; Hs.123125; integrin, beta 6; integrin\_B,EGF\_pp-binding;TM=Y;SS=M; 4.46  
 400263; ; Eos Control; GTP\_EFTU,EGF\_C,GTP\_EFTU\_D2,serpin;TM=M;; 4.46  
 441406; Z45957; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase;TM=M;; 4.45  
 434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; none;TM=M;; 4.45  
 413227; M79082; ; ESTs; none,none; 4.45  
 441321; H17182; Hs.7771; B-cell associated protein; Band\_7;TM=M;; 4.45  
 457194; H20669; Hs.35406; ESTs, Highly similar to unnamed protein product [H.sapiens]; none,pkinase,PBD; 4.45  
 414745; AA160511; Hs.5326; amino acid system N transporter 2; porcupine; none,none; 4.45  
 404276; ; NM\_002944;Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA.; fn3,pkinase,DUF139;TM=Y;SS=M; 4.45  
 426966; AL493134; ; sclerostin; DAN;TM=M;SS=M; 4.45  
 408873; AL046017; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none,none; 4.44  
 426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFZp586B0220 (from clone DKFZp586B0220); pkinase,none; 4.44  
 432798; AA565309; Hs.194015; ESTs; integrin\_B,Sema,PSI,TIG,none; 4.44  
 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm\_2,toxin\_2;TM=Y;SS=M; 4.44  
 417886; AA214584; ; ESTs; SPRY,7tm\_3,ANF\_receptor,none; 4.43  
 452098; AI858183; ; gb:wl46a12.x1 NCL\_CGAP\_Ut1 Homo sapiens cDNA clone 3' similar to contains Alu repetitive element,, mRNA sequence; SH3,none; 4.43  
 426874; N67325; Hs.347487; ESTs; SH3,TonB\_boxC,none; 4.43  
 422714; AB018335; Hs.119387; KIAA0792 gene product; DUF221;TM=Y;SS=M; 4.42  
 410741; Z11695; Hs.324473; mitogen-activated protein kinase 1; pkinase,none; 4.42  
 432193; AA372264; Hs.273193; hypothetical protein FLJ10706; pkinase;TM=M;; 4.41  
 409506; NM\_006153; Hs.54589; NCK adaptor protein 1; SH2,SH3;TM=M;; 4.41  
 429390; AB040942; Hs.201500; KIAA1509 protein; none;TM=M;; 4.41  
 421859; AA356620; Hs.108947; KIAA0050 gene product; ank,PH,ArfGap;SS=M; 4.41  
 451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none,none; 4.41  
 421748; NM\_014718; Hs.107809; KIAA0726 gene product; cadherin;TM=Y;; 4.40  
 410416; BE410072; Hs.63304; protein phosphatase methyltransferase-1; none;TM=M;; 4.40  
 450457; AA367701; Hs.6639; KIAA1624 protein; none;TM=M;SS=M; 4.40  
 433029; NM\_014322; Hs.279926; opsin 3 (encephalopsin); 7tm\_1,Monoxygenase;TM=Y;SS=M; 4.40  
 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase;TM=M;; 4.40  
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm\_1;TM=Y;SS=M; 4.40  
 440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; SPRY,BAG,UPF0001; 4.40  
 451154; AA015879; Hs.33536; ESTs; TIMP,none; 4.40  
 433895; AI287912; Hs.3628; mitogen-activated protein kinase kinase kinase kinase 4; pkinase,zf-C4,CNH,ERM;TM=M;; 4.40  
 422034; AC006486; Hs.333069; Ets2 repressor factor; Ets;TM=M;; 4.39  
 444009; AI380792; Hs.135104; ESTs; TNFR\_c6,TIL,none; 4.39  
 420020; BE295866; Hs.94382; adenosine kinase; pfkB;SS=M; 4.39  
 416207; NM\_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, complete cds; none;TM=Y;SS=M; 4.39  
 417655; AA780791; Hs.14014; hypothetical protein FLJ14813; pkinase,pkinase\_C;TM=M;; 4.39  
 402915; ; ENSP00000202587; Bicarbonate transporter-related protein BTR1.; HCO3\_cotransp;TM=Y;; 4.39  
 453199; AI336266; Hs.32353; mitogen-activated protein kinase kinase kinase 4; pkinase;TM=M;; 4.38  
 416033; NM\_012201; Hs.78979; Golgi apparatus protein 1; cys\_rich\_FGFR;TM=Y;SS=M; 4.38  
 453672; U73531; Hs.34526; G protein-coupled receptor; 7tm\_1;TM=Y;SS=M; 4.38  
 437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365O12.1 [H.sapiens]; GPS,7tm\_2;TM=Y;; 4.38  
 420039; NM\_004605; Hs.94581; sulfotransferase family, cytosolic, 2B, member 1; Sulfotransfer;SS=M; 4.38  
 412834; R77123; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone LNG00414; 7tm\_1,none; 4.38  
 452203; X57522; ; transporter 1, ATP-binding cassette, sub-family B (MDR/TAP); ABC\_tran,ABC\_membrane,SRP54,Thymidylate\_kin;TM=Y;SS=M; 4.37  
 425317; AW205118; Hs.210546; interleukin 21 receptor; none;TM=Y;SS=M; 4.37  
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 4.37  
 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fis, clone Y79AA1001384, highly similar to Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA; none,none; 4.37  
 434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M;; 4.37  
 412596; AA161219; Hs.799; diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor); EGF;TM=Y;SS=M; 4.36  
 440270; NM\_015986; Hs.7120; cytokine receptor-like molecule 9; fn3;SS=M; 4.36

- 432987; AI864771; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none; TM=Y; SS=M; 4.36
- 436943; AA773838; Hs.5353; caspase 10, apoptosis-related cysteine protease; ICE\_p10, ICE\_p20, DED; TM=M; 4.36
- 457897; AI356125; Hs.345168; ESTs, Weakly similar to HXA2\_HUMAN HOMEBOX PROTEIN HOX-A2 [H.sapiens]; homeobox; NA; NA; 4.36
- 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); Sema, kinase, TIG, PSI; none; 4.36
- 5 413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidylinositol-specific); SH2, SH3, C2, PH, PI-PLC-Y, PI-PLC-X, PDGF; SS=M; 4.35
- 408101; AW968504; Hs.123073; CDC2-related protein kinase 7; none; none; 4.35
- 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); Man-6-P\_recep; TM=M; SS=M; 4.35
- 10 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; aldo\_ket\_red; none; 4.35
- 438937; AW952654; Hs.244624; ESTs; EPH\_lbd, kinase, fn3, SAM; none; 4.35
- 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; none; lectin\_c; 4.35
- 436540; BE397032; Hs.14468; hypothetical protein MGC14226; rrm, 7tm\_1, SNF; TM=M; 4.34
- 435267; N23797; Hs.110114; ESTs; none; Syja\_N, Exo\_endo\_phos; 4.34
- 405616; ; Target Exon; none; SH3, BAR; 4.34
- 15 432141; BE410964; Hs.272736; nuclear receptor binding protein; kinase; TM=M; 4.33
- 417927; R73095; Hs.24122; ESTs; none; kinase; 4.33
- 429849; U33053; Hs.2499; protein kinase C-like 1; kinase, kinase\_C, HR1; TM=M; 4.33
- 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2; TM=Y; 4.33
- 435863; X02544; Hs.572; orosomucoid 1; lipocalin, aldehyd, ubiquitin, IRK; SS=M; 4.33
- 20 400847; ; NM\_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA; EGF, fn3, ldl\_recept\_a, ldl\_recept\_b, granulin, BNR; TM=Y; SS=M; 4.33
- 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT, FATC, PI3\_PI4\_kinase; TM=M; 4.33
- 413858; NM\_001610; Hs.75589; acid phosphatase 2, lysosomal; acid\_phosphat; TM=Y; SS=M; 4.33
- 442539; AL119506; Hs.58220; Homo sapiens cDNA: FLJ23005 fis, clone LNG00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP, adenylate kinase; 4.33
- 25 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; IMP4; TM=M; 4.32
- 436703; AW880614; Hs.146381; RNA binding motif protein, X chromosome; rrm, SH3, PH, CH, RhoGEF; 4.32
- 414899; AW975433; Hs.36288; ESTs; kinase, SH2, SH3; none; 4.32
- 444895; AI674383; Hs.22891; solute carrier family 7 (cationic amino acid transporter, y system), member 8; ASC, death, TNFR\_c6; 4.31
- 30 415135; AW673559; Hs.78040; KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1; ER\_lumen\_recept; none; 4.31
- 444070; NM\_015367; Hs.10267; MLI1 protein; Bcl-2; TM=Y; 4.31
- 422611; AA158177; Hs.118722; fucosyltransferase 8 (alpha (1,6) fucosyltransferase); SH3, K-box; TM=M; SS=Y; 4.31
- 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; bromodomain; TM=M; 4.30
- 440983; M20681; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; sugar\_tr; TM=Y; SS=M; 4.30
- 35 414080; AA135257; Hs.47783; B aggressive lymphoma gene; A1p; TM=M; 4.30
- 415072; BE253687; Hs.77876; Homo sapiens, clone IMAGE:3461982, mRNA, partial cds; Metallophos, Armadillo\_seg; TM=M; 4.30
- 442994; AI026718; Hs.16954; ESTs; ank, kinase, death, Ribosomal\_S14; 4.30
- 432328; AI572739; Hs.195471; 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3; PGAM, 6PF2K; TM=M; 4.29
- 439490; AW249197; Hs.100043; ESTs, Weakly similar to A46302 PTB-associated splicing factor, long form [H.sapiens]; none; TM=M; 4.29
- 422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (from clone DKFZp761E212); none; Na\_H\_Exchange; 4.29
- 40 415214; AI445236; Hs.125124; EphB2; fn3, kinase, SAM, EPH\_lbd; TM=Y; SS=M; 4.29
- 430316; NM\_000875; Hs.239176; insulin-like growth factor 1 receptor; fn3, Furin-like, kinase, Recep\_L\_domain; TM=M; SS=M; 4.29
- 429099; BE439952; Hs.196177; phosphorylase kinase, gamma 2 (testis); kinase, Bac\_DNA\_binding; TM=M; 4.29
- 425843; BE313280; Hs.159627; death associated protein 3; myb\_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; 4.28
- 45 437603; AW979259; Hs.293673; ESTs; death; none; 4.28
- 439975; AX328081; Hs.6817; inosine triphosphatase (nucleoside triphosphate pyrophosphatase); Ham1p\_like; TM=M; 4.28
- 424512; W53002; Hs.149846; integrin, beta 5; integrin\_B, EGF; TM=Y; SS=M; 4.28
- 442980; AA857025; Hs.8878; kinesin-like 1; kinesin, Luteo\_ORF3, DUF164; TM=M; 4.28
- 420166; AW732276; Hs.95583; transmembrane 4 superfamily member (tetraspan NET-7); transmembrane4; TM=Y; SS=M; 4.27
- 50 409582; R27430; Hs.271565; ESTs; none; Neur\_chan\_LBD, Neur\_chan\_memb; 4.27
- 439096; AA830185; ; ESTs; ras; none; 4.27
- 414561; AI064813; Hs.195155; Homo sapiens amino acid transport system N2 (SN2) mRNA, complete cds; Aa\_trans; TM=Y; 4.27
- 411835; U29343; Hs.72550; hyaluronan-mediated motility receptor (RHAMM); bZIP; SS=M; 4.27
- 428781; AF164799; Hs.193384; putative 28 kDa protein; kinase, DAG\_PE-bind, kinase\_C, OPR; SS=M; 4.27
- 55 430603; AA148164; Hs.247280; HBV associated factor; zf-C3HC4, zf-RanBP, kinase; 4.27
- 415149; X12451; Hs.78056; cathepsin L; Peptidase\_C1; SS=M; 4.26
- 444838; AV651680; Hs.208558; ESTs; Integrin\_A, FG-GAP; none; 4.26
- 402328; ; Target Exon; kinase; TM=M; 4.26
- 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none; none; 4.26
- 60 420942; H03514; Hs.15589; ESTs; none; kinase; 4.26
- 453902; BE502341; Hs.3402; ESTs; none; none; 4.26
- 425505; AL036458; ; gb:DKFZp564D2062\_r1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564D2062 5', mRNA sequence; arf, G-alpha; none; 4.26
- 427344; NM\_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor 3A; Neur\_chan\_LBD, Neur\_chan\_memb; TM=Y; SS=M; 4.26
- 432269; NM\_002447; Hs.2942; macrophage stimulating 1 receptor (c-met-related tyrosine kinase); kinase, Sema, PSI, TIG, A4\_EXTRA; TM=M; SS=M; 4.26
- 65 417007; AF224741; Hs.80768; chloride channel 7; CBS, voltage\_CLC; TM=Y; 4.26
- 447960; AW954377; Hs.26412; ring finger protein 26; zf-C3HC4; TM=Y; SS=M; 4.26
- 442300; AI765908; Hs.129166; ESTs; none; SS=M; 4.25
- 421856; NM\_016447; Hs.108931; MAGUK protein p57; Protein Associated with Lins 2; SH3, PDZ, Guanylate\_kin, L27; TM=M; 4.25
- 452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PLACE1010076; kinase, Activin\_recp; none; 4.25
- 70 422451; AA310753; Hs.42491; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; PDZ, SH2, STAT, STAT\_bind, STAT\_prot; none; 4.25
- 453955; AW579207; Hs.304666; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; fn3, ig, MAM; none; 4.25
- 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substrate; SH3; TM=M; 4.25
- 419133; U46116; Hs.89627; protein tyrosine phosphatase, receptor type, G; fn3, Y\_phosphatase, carb\_anhydrase, DSPc; TM=Y; SS=M; 4.25
- 419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; aa\_permeases; TM=Y; SS=M; 4.25
- 75 415198; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M; 4.24
- 416440; AI823912; Hs.79335; Homo sapiens, Similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1, clone MGC:15280, mRNA, complete cds; SWIB; TM=M; 4.24
- 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothetical protein [H.sapiens]; none, spectrin, SH3, PH, CH; 4.24
- 449444; AW818436; Hs.23590; solute carrier family 16 (monocarboxylic acid transporters), member 4; none; TM=Y; SS=M; 4.24
- 80 433848; AF095719; Hs.93764; carboxypeptidase A4; Zn\_carbOpept, Propep\_M14; SS=M; 4.24
- 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glucose transporter), member 10; sugar\_tr; TM=Y; SS=M; 4.24
- 412681; AW983655; Hs.172004; titin; fn3, ig, SGXXSG, kinase; TM=M; 4.24
- 424653; AW977534; Hs.151469; calcium/calmodulin-dependent serine protein kinase (MAGUK family); none; none; 4.24
- 421066; AU076725; Hs.101408; branched chain aminotransferase 2, mitochondrial; aminotran\_4; 4.23

- 428338; AF147765; Hs.232093; ESTs; fn2,CIMR;TM=M;SS=M; 4.23  
 443329; BE262943; Hs.9234; hypothetical protein MGC1936; none;TM=Y;SS=M; 4.23  
 432314; AA533447; Hs.312989; ESTs; Xlink;none; 4.23  
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 4.23  
 5 454166; AW993356; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 4.23  
 442596; AI457102; Hs.347970; Human glucose transporter pseudogene; none;none; 4.23  
 442549; AI751601; Hs.8375; TNF receptor-associated factor 4; MATH,zf-TRAF,zf-C3HC4;SS=M; 4.22  
 424154; AF026004; Hs.141660; chloride channel 2; voltage\_CLC,CBS,EPO\_TPO,PC\_rep; 4.22  
 433419; AI830342; Hs.211272; ESTs; transmembrane4;none; 4.22  
 10 421921; H83363; Hs.6820; translocase of inner mitochondrial membrane 10 (yeast) homolog; zf-Tim10\_DDP,efhand,CH,spectrin,serpin;TM=M;; 4.22  
 445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK;none; 4.22  
 424812; AF059252; Hs.153299; DOM-3 (C. elegans) homolog Z; none;TM=M; 4.22  
 410668; BE379794; Hs.65403; hypothetical protein; death,TNFR\_c6;TM=Y;SS=M; 4.22  
 15 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic acid transporters), member 6; none;none; 4.22  
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;; 4.21  
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; none;none; 4.21  
 400208; ; Eos Control; FCH,RhoGAP,SH3;TM=M;; 4.21  
 405369; ; NM\_005569; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA.; pkinase,LIM,PDZ;SS=M; 4.21  
 20 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase\_2;TM=M;; 4.21  
 441208; AI339704; Hs.150401; ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens];  
 ion\_trans,RYDR\_JTPR,MIR;none; 4.21  
 427217; AA399272; Hs.144341; ESTs; ANP,GHMP\_kinases;none; 4.21  
 400845; ; NM\_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA.;  
 EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 4.21  
 25 422667; H25642; ; ESTs; FMO-like,FMO-like; 4.21  
 450056; BE047394; Hs.8208; ESTs, Weakly similar to S71512 hypothetical protein T2 - mouse [M.musculus];  
 ABC\_tran,ABC\_membrane,ig,MHC\_II\_beta,SRP54,proteasome,ABC\_membrane,ABC\_tran; 4.20  
 448950; AF288687; Hs.9275; CGI-152 protein; E1-E2\_ATPase,Hydrolase;TM=Y;; 4.20  
 30 408634; AW407254; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none;none; 4.20  
 422335; AA375957; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none;none; 4.20  
 426754; NM\_014264; Hs.172052; serine/threonine kinase 18; pkinase;TM=M;; 4.20  
 435810; BE349853; Hs.2785; keratin 17; zf-Tim10\_DDP,SH2,SH3,pkinase,PH,BTK,Ribosomal\_L44; 4.20  
 446143; BE245342; Hs.306079; sec61 homolog; NUDIX,secY,E1\_dehydrog,transkel\_pyr;TM=Y;SS=M; 4.20  
 35 426626; AI124572; Hs.323879; inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma; zf-C2H2;TM=M;; 4.20  
 403716; ; Target Exon; Adap\_comp\_sub,PDZ,DEP,DIX,Dishevelled,hexapep,W2,ABC\_tran; 4.19  
 415749; BE262529; Hs.78771; phosphoglycerate kinase 1; PGK;none; 4.19  
 434599; AB002313; Hs.3989; plexin B2; PSI,Sema,TIG;NA;NA; 4.19  
 412600; L28824; Hs.74101; spleen tyrosine kinase; SH2,pkinase; 4.19  
 416738; N29218; Hs.40290; ESTs; ABC\_tran,ABC\_membrane;none; 4.19  
 40 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; DEAD,helicase\_C,PRK,AIP3;TM=M;; 4.19  
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none;none; 4.19  
 407305; AA715284; ; gb:nv35f03.r1 NCI\_CGAP\_Br5 Homo sapiens cDNA clone similar to contains Alu repetitive element, mRNA sequence; pkinase,integrin\_B,Sema,PSI,TIG;none;  
 4.18  
 45 452880; AA029332; Hs.87549; ESTs; none,integrin\_B; 4.18  
 428245; AF151048; Hs.183180; anaphase promoting complex subunit 11 (yeast APC11 homolog); none;SS=M; 4.18  
 421964; X73079; Hs.288579; polymetric immunoglobulin receptor; ig,Cobalamin\_bind;TM=M;SS=M; 4.18  
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M;; 4.18  
 421790; AW895201; Hs.22654; sodium channel, voltage-gated, type I, alpha polypeptide; ion\_trans,IQ,PEP-utilizers\_C;TM=Y;; 4.18  
 50 429668; AA626142; Hs.179991; ESTs, Weakly similar to S28942 protein kinase C [H.sapiens]; none;none; 4.18  
 443068; AI188710; ; ESTs; Endonuclease,pkinase,Activin\_rec;none; 4.18  
 418827; BE327311; Hs.47166; HT021; none;TM=M;; 4.18  
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine protease; ICE\_p10,ICE\_p20,DED;TM=M;; 4.18  
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M;; 4.18  
 55 422083; NM\_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; none;none; 4.18  
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ;SS=M; 4.18  
 413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like 1; SH2,SAM,Exo\_endo\_phos;SS=M; 4.18  
 424954; NM\_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,WD40,IRK;TM=M;; 4.17  
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none;none; 4.17  
 60 431544; AK000770; Hs.299329; Homo sapiens cDNA FLJ20763 fis, clone COL09911; none;none; 4.17  
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; CBS,IMPDH\_C,IMPDH\_N,NPD;TM=M;; 4.17  
 452012; AA307703; Hs.279766; kinesin family member 4A; kinesin,DNA\_topoisolV,K-box;TM=M;; 4.17  
 425606; U52112; Hs.158331; renin-binding protein; none; 4.16  
 416817; AA398045; Hs.104679; ESTs; Furin-like,pkinase,Recep\_L\_domain,fn3;none; 4.16  
 65 402447; ; C1000201.gij204416[gb]AAA02627.1| (L05195) fructose transporter [Rattus norvegicus] gjl44; none;TM=Y;SS=M; 4.16  
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; Euk\_porin;TM=M;SS=M; 4.15  
 426395; BE151985; Hs.5722; hypothetical protein FLJ23316; pkinase;none; 4.15  
 404140; ; NM\_006510; Homo sapiens ret finger protein (RFP), transcript variant alpha, mRNA.; zf-C3HC4,SPRY,zf-B\_box;SS=M; 4.15  
 432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate synthase 2; APS\_kinase,ATP-sulfurylase;TM=M;; 4.15  
 70 405516; ; ENSP00000200457; Thyroid receptor interacting protein 6 (TRIP6) (OPA-interacting protein 1) (Zyxin related protein 1) (ZRP-1); LIM;TM=M;; 4.15  
 448390; AL035414; Hs.21068; hypothetical protein; FGGY\_C;TM=M;; 4.15  
 435732; AF229178; Hs.123136; leucine rich repeat and death domain containing protein; none;none; 4.15  
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol\_BP,pkinase;TM=M;; 4.15  
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor, pi; Neur\_chan\_LBD,Neur\_chan\_memb;TM=Y;SS=M; 4.14  
 75 424339; BE257148; Hs.145416; endoglycan; none;TM=Y;SS=M; 4.14  
 427274; NM\_005211; Hs.174142; colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog; ig,pkinase;TM=Y;SS=M; 4.14  
 440524; BE171264; Hs.16798; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF;none; 4.14  
 436115; AW512033; Hs.102004; ESTs; pkinase;none; 4.14  
 447050; NM\_016314; Hs.17200; STAM-like protein containing SH3 and ITAM domains 2; SH3,VHS,UIM;SS=M; 4.14  
 80 418529; AW005695; Hs.250897; TRK-fused gene; Band\_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 4.14  
 420727; H75701; Hs.99886; complement component 4-binding protein, beta; sushi;SS=M; 4.14  
 433075; NM\_002959; ; sortilin 1; Exo\_endo\_phos,Atrophin-1,BNR,Kelch;TM=M;; 4.14  
 422783; AA598956; Hs.120439; ethanolamine kinase; Choline\_kinase;TM=Y;; 4.14  
 410726; AI623859; Hs.15936; ESTs; pkinase,pro\_isomerase;none; 4.14

417903; NM\_002342; Hs.1116; lympholoxin beta receptor (TNFR superfamily, member 3); TNFR\_c6; TM=M; SS=M; 4.14  
 428307; W27393; Hs.183648; protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1; SAM,SH3,HS1\_rep; 4.14  
 442434; AA995787; Hs.129583; ESTs; IRK; none; 4.13  
 438361; AA805666; Hs.146217; Homo sapiens cDNA: FLJ23077 fis, clone LNG05840; pkinase, pkinase\_C, none; 4.13  
 445580; AF167572; Hs.12912; skb1 (S. pombe) homolog; none; SS=M; 4.13  
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand, kaza, arf, ras, 7tm\_1; TM=M; 4.13  
 400252; ; NM\_004651; Homo sapiens ubiquitin specific protease 11 (USP11), mRNA. substrate 1 (PTPNS1), mRNA.; UCH-1, UCH-2; TM=M; 4.13  
 446641; AL049229; Hs.15787; Homo sapiens mRNA; cDNA DKFZp564O1016 (from clone DKFZp564O1016); none, pkinase, PBD; 4.13  
 400209; ; NM\_001666; Homo sapiens Rho GTPase activating protein 4 (ARHGAP4), mRNA. VERSION NM\_006083.2 GI; FCH, RhoGAP, SH3; TM=M; 4.13  
 429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm, BAG; SS=M; 4.13  
 411826; AW947946; Hs.26706; CGI-121 protein; none, DSPc; 4.13  
 423189; M59371; Hs.171596; EphA2; fn3, pkinase, SAM, EPH\_lbd; TM=Y; SS=M; 4.12  
 413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; integrin\_B, Glyco\_hydro\_56; SS=M; 4.12  
 414874; D26351; Hs.77515; inositol 1,4,5-triphosphate receptor, type 3; ion\_trans, MIR, RYDR, ITPR; TM=Y; 4.12  
 432047; NM\_016247; Hs.272380; interphotoreceptor matrix proteoglycan 200; EGF, SEA; TM=Y; SS=M; 4.12  
 451820; AW058357; Hs.199248; ESTs; 7tm\_1; TM=Y; SS=M; 4.12  
 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; zf-C2H2, BTB, K\_tetra, WD40, Syntaxin; 4.12  
 424539; L02911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK-2); pkinase, Activin\_rec; TM=M; SS=M; 4.12  
 405110; ; C7000199.gil12643960[sp]Q9Y6T7[KDGB\_HUMAN DIACYLGLYCEROL KINASE, BETA (DIGLYCERIDE KINASE); none, none; 4.12  
 441026; AW179058; Hs.99858; ribosomal protein L7a; pkinase, LRR, LRRCT, Ribosomal\_L7Ae, none; 4.11  
 434142; A1696513; Hs.108705; protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform; HEAT, Vitellinogenin\_N, HEAT\_PBS; SS=M; 4.11  
 450505; NM\_004572; Hs.25051; plakophilin 2; Armadillo\_seg; TM=M; 4.11  
 459601; AL044470; Hs.270604; ESTs, Weakly similar to ALU7\_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; none, SH3, PGAM, UBA; 4.10  
 417300; A1765227; Hs.55610; solute carrier family 30 (zinc transporter), member 1; Cation\_efflux; TM=Y; SS=M; 4.10  
 427315; A179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (from clone DKFZp564N0763); none, spectrin, SH3, PH, CH; 4.10  
 416239; AL038450; Hs.48948; ESTs; E1-E2\_ATPase, Cation\_ATPase\_C, Cation\_ATPase\_N, Hydrolase, none; 4.10  
 429311; AF080157; Hs.198998; conserved helix-loop-helix ubiquitous kinase; pkinase, none; 4.10  
 412146; M92444; Hs.37322; APEX nuclease (multifunctional DNA repair enzyme); Exo\_endo\_phos, Atrophin-1, BNR, Kelch; TM=M; 4.10  
 418420; AW604405; Hs.324874; hypothetical protein MGC3079; Phosphodiesterase; TM=Y; 4.10  
 434396; AA632270; Hs.162851; Homo sapiens cDNA FLJ14317 fis, clone PLACE3000401; pkinase, none; 4.10  
 454438; AA224053; Hs.172405; cell division cycle 27; SPRY, 7tm\_3, ANF\_receptor; 4.10  
 439578; AW263124; Hs.315111; nuclear receptor co-repressor/HDAC3 complex subunit; WD40; TM=M; 4.10  
 451995; A1827431; Hs.224645; ESTs, Weakly similar to IF16\_HUMAN GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 [H.sapiens]; none, PAAD\_DAPIN, HIN; 4.10  
 420340; NM\_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TIT3 complex); ITAM; TM=M; SS=M; 4.10  
 442942; AW167087; Hs.131562; ESTs; pkinase, none; 4.09  
 428187; A1687303; Hs.285529; G protein-coupled receptor 49; 7tm\_1, none; 4.09  
 418838; AW385224; Hs.35198; ecdonucleotide pyrophosphatase/phosphodiesterase 5 (putative function); Phosphodiesterase; TM=Y; SS=M; 4.09  
 416445; AL043004; Hs.79337; KIAA0135 protein; pkinase, PAS; TM=M; 4.08  
 427001; NM\_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2; pkinase; TM=M; 4.08  
 403608; ; C3001199.gil7494834[pilr]T15308 hypothetical protein B0286.2 - Caenorhabditis elegans [41]; 7tm\_1, 7tm\_2, GPS, WIF; TM=Y; SS=M; 4.08  
 427177; AB006537; Hs.173880; interleukin 1 receptor accessory protein; ig, TIR; TM=Y; SS=M; 4.08  
 401241; AB028989; ; mitogen-activated protein kinase 8 interacting protein 3; Cys\_knot, TGF-beta, vwa, vwc, vwd, TIL, DUF139; SS=M; 4.07  
 444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligase Rsp5; potential epithelial sodium channel regulator; WW, HECT, RNA\_pol\_A, none; 4.07  
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 4.06  
 426006; R49031; Hs.22627; ESTs; pkinase, TBC; 4.06  
 434521; NM\_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo\_seg, IBB; TM=M; 4.06  
 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not available 7496841) [C.elegans]; 7tm\_1, none; 4.05  
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD\_DAPIN, HIN; SS=M; 4.05  
 413109; AW389845; Hs.110855; ESTs; PHO4, none; 4.05  
 426457; AW894667; Hs.169965; chimerin (chimaerin) 1; DAG\_PE-bind, RhoGAP, SH2; TM=M; 4.05  
 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase, TrkA-N, 2-Hacid\_DH\_C; TM=M; 4.04  
 429747; M87507; Hs.2490; caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase); CARD, ICE\_p10, ICE\_p20; SS=M; 4.04  
 444378; R41339; Hs.12569; ESTs; ig, pkinase, LRR, LRRNT, LRRCT, none; 4.04  
 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; none; TM=Y; SS=M; 4.04  
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone LNG00414; 7tm\_1, none; 4.04  
 413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-related family, member 3; none, START; 4.04  
 418540; A1821597; Hs.90877; ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ank, CAP\_GLY, 7tm\_1; 4.03  
 442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; rrm, IRK; SS=M; 4.02  
 448659; AF191838; Hs.21712; TANK-binding kinase 1; pkinase; TM=M; 4.02  
 412935; BE267045; Hs.75064; tubulin-specific chaperone c; none; 4.02  
 414844; AA296874; Hs.77494; deoxyguanosine kinase; dNK; 4.02  
 445817; NM\_003642; Hs.13340; histone acetyltransferase 1; none; TM=M; 4.02  
 426728; NM\_007118; Hs.171957; triple functional domain (PTPRF interacting); SH3, ig, pkinase, PH, spectrin, RhoGEF; TM=M; 4.02  
 420676; A1434780; Hs.4248; vav 2 oncogene; RhoGEF, PH, CH, SH2, SH3, DAG\_PE-bind, none; 4.02  
 405102; ; C15001220.gil4469558[gb]AAD21311.1 [AF126008] breast cancer nuclear receptor-binding aux; DAG\_PE-bind, PH, RhoGEF, DC1; SS=M; 4.02  
 439964; A1732902; Hs.124652; Homo sapiens cDNA FLJ12376 fis, clone MAMMA1002494; pkinase, none; 4.01  
 429680; AL035754; Hs.2474; toll-like receptor 1; LRR, LRRCT, TIR; TM=M; SS=M; 4.01  
 453891; AB037751; Hs.36353; Homo sapiens mRNA full length insert cDNA clone EUROIIMAGE 1035904; none, none; 4.01  
 426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR motif, Y isoform [H.sapiens]; Kunitz\_BPTI, Kunitz\_BPTI, 7tm\_2, HRM; 3.99  
 424232; AB015982; Hs.143460; protein kinase C, nu; pkinase, DAG\_PE-bind, PH; TM=M; 3.99  
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none, none; 3.98  
 449517; AW500106; Hs.23643; serine/threonine protein kinase MASK; pkinase; TM=M; 3.98  
 404185; ; Target Exon; sugar\_tr; TM=Y; SS=M; 3.98  
 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; none; TM=M; 3.98  
 429638; A1916662; Hs.211577; kinesin 1 (kinesin receptor); bZIP, Tropomyosin, spectrin, LBP\_BPL\_CETP, B56, M; TM=Y; SS=M; 3.97  
 417386; AL037228; Hs.82043; D123 gene product; NUDIX, secY, E1\_dehydrog, transket\_pyr; TM=Y; SS=M; 3.97  
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; MORN, sugar\_tr; TM=Y; SS=M; 3.96  
 417183; R52089; Hs.172717; ESTs; pkinase, LRRCT, ig, LRR, LRRNT, none; 3.95  
 439176; A1446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; none; TM=M; 3.94  
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M; 3.94  
 422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, subfamily J, member 2; IRK; TM=Y; 3.94

- 450746; D82673; Hs.278589; general transcription factor II, i; none,SH3,PX; 3.94  
 418516; NM\_006218; Hs.85701; phosphoinositide-3-kinase, catalytic, alpha polypeptide; PI3\_PI4\_kinase,PI3Ka,PI3K\_C2,PI3K\_rbd,PI3K\_p85B,none; 3.94  
 414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone LNG09846; none,NA,NA; 3.93  
 416537; T99086; Hs.144904; nuclear receptor co-repressor 1; myb\_DNA-binding,RNA\_pol\_A,none; 3.93  
 450747; AI064821; Hs.318535; ESTs, Highly similar to 1818357A EWS gene [H.sapiens]; rrm,zf-RanBP,GAS2; 3.93  
 444825; AW167613; ; mitogen-activated protein kinase kinase kinase 8; pkinase;TM=M;; 3.93  
 408354; AI382803; Hs.159235; ESTs; none,none; 3.93  
 453945; NM\_005171; Hs.36908; activating transcription factor 1; rrm,zf-RanBP,pkinase,GST\_C,Ets,SAM\_PNT,ABC2\_membrane,myosin\_head,IQ,Myosin\_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT\_hook,SAM;TM=M;; 3.93  
 428532; AF157326; Hs.184786; TBP-interacting protein; Armadillo\_seg,VHS,HEAT;TM=M;; 3.92  
 413967; AW204431; Hs.117853; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Armadillo\_seg,IBB,PHD,DDT,none; 3.91  
 415906; AI751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fis, clone HRC02860; Ephrin,none; 3.91  
 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none,none; 3.91  
 440255; AI932285; Hs.160569; ESTs; none,pkinase; 3.90  
 421077; AK000061; Hs.101590; hypothetical protein; ank,pkinase,death,SPRY,SAP,Ribosomal\_L24e,SRP54,dDENN,DENN,uDENN;TM=M;; 3.90  
 433211; H11850; Hs.12808; MARK; pkinase,UBA,KA1,SS=M; 3.90  
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M;; 3.90  
 419609; U46415; Hs.270379; gb:HSU46415 Human pancreatic cancer cell line Patu 8988t Homo sapiens cDNA clone xs476, mRNA sequence; PWWP,none; 3.90  
 433198; AA992841; Hs.27263; KIAA1458 protein; none,none; 3.89  
 407721; Y12735; Hs.38018; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3; pkinase;TM=M;; 3.89  
 427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none;TM=M;; 3.89  
 453035; AW581943; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; none,none; 3.89  
 446329; NM\_013272; Hs.14805; solute carrier family 21 (organic anion transporter), member 11; kazal,OATP\_N,OATP\_C;TM=Y;SS=M; 3.89  
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker\_histone;TM=M;; 3.88  
 432074; AA525248; Hs.149723; ESTs; Y\_phosphatase,none; 3.88  
 435143; R12375; Hs.194600; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 3.87  
 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese,none; 3.87  
 428474; AB023182; Hs.184523; KIAA0965 protein; pkinase;TM=M;; 3.87  
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT2RP2002066, highly similar to Rattus norvegicus transmembrane receptor Unc5H2 mRNA; death,ZU5;SS=M; 3.86  
 415457; AW081710; Hs.7369; ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; MORN,sugar\_tr;TM=Y;SS=M; 3.86  
 447061; D86964; Hs.17211; dedicator of cyto-kinesis 2; SH3;TM=M;; 3.86  
 426490; NM\_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M;; 3.86  
 451961; NM\_003800; Hs.27345; RNA guanylyltransferase and 5'-phosphatase; mRNA\_cap\_enzyme,DSPc,DNA\_ligase,mRNA\_cap\_C;TM=M;; 3.86  
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-receptor type 2; Y\_phosphatase;TM=Y;; 3.86  
 446874; AW968304; Hs.56156; ESTs; none,RGS; 3.85  
 418630; AI351311; Hs.251946; poly(A)-binding protein, cytoplasmic 1-like; pkinase,none; 3.85  
 416140; AI918035; Hs.301198; roundabout (axon guidance receptor, Drosophila) homolog 1; none,none; 3.85  
 425474; Z48054; Hs.158084; peroxisome receptor 1; TPR;TM=M;; 3.85  
 413073; AL038165; Hs.75187; translocase of outer mitochondrial membrane 20 (yeast) homolog; MAS20,zf-A20,VPS9;TM=M;SS=M; 3.85  
 411770; NM\_014278; Hs.71992; heat shock protein (hsp110 family); HSP70;TM=M;; 3.84  
 428782; X12830; Hs.193400; interleukin 6 receptor; fn3,ig;TM=Y;SS=M; 3.84  
 450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig;TM=Y;SS=M; 3.84  
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine protease; CARD,ICE\_p10,ICE\_p20;SS=M; 3.83  
 440332; AI218517; Hs.188051; ESTs; fn3,pkinase,SAM,EPH\_bld,none; 3.83  
 445803; AV655264; Hs.4283; ESTs; pkinase,RGS,PH,myosin\_head,Myosin\_tail; 3.83  
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH;TM=M;; 3.83  
 414991; C17898; ; gb:C17898 Human placenta cDNA (Tfujiiwara) Homo sapiens cDNA clone GEN-554E10 5', mRNA sequence; Zip,none; 3.83  
 423067; AA321355; Hs.285401; colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage); fn3;TM=Y;SS=M; 3.82  
 419088; AI538323; Hs.52620; integrin, beta 8; integrin\_B,none; 3.82  
 411704; AI499220; Hs.71573; hypothetical protein FLJ10074; pkinase;TM=M;; 3.82  
 459346; AW510557; Hs.258016; EST; none;TM=M;; 3.82  
 445330; R52656; Hs.21691; ESTs; 7tm\_1,none; 3.82  
 451452; BE560065; Hs.26433; dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminophosphotransferase 1 (GlcNAc-1-P transferase); Glycos\_transf\_4;TM=Y;SS=M; 3.81  
 405545; ; Target Exon; ABC\_tran,SRP54,ABC\_membrane;TM=Y;SS=M; 3.81  
 448165; NM\_005591; Hs.20555; meiotic recombination (S. cerevisiae) 11 homolog B; Metallophos,Ribosomal\_L15e;SS=M; 3.81  
 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; ig;TM=Y;SS=M; 3.80  
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate transporter), member 1; PHO4,LIM;TM=M;; 3.80  
 421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo\_seg;SS=M; 3.80  
 438581; AW977766; Hs.292133; ESTs, Moderately similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; pkinase,RIO1,none; 3.79  
 439199; R40373; Hs.26299; ESTs; ion\_trans,none; 3.78  
 450931; N25156; Hs.25648; tumor necrosis factor receptor superfamily, member 5; TNFR\_c6;TM=Y;SS=M; 3.78  
 417691; AU076610; Hs.82399; low density lipoprotein receptor defect C complementing; none;SS=M; 3.78  
 430355; NM\_006219; Hs.239818; phosphoinositide-3-kinase, catalytic, beta polypeptide; PI3\_PI4\_kinase,PI3Ka,PI3K\_C2,PI3K\_rbd,PI3K\_p85B;TM=M;; 3.78  
 448119; H38587; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y;; 3.78  
 442013; AA506476; Hs.10600; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains the NIFS gene for cysteine desulfurase, two genes for novel proteins and the gene for the splicing factor CC1.3 with a second isoform (CC1.; none,none; 3.77  
 425481; AW978162; Hs.18571; ESTs; none,Oxysterol\_BP; 3.77  
 411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA1330 protein [H.sapiens]; RNA\_pol\_A,ig,MHCK\_EF2\_kinase;SS=M; 3.77  
 426866; U02330; Hs.172816; neuregulin 1; Peptidase\_M49,EGF,ig,Neuregulin;TM=M;; 3.77  
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 3.77  
 434398; AA121098; Hs.3838; serum-inducible kinase; pkinase,POLO\_box;TM=M;; 3.77  
 415485; AW272990; Hs.18571; ESTs; none,Oxysterol\_BP; 3.76  
 453226; AA641926; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase\_c,none; 3.76  
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RIO1;TM=M;; 3.76  
 424842; AA034127; Hs.153487; signal transducing adaptor molecule (SH3 domain and ITAM motif) 1; SH3,VHS,UIM;TM=M;; 3.75  
 426500; NM\_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M;; 3.75  
 419952; AK000967; Hs.93872; KIAA1682 protein; none;TM=M;; 3.75  
 425424; NM\_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;; 3.75  
 431696; AA259068; Hs.267819; protein phosphatase 1, regulatory (inhibitor) subunit 2; none;SS=M; 3.75



- 444184; T87841; Hs.282990; Human DNA sequence from clone RP1-28H20 on chromosome 20q13.1. Contains part of a gene for a novel protein similar to membrane transport proteins, the 5' end of a novel gene, ESTs, STSs, GSSs and three CpG islands; pkinase,RIO1,APH,KOW;TM=M;; 3.75
- 405411; ; ENSP00000252213:SODIUM BICARBONATE COTRANSPORTER.; none;TM=Y;SS=M; 3.75
- 405602; ; Target Exon; pkinase;SS=M; 3.75
- 5 429355; AW973253; Hs.292689; ESTs; pkinase,bZIP,Armadillo\_seg,none; 3.75
- 430153; AW968128; Hs.336679; ESTs; pkinase,none; 3.74
- 414180; AI863304; Hs.120905; Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391; PI3\_Pi4\_kinase,PI3Ka,PI3K\_C2,PI3K\_rbd,PI3K\_p85B,none; 3.74
- 432236; AA531132; ; gb:nj47h06.s1 NCI\_CGAP\_Pr9 Homo sapiens cDNA clone, mRNA sequence; pkinase,none; 3.74
- 10 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds; none,spectrin,SH3,PH,CH; 3.74
- 426485; NM\_006207; Hs.170040; platelet-derived growth factor receptor-like; ig;SS=M; 3.74
- 408414; AI114688; Hs.17998; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; fn3,ig;TM=Y;SS=M; 3.73
- 409793; AI825463; Hs.147996; protein kinase, X-linked; pkinase,pkinase\_C;TM=M;; 3.73
- 412456; T32689; Hs.7859; ESTs; BAG,none; 3.73
- 15 407894; AJ278313; Hs.41143; phosphoinositide-specific phospholipase C-beta 1; C2,PI-PLC-Y,PI-PLC-X;TM=M;; 3.73
- 442229; AI885776; Hs.8164; Multibrey nanism; MATH,DENN,GRAM,zf-B\_box,dDENN,uDENN;SS=M; 3.73
- 450161; AI088196; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA sequence; ig,pkinase,none; 3.72
- 408331; NM\_007240; Hs.44229; dual specificity phosphatase 12; DSPc;TM=M;; 3.72
- 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofillin\_ADF;SS=M; 3.72
- 20 403391; ; C3001164\*.gil1730196[sp]P50573[GAR3\_RAT GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-3 SUBUNIT PRE; none;TM=Y;; 3.72
- 417527; AA203524; ; gb:zx56e10.r1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone 5', mRNA sequence; SH3;SS=M; 3.71
- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase); pkinase;TM=M;; 3.71
- 428180; AI129767; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; G-alpha,arf;TM=M;; 3.71
- 422127; AW504286; Hs.112049; SET binding factor 1; dDENN,DENN,GRAM,PH;SS=M; 3.70
- 25 430570; AI417881; Hs.292464; ESTs; 7tm\_2,Fz,Frizzled,none; 3.70
- 452561; AI692181; Hs.49169; KIAA1634 protein; TPR,PDZ,WW,Guanylate\_kin;TM=M;; 3.69
- 432336; NM\_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm,pkinase;TM=M;; 3.69
- 419945; AW290975; Hs.118923; ESTs; SH3,PDZ,Guanylate\_kin,transferrin; 3.69
- 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3,PDZ,Guanylate\_kin;TM=M;; 3.68
- 30 436534; AA721628; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; ig;TM=Y;SS=M; 3.68
- 407202; NS8172; Hs.109370; ESTs; F5\_F8\_type\_C,pkinase,Ets,none; 3.67
- 420297; AI628272; Hs.88323; ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; pkinase,TUDOR,none; 3.67
- 417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase;TM=M;; 3.67
- 35 425304; AA463844; Hs.31339; fibroblast growth factor 11; FGF,Neur\_chan\_LBD,Neur\_chan\_memb,none; 3.67
- 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 3.67
- 419511; AA429750; Hs.75113; general transcription factor IIA; Glypican,none; 3.66
- 424315; AW614850; Hs.193384; putative 28 kDa protein; none,none; 3.66
- 413076; U10564; Hs.75188; weel (S. pombe) homolog; pkinase;TM=M;; 3.66
- 40 425838; NM\_014071; Hs.159613; nuclear receptor coactivator RAP250; peroxisome proliferator-activated receptor interacting protein; thyroid hormone receptor binding protein; none;TM=M;; 3.65
- 446983; AA157484; Hs.97199; complement component C1q receptor; EGF,lectin\_c,Tissue\_fac,Xlink,TIL;TM=Y;SS=M; 3.65
- 434350; AL042940; Hs.93872; KIAA1682 protein; none,none; 3.65
- 45 457317; AA683016; Hs.12210; hypothetical protein FLJ13732 similar to tensin; SH2;TM=M;; 3.65
- 434416; AA805903; Hs.59498; cell division cycle 2-like 5 (cholinesterase-related cell division controller); pkinase,none; 3.65
- 410174; AA306007; Hs.59461; DKFZP434C245 protein; none,DSPc; 3.65
- 423598; BE247600; Hs.155538; ESTs; 7tm\_1;TM=Y;SS=M; 3.65
- 440861; BE244115; Hs.7482; KIAA0682 gene product; rrm,Guanylate\_kin;TM=M;; 3.64
- 454954; AW993013; Hs.49169; KIAA1634 protein; TPR,PDZ,WW,Guanylate\_kin;TM=M;; 3.64
- 50 430250; NM\_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;; 3.64
- 450587; AI828854; Hs.258538; striatin, calmodulin-binding protein; pkinase,WD40;TM=Y;; 3.64
- 424893; AW295112; Hs.153648; Homo sapiens cDNA FLJ13303 fis, clone OVARC1001372, highly similar to Homo sapiens liprin-alpha4 mRNA; SAM;SS=M; 3.64
- 425645; AA361027; ; gb:EST70242 T-cell lymphoma Homo sapiens cDNA 5' end, mRNA sequence; HMG\_box,DNA\_mis\_repair,HATPase\_c,none; 3.64
- 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin\_EGF,laminin\_Nterm,Integrin\_B;SS=M; 3.63
- 55 415292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;; 3.63
- 412314; AA825247; Hs.250899; heat shock factor binding protein 1; 7tm\_1;TM=Y;SS=M; 3.63
- 418303; AA215701; Hs.186541; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; eIF5\_eIF2B,W2,pkinase,UBA,KA1; 3.63
- 452716; AI914925; Hs.222240; ESTs; SH2,STAT,STAT\_bind,STAT\_prot,none; 3.63
- 403869; ; NM\_004520\*.Homo sapiens kinesin heavy chain member 2 (KIF2), mRNA. member 3 (KCNQ3), mRNA.; kinesin;TM=M;; 3.63
- 60 450377; AB033091; Hs.74313; KIAA1265 protein; Zip;TM=M;SS=M; 3.63
- 417793; AW405434; Hs.82575; small nuclear ribonucleoprotein polypeptide B'; rrm;TM=M;; 3.63
- 404942; U30825; ; splicing factor, arginine/serine-rich 9; CD36;TM=Y;SS=M; 3.63
- 429554; NM\_012275; Hs.207224; interleukin 1, delta; IL1;TM=M;; 3.63
- 417871; AA521368; Hs.24252; ESTs; IBB,Armado\_seg,none; 3.62
- 437672; AW748265; Hs.5741; flavohemoprotein b5'; hema\_1,NAD\_binding,lipoxygenase,FAD\_binding\_6;TM=M;; 3.62
- 65 438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; lipoxygenase,PLAT,none; 3.62
- 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5\_F8\_type\_C;TM=M;SS=M; 3.61
- 407961; AW672939; Hs.41694; origin recognition complex, subunit 2 (yeast homolog)-like; none,pkinase,pro\_isomerase; 3.61
- 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1; SH2,SH3,pkinase;SS=M; 3.61
- 70 455608; BE011437; ; gb:CM4-BN0220-080500-170-f03 BN0220 Homo sapiens cDNA, mRNA sequence; none,CDK5\_activator; 3.61
- 407748; AL079409; Hs.38176; KIAA0606 protein; SCN Circadian Oscillatory Protein (SCOP); PP2C,LRR,PH;TM=M;; 3.60
- 421474; U76362; Hs.104637; solute carrier family 1 (glutamate transporter), member 7; SDF;TM=Y;SS=M; 3.60
- 449987; AW079749; Hs.184719; ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ABC\_tran,ABC\_membrane,ion\_trans; 3.60
- 75 403142; ; NM\_002706\*.Homo sapiens protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform (PPM1B), mRNA.; PP2C;TM=M;; 3.60
- 400844; ; NM\_003105\*.Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA.; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 3.59
- 450152; AI138635; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA sequence; ig,pkinase,none; 3.59
- 429782; NM\_005754; Hs.220689; Ras-GTPase-activating protein SH3-domain-binding protein; rrm,NTF2;TM=M;; 3.59
- 80 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none;SS=M; 3.59
- 437400; AB011542; Hs.5599; EGF-like-domain, multiple 5; TNFR\_c6,laminin\_EGF;TM=Y;; 3.58
- 426797; AW936258; Hs.342849; ADP-ribosylation factor-like 5; arf,Ca\_channel\_B,SH3; 3.58
- 431170; AW971246; Hs.291022; ESTs; LRR,CARD,none; 3.58
- 434542; AA769310; Hs.61260; hypothetical protein FLJ13164; PH,Oxysterol\_BP;TM=M;SS=M; 3.58



- 420181; A1380089; Hs.158951; ESTs; none,ig, pkinase,LRR,LRRCT; 3.57  
 450572; A1700863; Hs.202494; Homo sapiens cDNA FLJ13245 fis, clone OVARC1000681; Na\_sulph\_symp,none; 3.57  
 433618; AA602539; Hs.345494; ESTs; G-alpha,A\_deaminase; 3.57  
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; pkinase,none; 3.57  
 418512; AW498974; ; diacylglycerol kinase, zeta (104kD); ras,none; 3.57  
 451752; AB032997; Hs.26966; KIAA1171 protein; ATP-synt\_C,TBC;TM=Y;SS=M; 3.57  
 417129; A1381800; Hs.300684; calcitonin gene-related peptide-receptor component protein; none,none; 3.57  
 449474; AA019344; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing); ThiF,UBACT, pkinase,UCH-2,UCH-1,rrm,zf-C2H2,zf-RanBP,G-patch; 3.57  
 412124; H43378; Hs.288550; Homo sapiens cDNA: FLJ23156 fis, clone LNG09609; none,none; 3.56  
 435021; AA922192; Hs.54709; ESTs; EPH\_Lbd, pkinase,fn3,SAM,none; 3.56  
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit, alpha type, 4; proteasome;TM=M; 3.56  
 437387; A1198874; Hs.28847; AD026 protein; none,7tm\_1,WD40; 3.56  
 422583; AA410506; Hs.27973; KIAA0874 protein; ank,G-alpha;TM=M; 3.55  
 452102; U04343; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none;TM=Y;SS=M; 3.56  
 420112; NM\_005109; Hs.95220; oxidative-stress responsive 1; pkinase;TM=M; 3.55  
 437639; AA827712; Hs.291880; ESTs; SH3,none; 3.55  
 457500; NM\_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm, pkinase;TM=M; 3.55  
 415660; A1909007; Hs.78563; ubiquitin-conjugating enzyme E2G 1 (homologous to C. elegans UBC7); UQ\_con;TM=M; 3.55  
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD;TM=M; 3.55  
 428727; AF078847; Hs.191356; general transcription factor IIH, polypeptide 2 (44kD subunit); PHO4,LIM;TM=M; 3.55  
 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase, pkinase\_C,HR1;TM=M; 3.55  
 408683; R58665; Hs.46847; TRAF and TNF receptor-associated protein; Exo\_endo\_phos;TM=M; 3.55  
 412350; A1659306; Hs.73826; protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte); Y\_phosphatase,Band\_41,PDZ;TM=M; 3.55  
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 3.55  
 427283; AL119796; Hs.174185; ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin); Sulfatase,Somatomedin\_B,Phosphodiesterase,Endonuclease;TM=M;SS=Y; 3.55  
 414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14\_17,none; 3.55  
 424848; A1263231; Hs.327090; EST; SH3,PDZ,Guanylate\_kin,none; 3.54  
 402704; ; C1001099; gi|6005896|ref|NP\_009101.1| testis-specific protein kinase 2 [Homo sapiens] gil4; none,none; 3.54  
 444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; aa\_permeases;TM=Y;SS=M; 3.54  
 429687; A165749; Hs.211608; nucleoporin 153kD; zf-RanBP,integrin\_B;TM=M; 3.53  
 413879; AA132961; Hs.212533; Homo sapiens cDNA: FLJ22572 fis, clone HSI02313; none,none; 3.53  
 431045; AW968560; Hs.301957; nudix (nucleoside diphosphate linked moiety X)-type motif 5; NUDIX,secY,E1\_dehydrog,transket\_pyr;TM=Y;SS=M; 3.53  
 423855; AA331761; Hs.254859; ESTs; none, pkinase,UQ\_con,vwa,FG-GAP,integrin\_A; 3.53  
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin,bZIP;TM=M; 3.52  
 410686; A1733735; Hs.114905; IRE1, S. cerevisiae, homolog of; pkinase,Bacterial\_PQ;TM=M;SS=M; 3.52  
 449810; AB008681; Hs.23994; activin A receptor, type IIB; pkinase,Activin\_recpt;TM=Y;SS=M; 3.52  
 418755; Y14443; Hs.88219; zinc finger protein 200; zf-C2H2,zf-BED;TM=M; 3.52  
 448804; AW512213; Hs.342849; ADP-ribosylation factor-like 5; arf,Ca\_channel\_B,SH3; 3.52  
 438507; AA809052; Hs.182018; ESTs; none,none; 3.52  
 456559; A1336273; Hs.102548; glucocorticoid receptor DNA binding factor 1; none,PAS; 3.51  
 410054; AL120050; Hs.58220; Homo sapiens cDNA: FLJ23005 fis, clone LNG00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP,adenylatekinase; 3.51  
 422321; AA906427; Hs.181035; hypothetical protein MGC11296; none;TM=M; 3.51  
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2,PH;TM=M; 3.50  
 407393; AB038237; ; gb:Homo sapiens mRNA for G protein-coupled receptor C5L2, complete cds.; 7tm\_1;TM=Y;SS=M; 3.50  
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine protease; pkinase,ICE\_p10,ICE\_p20;TM=M;SS=M; 3.50  
 420673; AB008112; Hs.99847; peroxisome biogenesis factor 1; AAA,APS\_kinase;TM=M;SS=M; 3.49  
 424663; NM\_002351; Hs.151544; SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome); SH2;TM=M; 3.49  
 429327; AA283981; Hs.199248; prostaglandin E receptor 4 (subtype EP4); 7tm\_1;TM=Y;SS=M; 3.49  
 400178; ; Eos Control; none,Somatomedin\_B; 3.49  
 439549; AW937885; Hs.137314; ESTs; SH2,none; 3.49  
 436345; AA873008; Hs.121572; ESTs; CARD,BIR,zf-C3HC4,CARD,BIR,zf-C3HC4; 3.49  
 427658; H61387; Hs.30868; nogo receptor; LRR,LRRNT,LRRCT;SS=M; 3.48  
 402833; ; C1002508; gi|6691937|emb|CAB65797.1| (AL096770) bA150A6.2 (novel 7 transmembrane receptor; none,none; 3.48  
 442363; A1337304; Hs.23120; PIST; fn3, pkinase,PDZ,DUF139;TM=Y;SS=M; 3.48  
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; none;TM=M; 3.47  
 417971; Y08991; Hs.83050; phosphoinositide-3-kinase, regulatory subunit 4, p150; pkinase,WD40,HEAT;SS=M; 3.47  
 432169; Y00971; Hs.2910; phosphoribosyl pyrophosphate synthetase 2; Pribosylran; 3.47  
 447425; A1963747; Hs.18573; acylphosphatase 1, erythrocyte (common) type; Acylphosphatase;SS=M; 3.47  
 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 3.46  
 401851; ; NM\_002401; Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP3K3), mRNA.; pkinase;SS=M; 3.46  
 407877; AW016811; Hs.234478; Homo sapiens cDNA: FLJ22648 fis, clone HSI07329; pkinase, pkinase\_C,none; 3.45  
 432279; N95104; Hs.274260; ATP-binding cassette, sub-family C (CFTR/MRP), member 6; ABC\_tran,ABC\_membrane,none; 3.45  
 437103; AW139408; Hs.152940; ESTs; Choline\_kinase,none; 3.45  
 420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339, mRNA, complete cds; 7tm\_1;TM=Y;SS=M; 3.44  
 422209; AF005210; Hs.113222; chemokine (C-C motif) receptor 8; 7tm\_1,7tm\_2;TM=Y;SS=M; 3.44  
 410781; A1375672; Hs.165028; ESTs; pkinase,laminin\_Nterm,laminin\_EGF,cyclin,F-box,cyclin\_C,serpin,ATP-synt\_C; 3.44  
 437296; AA350994; Hs.20281; KIAA1700; Rhodanese,DSF;TM=M; 3.43  
 419855; A1935182; Hs.144139; ESTs; zf-C3HC4,UBA,Cbl\_N,Cbl\_N3,zf-C3HC4,UBA,Cbl\_N,Cbl\_N2,Cbl\_N3; 3.43  
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2; Fz,NTR;SS=M; 3.43  
 428483; A1908539; Hs.184592; KIAA0344 gene product; none,none; 3.43  
 445119; AF035121; Hs.12337; kinase insert domain receptor (a type III receptor tyrosine kinase); ig, pkinase;TM=Y;SS=M; 3.42  
 454468; A1590319; Hs.19122; eukaryotic translation initiation factor 4E-like 3; none,Neur\_chan\_LBD,Neur\_chan\_memb,IF4E; 3.42  
 410386; W26187; Hs.3327; Homo sapiens cDNA: FLJ22219 fis, clone HRC01637; pkinase,Guanylate\_kin,PDZ,SH3,L27,none; 3.42  
 422907; A1879263; Hs.77273; Human glucose transporter pseudogene; none,none; 3.42  
 449816; A1701457; Hs.38694; ESTs; SET,BAH,PK,PK\_C; 3.42  
 440074; AA863045; Hs.10669; ESTs, Weakly similar to T00050 hypothetical protein KIAA0400 [H.sapiens]; SH3,ank,tubulin-binding,ArfGap,PH;TM=M;SS=M; 3.42  
 425475; W56339; Hs.107057; ESTs; pkinase,none; 3.42  
 410242; AB028989; ; mitogen-activated protein kinase 8 interacting protein 3; Cys\_knot,TGF-beta,vwa,vcv,vwd,TIL,DUF139;SS=M; 3.41  
 429276; AF056085; Hs.198612; G protein-coupled receptor 51; 7tm\_3,ANF\_receptor,bZIP;TM=Y; 3.41  
 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, type I, 107kD; none,none; 3.41  
 410908; AA121686; Hs.10592; ESTs; GTP\_EFTU,GTP\_EFTU\_D3,GTP\_EFTU\_D2,none; 3.41

- 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor type, E; Y\_phosphatase:none; 3.40  
 447898; AW969638; Hs.112318; 6.2 kd protein; none:none; 3.40  
 450402; BE218027; Hs.89969; ESTs; SH3:none; 3.40  
 5 441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB:none; 3.40  
 408546; W49512; Hs.46348; bradykinin receptor B1; 7tm\_1;TM=Y;SS=M; 3.40  
 410927; T77635; ; gb:yc91h06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone 5', mRNA sequence; none:none; 3.40  
 10 409646; AW161391; Hs.709; deoxycytidine kinase; dNK;SS=M; 3.39  
 417165; R80137; Hs.302738; Homo sapiens cDNA; FLJ21425 fis, clone COL04162; Sulfate\_transp,STAS,HMG\_box; 3.39  
 449343; AI151418; ; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); none:none; 3.39  
 450511; R07423; Hs.85092; thyroid hormone receptor interactor 11; Myosin\_tail,EGF; 3.39  
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M;; 3.38  
 418428; Y12490; Hs.85092; thyroid hormone receptor interactor 11; bZIP,kinesin,GTP\_cyclohydrol,M;TM=M;; 3.37  
 422369; AF005216; Hs.115541; Janus kinase 2 (a protein tyrosine kinase); SH2,pkinase;TM=M;; 3.37  
 15 456451; AI761180; Hs.94211; rcd1 (required for cell differentiation, S.pombe) homolog 1; none;TM=M;; 3.37  
 438543; AA810141; Hs.192182; ESTs; SH2,pkinase:none; 3.37  
 401943; NM\_012434; ; solute carrier family 17 (anion/sugar transporter), member 5; none;TM=M;; 3.36  
 415276; U88666; Hs.78353; SFRS protein kinase 2; pkinase;TM=M;; 3.36  
 447881; BE620886; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; pkinase,pkinase; 3.35  
 434533; AA639257; Hs.292549; ESTs; SH3,PDZ,Guanylate\_kin:none; 3.35  
 20 432639; AW973785; ; gb:EST385886 MAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence; none,IRK; 3.35  
 410678; BE540516; Hs.293732; hypothetical protein MGC3195; Armadillo\_seg;TM=M;SS=Y; 3.35  
 402807; ; ENSP00000235229:SEMB; integrin\_B,Sema,PSI;TM=Y;; 3.35  
 420189; AW296380; Hs.95821; osteoclast stimulating factor 1; SH3,ank;; 3.34  
 25 437389; AL359587; Hs.271586; hypothetical protein DKFZp762M115; secY,E1\_dehydrog,transket\_pyr:none; 3.34  
 453423; NM\_002647; Hs.32971; phosphoinositide-3-kinase, class 3; PI3\_Pi4\_kinase,PI3Ka,PI3K\_C2;TM=M;; 3.34  
 414270; L20852; Hs.347527; solute carrier family 20 (phosphate transporter), member 2; Enterotoxin\_A,PHO4;TM=Y;SS=M; 3.33  
 417479; AI057052; ; ESTs, Weakly similar to Z195\_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]; LRR,CARD:none; 3.33  
 424946; M64572; Hs.153932; protein tyrosine phosphatase, non-receptor type 3; Band\_41,PDZ,Y\_phosphatase:none; 3.33  
 452681; AF153330; Hs.30246; solute carrier family 19 (thiamine transporter), member 2; Folate\_carrier;TM=Y;SS=M; 3.33  
 30 426477; AA379464; ; gb:EST92386 Skin tumor I Homo sapiens cDNA 5' end, mRNA sequence; DUF6,MATH,BTB; 3.33  
 438283; AI458931; Hs.37282; ESTs; none,transmembrane4; 3.33  
 421327; AA837295; Hs.188802; ESTs; none,IMP4,Y\_phosphatase; 3.33  
 432481; AW451645; Hs.151504; Homo sapiens cDNA FLJ11973 fis, clone HEMBB1001221; laminin\_G,Collagen,COLFI,CorA,TSPN:none; 3.33  
 452682; AA456193; Hs.9071; progesterone membrane binding protein; homeobox:none; 3.32  
 35 428997; AF065391; Hs.194718; zinc finger protein 265; zf-RanBP;TM=M;; 3.32  
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY\_C;TM=M;; 3.31  
 443601; AI078554; Hs.15682; ESTs; ank,pkinase,death,Ribosomal\_S14; 3.31  
 430597; AF062006; Hs.285529; G protein-coupled receptor 49; 7tm\_1,LRR,LRRNT;TM=Y;SS=M; 3.31  
 419912; AF249745; Hs.6086; Rho guanine nucleotide exchange factor (GEF) 4; SH3,PH,RhoGEF;TM=M;; 3.31  
 40 400380; NM\_018486; Hs.283079; G protein-coupled receptor C5L2; 7tm\_1;TM=Y;SS=M; 3.31  
 415983; AI436798; Hs.117078; Homo sapiens cDNA: FLJ23028 fis, clone LNG01852, highly similar to HSU08023 Human cellular proto-oncogene (c-mer) mRNA; fn3,ig,pkinase;TM=Y;SS=M; 3.31  
 441054; AA913591; Hs.126480; ESTs; none,7tm\_1; 3.31  
 418342; BE002723; ; leptin receptor; ICE\_p20,DED,ICE\_p20,DED; 3.31  
 45 446128; AW836779; Hs.113029; ribosomal protein S25; none,7tm\_1; 3.31  
 425086; AW957571; Hs.12319; Homo sapiens cDNA FLJ12774 fis, clone NT2RP2001663, moderately similar to ENOLASE (EC 4.2.1.11); none,Guanylate\_kin,PDZ,SH3; 3.31  
 425725; NM\_012243; Hs.159322; solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3; DUF6;TM=Y;SS=M; 3.30  
 422608; AW160644; Hs.118695; potassium voltage-gated channel, subfamily G, member 1; ion\_trans,K\_tetra;TM=Y;; 3.30  
 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE\_p20,DED;TM=M;; 3.30  
 50 433656; AW974941; Hs.292385; ESTs, Weakly similar to T78885 serine/threonine-specific protein kinase [H.sapiens]; pkinase,ABC1:none; 3.30  
 413132; NM\_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic) inhibitor alpha; PKI;SS=M; 3.30  
 402603; ; ENSP00000251206:KIAA0778 PROTEIN (FRAGMENT).; none;TM=Y;; 3.30  
 418801; AA228366; Hs.115122; ESTs; Integrin\_A,FG-GAP:none; 3.30  
 55 400275; ; NM\_006513:Homo sapiens seryl-IRNA synthetase (SARS), mRNA. (SAM68), mRNA.; tRNA-synt\_2b,Seryl\_IRNA\_N;TM=M;; 3.29  
 440286; U29589; Hs.7138; cholinergic receptor, muscarinic 3; 7tm\_1;TM=Y;; 3.29  
 409101; NM\_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; G-alpha:none; 3.29  
 432736; AA788898; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 3.29  
 408738; NM\_014785; Hs.47313; KIAA0258 gene product; none;TM=M;; 3.29  
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955; Aa\_trans:none; 3.29  
 60 405328; ; NM\_005391:Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3), mRNA.; HATPase\_c;SS=M; 3.28  
 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit 6; none:none; 3.28  
 408756; AA524743; Hs.44883; ESTs; Armadillo\_seg,IBB,DEAD,helicase\_C,Sec63,DDT,PHD,bromodomain;TM=M;; 3.28  
 415474; NM\_014252; Hs.78457; solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15; mito\_carr;TM=M;; 3.28  
 417805; U38545; Hs.82587; phospholipase D1, phosphatidylcholine-specific; PH,PLDc,PX;TM=M;; 3.28  
 65 410254; BE004131; Hs.318510; Homo sapiens cDNA FLJ13682 fis, clone PLACE2000015, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15; ehand:none; 3.28  
 443968; AA287702; Hs.10031; KIAA0955 protein; CARD;TM=M;SS=M; 3.28  
 438899; AF085833; Hs.135624; ESTs; none,PI3\_Pi4\_kinase,PI3Ka,PI3K\_C2,PI3K\_rbd,PI3K\_p85B; 3.27  
 415663; AW296841; Hs.313332; ESTs; UQ\_con,Neur\_chan\_LBD,Neur\_chan\_memb; 3.27  
 70 414087; W19712; ; gb:zb36603.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 5', mRNA sequence; pkinase:none; 3.27  
 442833; AA328153; Hs.88201; ESTs, Weakly similar to A Chain A, Crystal Structure Of The Human Acyl Protein Thioesterase 1 At 1.5 A Resolution [H.sapiens]; abhydrolase\_2;TM=M;; 3.27  
 444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none;TM=Y;SS=M; 3.26  
 432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis repressor with CARD domain); CARD;TM=M;; 3.26  
 75 458943; AW249181; Hs.19954; ESTs, Weakly similar to T19873 hypothetical protein C41C4.2 - Caenorhabditis elegans [C.elegans]; none,pkinase,RGS; 3.26  
 411974; AW880414; Hs.84264; acidic protein rich in leucines; E1-E2\_ATPase,Cation\_ATPase\_C,Cation\_ATPase\_N,Hydrolase,asp; 3.26  
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbonate cotransporter, member 4; HCO3\_cotransp;TM=Y;; 3.26  
 423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7tm\_2,HRM,CSD;TM=Y;SS=M; 3.25  
 442643; U82756; Hs.3991; PRP4/STK/WD splicing factor; WD40;SS=M; 3.25  
 80 417525; R93355; Hs.192991; ESTs, Weakly similar to ALUB\_HUMAN !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]; SH3,ig,pkinase,PH,spectrin,RhoGEF;SS=M; 3.25  
 412283; BE06084; ; gb:QV3-BT0379-140100-058-g12 BT0379 Homo sapiens cDNA, mRNA sequence; ion\_trans,RYDR,ITPR,MIR:none; 3.25  
 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5\_F8\_type\_C,CUB,CUB,MAM,F5\_F8\_type\_C; 3.25  
 400352; AF227133; ; taste receptor, type 2, member 7; none;TM=Y;SS=M; 3.25

- 402974; ; ; Target Exon; Y\_phosphatase, GnRH, hormone5, hormone4; 3.25  
 407644; D16815; Hs.37288; nuclear receptor subfamily 1, group D, member 2; hormone\_rec.zf-C4; TM=M; SS=M; 3.25  
 421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; helicase\_C; SS=M; 3.25  
 438022; AW517524; Hs.135201; NOD2 protein; LRR, CARD, GTP\_CDC, Viral\_helicase1; TM=M; 3.24  
 449964; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase; TM=M; 3.24  
 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; EGF\_sushi, trypsin, CUB, ABC\_tran, ABC\_membrane; SS=M; 3.24  
 427319; AW631495; Hs.27135; B-cell receptor-associated protein BAP29; filament; TM=Y; SS=M; 3.24  
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RRN3;  
 aa\_permeases, pyridoxal\_deC, bromodomain, PHD, MBD, AT\_hook, DDT, PI3\_PI4\_kinase, FAT, FATC, BoIA, RUN; TM=M; 3.24  
 411887; AW182924; Hs.128790; ESTs; pkinase; TM=M; 3.24  
 430180; AA331406; Hs.75456; A kinase (PRKA) anchor protein 10; RGS; SS=M; 3.24  
 410267; AW978005; Hs.12600; N-ethylmaleimide-sensitive factor attachment protein, beta; none, NTF2; 3.23  
 410240; AL157424; Hs.61289; synaptojanin 2; Exo\_endo\_phos, Syja\_N, rrm, Gram-ve\_porins; TM=M; 3.23  
 434510; AF143885; Hs.18190; EST; SH3, FCH, none; 3.22  
 422592; BE081857; Hs.94211; rcd1 (required for cell differentiation, S.pombe) homolog 1; none, PI-PLC-X, PH, PI-PLC-Y, C2; 3.22  
 439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none, none; 3.22  
 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase, DCX; TM=M; 3.22  
 409245; AA361037; Hs.288036; IRNA isopentenylpyrophosphate transferase; Armadillo\_seg; TM=M; 3.22  
 458946; AA009716; Hs.42311; ESTs; none, DSPC, Y\_phosphatase; 3.22  
 409048; H59990; Hs.37699; ESTs; Armadillo\_seg, IBB, none; 3.22  
 420357; U94333; Hs.97199; complement component C1q receptor; EGF, lectin\_c, Tissue\_fac, Xlink, TIL; TM=Y; SS=M; 3.22  
 426230; AA367019; Hs.241395; protease, serine, 1 (trypsin 1); trypsin, toxin\_4; SS=M; 3.21  
 411352; NM\_002890; Hs.758; RAS p21 protein activator (GTPase activating protein) 1; SH2, SH3, C2, PH, RasGAP; TM=M; SS=M; 3.21  
 438333; R39382; Hs.25283; cyclin-dependent kinase 8; pkinase, none; 3.20  
 414202; BE275653; Hs.270379; transmembrane 6 superfamily member 1; 7tm\_5, none; 3.20  
 429651; D79248; Hs.279870; ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; MgtE, none; 3.20  
 400987; ; C11000939.gi11464993[ref|NP\_065260.1] gene for odorant receptor MOR83 [Mus musculus] glif6; none; TM=Y; SS=M; 3.20  
 413760; Z25101; Hs.25127; Homo sapiens mRNA for KIAA1725 protein, partial cds; none, ank, ArfGAP; 3.20  
 408468; AI909712; Hs.93837; phosphatidylinositol transfer protein, membrane-associated; PX, PH, PLDc, PH, PLDc, PX; 3.20  
 409463; AI458165; Hs.17296; hypothetical protein MGC2376; K\_tetra; TM=M; 3.20  
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none; TM=M; 3.19  
 423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbonate cotransporter, member 7; HCO3\_cotransp; TM=Y; SS=M; 3.19  
 407753; AL045916; Hs.293419; ESTs; Ephrin, none; 3.19  
 419355; AA428520; Hs.90061; progesterone binding protein; heme\_1; TM=Y; SS=M; 3.19  
 454128; AL031259; Hs.41639; programmed cell death 2; zf-MYND; TM=M; 3.19  
 421202; AF193339; Hs.102506; eukaryotic translation initiation factor 2-alpha kinase 3; pkinase; TM=Y; SS=M; 3.19  
 446360; N42553; Hs.267914; homolog of mouse transient receptor potential-phospholipase C-interacting kinase CHaK; hypothetical protein FLJ20117;  
 ion\_trans, MHCK\_EF2\_kinase; TM=M; 3.18  
 458882; R34993; Hs.226666; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; CRAL\_TRIO, PKI; 3.18  
 424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; pkinase, TBC; 3.18  
 444745; AF117754; Hs.11861; thyroid hormone receptor-associated protein, 240 kDa subunit; none; TM=M; 3.18  
 426399; AA652588; Hs.301348; Homo sapiens cDNA FLJ13271 fis, clone OVARC1001000; SH3, HS1\_rep, none; 3.18  
 425836; AW955696; Hs.90960; ESTs; Cbl\_N, Cbl\_N2, Cbl\_N3, UBA, zf-C3HC4, none; 3.18  
 403335; ; NM\_021815; Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA.; SSF; TM=Y; SS=M; 3.17  
 428788; AF082283; Hs.193516; B-cell CLL/lymphoma 10; CARD; TM=M; 3.17  
 429558; AI391454; Hs.207251; nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein; none; SS=M; 3.17  
 440248; AA876138; Hs.153136; ESTs; SH2, none; 3.17  
 423706; U95218; Hs.131924; G protein-coupled receptor 65; 7tm\_1; TM=Y; SS=M; 3.17  
 429752; H52348; Hs.36636; ESTs; pkinase, pkinase; 3.17  
 446163; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 fis, clone PLACE1010270; none; NA; NA; 3.17  
 456773; AI038192; Hs.129764; EGF-like repeats and discoidin I-like domains 3; rrm, SH3, myosin\_head, IQ, MyTH4, EGF, F5\_F8\_type\_C, Band\_41; TM=M; 3.17  
 434392; AW983709; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone HRC12631; pkinase, none; 3.16  
 435972; W95088; Hs.114198; ESTs; pkinase, OPR, none; 3.16  
 441401; AI824338; Hs.126891; ESTs; Tissue\_fac; TM=M; SS=M; 3.16  
 410497; AL157648; Hs.157078; Homo sapiens cDNA FLJ12793 fis, clone NT2RP2002033; none, none; 3.16  
 401113; H25530; ; solute carrier family 22 (organic cation transporter), member 1-like; none; SS=M; 3.16  
 424833; NM\_003894; Hs.153405; period (Drosophila) homolog 2; PAS; SS=M; 3.15  
 453880; AI803166; Hs.28462; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; HSP70, none; 3.15  
 435391; AA704588; Hs.58934; ESTs; PIP5K, none; 3.15  
 428065; AI634046; Hs.157313; ESTs; ICE\_p20, DED, ICE\_p10, ICE\_p20, DED; 3.15  
 452688; AA721140; Hs.49930; ESTs, Weakly similar to putative p150 [H.sapiens]; SH3, none; 3.15  
 426839; M74782; Hs.172689; interleukin 3 receptor, alpha (low affinity); none; TM=M; SS=M; 3.15  
 421247; BE391727; Hs.102910; general transcription factor IIH, polypeptide 4 (52kD subunit); none; TM=M; 3.14  
 440249; AI246590; Hs.249175; ESTs; TatD\_DNase, pkinase, death, none; 3.14  
 409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG; TM=M; 3.13  
 446135; AW130288; Hs.170318; hypothetical protein FLJ10147; hormone\_rec.zf-C4; SS=M; 3.13  
 400440; X83957; Hs.83870; nebulin; SH3, Nebulin; 3.12  
 409099; AK000725; Hs.50579; hypothetical protein FLJ20718; Armadillo\_seg; TM=M; 3.12  
 434237; AF119908; Hs.235516; hypothetical protein PRO2955; none; SS=M; 3.12  
 428179; AI127772; Hs.279696; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; pkinase, PX, pkinase\_C; SS=M; 3.12  
 422824; NM\_012108; Hs.121128; BCR downstream signaling 1; SH2, PH; TM=M; 3.11  
 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B14E12, mRNA sequence; 7tm\_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B\_box; TM=Y; SS=M; 3.11  
 435411; AW444619; Hs.138211; ESTs; none, pkinase; 3.11  
 424852; AI222779; Hs.144848; ESTs; adenylatekinase, SH2, pkinase, none; 3.11  
 441970; AW959918; Hs.155160; ESTs; rrm, zf-C2H2; 3.11  
 433370; AI470523; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC\_tran, ABC\_membrane; TM=Y; 3.11  
 413285; BE078405; ; gb:QV2-BT0617-080300-071-g03 BT0617 Homo sapiens cDNA, mRNA sequence; GCV\_T; SS=M; 3.10  
 429458; BE161832; Hs.292689; ESTs; pkinase, bZIP, Armadillo\_seg, none; 3.10  
 401185; ; NM\_021625; Homo sapiens vanilloid receptor-related osmotically activated channel; OTRPC4 protein (OTRPC4), mRNA.; ank, ion\_trans; TM=Y; 3.10  
 404537; Z25884; ; chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant); none; TM=Y; 3.10  
 417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone HEP03834; voltage\_CLC, CBS, none; 3.09  
 450792; AA400323; Hs.183041; ESTs; none, ABC\_tran; 3.09

420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP,7tm\_1; 3.09  
 444040; AF204231; Hs.182982; golgin-67; SH3,C2,PH,RhoGEF,efhand;TM=M;; 3.09  
 416990; AF124145; Hs.80731; autocrine motility factor receptor; zf-C3HC4,CUE;TM=Y;; 3.09  
 442215; AI703172; Hs.129005; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; none,none; 3.09  
 424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK,none; 3.09  
 426623; AA382826; Hs.132793; ESTs; none;TM=M;; 3.08  
 419577; L36531; Hs.91296; integrin, alpha 8; integrin\_A,FG-GAP;TM=Y;; 3.08  
 426618; AL036456; Hs.171374; smg GDS-ASSOCIATED PROTEIN; Armadillo\_seg;TM=M;; 3.08  
 445133; AW157646; Hs.153506; ESTs; ehband,spectrin,GAS2,SH3,Plectin,RA,Xylose\_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,Idh\_C,CH,AIP3;TM=M;; 3.08  
 423681; AB023215; Hs.131525; Homo sapiens mRNA; cDNA DKFZp434E199 (from clone DKFZp434E199); partial cds; TTL;TM=M;; 3.08  
 428730; AA625947; Hs.25750; ESTs; HECT,none; 3.08  
 427976; AW977808; Hs.80545; mitogen-activated protein kinase 8 interacting protein 2; Ribosomal\_L37e,pkinase; 3.08  
 412448; L12964; Hs.73895; tumor necrosis factor receptor superfamily, member 9; TNFR\_c6;TM=Y;SS=M; 3.08  
 416814; AW192307; Hs.80042; dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylglucosyltransferase; Alg6\_Alg8,7tm\_1;TM=Y;SS=M; 3.08  
 427395; AW298741; Hs.97861; ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens]; none,aldedh,aakinas; 3.08  
 436267; AW450938; Hs.180115; ESTs; none,PFK; 3.07  
 422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic acid transporters), member 6; sugar\_tr;TM=Y;SS=M; 3.07  
 439238; N47305; Hs.46668; ESTs; 7tm\_1;TM=Y;SS=M; 3.07  
 458760; AL498631; Hs.111334; ferritin, light polypeptide; cystatin,ferritin,histone,HCO3\_cotransp,SH3,RhoGAP,xan\_ur\_permease,FCH;SS=M; 3.07  
 424236; AW058114; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase;TM=M;; 3.06  
 427286; AW732802; Hs.2132; epidermal growth factor receptor pathway substrate 8; SH3,TonB\_boxC;TM=M;; 3.06  
 423878; AI907090; Hs.52891; hypothetical protein PRO1853; cystatin,ferritin,histone,HCO3\_cotransp,SH3,RhoGAP,xan\_ur\_permease,FCH;SS=M; 3.06  
 419270; NM\_005232; Hs.89839; EphA1; fn3,pkinase,SAM,EPH\_lbd;TM=M;SS=M; 3.06  
 450407; NM\_000810; Hs.24969; gamma-aminobutyric acid (GABA) A receptor, alpha 5; Neur\_chan\_LBD,Neur\_chan\_memb;TM=Y;; 3.06  
 456249; AI206144; Hs.82508; HRIHFB2206 protein; none;SS=M; 3.06  
 441560; F13386; Hs.7888; Homo sapiens clone 23736 mRNA sequence; pkinase,Recep\_L\_domain,Furin-like,YLP,none; 3.05  
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;SS=M; 3.05  
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); pyr\_redox;TM=M;; 3.05  
 425390; AI092634; Hs.156114; protein tyrosine phosphatase, non-receptor type substrate 1; ig;TM=Y;SS=M; 3.04  
 409705; M37762; Hs.56023; brain-derived neurotrophic factor; NGF;SS=M; 3.04  
 413962; AA331563; Hs.24678; sphingosine-1-phosphatase; PAP2;TM=Y;; 3.04  
 426578; R23027; ; gb:yh27e07.r1 Soares placenta Nb2HP Homo sapiens cDNA clone 5', mRNA sequence; pkinase,none; 3.04  
 438005; BE151746; ; gb:PM1-HT0305-061299-003-a06 HT0305 Homo sapiens cDNA, mRNA sequence; pkinase,UBA,KA1,none; 3.04  
 438316; AA789249; Hs.80042; gb:aj27g08.s1 Soares testis\_NHT Homo sapiens cDNA clone 1391582 3', mRNA sequence; none,none; 3.04  
 452850; H23230; Hs.22481; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; CBS,voltage\_CLC,none; 3.03  
 405266; ; Target Exon; arf,G-alpha;SS=M; 3.03  
 402615; ; C1003844\*gi16912550[ref]NP\_036483.1| olfactory receptor, family 10, subfamily J, member 1; none;TM=Y;SS=M; 3.03  
 422803; W28669; Hs.139041; ESTs; transmembrane4,none; 3.02  
 439325; AF086139; Hs.150423; cyclin-dependent kinase 9 (CDC2-related kinase); pkinase,Mur\_ligase,Mur\_ligase\_C; 3.02  
 416389; AA180072; Hs.149846; integrin, beta 5; integrin\_B,none; 3.02  
 418836; AI655499; Hs.161712; ESTs; pkinase,Activin\_recpt,PDZ,ZU5,death; 3.02  
 438996; AW748336; Hs.110613; KIAA0421 protein; none;TM=M;; 3.02  
 422676; D28481; Hs.1570; histamine receptor H1; 7tm\_1;TM=Y;SS=M; 3.02  
 450267; AW505538; Hs.243620; ESTs; pkinase,none; 3.01  
 400566; ; Target Exon; none;TM=Y;; 3.01  
 407816; AW500857; Hs.40137; anaphase-promoting complex 1; meiotic checkpoint regulator; PI-PLC-X,C2,SH2,PH,SH3,PI-PLC-Y,PAN,none; 3.01  
 429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase); Y\_phosphatase,Band\_41,PDZ;SS=M; 3.01  
 417067; AJ001417; Hs.81086; solute carrier family 22 (extraneuronal monoamine transporter), member 3; sugar\_tr;TM=Y;SS=M; 3.00  
 403212; ; NM\_019595:Homo sapiens intersectin 2 (ITSN2), mRNA. (CHRNA9), mRNA.; SH3,efhand,C2,PH,RhoGEF;TM=M;; 3.00  
 410141; R07775; Hs.287657; Homo sapiens cDNA: FLJ21291 fis, clone COL01963; F5\_F8\_type\_C,pkinase,Ets,none; 3.00  
 421059; AI654133; Hs.30212; thyroid receptor interacting protein 15; none,none; 3.00  
 452335; AW188944; Hs.61272; ESTs; none,IRK; 2.99  
 437644; AA748575; Hs.136748; lectin-like NK cell receptor; lectin\_c;TM=Y;SS=M; 2.99  
 435876; AW612586; Hs.160271; G protein-coupled receptor 48; 7tm\_1,LRR,LRRNT;TM=Y;SS=M; 2.99  
 429177; AA447527; Hs.207429; ESTs; 7tm\_1,none; 2.99  
 449289; BE466067; Hs.225660; ESTs; 3Beta\_HSD,pkinase; 2.99  
 454701; AW854930; ; gb:PM0-CT0263-201099-003-f06 CT0263 Homo sapiens cDNA, mRNA sequence; SH2,STAT,STAT\_bind,STAT\_prot,none; 2.99  
 409995; AW960597; Hs.129206; ESTs; pkinase,none; 2.98  
 446860; AV660685; Hs.282953; ESTs; none,PP2C; 2.98  
 438684; AA830105; Hs.194976; SH2 domain-containing phosphatase anchor protein 1; ig;TM=Y;SS=M; 2.98  
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;; 2.98  
 403290; ; C10001011\*gi14758212[ref]NP\_004411.1| dual specificity phosphatase 8 [Homo sapiens] gi1601; none;TM=M;; 2.97  
 433556; W56321; Hs.111460; calcium/calmodulin-dependent protein kinase (CaM kinase) II delta; pkinase,none; 2.97  
 421990; T31811; Hs.110480; DC12 protein; GKAP,DUF159;TM=M;; 2.97  
 428315; AA688152; Hs.98505; ESTs; pkinase,none; 2.97  
 411140; AW819463; ; gb:RC5-ST0293-061299-031-C07 ST0293 Homo sapiens cDNA, mRNA sequence; Choline\_kinase,Carn\_acyltransf,Sulfatase,Carn\_acyltransf; 2.97  
 453998; H47802; Hs.7557; FK506-binding protein 5; none,none; 2.97  
 401342; ; Target Exon; none,none; 2.97  
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); dNK,none; 2.96  
 410976; R36207; Hs.25092; hypothetical protein MGC10744; none;TM=M;SS=M; 2.96  
 431074; BE072772; Hs.153279; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; none,serpin; 2.96  
 443829; AI087954; Hs.23348; S-phase kinase-associated protein 2 (p45); F-box,none; 2.96  
 400356; AF227137; ; taste receptor, type 2, member 13; none;TM=Y;SS=M; 2.95  
 422559; AW247696; Hs.155839; hypothetical protein MGC12934; adh\_zinc,PGK,Semialdehyde\_dh;SS=M; 2.95  
 423482; BE280172; Hs.129228; galactokinase 2; GHMP\_kinases;TM=M;; 2.95  
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 2.95  
 414581; AA256213; Hs.72010; ESTs; none,Carn\_acyltransf,Choline\_kinase,SCO1-SenC,Glycos\_transf\_3,Glycos\_trans\_3N; 2.95  
 453058; AW612293; Hs.288684; Homo sapiens cDNA FLJ11750 fis, clone HEMBA1005568; SH2,SH3,C2,PH,RasGAP,none; 2.95  
 430556; AW967807; Hs.13797; ESTs; HECT,none; 2.94  
 400471; ; Target Exon; none;TM=M;; 2.94  
 419459; AW291128; Hs.278422; DKFZP586G1122 protein; Metallophos,7tm\_1; 2.94  
 407013; U35637; ; gb:Human nebulin mRNA, partial cds; SH3,Nebulin; 2.94  
 421476; AW953805; Hs.21887; ESTs; Piwi,PAZ,Piwi; 2.94

- 426806; T19228; Hs.172572; hypothetical protein FLJ20093; ank,pkinase,UPF0073;SS=M; 2.94  
 405588; ; NM\_000299\*:Homo sapiens plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) (PKP1), mRNA.; Armadillo\_seg;TM=M; 2.94  
 443614; AV655386; Hs.7645; fibrinogen, B beta polypeptide; none,none; 2.94  
 416737; AF154335; Hs.79691; LIM domain protein; LIM,PDZ;TM=M; 2.93  
 5 428522; R10184; Hs.191987; ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; none,ArfGap,PH,TNFR\_c6; 2.93  
 447818; W79940; Hs.21906; Homo sapiens clone 24670 mRNA sequence; none,pkinase; 2.93  
 432925; AA878324; ; ESTs; none,none; 2.93  
 10 443670; AW178935; Hs.238707; ESTs; RmaAD,DENN,dDENN,uDENN;TM=M; 2.93  
 447555; A1391662; Hs.160963; Homo sapiens, clone MGC:12318, mRNA, complete cds; none;TM=M; 2.93  
 435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; none;TM=M; 2.93  
 417670; R07785; ; gb:yf15c06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 5' similar to contains Alu repetitive element;contains MSR1 repetitive element ;, mRNA sequence; XYPPX,ABC\_membrane,ABC\_tran; 2.93  
 15 424148; BE242274; Hs.1741; integrin, beta 7; integrin\_B,EGF,metalthio,PSI;TM=Y;SS=M; 2.92  
 439090; H65724; Hs.347158; gb:yr76a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 5', mRNA sequence; pkinase,none; 2.92  
 408048; NM\_007203; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemm;TM=M; 2.92  
 428796; A0076734; Hs.193665; solute carrier family 28 (sodium-coupled nucleoside transporter), member 2; Nucleoside\_tra2,BPD\_transp\_2;TM=Y; 2.92  
 415272; AA164215; Hs.203186; ESTs; none,Exo\_endo\_phos,BNR,Atrophin-1,B56,pkinase,ig,TPR; 2.92  
 20 424775; AB014540; Hs.153026; SWAP-70 protein; efhand,PH,Neuregulin;TM=M; 2.92  
 439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR\_c6,granulin,CUB,Keratin\_B2,TIL;TM=M;SS=M; 2.92  
 441680; AW444598; Hs.7940; RAP1, GTP-GDP dissociation stimulator 1; Armadillo\_seg;TM=M; 2.91  
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1; Somatomedin\_B,Endonuclease,Phosphodiester;TM=Y;SS=M; 2.91  
 400398; AF137396; Hs.283879; ubiquitin 3; 7tm\_1,Abi;TM=Y;SS=M; 2.91  
 25 435592; A1830490; Hs.1466; glycerol kinase; FGGY,FGGY\_C;TM=M; 2.90  
 400539; ; Target Exon; none;TM=M; 2.90  
 403743; ; C1002604:gil8393668[ref]NP\_058989.1] kinase interacting with leukemia-associated gene (st; none;TM=M; 2.90  
 418913; BE046745; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Y\_phosphatase,IMP4,none; 2.90  
 428169; A1928984; Hs.182793; golgi phosphoprotein 2; photoRC,UPF0118;TM=Y; 2.90  
 403912; ; C5000394\*:gil12737280[ref]XP\_006682.2] keratin 18 [Homo sapiens]||6633; none;TM=M; 2.89  
 30 431868; BE246400; Hs.285176; acetyl-Coenzyme A transporter; none;TM=Y; 2.89  
 421558; AB011125; Hs.105749; KIAA0553 protein; none;TM=M; 2.89  
 444100; AA383343; Hs.22116; CDC14 (cell division cycle 14, S. cerevisiae) homolog B; Y\_phosphatase,DSPC;TM=M; 2.89  
 47437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupled, 2; 7tm\_1,SH2;TM=Y;SS=M; 2.89  
 35 431512; BE270734; Hs.2795; lactate dehydrogenase A; ldh,ldh\_C,SH3,pkinase,UBA;TM=M; 2.89  
 446601; A132783; Hs.155772; Homo sapiens thymic stromal co-transporter mRNA, complete cds; sugar\_tr;TM=Y; 2.89  
 420747; BE294407; Hs.99910; phosphofructokinase, platelet; PFK;TM=M; 2.88  
 449459; BE546846; Hs.195048; ESTs; ank,ras,PH,ArfGap,HCO3\_cotransp; 2.88  
 405099; ; Target Exon; C2,PI-PLC-Y,PI-PLC-X;TM=M; 2.88  
 445890; AF055019; Hs.21906; Homo sapiens clone 24670 mRNA sequence; pkinase,pkinase; 2.88  
 40 401445; ; NM\_021161\*:Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA.; ion\_trans;TM=Y;SS=M; 2.87  
 405480; ; Target Exon; none,none; 2.87  
 400189; ; Eos Control; LRR,PPTA;TM=M; 2.87  
 45 450125; AA005418; Hs.158186; ESTs; CIDE-N,7tm\_1,none; 2.87  
 432056; AB040973; Hs.272385; G protein-coupled receptor 72; 7tm\_1;TM=Y;SS=M; 2.86  
 423619; T48691; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm\_1,7tm\_2;TM=Y;SS=M; 2.86  
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; xan\_ur\_permease,RA; 2.86  
 420035; F26725; Hs.187908; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; HATPase\_c,MOZ\_SAS,zf-C2H2; 2.86  
 425480; AB023198; Hs.158135; KIAA0981 protein; PIP5K;SS=M; 2.86  
 50 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc finger protein, ESTs, STSs, GSSs and a putative CpG; none;TM=M; 2.86  
 444595; AL121094; Hs.83572; hypothetical protein MGC14433; Y\_phosphatase,SH2,Y\_phosphatase,SH2; 2.85  
 411331; AW837178; ; gb:QV1-LT0037-070300-100-d11 LT0037 Homo sapiens cDNA, mRNA sequence; SH2,none; 2.85  
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; none,none; 2.85  
 55 440617; AA894880; Hs.181181; ESTs; none,none; 2.85  
 454071; A1041793; Hs.42502; ESTs; 7tm\_1,none; 2.85  
 411040; AF007393; Hs.177574; protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor); HLH;TM=M; 2.85  
 402183; ; NM\_004491\*:Homo sapiens glucocorticoid receptor DNA binding factor 1 (GRLF1), mRNA.; none;SS=M; 2.85  
 428753; AW939252; Hs.192927; hypothetical protein FLJ20251; none;TM=M; 2.84  
 60 417070; Z19077; Hs.172004; titin; fn3,ig,SGXXSG,pkinase;TM=M; 2.84  
 458456; A1122709; Hs.153609; ESTs; bZIP,Armadillo\_seg,rrm,NTF2,none; 2.84  
 421226; A1096748; Hs.102708; DKFZP434A043 protein; Armadillo\_seg,integrin\_B,PSI,TIG;TM=M;SS=M; 2.84  
 436733; BE327477; Hs.166941; ESTs; 7tm\_3,oxidored\_q5\_N,Presenilin,PWI; 2.84  
 427161; A1024595; Hs.97508; a disintegrin and metalloproteinase domain 6; ig;TM=Y;SS=M; 2.84  
 419462; AF071076; Hs.112255; nucleoporin 98kD; DEAD,helicase\_C,Nucleoporin\_FG,homeobox;SS=M; 2.83  
 65 413658; AA055369; Hs.75456; A kinase (PRKA) anchor protein 10; none,none; 2.83  
 400749; ; NM\_003105\*:Homo sapiens sorilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA.; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 2.83  
 447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; TB2\_DP1\_HVA22;TM=Y;SS=M; 2.83  
 413243; AA769266; Hs.193657; ESTs; pkinase,zf-C4,ERM,CNH,none; 2.83  
 70 423690; AA329648; Hs.23804; ESTs, Weakly similar to PN0099 son3 protein [H.sapiens]; ion\_trans,IQ,none; 2.82  
 447993; AW139525; Hs.170362; ESTs; none,none; 2.82  
 423061; A1290473; Hs.44807; ESTs; integrin\_B,Sema,PSI,TIG,none; 2.82  
 440619; AW408586; Hs.91052; ESTs, Moderately similar to ALU5\_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; abhydrolase\_2,none; 2.82  
 75 423497; U92642; Hs.129701; G protein-coupled receptor 45; 7tm\_1;TM=Y;SS=M; 2.81  
 446126; AW085909; Hs.10177; pleckstrin homology domain interacting protein; none,none; 2.81  
 452488; N74921; Hs.184389; ESTs; none;TM=M; 2.80  
 449515; A1653378; Hs.302012; ESTs; ion\_trans;TM=Y;SS=M; 2.79  
 80 443881; R64512; Hs.237146; hypothetical protein FLJ12752; none,none; 2.79  
 449636; A1656608; Hs.281328; ESTs, Weakly similar to T00378 KIAA0641 protein [H.sapiens]; pkinase,hormone3;TM=Y;SS=M; 2.78  
 424348; AB020523; Hs.266258; endonuclease G-like 1; Endonuclease;TM=M;SS=M; 2.78  
 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase,PLAT;TM=M; 2.78  
 442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; MIF,sugar\_tr,none; 2.78

450010; AW293801; Hs.255052; ESTs; ARID,7tm\_1; 2.78  
 452813; U54727; Hs.191445; ESTs; pkinase,Activin\_recpt,none; 2.78  
 418177; N44967; ; ESTs; pkinase,none; 2.78  
 408014; AA723782; Hs.41749; protein kinase, cGMP-dependent, type II; cNMP\_binding,pkinase;SS=M; 2.77  
 448362; AA641767; Hs.21015; hypothetical protein DKFZp564L0864 similar to HIAT1; sugar\_tr;TM=Y;SS=M; 2.77  
 423994; X01057; Hs.1724; interleukin 2 receptor, alpha; sushi;TM=Y;SS=M; 2.77  
 427342; AL110150; Hs.176680; Homo sapiens mRNA; cDNA DKFZp586D0724 (from clone DKFZp586D0724); none;NA;NA; 2.76  
 447574; AF162666; Hs.18895; tousel-like kinase 1; pkinase;TM=M; 2.76  
 442681; A1809182; Hs.130907; ESTs; transketolase,E1\_dehydrog,transket\_pyr,transketolase\_C,pkinase; 2.75  
 433637; AW024214; Hs.102307; ESTs; Na\_sulph\_symp,aa\_permeases;TM=Y;SS=M; 2.75  
 458997; AW937420; Hs.69662; ESTs; SH3,RhoGAP,FCH;TM=M; 2.75  
 432284; AA532807; Hs.105822; ESTs; pkinase,none; 2.74  
 406139; ; Target Exon; ig,Tub;TM=Y;SS=M; 2.74  
 439518; W76326; ; gb:zd60d04.r1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone 5' similar to contains Alu repetitive element; mRNA sequence; Armadillo\_seg,none; 2.74  
 428536; A1143139; Hs.2288; visinin-like 1; efhand;SS=M; 2.73  
 400211; ; NM\_003899; Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. VERSION NM\_003897.1 GI; SH3,PH,RhoGEF,Terpene\_synt;TM=M; 2.73  
 402129; ; Target Exon; SH2,Peptidase\_C9;TM=M; 2.73  
 424238; AA337401; Hs.137635; ESTs; none;TM=M;SS=M; 2.73  
 433834; AA620742; Hs.130786; ESTs; SPX,EXS;TM=Y; 2.73  
 409339; AB020686; Hs.54037; ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function); Sulfatase,Phosphodiester;TM=M;SS=M; 2.73  
 408163; AW779842; Hs.258217; ESTs; 7tm\_1,zf-B\_box,zf-C3HC4,7tm\_1,zf-B\_box,zf-C3HC4; 2.73  
 422358; AL133030; Hs.115429; Homo sapiens mRNA for KIAA1666 protein, partial cds; SH3;TM=M; 2.73  
 426409; AA594207; ; gb:nn29e01.s1 NCL\_CGAP\_Gas1 Homo sapiens cDNA clone 3', mRNA sequence; pkinase,Fibrillarin,none; 2.72  
 400645; ; Target Exon; lig\_chan,SBP\_bac\_3,ANF\_receptor,none; 2.72  
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; adenylatekinase,none; 2.71  
 442572; A1001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 2.71  
 409317; U20165; Hs.53250; bone morphogenetic protein receptor, type II (BMPR2); pkinase,Activin\_recpt;TM=M;SS=M; 2.71  
 403201; ; Target Exon; none; 2.71  
 459357; AW848421; ; gb:IL3-CT0214-150200-075-B11 CT0214 Homo sapiens cDNA, mRNA sequence; ABC\_tran,ABC\_membrane,ion\_trans; 2.70  
 439935; S75105; Hs.8358; glutamate receptor, ionotropic, kainate 2; ANF\_receptor,lig\_chan,none; 2.70  
 414924; C06267; Hs.44247; ESTs; none,none; 2.69  
 421008; BE259378; Hs.103147; hypothetical protein FLJ21347; DUF255; 2.69  
 449951; AA004982; Hs.120904; ESTs; DED,Calsequestrin; 2.69  
 411226; AW833022; ; gb:RC3-TT0005-191099-012-d04 TT0005 Homo sapiens cDNA, mRNA sequence; pkinase,none; 2.68  
 417625; U59305; Hs.44708; Ser-Thr protein kinase related to the myotonic dystrophy protein kinase; pkinase,bZIP,G-gamma,K-box,pkinase\_C;SS=M; 2.68  
 408051; A1623351; Hs.172148; ESTs; PH,RhoGAP,none; 2.68  
 412521; AW753481; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 2.68  
 413922; A1535895; Hs.221024; ESTs; ion\_trans,RYDR\_ITPR,MIR,UDPGT; 2.68  
 432188; A1362952; Hs.2928; solute carrier family 7 (cationic amino acid transporter, y system), member 1; aa\_permeases;TM=Y;SS=M; 2.67  
 415516; F11411; ; gb:HSC2WF081 normalized infant brain cDNA Homo sapiens cDNA clone c-2wf08, mRNA sequence; ion\_trans,none; 2.67  
 419749; X73608; Hs.93029; sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican); kazal,thyroglobulin\_1;SS=M; 2.66  
 416095; AW014327; Hs.221951; ESTs; Weakly similar to I38022 hypothetical protein [H.sapiens]; ig,zf-C3HC4,Cbl\_N,Cbl\_N2,Cbl\_N3,none; 2.66  
 403609; ; C3001199:gil7494834[pir][T15308 hypothetical protein B0286.2 - Caenorhabditis elegans][41; 7tm\_1,7tm\_2,GPS,WIF;TM=Y;SS=M; 2.66  
 458213; AL047521; Hs.12210; hypothetical protein FLJ13732 similar to tensin; pkinase,none; 2.66  
 426158; NM\_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3; Furin-like,pkinase,Recep\_L\_domain,Furin-like,pkinase,Recep\_L\_domain,Peptidase\_M24; 2.66  
 435410; AL135067; Hs.117182; ESTs; none,pkinase,RBD,DAG\_PE-bind; 2.66  
 437838; A1307229; Hs.184304; ESTs; CARD,ICE\_p20,ICE\_p10,HIT,voltage\_CLC,CBS,HCCA\_isomerase; 2.66  
 430293; A1416988; Hs.238272; inositol 1,4,5-trisphosphate receptor, type 2; ion\_trans,RYDR\_ITPR,MIR,none; 2.65  
 433090; A1720050; ; immortalization-upregulated protein; none;SS=M; 2.65  
 432103; T15803; Hs.272458; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); Metallophos;TM=M; 2.65  
 435852; H72303; Hs.36011; ESTs; pkinase,none; 2.64  
 433327; A1674779; Hs.126744; ESTs; none,7tm\_1; 2.64  
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; none,FMO-like; 2.64  
 432251; AW972983; Hs.232165; polycythemia rubra vera 1; cell surface receptor; none;TM=M;SS=M; 2.63  
 446963; A1862668; Hs.176333; ESTs; OMPdecase,Pribosyltran,pkinase,RhoGEF,PH; 2.63  
 444821; AA053564; Hs.12040; STE20-like kinase; pkinase;TM=M; 2.63  
 436206; AK001451; ; CD2-associated protein; none,none; 2.63  
 434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic receptor; death,Kunitz\_BPTI;TM=Y;SS=M; 2.63  
 439039; A1656707; Hs.48713; ESTs; pkinase,none; 2.63  
 449656; AA002008; Hs.188633; ESTs; PIP5K,none; 2.63  
 429341; X73874; Hs.2393; phosphorylase kinase, alpha 1 (muscle); none;TM=M; 2.62  
 445174; AV652850; Hs.172004; titin; fn3,ig,SGXXSG,none; 2.62  
 424950; AA602917; Hs.156974; ESTs; none,CDP-OH\_P\_transf; 2.62  
 438141; AW946871; ; gb:RC2-ET0022-080500-012-d02 ET0022 Homo sapiens cDNA, mRNA sequence; SH2,STAT,STAT\_bind,STAT\_prot,none; 2.61  
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, complete cds; pkinase,TBC,Rhodanese;TM=M; 2.61  
 409264; NM\_014937; Hs.52463; KIAA0966 protein; Syja\_N;TM=M; 2.60  
 458438; A1141520; Hs.151464; ESTs; Weakly similar to ALUC\_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]; pkinase,none; 2.60  
 400719; ; NM\_004055; Homo sapiens calpain 5 (CAPN5), mRNA. VERSION NM\_004335.2 GI; C2,Peptidase\_C2,Calpain\_III;TM=M; 2.60  
 427318; AF186081; Hs.175783; zinc transporter; Zip;TM=Y;SS=M; 2.59  
 426086; T94907; Hs.188572; ESTs; PH,Ets,CH,spectrin,Ca\_channel\_B,none; 2.59  
 430105; X70297; Hs.2540; cholinergic receptor, nicotinic, alpha polypeptide 7; Neur\_chan\_LBD,Neur\_chan\_memb,pkinase;TM=Y;SS=M; 2.58  
 411495; AP000693; Hs.70359; KIAA0136 protein; HATPase\_c,bZIP;TM=M; 2.58  
 438167; R28363; Hs.24286; ESTs; none;TM=Y;SS=M; 2.58  
 418749; N75147; Hs.22488; ESTs; none,zf-C2H2,KRAB,pkinase; 2.58  
 454289; AL137554; Hs.49927; protein kinase NYD-SP15; dCMP\_cyt\_deam;TM=M; 2.58  
 443605; H06865; Hs.134131; ESTs; efhand,ion\_trans,none; 2.57  
 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 2.57  
 403088; ; NM\_003319; Homo sapiens titin (TTN), mRNA. mRNA; ; fn3,ig,SGXXSG;TM=M; 2.57  
 409190; AU076536; Hs.50984; sarcoma amplified sequence; transmembrane4;TM=Y;SS=M; 2.57  
 426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 fis, clone HRC04468; ig;TM=Y;SS=M; 2.56  
 403328; ; Target Exon; Glyco\_hydro\_35;TM=M; 2.56

- 426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo\_seg,HEAT\_PBS;; 2.56  
 428695; A1355647; Hs.189999; purinergic receptor (family A group 5); 7tm\_1,TM=Y;SS=M; 2.54  
 419285; D31887; Hs.89968; KIAA0062 protein; Zip;TM=Y;SS=M; 2.54  
 415740; N80486; Hs.39911; Homo sapiens mRNA for FLJ00089 protein, partial cds; CBM\_21;TM=M;; 2.53  
 403305; NM\_006825; ; transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment; pkinase;TM=Y;SS=M; 2.53  
 443804; AL135352; Hs.255883; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Peptidase\_M18,Peptidase\_M18,Y\_phosphatase; 2.53  
 450425; H06607; Hs.6099; ESTs; E1-E2\_ATPase,Cation\_ATPase\_C,Cation\_ATPase\_N,Hydrolase,none; 2.51  
 401702; ; NM\_001171;Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 6 (ABCC6), mRNA.; ABC\_tran,ABC\_membrane;TM=Y;SS=M; 2.50  
 439463; W69304; ; gb:zd46f01.r1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone 5', mRNA sequence; fn3,Y\_phosphatase,none; 2.50  
 425975; AB011082; Hs.165559; organic cationic transporter-like 4; sugar\_tr;TM=Y;; 2.50  
 443259; AW090601; Hs.69171; protein kinase C-like 2; pkinase,pkinase\_C,HR1,none; 2.50  
 400777; ; NM\_007325;Homo sapiens glutamate receptor, ionotropic, AMPA 3 (GRIA3), transcript variant flp, mRNA.; lig\_chan,SBP\_bac\_3,ANF\_receptor;TM=M;SS=Y; 2.49  
 426044; AA502490; Hs.170290; ESTs; none,none; 2.48  
 454564; AW807573; ; gb:MR1-ST0088-021299-004-g01 ST0088 Homo sapiens cDNA, mRNA sequence; pkinase,none; 2.48  
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; KH-domain,TUDOR;TM=M;SS=M; 2.47  
 426481; AW963941; ; gb:EST376014 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence; Y\_phosphatase,Band\_41,DSpc,none; 2.46  
 426005; AA377499; ; gb:EST90341 Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence; tubulin,FKBP,COX6B,7tm\_1,tubulin\_C;SS=M; 2.46  
 424879; AA348013; Hs.273385; ESTs; arf,G-alpha,none; 2.46  
 415156; X84908; Hs.78060; phosphorylase kinase, beta; none;TM=M;; 2.46  
 416508; R39769; ; ESTs, Moderately similar to ALU8\_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; SH3,PDZ,Guanylate\_kin,ZU5,none; 2.46  
 408087; AW150645; ; gb:xcg54407.x1 NCL\_CGAP\_Ut4 Homo sapiens cDNA clone 3', mRNA sequence; XYPPX,ABC\_membrane,ABC\_tran; 2.46  
 433434; AA588429; ; gb:nc22b03.s1 NCL\_CGAP\_Pr22 Homo sapiens cDNA clone 3', mRNA sequence; pkinase,DNA\_mis\_repair,HATPase\_c; 2.45  
 446768; AV660305; Hs.110286; ESTs; ICE\_p20,DED,ICE\_p10,ICE\_p20,DED; 2.45  
 437158; AW090198; ; KIAA1150 protein; none;NA;NA; 2.45  
 430177; AW969233; Hs.302746; MSTP028 protein; K\_tetra,none; 2.45  
 422270; AF114494; Hs.114062; protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a; none;TM=Y;; 2.45  
 430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7\_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; Y\_phosphatase,Adaptin\_N,Y\_phosphatase; 2.44  
 446569; AW248031; Hs.155839; hypothetical protein MGC12934; adh\_zinc,PGK,Semialdehyde\_dh;SS=M; 2.44  
 411902; AW875344; ; gb:RC1-PT0009-220300-013-f06 PT0009 Homo sapiens cDNA, mRNA sequence; none,pkinase,ank; 2.43  
 430057; AW450303; Hs.2534; bone morphogenetic protein receptor, type IA (BMPRI1A) (ALK-3); Activin\_rec,pkinase;TM=Y;SS=M; 2.43  
 446338; AI289121; Hs.206978; ESTs; none,SH3; 2.42  
 426221; AB007881; Hs.110613; KIAA0421 protein; none,Ribosomal\_S8; 2.42  
 446796; AI652497; Hs.110103; RNA polymerase I transcription factor RRN3; none,none; 2.41  
 428360; H10291; Hs.30974; ESTs; pkinase,PBD,none; 2.40  
 428379; X06026; Hs.2259; CD3G antigen, gamma polypeptide (TIT3 complex); ITAM;TM=Y;SS=M; 2.40  
 432488; AA551010; Hs.216640; ESTs; Na\_sulph\_symp,none; 2.40  
 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, yeast, homolog)-like; none,Ribosomal\_S13,Galactosyl\_T,Zip,adh\_short,zf-C3HC4; 2.40  
 448595; AB014544; Hs.21572; KIAA0644 gene product; LRR,LRRCT;TM=Y;SS=M; 2.40  
 428283; AI439096; Hs.323079; Homo sapiens mRNA; cDNA DKFZp564P116 (from clone DKFZp564P116); Y\_phosphatase,fn3,ig,none; 2.39  
 432460; H12912; Hs.274691; adenylate kinase 3; adenylatekinase,none; 2.38  
 429549; AI333013; Hs.250505; retinoic acid receptor, alpha; none,zf-C3HC4,BRCT,lig\_chan; 2.38  
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; Phosphodiester,Somatostatin\_B,Endonuclease,none; 2.36  
 417473; M55268; Hs.82201; casein kinase 2, alpha prime polypeptide; pkinase,ABC1;TM=M;; 2.35  
 453186; AK001708; Hs.32271; hypothetical protein FLJ10846; TK,DUF300;TM=Y;SS=M; 2.33  
 447276; AL049795; Hs.17987; hypothetical protein MGC1203; none;TM=M;; 2.33  
 445310; AI242490; Hs.153290; Homo sapiens cDNA FLJ14318 fis, clone PLACE3000402; none,pkinase; 2.31  
 432942; AF083955; Hs.279852; G protein-coupled receptor; 7tm\_1,globin;TM=Y;SS=M; 2.30  
 434693; AW976001; Hs.337603; ESTs; none,none; 2.26  
 452034; F12234; Hs.75893; ankyrin 3, node of Ranvier (ankyrin G); ZU5,death,none; 2.25  
 423732; AF058056; Hs.132183; solute carrier family 16 (monocarboxylic acid transporters), member 7; sugar\_tr;TM=Y;SS=M; 2.25  
 404956; ; C1003210\*gi16912582[ref][NP\_036524.1] peflin [Homo sapiens] gi16009487[dbj][BAA84922.1] (AB; none,PI3\_P14\_kinase,PI3K\_C2,PI3K\_rbd,PX,PI3Ka,C2; 2.24  
 452183; NM\_006594; Hs.28298; adaptor-related protein complex 4, beta 1 subunit; Adaptin\_N,Y\_phosphatase; 2.23  
 420529; D25259; Hs.319844; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; pkinase,DAG\_PE-bind,RBD,ras,DC1,GFP;TM=M;; 2.21  
 408808; BE074219; Hs.17230; hypothetical protein FLJ22087; Armadillo\_seg;TM=M;SS=M; 2.21  
 451932; AA360954; Hs.27268; Homo sapiens cDNA: FLJ21933 fis, clone HEP04337; SH3,PH,RhoGEF;TM=M;; 2.21  
 432008; AW296791; Hs.193170; hypothetical protein FLJ21687; LIM,Synaptophysin,ion\_trans,KOW; 2.20  
 455840; BE145897; ; gb:MR0-HT0208-221299-204-b07 HT0208 Homo sapiens cDNA, mRNA sequence; PI3\_P14\_kinase,PI3Ka,PI3\_P14\_kinase,PI3Ka; 2.19  
 429238; NM\_002849; Hs.198288; protein tyrosine phosphatase, receptor type, R; Y\_phosphatase;TM=Y;SS=M; 2.19  
 430975; AA490055; ; gb:ab05b09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 3', mRNA sequence; adenylatekinase,Thymidylate\_kin;TM=M;; 2.17  
 407174; T79938; Hs.77062; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5; ig,none; 2.16  
 450921; AA098790; Hs.146245; ESTs, Moderately similar to T17242 hypothetical protein DKFZp586B1417.1 [H.sapiens]; none;NA;NA; 2.15  
 427209; H06509; Hs.92423; KIAA1566 protein; pkinase;TM=M;; 2.14  
 401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT\_bind,STAT\_prot,ion\_trans,PAC,PAS,none; 2.12  
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; adenylatekinase,none; 2.07  
 439520; W76548; Hs.336621; ESTs, Moderately similar to ALU5\_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ion\_trans,none; 2.06  
 410439; R35943; Hs.63758; transferrin receptor 2; PA;TM=Y;; 2.05  
 448696; AI564769; Hs.173070; EST, Weakly similar to ZN42\_HUMAN ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1) [H.sapiens]; none,zf-C2H2; 2.04  
 449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K\_tetra,ion\_trans,none; 2.04  
 453496; AA442103; Hs.33084; solute carrier family 2 (facilitated glucose/fructose transporter), member 5; sugar\_tr;TM=Y;SS=M; 2.02  
 443952; AI149106; Hs.143530; ESTs; pkinase,none; 2.02  
 437589; AA761322; Hs.269662; ESTs; SH2,SH3,C2,PH,RasGAP,none; 2.02  
 422637; AA399024; Hs.118836; myoglobin; globin;TM=M;; 2.01  
 450253; AL133047; Hs.24715; Homo sapiens mRNA; cDNA DKFZp434D0215 (from clone DKFZp434D0215); partial cds; SH3;TM=M;; 1.97  
 401984; ; C17000146\*gi12143629[pir][A57156 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) l; pkinase;; 1.96  
 453464; AI884911; Hs.32989; receptor (calcitonin) activity modifying protein 1; none;TM=Y;; 1.95  
 417733; AL048678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown protein; none;NA;NA; 1.94  
 411450; H49619; Hs.127301; ESTs; pkinase,none; 1.82  
 406303; ; C16000922:gi17499103[pir][T20903 hypothetical protein F14F4.3b - Caenorhabditis elegans gi; ABC\_tran,GTP\_EFTU,PRK,ABC\_membrane;TM=Y;; 1.80  
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor type, M; fn3,ig,Y\_phosphatase,MAM;TM=Y;SS=M; 1.74



425280; U31519; Hs.1872; phosphoenolpyruvate carboxykinase 1 (soluble); PEPCK;TM=M;; 1.65  
425958; AW163271; Hs.301839; intracellular antigen detected by monoclonal antibody Ki-1; intracellular hyaluronan-binding protein; Y\_phosphatase,DSPC;TM=M;; 1.63  
432563; NM\_013261; Hs.198468; peroxisome proliferative activated receptor, gamma, coactivator 1; rrm;TM=M;; 1.51

TABLE 49B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 BI22204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581 BI009308 BI009893 BF922203 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291 AW905577 AW975593 AA713730 AW836781 AA666384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555 AA586369 AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389 AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680 AF086101 AL133916 AW955684 AW950828 AI346341 AI867454 BM263376 BF432231 AI421279 AI655270 AW014882 BF439949 AA775552 N62351 AA626243 N59253 AI341407 AA456968 AA457077 AI358918 AA364013 N79113 N54784 BE175639 N76721 AV727392 Z45529 Z44343 F05908 F05403 F05398 BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701 BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592 AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AI072248 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA459292 AI494230 BF057531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363 AK057826 AI631982 AA224195 AI701458 AA890570 AW966562 AW071907 AI671352 AI375892 T03517 AI124088 R88265 AI084316 BF223720 AI354686 T33652 AW205836 BE931115 AI720211 T03490 BF084055 AI372637 T15415 BG054890 AA630384 F26326 AI140719 AA443303 T33230 T33623 T33511 T33785 AW118072 W20198 AI657180 T15734 AI419606 N90552 AA224388 T15909 T03515 D55612 W27899 NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355 AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205 BE090841 AW163750 BF747730 BF898637 AI206506 AV660870 AV692110 AW386830 AV656831 N84710 AW993470 BF086802 BF758454 BG960772 BF757769 BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE909924 AA708208 BG530266 BF968015 AW992390 BF888862 BG536628 AA143164 AW748953 BG498922 BF885190 BF889005 BF754781 BF800003 BM476529 AI627668 AW028126 AL046011 BF590668 AI017447 AA579936 AI367597 AA699622 BE280597 AI124620 AI082548 AW274985 AA677870 AI056767 BE551689 AA287642 H94499 AI752427 AI652365 AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813 AI092115 BF312771 BF242859 BG533616 BG533761 BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353 AU155318 BE302211 AI375022 AA085641 AU157923 H88858 AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296 AI184820 AI469178 AA782432 H92184 AA340562 BF195818 AA852821 AW576342 AA827107 AA173317 AW190014 AI918514 AA729372 AA729718 AI055958 AA331424 BE328601 AA515690 BI018896 AW628277 AA748368 AA626222 BG492636 AW380620 BF800058 AW370956 AA290909 R25857 BG952995 BF801437 AA172077 AU155890 AU149783 AI720904 AA902936 AA865727 AI470830 AV740677 AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427 BE928472 D25910 BF758439 BF968785 BE565238 AA355981 AI905607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471 BG574501 AA187596 AA361196 T95557 BG531446 BG527242 BG527513 BG611106 AA085995 BF847252 BG024608 BE540261 BG531236 AL579993 BG108733 BG483503 BG571032 BG492505 BC014030 NM_004068 BC004996 AK057883 D63475 BM468205 BG386792 BG750447 BG755842 BG479084 BG741027 AU118129 BE901043 AU141281 BG825395 BG338276 BE396231 AU121493 AU131489 BF341132 BG335659 BI769251 AU142779 AU124483 BG480828 AU121353 BG702326 AU137866 BG759046 BI460601 BE887290 BG750415 BF127710 BG757819 BI160266 AU122086 BG824046 BG744180 BE884943 BM006610 BG702599 BI870749 BF307033 BI334771 BG480606 AU142599 AU141336 BM018563 BI335565 AU138308 BE391241 BG774488 BE278025 BG717959 BG706920 BE312567 AU138300 BE303034 BE303016 AU139252 BE336797 BG470940 BE336735 BF305197 AU134288 AU139907 BE261245 BE208718 BG761912 BF212890 AW732692 BM011258 AW247629 AU136696 BF530078 BF204146 AL048752 BG328927 BE388385 BE260122 AU138789 BE253465 BF733914 AW249415 AW239535 BE311791 BE256236 BF529742 BG770465 AW245777 AW245813 BE296677 BE266852 BE168115 BE396596 BE280057 BE168229 AI750820 AU134137 BF792191 AI272215 AI907348 AW238875 BF805152 BF568397 BE712727 BE081443 BE001805 BF724536 BF744705 AW247385 BE796369 AU133759 AV705142 BE794402 BM465821 BG281284 AW384831 BM450689 AU134125 BE311650 BF356318 BM462831 BG420555 BE749127 AU134590 BM019438 BC013796 BG761223 BG122058 BE872076 BG748496 BG821374 BE619159 BG423244 AU137110 AU127210 BE270081 AA496860 AA351380 AA356303 AU099781 AA355912 AA371411 AA325535 U36188 AL569574 AL577204 AL525543 AL567342 AL567334 AL567122 AL536527 AL567098 BG681585 BG824951 BI870652 BI225855 AW393878 BG750632 BI223803 BE877552 BE270473 BE389392 BE779021 BM017845 BI117816 BE396513 BM049006 AW393945 BE786941 BE267724 BE562981 BE314236 BF744102 BM019781 BF806063 BF828673 BF829178 BF829175 BF433802 BE909928 BF839784 AW578564 BF943095 AW328030 AA448596 AW882688 AA909846 BF924341 AW361460 AA425174 BE940557 BF761585 BF931276 BF934886 W68597 BF933977 BI035906 BE836064 BF837576 BI018368 AA205908 H54612 R88902 BE812330 BE932300 BF924562 AW805376 BE769859 R87381 AA371901 BE838855 AA326381 W56191 AA341231 AA464093 AL575977 AL518650 AL547393 BG338327 AL517563 AL536921 BG207096 BG207589 BG199290 BG220159 BG744842 BG104730 AA555035 AA618009 AA861062 AA610582 AW245418 AI040983 AA521380 AW245455 AU147292 AU155236 BE620286 AW250767 BF888236 BE620819 AU154343 AU150827 AU148334



5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

AW069495 AA701091 AU155225 AW250019 AA666235 AU147764 AA449739 BF907598 AW043731 AU144390 AI924565 BE300631 AW874021  
 BE208088 BF732773 BF594057 AI159873 AU143930 N24100 AI052499 AI989370 AI366151 AI139248 AA4838250 AI095433 AI269227  
 BF811358 AU151352 AA477554 AI131290 AI049797 AU157349 AA620559 AA581533 AI338299 AA402755 AI050079 AU157614 AI280691  
 AA706590 BE206615 AA861056 AU153214 AU155712 AW069554 AI081124 AU155846 AI081123 AA719876 AI754976 AI027763 AA723095  
 BI518782 AW050706 F37521 R79062 AA565530 H39826 AA404670 AU158884 AI139682 AA513633 AI283202 AA651856 AI623515 AA427413  
 AW248474 BF841432 BM453246 AI302390 AA808269 AI249357 AA132775 AA716732 AA479932 AI198296 AI208674 AI088433 F36977 AA496899  
 AW615762 AA602541 AA341161 D58785 T15399 AI286077 W69152 F28418 AI272156 AA338034 AA568455 BE206121 AI080033 AI699680  
 AA861255 AI953465 AI613240 AL581773 AL531577 BF526361 AA657809 AW152670 BE621523 AW078705 AW673719 AA102613 AA195604  
 R72209 AA402208 AA404305 N24999 AI963535 D54741 BI461415 BM475959 BI260926 BI116213 BE280120 BE940258 BE280044 AI905744  
 BG001474 BE937718 BF799283 BI091621 BG421006 BG289235 BF736825 BI253429 BG170064 R72512 T92815 BF931257 BM455183 BG033362  
 BG574220 N31395 BF739185 AA371995 BE879011 BI198754 BF378989 T12266 BM019421 BI194570 BF378992 AW996595 BI858649 W94605  
 W61345 AA122384 AA171923 T92736 AA761504 AI819039 AI439358 AL517777 AL565919 AA622001 AA642695 AA704144 AA081465 AA070621  
 AA375562 AA700011 AA926863 W37310 AL566236 BF677809 BG760021 AW361433 BE828605 BE268449 BF805977 BG292452 BF981071  
 BF217108 BF928698 R33993 AW882841 AI857453 AW078733 AI433035 AI018103 R90927 AA804720 AA551734 R33835 H19741 R78754  
 BF930494 BG109583 AA631926 BE834008 BG996533  
 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796  
 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033  
 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AA4572531 AW015724 BE349186  
 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA057070 AI075878 W38161 AI972739  
 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827  
 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817  
 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693  
 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453  
 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301  
 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398  
 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071  
 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414  
 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AI576200 AL571074 AL574525  
 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574  
 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437  
 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510  
 AE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307  
 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954  
 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896  
 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027  
 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821  
 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AI556586  
 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578  
 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365  
 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA151188 AI466615 C06300 BG497644  
 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120  
 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148  
 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525  
 BC015334 AA805670 AW014686 N66615 BG029745 AA481269 H91728  
 AJ420458 AI018523 AA708686 BF949633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI654847 AW874199 AI206120  
 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350  
 W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199  
 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366466 N64350 AA779107 AW025969 R49056  
 AA347011 R55722 AW771106 F04969 Z38381 F16559 H17396 BI493714 AI880103 AW771447 AI202561 AW778851 AI494436 BF856114 H22570  
 AW957244 AA370585 AW957239  
 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796  
 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033  
 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AA4572531 AW015724 BE349186  
 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA04570 AI075878 W38161 AI972739  
 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827  
 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817  
 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693  
 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453  
 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301  
 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398  
 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071  
 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414  
 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AI576200 AL571074 AL574525  
 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574  
 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437  
 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510  
 AE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307  
 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954  
 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896  
 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027  
 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821  
 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AI556586  
 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578  
 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365  
 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA151188 AI466615 C06300 BG497644  
 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120  
 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148  
 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525  
 AW975503 BE763276 H74234 AA687376  
 AA229762 AA230035  
 BC006097 X03066 NM\_002120 M26040 AW469119 AW469127 AI299772 AW518149 AI144456 AW628070 AI629032 AI358810 AI880433 AI440472  
 AI357070 AI865365 AW014799 AI767973 AW518041 AA909398 AW768606  
 BC012771 BG397153 BF366196 AA337277 AA319285 AW843252

5	410032 400263	1490765_1 18977_1	BE065985 BE066083 BE066008 BE066093 BE065944 Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG988348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084 BE072622 M79082 NM_025237 AF326739 AW771508 AI498457 AI493134 AI383985 AI498691 BF431247 AI580267 D79813 AF331844 AA393939 AI783624 AA969408 AI768408 AA393768 AA210987 D57294 AA214584 AA207006 D56572 BG028348 BF772844 H83066 AW817969 H90985 BF755039 AI858183 BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57522 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AI574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586 AW978432 AA830185 N67023 R80000 AL036458 AA358606 AW962990 X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 AI910663 BF905778 BG251264 AL562106 AI890538 AW769258 AI590391 AI913055 AW083235 AI078474 AI925022 AW504628 AW129725 BE466589 AW002786 AW591760 AI968816 AW006268 AW593787 BG236814 AW769893 AW407608 AW075982 AI248207 AI762509 AI812070 AI249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245 BI014177 AL519126 BE675314 AW806520 BI870778 BF879549 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893 BE798121 R09703 BI013066 AI758223 AW469334 BF940841 AW080348 AI270363 AI055892 BE464168 BF431797 BE350144 BF448739 AI693409 BF432999 D62848 AA398070 AI383375 AW611490 AA715338 AA715284 AA715344 AV752763 AI032142 N30308 N22181 H95390 AW675632 X98248 NM_002959 AU127082 AU143346 BE327147 AI168442 AA426361 BF056336 AA418378 AI470560 AI365213 BI032745 BI032986 AA969895 AA233278 AW291971 AA418326 AI198417 AI337018 BI032747 AA888000 AU099083 AU129681 AI036861 AA418275 BF887436 BF767448 AA232975 BI094065 BI859449 AL079651 BF877391 AW902319 BF878798 BG281450 AA418268 BG770672 BE890328 BI520437 BE387505 AW375004 BI020046 BI033747 BF800905 BF869732 N99710 BF905459 BE715637 BE746496 BF918537 BF751392 BF751390 BF369123 BG949840 AA984366 H85743 AW593418 AI990196 T92267 AA018359 H38111 BM050097 BF692315 AW805907 AI547305 AA631091 BF845219 BG949806 T92310 BE277220 U44839 NM_004651 BC000350 BI458316 AU117940 BG759024 BG749694 BE799505 BG831537 AI816335 AA325352 AL547005 AW157038 AI859331 AI816186 AU150786 AL043549 AW162880 AU159233 AI143169 T03478 BE727648 AA764725 BE206603 AI369814 AI984369 AW157545 BE221486 H99016 AU159025 AI074496 AI494516 BE245950 AA704385 AA280862 AI479595 AI369776 BE671398 T05538 AA682249 BI677303 BE645335 AI359434 H92868 D52599 D53609 D54715 T06015 BE222174 AI954706 D53218 D53787 R69889 W86896 AI497670 R70771 BF309414 BE620147 BG910597 AW964968 BE836120 AL579715 H56512 D55956 BI044097 AL555239 BF220278 AA081991 AI819544 AW001573 AW131600 AI858764 D52367 W22034 BG818979 BG024561 BE702779 BI458863 BI910399 BG707755 BF348284 H10055 BI086315 BE620574 H41088 BG119517 W23267 W21941 AA328817 X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 AI910663 BF905778 BG251264 AL562106 AI890538 AW769258 AI590391 AI913055 AW083235 AI078474 AI925022 AW504628 AW129725 BE466589 AW002786 AW591760 AI968816 AW006268 AW593787 BG236814 AW769893 AW407608 AW075982 AI248207 AI762509 AI812070 AI249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245 BI014177 AL519126 BE675314 AW806520 BI870778 BF879549 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893 BE798121 R09703 BI013066 AV659361 BE075267 BF743302 AL549208 AI950002 AI224961 AI471552 AI356537 AA768943 AA677028 AI358509 AI147596 AI208057 AI042009 AA156840 AA156603 AA151281 AA151341 N73171 AL540476 AI950893 BG960775 AL573355 D78831 C17898 D78863 AW747857 BI062758 AW629481 AA837630 AA557850 AA531132 AW973966 AW747856 AA203524 W88451 BE539344 AA361027 BF328781 BE011406 BE011437 BE011402 BE011395 BE011428 BE011421 BE011407 BM046773 AA224297 T33786 T08951 T09274 T08592 T30936 AA350905 NM_018485 AB038237 U69668 AA448366 X63105 BC016514 BE694436 AI655840 AW235355 BG427984 AA612862 AA448223 BM145813 BM194565 AI870824 BE973573 BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687 BF908518 BF907890 R11490 AL536642 BF109180 AA953881 AI783716 BE622908 AI621005 AW148784 AI690114 AW275000 AI765790 BF222859 AW167268 AI990460 AW300443 AA779660 AI620568 BF115024 BE504703 AW628332 AI922851 BE006636 AU158376 AI168279 AA809916 AI469757 AA830828 AA830388 N64324 AI049683 AA970275 BF477364 BG261301 AA326388 AU150565 AU158374 AA687967 N58510 AI650450 AL549572 BF349280 BF349269 BM463016 AW836798 AL120958 AW836891 AW385525 BE175733 BE175727 BE175723 BF092430 BI061782 AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW847833 AL536643 AW366516 AW391532 BE934857 BF925057 AW438446 R86246 AW179270 BE087782 BE832144 AW956025 AW956024 BE550261 BF747649 BF802668 AA369961 AV747207 AW973072 BE467756 N51927 AA531539 AW241296 AI797097 BI492823 AW021896 F10837 BE715542 BE715487 AW087443 AA533638 R51354 AW131541 R51852 N53741 R39257 T77635 BF955795 BF331656 F13236 AW810749 AK055378 BE896063 AV722833 BI032095 BF952019 BG547204 AI151418 W03542 W60401 AI346936 AA862855 W60310 N72501 BF963436 C04881 H90060 AA001203 AI863984 AI932612 AI499771 AI187944 AA501896 AA714924 H00689 AA918680 AA573996 AA521308 AW182868 BF996707 AA908959 AI628880 AW173363 AW665845 AA130178 AI818267 AI653663 AI828924 AA746655 AI951984 AI635625 AI093113 AI377976 AI624029 AI418242 R76291 W92652 AI207798 AV706224 AA742467 AA641806 W61229 AA130170 AA160170 H85007 W72474 W61163 H97873 AI047509 R76567 AA812071 H81599 AA021275 H85004 H85894 BG537537 BF830518 W76228 W46673 Z43839 R78710 C01747 H00789 BL063345 W92828 BE150445 AW380821 AW173095 H85630 H81598 H86032 R84855 R13223 AA774992 AW973785 H60163 AA557608 AI057052 AI241633 T89416 AA379611 AA379464 AA379463 BG025680 AW890852 BE002723 BE763824
10	413227 426966	25501_86 349_1	
15	417886 452098 452203	1031334_1 161393_1 2630_1	
20			
25	439096 425505 400208	1241997_1 1228213_1 16640_1	
30			
35	422667 407305 443068 433075	224778_1 2466680_1 18695_17 78_6	
40			
45	400252	2656_2	
50	400209	16640_1	
55	444825	19904_1	
60	414991 432236 417527 425645 455608 418512 407393 400178	1785136_1 1001131_1 2431831_1 1283068_1 1478902_1 12225_6 6807_1 840_4	
65			
70	410927	3618_2	
75	449343	14470_1	
80	432639 417479 426477 418342	1237887_1 2356588_1 1296538_1 295203_2	

400275	18707_1	NM_006513 BC009390 X91257 BC000716 BM450041 BI771139 AV710955 AU120415 AU141179 AU121081 BE409287 AU141397 AU122238 BI256788 BE386217 AU143368 AU133780 AU139704 BG531086 BE268235 BE545230 AU143414 AV761720 AU129842 AU143343 BE270064 BG473378 BE298813 BI772360 BE617354 AU140124 BE277005 BG746716 BE814960 AW161287 AV762084 BG989885 AW674875 AA313975 AV749916 AA374328 BM011248 AU098465 AW238888 BG940091 BG284599 AW410037 AA378483 D49914 AL573323 AL549819 AL572282 AL572871 AL568117 AL571945 AL547790 AL581217 AL514659 AL573926 AL540816 AW410038 BI262249 BG284713 AI659394 AI093582 AW965846 AA652206 AI686014 AA654357 AU146982 AW273447 AW157715 AW574750 BG683509 AW887824 AI818522 AA703770 BE542873 AA515504 AU154982 AA831254 AA828521 AI088602 AA854654 AA190869 BF062816 AA464944 BG261335 AI003584 BG402820 AA932098 W68695 AW182900 W37334 AI073864 C17924 C18528 AI299318 BF154399 BG319570 BF764242 BF764209 AI620320 T06029 BF447193 F29285 AL548949 BI333775 BE743602 BE618230 BE268139 BF036434 BE562718 BG774381 AA659833 AA297649 AA010945 BG105512 BE269205 T32623 BG015679 AL518518 AL517118 AL538396 AI049861 AL581976 AV752041 W26586 BE181609 AI963016 BG057603 AI720256 AA844560 AA055570 BE619606 C17428 AI042174 N93945 N69743 BF795208 AW057940 BI091399 AW975179 AA909936 H28712 W65445 AL515439 W37117 H66514 T85737 W37369 W19712 BE247277 L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138 AW936035 AW935951 AW935789 AW935881 AW936018 AW935892 BE069084 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006691 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445 BE078405 BE078404 BE168534 AV742719 R23027 R63874 AA381749 BG542693 D63271 T94955 AA8774994 BF697879 BG984482 AW854930 AW854941 AW814115 AW814431 AW814190 BF325887 BF325890 BF985536 AW819463 AW819514 AW819617 AW819618 AW819609 U35637 AA192323 AA194508 BG011583 F25712 AL596820 BE185376 AA878324 AI619686 AI014377 T85948 R07785 T86972 Y08200 NM_004581 BC003093 BE733834 BI753321 BG773890 BF091906 BI917541 AI023762 AA587230 BF435086 AI264262 AI687392 AI810536 AW589886 AI244419 AA749261 AA535435 AW205689 AI765770 AI765431 C02465 AW305347 AI818456 AA322111 AW381845 AW381829 AV749407 AA811636 AU159893 AA603065 AA652542 AI468678 R49616 AW381863 BE389867 BE182387 BF087771 AA527551 AA134051 AA831504 AA134052 AI871759 AW089048 BI913532 AA367709 BG828155 BF093014 AW837178 T77002 F13038 AK056654 AJ420421 AI127111 AA705921 AA749298 AA776967 AI343768 AW070583 AA766587 AA804876 AA460658 AA394137 W72279 AW071467 AI343843 AA393817 AW769379 AA861873 AA715043 AW512448 AI452856 AI819873 T17354 AW779778 BF477620 AI783605 AI624523 AA261906 AA514931 BI964124 AW576481 AI864544 AA490863 AA860972 BI963076 AI632879 AA291985 AA255873 BI966876 BI963833 Z38970 BI495302 BI495301 AI784395 AU185472 AA652150 AA652026 D20449 BI088167 BI260636 BE869946 AI935271 BI792882 AI762915 AI809275 AI813351 BF447139 AI052069 AI057127 AA398950 AA291984 AA292934 AA262543 BF760287 R64455 R72980 H90786 BE698016 AW959314 BI031449 AL574617 AA776284 AA393770 BM455617 BI602104 BI793150 N36710 H59529 BI005937 BI600748 BF085914 BF085907 BF835429 BF835210 BF085926 AA226136 BF836829 BF836606 BM007373 AI369807 BF085930 W25119 BI252884 BI001270 BE549079 BF238403 R56934 AF086341 W76326 W72300 NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI855378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW44935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030 AW964027 AA377709 AW848421 T71427 T62567 AW833022 AW833054 H20760 R15237 Z43915 BF372479 F11411 AB038318 BC008888 BE905346 BE301941 AA705936 AW014954 BE378742 AI720050 BE395327 BG951204 AK001451 AU151098 AW515640 AW439618 AI671555 AW304963 AA565885 AI829434 AW590882 AI889234 AW117522 AA847824 AI636224 AA883540 AA169387 AW771571 AI130803 BF438773 AA088710 AI972691 AI972638 AI762358 AI473907 AI925905 AA502277 BG943806 BG218468 AA194853 AU128875 AA306025 BG986896 AA778849 AW946871 AW946782 AW946955 AF086283 W69200 W69304 AW807573 AW807572 AW963941 AA379825 AW963944 AA379564 NM_054014 X52220 BC005147 BI551326 AI393601 AW592611 AA608921 AA731598 W96331 AW590007 AI076813 AI022644 AA158365 AI699321 AI146747 AW296894 H85337 AA017692 AA354519 AA018512 D20081 R02704 AA825671 AA017651 AL135600 R02585 AA018849 BG749616 BF689840 R85326 AA677955 AA702354 AI076645 AI057359 H53178 W86484 H53074 BG988909 AW962456 AA367326 AA377499 R39769 T53143 H60012 AW150645 AW811024 AW811148 AW811068 BF812525 AW504832 AI972567 AA588429 AI299694 AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847 AW875344 AW875287 AW875285 AW875286 BF361295 AW875402 AW875400 BE145816 BE145897 BF349721 BE145885 AK057266 BI767614 BI828586 AW069362 BI829572 AI826091 BI819382 AL040402
--------	---------	--

TABLE 49C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
5				
10	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	401027	7230983	Minus	70407-70554,71060-71160
	400991	8096825	Plus	159197-159320
	406137	9166422	Minus	30487-31058
	404083	9944029	Minus	16650-17082
15	404440	7528051	Plus	80430-81581
	400792	7382433	Plus	134339-134593
	404289	2769644	Plus	15049-15286,30267-30457
	401083	3242744	Plus	33192-33360
	402211	7689783	Minus	67414-68229
20	402705	8782736	Plus	89961-90114,90773-90895,91131-91261
	402233	7690102	Plus	90281-91477
	405370	2078469	Minus	38980-39111
	400846	9188605	Plus	39310-39474
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
25	401345	9926424	Plus	148042-148392
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
	406364	9256114	Minus	50715-50833
	405490	7705240	Plus	20683-20850
	400755	8119083	Minus	120084-120889
30	404276	9885189	Plus	127624-127856
	402915	7406502	Minus	140-276
	405616	5649378	Minus	2782-3308
	400847	9188605	Plus	44643-44835
	402328	4464283	Minus	13758-13922,14558-14752
35	405369	2078469	Minus	34183-34357,35686-35751
	400845	9188605	Plus	34428-34612
	403716	7239669	Plus	86899-87122
	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
	404140	9843520	Plus	37761-38147
40	405516	9454624	Plus	112707-112876,113676-113854
	405110	8096888	Minus	118940-119100
	403608	8308266	Minus	121321-121476
	401241	4827300	Minus	30503-30844,31056-31248
	405102	8076881	Minus	120922-121296
45	404185	4572584	Minus	129171-129327
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405411	3451356	Minus	17503-17778,18021-18290
	405602	4753260	Plus	44647-44778
	403391	9438337	Plus	42410-42544,83317-83540,86840-86922,8797
50	403869	7280046	Minus	34379-34583
	404942	7382153	Plus	92095-92252
	403142	9444521	Plus	89286-90131
	400844	9188605	Plus	24746-24872,25035-25204
	402704	8782736	Plus	37368-37493
55	402833	8918545	Plus	26987-27778
	401851	7770425	Minus	146443-146664,147794-147971,148351-14848
	401242	4827300	Minus	32616-32863
	401943	4914397	Plus	65925-66371
	402807	6456148	Minus	101542-101660,103476-103656
60	402603	9909396	Minus	141663-141852
	405328	3253114	Plus	21399-21583
	402974	9663349	Plus	124035-124321
	400987	8086488	Minus	22052-22185
	403335	8568884	Plus	112307-112524,114074-114703
65	401113	9966541	Minus	19419-19959
	401185	9625304	Minus	177393-177691
	404537	8247909	Minus	188775-189573
	405266	4156171	Minus	63337-63552
	402615	9926801	Plus	131390-132157
70	400566	9884730	Plus	64486-64714
	403212	7630897	Minus	156037-156210
	403290	8083176	Plus	19288-20076
	401342	9908882	Plus	3096-3242
	400471	9931670	Minus	105629-105760
75	405588	5002511	Plus	46180-46366
	400539	7574902	Plus	8559-8721
	403743	7652003	Minus	136463-136646
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	405099	8074292	Minus	114365-114514,128635-128831
80	401445	8218584	Minus	93700-93886
	405480	2766593	Plus	33325-33659
	402183	7658390	Minus	100618-104298
	400749	7331445	Minus	9162-9293
	406139	9166768	Minus	72397-72602

402129	7704953	Minus	166156-166365
400645	8117693	Minus	58471-58716
403201	9958297	Minus	109782-109934
403609	8308266	Minus	125974-126320
400719	8118911	Minus	44579-44656,45294-45487,46449-46641
403088	8954241	Plus	169894-170193,170504-170806
403328	8469086	Minus	120428-120703
403305	8099945	Plus	114632-114805
401702	1871197	Minus	68182-68325
400777	8131663	Plus	70745-71121
404956	7387343	Plus	55883-56203
401917	9502466	Plus	25054-25229
401984	4454511	Plus	103825-104024
406303	8575868	Plus	173622-173786

Table 50A lists about 414 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 85th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 51A lists about 518 genes up-regulated in seminomatous testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" seminomatous testicular cancer level was set to the 85th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 52A lists about 673 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal testicular adult tissues was greater than or equal to 6. The "average" testicular cancer level was set to the 75th percentile amongst testicular cancers. The "average" normal adult testicular tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 53A lists about 735 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal adult tissues was greater than or equal to 3. The "average" testicular cancer level was set to the 95th percentile amongst testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 54A lists about 476 testis-specific genes downregulated in testicular cancer (non-seminomatous and seminomatous). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio (R1) of normal testis to normal adult tissues was greater than or equal to 3. R1 was calculated as the mean number of interquartile range values over the median normal adult body tissue expression among normal testicular samples. The ratio (R2) of "average" normal testis to "average" testicular cancer among these genes was greater than or equal to 2. The "average" normal testis level was set to the 50th percentile amongst normal testis. The "average" normal testicular cancer level was set to the 95th percentile amongst testicular cancer samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 55A lists about 586 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 95th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult testicular tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Table 56A lists about 812 genes up-regulated in seminomatous testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" seminomatous testicular cancer level was set to the 50th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 50A:

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues

Pkey	ExAccn	UniGene	Unigene Title	R1
432666	AW204069		ESTs, Weakly similar to unnamed protein	74.60
432730	AI066520	Hs.131358	ESTs	50.55
450581	AF081513	Hs.25195	TGF-beta 4	47.85
418696	AW959433	Hs.326290	hypothetical protein FLJ12581	44.05
423458	AI204212		ESTs	36.60
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	30.60
448981	AI968719	Hs.195387	ESTs	26.40
407710	AW022727	Hs.23616	ESTs	24.00
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	19.35
451106	BE382701	Hs.25960	N-MYC oncogene	18.85
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	18.40
420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	18.25

	424578	AK001973	Hs.150890	hypothetical protein	17.86
	418756	AA252254	Hs.226949	ESTs	17.20
	404996			Target Exon	16.15
5	447534	AW953935	Hs.288655	ESTs	15.80
	456847	AI360456	Hs.37776	ESTs	15.00
	446979	AI654443	Hs.197683	ESTs	14.80
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	14.75
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	14.70
10	449322	AI638616	Hs.196566	ESTs	14.35
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	14.20
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	12.95
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	12.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	12.55
15	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.43
	406547			Target Exon	12.35
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	12.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	11.65
	408908	BE296227	Hs.250822	serine/threonine kinase 15	11.55
20	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	11.05
	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (	10.08
	426866	U02330	Hs.172816	neuregulin 1	10.05
	446791	AI632278	Hs.195922	ESTs	10.05
	433159	AB035898	Hs.150587	kinesin-like protein 2	9.85
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.95
25	427521	AW973352		ESTs	8.92
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	8.90
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.52
	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
30	408465	AW196940	Hs.253277	ESTs	8.47
	444971	AI651116	Hs.148659	ESTs	8.35
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	8.35
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	8.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.95
35	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	7.75
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	7.65
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	7.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	7.36
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	7.25
40	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.25
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	7.22
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.13
	435918	AF263538	Hs.86232	growth differentiation factor 3	7.13
	412537	AL031778		nuclear transcription factor Y, alpha	7.08
45	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	7.05
	428916	AF003001	Hs.194562	telomeric repeat binding factor (NIMA-in	6.88
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.75
	437052	AA861697	Hs.120591	ESTs	6.75
50	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.72
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.71
	457465	AW301344	Hs.122908	DNA replication factor	6.62
	442832	AW206560	Hs.253569	ESTs	6.54
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	6.30
55	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	6.30
	448588	AI970276	Hs.156905	KIAA1676	6.12
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	6.09
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	5.95
	412642	BE244598	Hs.809	hepatocyte growth factor (hepatopoietin A;	5.85
60	443068	AI188710		ESTs	5.85
	438450	AI050866	Hs.65853	nodal, mouse, homolog	5.81
	441287	AW293132	Hs.131373	ESTs	5.80
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	5.76
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
65	436902	AW247145	Hs.192729	ESTs	5.70
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
70	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	5.56
	436812	AW298067		gb:UI-H-BW0-ajp-g-09-0-UI.s1 NCL_CGAP_Su	5.55
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	5.51
	431354	BE046956	Hs.251673	DNA (cytosine-5)-methyltransferase 3 be	5.51
	430044	AA464510	Hs.152812	ESTs	5.47
	437036	AI571514	Hs.133022	ESTs	5.45
	435663	AI023707	Hs.134273	ESTs	5.40
75	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.40
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.21
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	5.15
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	5.15
	430272	X04898	Hs.237658	apolipoprotein A-II	5.12
80	427961	AW293165	Hs.143134	ESTs	5.05
	424315	AW614850	Hs.193384	putative 28 kDa protein	5.05
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!!	5.00
	418477	AW022983		gb:df46h12.y1 Morton Fetal Cochlea Homo	5.00
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	4.95

	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.94
	443537	D13305	Hs.203	cholecystokinin B receptor	4.92
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	4.90
5	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	4.80
	449592	AI655494	Hs.195718	ESTs	4.75
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 s3	4.73
10	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.68
	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	4.61
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.60
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	4.48
15	402145			Target Exon	4.48
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	4.47
	453289	AI188161	Hs.144627	ESTs	4.45
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	4.40
	422689	AW856655		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	4.32
20	426427	M86699	Hs.169840	TTK protein kinase	4.30
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	4.20
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.18
	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (	4.15
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.10
25	438188	AA779975	Hs.128859	ESTs	4.10
	435514	AW592804		ESTs	4.10
	442333	AI650877	Hs.129302	ESTs	4.05
	413627	BE182082	Hs.246973	intron of Bicaudal D homolog 1	4.00
	445140	AI650599	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
30	448038	AW015073	Hs.232026	ESTs, Weakly similar to ROS2_HUMAN 52 KD	4.00
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.95
	419423	D26488	Hs.90315	KIAA0007 protein	3.95
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	3.95
	441553	AA281219	Hs.121296	ESTs	3.95
35	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.91
	409757	NM_001898	Hs.123114	cystatin SN	3.89
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.88
	450351	BE547267	Hs.59791	hypothetical protein MGC13183	3.85
40	403780			C4001759:glj133250[sp]P19474[RO52_HUMAN	3.84
	421917	AB028943	Hs.109445	KIAA1020 protein	3.84
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	3.84
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	3.82
	410193	AJ132592	Hs.59757	zinc finger protein 281	3.80
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.80
45	415829	AW450198	Hs.163742	ESTs	3.78
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.77
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.70
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.68
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.66
50	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	3.65
	420900	AL045633	Hs.44269	ESTs	3.65
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.65
	426496	D31765	Hs.170114	KIAA0061 protein	3.60
	452461	N78223	Hs.108106	transcription factor	3.60
55	418379	AA218940	Hs.137516	fidgetin-like 1	3.50
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.48
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.45
	419384	AA490866	Hs.39429	ESTs	3.44
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	3.43
60	446293	AI420213	Hs.149722	LIM domain transcription factor LIM-1 (h	3.41
	422094	AF129535	Hs.272027	F-box only protein 5	3.40
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.40
	423198	M81933	Hs.1634	cell division cycle 25A	3.39
	424153	AA451737	Hs.141496	MAGE-like 2	3.38
65	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.37
	443715	AI583187	Hs.9700	cyclin E1	3.34
	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.34
	449571	AW016812	Hs.200266	ESTs	3.34
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.31
70	452807	AA028933	Hs.162434	ESTs	3.31
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	3.30
	421650	AA781795	Hs.122587	ESTs	3.30
	418355	L42563	Hs.1165	ATPase, H? transporting, nongastric, alp	3.28
	438494	AA908678	Hs.130183	ESTs	3.23
75	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.22
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	3.20
	427642	R40761	Hs.9834	ESTs	3.20
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosi	3.18
	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.18
80	442618	R56222	Hs.26514	ESTs	3.17
	415799	AA653718	Hs.225841	DKFZP434D193 protein	3.17
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.15
	450431	AW136797	Hs.266041	ESTs	3.13
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.12

	430835	AI240006	Hs.192326	ESTs	3.12
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.10
	417791	AW965339	Hs.111471	ESTs	3.10
5	434609	R76593		gb:yi60c11.1 Soares placenta Nb2HP Homo	3.05
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.04
	411975	AI916058	Hs.144583	ESTs	3.01
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	2.99
10	440207	AI371978	Hs.128326	ESTs	2.98
	435726	BE535787	Hs.113170	ESTs	2.97
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.97
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	2.95
	435373	AW665538	Hs.117689	ESTs	2.93
15	452571	W31518	Hs.34665	ESTs	2.93
	454679	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo	2.91
	414972	BE263782	Hs.77695	KIAA0008 gene product	2.90
	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.90
	420092	AA814043	Hs.88045	ESTs	2.89
20	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	2.89
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	2.87
	422746	NM_004484	Hs.119651	glypican 3	2.87
	446258	AI283476	Hs.263478	ESTs	2.86
	444371	BE540274	Hs.239	forkhead box M1	2.86
25	409517	X90780		tropoin I, cardiac	2.85
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	2.84
	443169	AI038687	Hs.133338	ESTs	2.84
	447519	U46258	Hs.339665	ESTs	2.84
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.84
30	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.83
	416201	AA467752	Hs.195161	ESTs	2.83
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.83
	457191	AI376228		Friend leukemia virus integration 1	2.82
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	2.81
35	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.80
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	2.75
	427719	AI393122	Hs.134726	ESTs	2.75
	451684	AF216751	Hs.26813	CDA14	2.75
	414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	2.74
40	442032	AW016786		ESTs	2.73
	437123	AL049285	Hs.302053	Homo sapiens mRNA; cDNA DKFZp564M193 (fr	2.72
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	2.72
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	2.71
	438180	AA808189	Hs.272151	ESTs	2.70
45	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.70
	423765	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.69
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	2.69
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	2.68
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.67
50	445413	AA151342	Hs.12677	CGI-147 protein	2.66
	448769	N66037	Hs.38173	ESTs	2.66
	411022	AW936378		gb:QV4-DT0021-301299-071-f05 DT0021 Homo	2.65
	423600	AI633559	Hs.310359	ESTs	2.65
	447175	AI365208	Hs.293606	ESTs	2.65
55	414151	AW976468	Hs.257245	ESTs	2.65
	448877	AI583696	Hs.253313	ESTs	2.62
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.61
	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	2.61
	449665	AI655391	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.61
60	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.60
	429228	AI553633		ESTs	2.60
	410929	H47233	Hs.30643	ESTs	2.59
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.58
	446142	AI754693	Hs.145968	ESTs	2.56
65	445093	AI207197		ESTs	2.56
	413686	AI469213	Hs.71404	ESTs	2.55
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	2.55
	420218	AW958037		ribosomal protein L4	2.55
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	2.55
70	414312	AA155694	Hs.191060	ESTs	2.55
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synth	2.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.52
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.51
	435096	AA664977		gb:nu73b07.s1 NCI_CGAP_Alv1 Homo sapiens	2.50
75	422468	AA355210		gb:EST63589 Jurkat T-cells V Homo sapien	2.50
	449576	AW014631	Hs.225068	ESTs	2.50
	415684	D59356		sorbitol dehydrogenase	2.50
	452226	AA024898	Hs.157103	ESTs	2.50
	421451	AA291377	Hs.50831	ESTs	2.50
80	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.50
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.49
	453941	U39817	Hs.36820	Bloom syndrome	2.49
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.49
	449655	AI021987	Hs.59970	ESTs	2.49



	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.49
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	2.48
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.48
5	445363	NM_005993	Hs.12570	tubulin-specific chaperone d	2.47
	452404	AW450675	Hs.212709	ESTs	2.46
	444823	BE262989	Hs.12045	putative protein	2.46
	427675	AW138190	Hs.180248	zinc finger protein 124 (HZF-16)	2.45
	444159	AF116846	Hs.10431	dead ringer (Drosophila)-like 2 (bright	2.45
10	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	2.45
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.45
	433183	AF231338	Hs.222024	transcription factor BMAL2	2.45
	447350	AI375572		v-erb-a avian erythroblastic leukemia vi	2.45
	428728	NM_016625	Hs.191381	hypothetical protein	2.43
15	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	2.43
	410276	AI554545		angiopoietin-2	2.42
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.42
	419029	AA233397	Hs.326290	hypothetical protein FLJ12581	2.42
	437908	AI082424		ESTs	2.41
20	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.41
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	2.40
	425212	AW962253	Hs.171618	ESTs	2.39
	423787	AJ295745	Hs.236204	nuclear pore complex protein	2.38
	425601	AW629485	Hs.140720	GSK-3 binding protein FRAT2	2.38
25	449676	AW380579	Hs.209657	ESTs	2.38
	429467	NM_004477	Hs.203772	FSHD region gene 1	2.37
	453227	AW135862	Hs.243991	ESTs	2.37
	417833	AW003251	Hs.86264	hypothetical protein FLJ14549	2.36
	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.36
30	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.35
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	2.35
	410060	NM_001448	Hs.58367	glypican 4	2.35
	449138	AW294215	Hs.195631	ESTs	2.35
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.35
35	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	2.35
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.34
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	2.34
	407818	AL021938	Hs.40154	jumonji (mouse) homolog	2.34
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	2.33
40	401704			NM_021195*:Homo sapiens claudin 6 (CLDN6	2.33
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	2.32
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.32
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	2.31
	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.30
45	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.30
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	2.30
	448755	AW503807	Hs.21907	histone acetyltransferase	2.30
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	2.29
50	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	2.29
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.28
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	2.27
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.26
	401220			branched chain aminotransferase 1, cytos	2.26
55	453985	N44545	Hs.251865	ESTs	2.25
	414890	BE281095	Hs.77573	uridine phosphorylase	2.25
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.25
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	2.25
	424765	AA428211		hypothetical protein FLJ14033 similar to	2.25
60	419278	AU076799	Hs.1247	apolipoprotein A-IV	2.24
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	2.24
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	2.23
	417273	AK002209	Hs.81831	Homo sapiens cDNA FLJ11347 fis, clone PL	2.23
	449722	BE280074	Hs.23960	cyclin B1	2.22
65	443184	AI638728	Hs.131973	ESTs	2.22
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	2.21
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	2.21
	435045	BE297155	Hs.143698	ESTs	2.21
	414883	AA926960		CDC28 protein kinase 1	2.21
70	446323	AI288274	Hs.345792	ESTs	2.20
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.20
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	2.20
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor;	2.20
	418973	AA233056	Hs.191518	ESTs	2.20
75	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.20
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.20
	443748	AW206447		gb:UL-H-B1-afg-g-02-0-UL.s1 NCI_CGAP_Su	2.20
	415989	AI267700		ESTs	2.20
	400195			NM_007057*:Homo sapiens ZW10 interactor	2.20
80	428878	AA436884	Hs.48926	ESTs	2.20
	431805	NM_014053	Hs.270594	FLVCR protein	2.19
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.19
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	2.18
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.18

5	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	2.18
	413992	W26276	Hs.104557	RNA, U2 small nuclear	2.18
	412722	AI343300	Hs.15091	ESTs	2.18
	409089	NM_014781	Hs.50421	KIAA0203 gene product	2.17
	430809	AI791150	Hs.262009	ESTs, Moderately similar to I38022 hypot	2.17
	406542			C19000728*:gi12585552 sp Q9Y2Q1 Z257_HU	2.17
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfami	2.17
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	2.17
10	425580	L11144	Hs.1907	galanin	2.16
	439398	AA284267	Hs.221504	ESTs	2.16
	452833	BE559681	Hs.30736	KIAA0124 protein	2.15
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	2.15
	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	2.15
	449410	AA001356	Hs.18159	ESTs	2.15
15	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.15
	427953	AA417944	Hs.44331	ESTs	2.15
	422281	M36803	Hs.346935	hemopexin	2.15
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.14
20	444960	AI611317	Hs.341531	ESTs	2.14
	415890	H08225	Hs.268712	ESTs	2.14
	402099			ENSP00000217725*:Laminin alpha-1 chain p	2.14
	427779	AA906997	Hs.180780	TERA protein	2.14
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	2.14
25	422170	AI791949	Hs.112432	anti-Mullerian hormone	2.14
	414161	AA136106	Hs.184852	KIAA1553 protein	2.14
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	2.13
	449810	AB008681	Hs.23994	activin A receptor, type IIB	2.11
	450663	H43540	Hs.25292	ribonuclease HI, large subunit	2.11
30	419525	T79257	Hs.1259	asialoglycoprotein receptor 2	2.11
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.10
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.10
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.10
	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr	2.09
35	418552	AF198254	Hs.86088	IGF-II mRNA-binding protein 1	2.09
	408291	AB023191	Hs.44131	KIAA0974 protein	2.09
	425474	Z48054	Hs.158084	peroxisome receptor 1	2.09
	453028	AB006532	Hs.31442	RecQ protein-like 4	2.09
	447831	AI433293	Hs.164115	ESTs	2.08
40	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.08
	429166	AB033096	Hs.197668	KIAA1270 protein	2.08
	432446	AA542845	Hs.294088	GAJ protein	2.08
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.07
	431093	AB031038	Hs.301704	eomesodermin (Xenopus laevis) homolog	2.07
45	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.07
	449569	AI656634	Hs.195389	ESTs	2.07
	429999	AI761902	Hs.99597	ESTs	2.06
	420552	AK000492	Hs.98806	hypothetical protein	2.06
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	2.05
50	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.05
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.05
	450375	AA009647		a disintegrin and metalloproteinase doma	2.05
	409066	AA062980	Hs.66960	ESTs	2.05
	425700	AF076292	Hs.159251	forkhead box H1	2.05
55	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	2.05
	409093	BE243834	Hs.50441	CGI-04 protein	2.05
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.04
	408446	AW450669	Hs.45068	hypothetical protein DKFZp434I143	2.04
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.04
60	429840	AA459699	Hs.99496	ESTs	2.03
	409717	AW452871	Hs.56043	CGI-115 protein	2.02
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.02
	448275	BE514434	Hs.20830	kinesin-like 2	2.02
	432731	R31178	Hs.287820	fibronectin 1	2.02
65	405157			NM_003213*:Homo sapiens TEA domain famil	2.02
	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	2.01
	423739	AA398155	Hs.97600	ESTs	2.01
	421310	AW630087	Hs.103315	trinucleotide repeat containing 1	2.00
	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	2.00
70	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	2.00
	407259	L02256		gb:Human Fab fragment binding syncytial	2.00

TABLE 50B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
------	------------	-----------

80	432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
	423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
			BG215094 BG198867 BG196332 BG208220 BG212418

5	430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603
	427521	513212_1	AI352469 BE061601 BI062752 AW818206 BF887722
	427486	684159_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165
	412537	14066_1	AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
10	43068	18695_17	BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433
	436812	659779_1	AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114
	418477	4172_1	AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364
			BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793
15	418378	1227421_1	AA382556 AW235763 AA927051 AI862075 BE886691 BE619282
	422689	874209_1	AV752763 AI032142 N30308 N22181 H95390 AW675632
	435514	132288_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673
	439780	49082_1	BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092
20	434609	14739_1	AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
	454679	174325_1	AA218925 AW962081 AA354237
	434414	35978_1	AW954733 AA315006 AW856665
			AA683356 AW592804 AI150287
25	409517	4537_1	AL109688 R23665 R26578
	406687	0_0	AF147390 R76593 R76594
	457191	1389182_1	AW813110 BF771370 BF771371 AW813113 AW003381
	410704	1054673_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422
30			AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298
			AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175
			BF854337
			NM_000363 X54163 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI657074 C03333 AI199911 C05024 C03193 AI950215 C05070
35	445093	175963_1	C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255
	420218	191547_1	T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339
			M31126
			AI216469 AI354789 AA446136 H24336 AA446443 AI376228 R48940
40	443748	669881_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
	415989	10194_1	BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
			AW840571
			BE155042 BE155040 BE154987 BE155012
45	440195	16894_2	BF223060 BF222818 AI950472 AW016786 AI207136 AI969730 BF222890 AI633857 AI968711 AA974235 AI352637
			AW936378 AW936544 AW813513
			BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620
			AW969605 AI553633
50	443748	669881_1	AI207197 BF773544 AW196462
	415989	10194_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756
			AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
			H30075 AA664977 AW975278
55	440195	16894_2	AW962701 AA310998 AW962699
			BF666746 D59356 BG678312 N56640 AA166861
			AI375572 AI480404 BF430912 T06882
			AA083514 AI554545 AW169852 AI363822 AI633826 AI656026 AI765624 AA147545 AA147552
60	443748	669881_1	AI740586 AA771806 BE500996 AW204531 AI082424 AI033879 BF093176 AA771764 D38676
	415989	10194_1	T65754 AA229658 AA229857
			AK021881 AU145974 AU145787 C16964 AA428211 AU119698 AA993264 BF999192 AW903017 AA346559 AU119446 AW581679 AA991677
			AW898165 AW386878 AW890957 Z18340
65	440195	16894_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI813360
			AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871
			AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887
			AA459292 AI494230 BF057531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407
70	443748	669881_1	AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
	415989	10194_1	BM467830 AI084433 AW206447 AI400976 AI248530 R16553
			BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF090208 BF090960 BF095153
			BG285837 AI720344 BF541715 AA355086 AA172236
75	440195	16894_2	BM477554 BM423967 BC020979 AF067656 NM_007057 BI869291 BG468263 BG760599 BI261788 AA855060 BE257094 BF212452 BE888249
			BI259219 AW409765 BE089556 AL564377 BI258884 AW440401 AL578460 AL578434 AL556136 BG036804 AL531381 AW371767 BG610641
			BF102552 BE294929 BF792282 BG121657 BG502285 BG777493 AL564510 AW770358 AA573448 AA564001 AA969560 AW078946 AW750065
			AL573860 AA143778 H99221 AA969210 AW103401 AW750073
80	450375	16559_3	BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410
			H59605 BE157601 AA113758
65	TABLE 50C		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
70	NL_position:	Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand
	404996	6007890	Plus
	406547	7711513	Minus
75	402145	8018280	Plus
	403780	8076989	Plus
	403432	9719611	Minus
	401704	3097841	Plus
	403433	9719611	Minus
80	401220	9929324	Minus
	406542	7711499	Plus
	402099	8117697	Plus
	406137	9166422	Minus

405157 9966228 Plus 156363-156502,157573-157746

5

TABLE 51A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of seminomatous testicular cancer compared to normal adult tissues

10

Pkey	ExAccn	UnigenelD	Unigene Title	R1
418696	AW959433	Hs.326290	hypothetical protein FLJ12581	56.62
432666	AW204069		ESTs, Weakly similar to unnamed protein	49.00
432730	AI066520	Hs.131358	ESTs	37.64
426534	U58096	Hs.2051	testis specific protein, Y-linked	37.60
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	32.70
420367	AA259090	Hs.257028	ESTs	29.98
420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	26.50
437052	AA861697	Hs.120591	ESTs	26.42
407710	AW022727	Hs.23616	ESTs	23.85
420528	AF130728	Hs.98586	doublesex and mab-3 related transcriptio	23.12
424578	AK001973	Hs.150890	hypothetical protein	22.27
420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	22.06
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	20.46
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	18.44
434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	15.92
430252	AI638774	Hs.105328	testes development-related NYD-SP20	15.44
423458	AI204212		ESTs	15.28
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	15.26
427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	14.84
427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	12.98
426427	M86699	Hs.169840	TTK protein kinase	12.44
420401	AK001907	Hs.97464	hypothetical protein	12.40
406937	U14622		gb:Human transketolase-like protein gene	11.60
430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	11.55
425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	11.52
418477	AW022983		gb:df46h12.y1 Morton Fetal Cochlea Homo	10.94
434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	10.78
436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-U1.s1 NCL_CGAP_Su	10.54
437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	10.40
433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	10.32
421241	X91817	Hs.102866	transketolase-like 1	10.14
410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	10.02
418134	AA397769	Hs.86617	ESTs	9.76
433159	AB035898	Hs.150587	kinesin-like protein 2	9.56
433975	AA971953	Hs.122055	ESTs	9.36
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	9.30
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	9.22
431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	9.16
436899	AA764852		ESTs	8.76
426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.76
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	8.64
408908	BE296227	Hs.250822	serine/threonine kinase 15	8.50
413627	BE182082	Hs.246973	intron of Bicaudal D homolog 1	8.42
425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	8.30
415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.14
408728	AL137379	Hs.47125	hypothetical protein FLJ13912	8.14
406547			Target Exon	8.02
424153	AA451737	Hs.141496	MAGE-like 2	7.90
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.64
437421	AA917062		ESTs	7.53
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.50
419423	D26488	Hs.90315	KIAA0007 protein	7.38
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.38
431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.32
430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (	7.29
436608	AA628980	Hs.192371	down syndrome critical region protein DS	7.25
435206	AI432364	Hs.160594	ESTs	7.20
414972	BE263782	Hs.77695	KIAA0008 gene product	7.12
407340	AA810168	Hs.284289	vittigo-associated protein VIT-1	7.10
426518	Z43039	Hs.170198	KIAA0009 gene product	7.10
436513	AJ278110	Hs.125507	DEAD-box protein	7.04
427521	AW973352		ESTs	6.96
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	6.92
422232	D43945	Hs.113274	transcription factor EC	6.90
420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	6.83
431041	AA490967	Hs.197955	KIAA0704 protein	6.76
427335	AA448542	Hs.251677	G antigen 7B	6.58
422797	AB033064	Hs.236463	KIAA1238 protein	6.55
418379	AA218940	Hs.137516	fidgetin-like 1	6.46

5	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	6.45
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	6.44
	422665	AJ011812	Hs.119018	transcription factor NRF	6.38
	433701	AW445023	Hs.15155	ESTs	6.34
	436909	AA907120		ESTs	6.28
10	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	6.27
	429228	AI553633		ESTs	6.26
	419384	AA490866	Hs.39429	ESTs	6.23
	435514	AW592804		ESTs	6.08
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	5.90
15	430835	AI240006	Hs.192326	ESTs	5.89
	438188	AA779975	Hs.128859	ESTs	5.88
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	5.80
	408758	NM_003686	Hs.47504	exonuclease 1	5.78
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	5.70
20	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.67
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	5.64
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	5.58
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothei	5.58
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	5.55
25	438494	AA908678	Hs.130183	ESTs	5.52
	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	5.52
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	5.48
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	5.45
	413623	AA825721	Hs.246973	intron of Bicaudal D homolog 1	5.36
30	402145			Target Exon	5.30
	414136	AA812434		SMC2 (structural maintenance of chromoso	5.28
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	5.22
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	5.16
	408460	AA054726	Hs.285574	ESTs	5.14
35	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.12
	420900	AL045633	Hs.44269	ESTs	5.08
	426496	D31765	Hs.170114	KIAA0061 protein	5.01
	407122	H20276	Hs.31742	ESTs	5.00
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	4.95
40	402199			Target Exon	4.90
	409103	AF251237	Hs.112208	XAGE-1 protein	4.90
	416859	H43437	Hs.80305	hypothetical protein MGC14258	4.84
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	4.82
	410929	H47233	Hs.30643	ESTs	4.73
45	417886	AA214584		ESTs	4.73
	426223	AW977812	Hs.130391	ESTs	4.72
	409421	AA199883	Hs.67624	ESTs	4.72
	428249	AA130914	Hs.183291	zinc finger protein 268	4.71
	429999	AI761902	Hs.99597	ESTs	4.68
50	431721	AB032996	Hs.268044	KIAA1170 protein	4.68
	408321	AW405882	Hs.44205	cortistatin	4.67
	419197	N48921	Hs.27441	KIAA1615 protein	4.66
	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	4.64
	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	4.64
55	427119	AW880562	Hs.272525	ESTs	4.64
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.64
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.64
	409066	AA062980	Hs.66960	ESTs	4.62
	416201	AA467752	Hs.195161	ESTs	4.53
60	433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.52
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.50
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	4.46
	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.46
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.34
65	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	4.32
	418971	AA360392	Hs.87113	ESTs	4.30
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	4.29
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.21
	415717	AA167270	Hs.130435	ESTs	4.18
70	423198	M81933	Hs.1634	cell division cycle 25A	4.12
	433849	BE465884	Hs.280728	ESTs	4.12
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.11
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	4.07
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.07
75	414725	AA769791		ring finger protein 21, interferon-respo	4.05
	408291	AB023191	Hs.44131	KIAA0974 protein	4.05
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.04
	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.04
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.03
80	421917	AB028943	Hs.109445	KIAA1020 protein	4.02
	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	4.02
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.01
	436360	AI962796	Hs.156100	ESTs	4.00
	438624	AA889055	Hs.123468	ESTs	3.99
	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	3.92
	411945	AL033527	Hs.92137	L-myc-2 protein(MYCL2)	3.90
	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.90

	413833	Z15005	Hs.75573	centromere protein E (312kD)	3.90
	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.88
	438456	AA913381	Hs.20594	ESTs	3.88
5	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.87
	412537	AL031778		nuclear transcription factor Y, alpha	3.86
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.85
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	3.83
	422094	AF129535	Hs.272027	F-box only protein 5	3.82
10	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.80
	416350	AF188625	Hs.189507	phospholipase A2, group IID	3.78
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.76
	401435			C14000397*.gi 7499898 pir T33295 hypoth	3.76
	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	3.74
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	3.70
15	409089	NM_014781	Hs.50421	KIAA0203 gene product	3.70
	426067	AW664691	Hs.97053	ESTs	3.67
	415684	D59356		sorbitol dehydrogenase	3.66
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.62
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	3.62
20	427761	AA412205	Hs.140996	ESTs	3.61
	433641	AF080229		gb:Human endogenous retrovirus K clone 1	3.60
	418216	AA662240	Hs.283099	AF15q14 protein	3.59
	438180	AA808189	Hs.272151	ESTs	3.58
	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	3.56
25	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.55
	428878	AA436884	Hs.48926	ESTs	3.54
	438885	AI886558	Hs.184987	ESTs	3.53
	416445	AL043004	Hs.79337	KIAA0135 protein	3.52
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.51
30	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.49
	427298	AA400495		ESTs	3.48
	420218	AW958037		ribosomal protein L4	3.40
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	3.40
	410420	AA224053	Hs.172405	cell division cycle 27	3.40
35	432809	AA565509	Hs.131703	ESTs	3.36
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.34
	421373	AA808229	Hs.46677	ESTs	3.34
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.31
40	418830	BE513731	Hs.88959	hypothetical protein MGC4816	3.30
	431077	AI669133	Hs.115660	hypothetical protein FLJ12810	3.30
	418049	AA211467		Homo sapiens, Similar to nuclear localiz	3.26
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.22
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	3.21
45	434288	AW189075	Hs.116265	fibrillin3	3.20
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.19
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.17
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.17
	420161	AI683069	Hs.120817	ESTs	3.17
50	414618	AI204600	Hs.95978	hypothetical protein MGC10764	3.16
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.14
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosi	3.14
	423419	R55336	Hs.23539	ESTs	3.13
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.12
55	408092	NM_007057	Hs.42650	ZW10 interactor	3.12
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	3.12
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	3.12
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.12
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.11
60	420552	AK000492	Hs.98806	hypothetical protein	3.11
	402408			NM_030920*:Homo sapiens hypothetical pro	3.10
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.10
	415829	AW450198	Hs.163742	ESTs	3.09
	423739	AA398155	Hs.97600	ESTs	3.07
65	418459	R85436	Hs.268814	ESTs	3.07
	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.07
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	3.06
	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.06
	420524	AB010575	Hs.98547	amiloride-sensitive cation channel 3, te	3.06
70	433023	AW864793		thrombospondin 1	3.04
	421633	AF121860	Hs.106260	sorting nexin 10	3.04
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.04
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	3.03
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.03
75	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (	3.03
	425312	AA354940	Hs.145958	ESTs	3.02
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.01
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.01
	432446	AA542845	Hs.294088	GAJ protein	3.01
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	3.00
80	436902	AW247145	Hs.192729	ESTs	3.00
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.00
	430056	X97548	Hs.228059	KRAB-associated protein 1	2.98
	427617	D42063	Hs.199179	RAN binding protein 2	2.98

	406367		NM_022357:Homo sapiens putative metallo	2.97
	418866	T65754	gb:yc11c07.s1 Stratagene lung (937210) H	2.97
	435918	AF263538	Hs.86232 growth differentiation factor 3	2.97
5	436511	AA721252	Hs.291502 ESTs	2.96
	402680		Target Exon	2.96
	414161	AA136106	Hs.184852 KIAA1553 protein	2.95
	427239	BE270447	ubiquitin carrier protein	2.95
	433683	AI817723	Hs.22678 hypothetical protein FLJ21832	2.94
10	417576	AA339449	Hs.82285 phosphoribosylglycinamide formyltransfer	2.94
	402299		Target Exon	2.92
	420697	AA827705	Hs.26605 ESTs	2.90
	427719	AI393122	Hs.134726 ESTs	2.90
	419131	AA406293	Hs.109526 ESTs	2.89
15	410048	W76467	Hs.343874 proline oxidase homolog	2.89
	427314	AB033024	Hs.175475 KIAA1198 protein	2.89
	424315	AW614850	Hs.193384 putative 28 kDa protein	2.88
	430335	D80007	Hs.239499 KIAA0185 protein	2.87
	410361	BE391804	Hs.62661 guanylate binding protein 1, interferon-	2.87
20	413686	AI469213	Hs.71404 ESTs	2.87
	429183	AB014604	Hs.197955 KIAA0704 protein	2.86
	430292	AK000634	Hs.238270 hypothetical protein FLJ20627	2.86
	422726	U11690	Hs.1572 faciogenital dysplasia (Aarskog-Scott sy	2.86
	437834	AA769294	gb:nz36g03.s1 NCL_CGAP_GCB1 Homo sapiens	2.86
25	435159	AA668879	Hs.116649 ESTs	2.84
	428361	NM_015905	Hs.183858 transcriptional intermediary factor 1	2.84
	430388	AA356923	Hs.240770 nuclear cap binding protein subunit 2, 2	2.84
	434070	AF116652	Hs.270087 hypothetical protein PRO0813	2.83
	429323	NM_001649	Hs.2391 apical protein, Xenopus laevis-like	2.83
30	433247	AB040948	Hs.142856 KIAA1515 protein	2.82
	415884	H22966	Hs.13471 ESTs	2.82
	427668	AA298760	Hs.180191 hypothetical protein FLJ14904	2.82
	437162	AW005505	Hs.5464 thyroid hormone receptor coactivating pr	2.81
	401091		decay accelerating factor for complement	2.81
35	425601	AW629485	Hs.140720 GSK-3 binding protein FRAT2	2.79
	428597	AK000147	Hs.295909 hypothetical protein FLJ10700	2.79
	417705	AW134952	Hs.175220 hypothetical protein FLJ14541	2.79
	438243	AI581311	ESTs	2.78
	418203	X54942	Hs.83758 CDC28 protein kinase 2	2.78
40	410704	BE076754	gb:CM1-BT0601-180200-121-b10 BT0601 Homo	2.77
	429063	AW363845	Hs.322903 ESTs, Weakly similar to A46010 X-linked	2.76
	427147	AA398587	Hs.97414 ESTs	2.76
	430552	AA176374	Hs.243886 nuclear autoantigenic sperm protein (his	2.76
	437660	W31708	Hs.55304 ESTs	2.74
45	425237	U07695	Hs.155227 EphB4	2.72
	419335	AW960146	Hs.284137 hypothetical protein FLJ12888	2.72
	426386	AA748850	Hs.125830 bladder cancer overexpressed protein	2.70
	423123	NM_012247	Hs.124027 SELENOPHOSPHATE SYNTHETASE ; Human selen	2.70
	430968	AW972830	gb:EST384925 MAGE resequences, MAGL Homo	2.70
50	420596	NM_002692	Hs.99185 polymerase (DNA directed), epsilon 2	2.68
	419741	NM_007019	Hs.93002 ubiquitin carrier protein E2-C	2.68
	401464		histone deacetylase 5	2.68
	411856	H67899	Hs.4190 Homo sapiens cDNA: FLJ23269 fis, clone C	2.68
	411365	M76477	Hs.289082 GM2 ganglioside activator protein	2.68
55	419029	AA233397	Hs.326290 hypothetical protein FLJ12581	2.67
	421654	AW163267	Hs.106469 suppressor of var1 (S.cerevisiae) 3-like	2.66
	421535	AB002359	Hs.105478 phosphoribosylformylglycinamide synthase	2.66
	423453	AW450737	Hs.128791 CGI-09 protein	2.66
	412673	AL042957	Hs.31845 ESTs	2.65
60	410006	AW732308	Hs.57783 eukaryotic translation initiation factor	2.65
	434159	AW135214	Hs.191828 ESTs	2.65
	427260	AA663848	gb:ae70b06.s1 Stratagene schizo brain S1	2.64
	439053	BE244588	Hs.6456 chaperonin containing TCP1, subunit 2 (b	2.64
	414706	AW340125	Hs.76989 KIAA0097 gene product	2.64
65	433979	AA620999	gb:ag03a08.s1 Soares_testis_NHT Homo sap	2.64
	403969		ENSP00000034663:Zinc finger protein 131	2.64
	420582	BE047878	Hs.99093 Homo sapiens chromosome 19, cosmid R2837	2.64
	418355	L42563	Hs.1165 ATPase, H <sup>+</sup> transporting, nongastric, alp	2.63
	411127	AA668995	Hs.218329 hypothetical protein	2.62
70	437205	AL110232	Hs.279243 Homo sapiens mRNA; cDNA DKFZp564D2071 (f	2.62
	412123	BE251328	Hs.73291 hypothetical protein FLJ10881	2.61
	436481	AA379597	Hs.5199 HSPC150 protein similar to ubiquitin-con	2.60
	408446	AW450669	Hs.45068 hypothetical protein DKFZp434I143	2.59
	437033	AW248364	Hs.5409 RNA polymerase I subunit	2.58
75	418592	X99226	Hs.284153 Fanconi anemia, complementation group A	2.58
	415585	R59946	Hs.184852 KIAA1553 protein	2.57
	424800	AL035588	Hs.153203 MyoD family inhibitor	2.57
	426470	AA528794	Hs.128644 ESTs	2.57
	426919	AL041228	ELAV (embryonic lethal, abnormal vision,	2.56
80	421209	AJ010230	Hs.102576 ret finger protein-like 1 antisense	2.56
	437496	AA452378	Hs.146668 Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.56
	401837		NM_025109:Homo sapiens hypothetical prot	2.56
	428743	AL080060	Hs.301549 Homo sapiens mRNA; cDNA DKFZp564H172 (fr	2.56
	422809	AK001379	Hs.121028 hypothetical protein FLJ10549	2.55

	418648	AW979223	Hs.292478	ESTs	2.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.54
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.54
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	2.54
5	428728	NM_016625	Hs.191381	hypothetical protein	2.53
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	2.52
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	2.52
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.52
10	422406	AF025441	Hs.116206	Opa-interacting protein 5	2.52
	433228	F28212	Hs.14953	KIAA1491 protein	2.51
	411943	BE502436	Hs.7962	ESTs, Weakly similar to S44608 C02F5.6 p	2.51
	426181	AA371422	Hs.334371	hypothetical protein MGC13096	2.50
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	2.50
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.48
15	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	2.48
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.47
	435726	BE535787	Hs.113170	ESTs	2.47
	404068			Target Exon	2.46
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	2.46
20	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	2.46
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.46
	429652	AA766810	Hs.259290	ESTs	2.45
	416204	AW972270	Hs.195161	ESTs	2.45
	414713	BE465243	Hs.12684	ESTs	2.44
25	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.44
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.44
	435244	N77221	Hs.187824	ESTs	2.44
	402679			NM_000478:Homo sapiens alkaline phosphat	2.43
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	2.42
30	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.41
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisqu	2.41
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.41
	423232	BE244625	Hs.125742	leucine-rich neuronal protein	2.40
	427578	AI591305	Hs.169084	ESTs, Highly similar to TUL3_HUMAN TUBBY	2.40
35	409934	R91601	Hs.190466	hypothetical protein FLJ22584	2.39
	423787	AJ295745	Hs.236204	nuclear pore complex protein	2.39
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	2.39
	438869	AF075009		gb:Homo sapiens full length insert cDNA	2.38
40	434981	AW182577	Hs.293077	ESTs	2.38
	417911	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (	2.38
	409210	AA251812	Hs.51120	cathelicidin antimicrobial peptide	2.37
	424425	AB031480	Hs.146824	SPR1 protein	2.37
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	2.37
45	421567	AJ272137	Hs.198265	matrix metalloproteinase 25	2.37
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.37
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	2.36
	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	2.36
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	2.36
50	410968	AA199907	Hs.67397	homeo box A1	2.36
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	2.36
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	2.36
	412389	AW947655		gb:RC0-MT0003-140300-031-b07 MT0003 Homo	2.35
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.35
55	403780			C4001759:gi133250[sp]P19474[RO52_HUMAN	2.34
	437681	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	2.34
	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	2.34
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	2.34
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.34
60	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	2.33
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.33
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.32
	418821	AA436002	Hs.183161	ESTs	2.32
	437437	AA226869		hypothetical protein DKFZp762L0311	2.32
65	413437	BE313164	Hs.75361	gene from NF2/meningioma region of 22q12	2.31
	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	2.30
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	2.30
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	2.30
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	2.29
70	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	2.29
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	2.29
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.28
	412721	AW183165	Hs.95600	ESTs	2.28
	404071			C12000514*:gi17302471[gb]AAF57556.1 (AE	2.27
75	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.26
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.26
	424935	AI655010	Hs.120363	hypothetical protein MGC15634	2.26
	415791	H09366	Hs.78853	uracil-DNA glycosylase	2.26
	431667	AA812573	Hs.246787	ESTs	2.26
80	424169	AA336399	Hs.153797	ESTs	2.25
	436540	BE397032	Hs.14468	hypothetical protein MGC14226	2.25
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.24
	403242			Target Exon	2.24
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.24



	421002	AF116030	Hs.100932	transcription factor 17	2.24
	438833	BE612940	Hs.88252	ESTs	2.24
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	2.23
5	433844	AA610175	Hs.179647	Homo sapiens cDNA FLJ12195 fis, clone MA	2.23
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.23
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	2.23
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.23
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.23
10	418826	AK000375	Hs.88820	HDCMC28P protein	2.23
	428612	AA770001		ESTs	2.22
	433220	AI076192	Hs.131933	ESTs	2.22
	422225	BE245652	Hs.118281	zinc finger protein 266	2.22
	437549	AA759149	Hs.128757	gb:ah70e03.s1 Soares_testis_NHT Homo sap	2.22
15	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.22
	408665	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.22
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.21
	420062	AW411096	Hs.94785	TGF(beta)-induced transcription factor 2	2.21
	432820	AI554057	Hs.152477	ESTs	2.21
20	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	2.21
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.20
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	2.20
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	2.20
	423675	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	2.20
25	433698	H24201	Hs.247423	adducin 2 (beta)	2.19
	409101	NM_004297	Hs.50612	guanine nucleotide binding protein (G pr	2.19
	435541	AA687361	Hs.221318	ESTs	2.19
	412019	AA485890	Hs.69330	Homo sapiens cDNA FLJ13835 fis, clone TH	2.19
	418753	BE217818	Hs.87016	hypothetical protein FLJ22938	2.19
30	435461	AI075846	Hs.133996	ESTs	2.19
	402260			NM_001436*:Homo sapiens fibrillarin (FBL	2.18
	421098	AI697901	Hs.192425	ESTs	2.18
	400587			C10000649*:gil7296574[gb]AAF51857.1 (AE	2.18
	407832	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.18
35	427159	U80735	Hs.173854	PAX transcription activation domain inte	2.17
	405770			NM_002362:Homo sapiens melanoma antigen,	2.17
	412722	AI343300	Hs.15091	ESTs	2.16
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	2.16
	438192	AI859065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.16
40	417420	T85150	Hs.268814	ESTs	2.16
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	2.16
	412851	AI826502	Hs.97269	ESTs	2.16
	414702	L22005	Hs.76932	cell division cycle 34	2.16
	409670	AI368109		KIAA1856 protein	2.16
45	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.15
	417863	AB000450	Hs.82771	vaccinia related kinase 2	2.15
	434750	BE019254	Hs.4112	t-complex 1	2.15
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	2.15
	418574	N28754		M-phase phosphoprotein 9	2.15
50	409019	AW385412		myosin regulatory light chain 2, smooth	2.15
	416608	R11499	Hs.189716	ESTs	2.14
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	2.14
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	2.13
	422805	AA436989	Hs.121017	H2A histone family, member A	2.13
55	410284	U50939	Hs.61828	amyloid beta precursor protein-binding p	2.13
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	2.12
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	2.12
	433252	AB040957	Hs.151343	KIAA1524 protein	2.12
	416819	U77735	Hs.80205	pim-2 oncogene	2.12
60	437218	AL117497	Hs.58185	ESTs, Weakly similar to T42727 prolifera	2.12
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	2.12
	433947	AA927996	Hs.112876	ESTs, Weakly similar to AF129535 1 F-box	2.11
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.11
	435703	AW630133	Hs.83313	GK003 protein	2.11
65	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.11
	422192	AA305159	Hs.113019	fls485	2.11
	407961	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	2.10
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.10
	414151	AW976468	Hs.257245	ESTs	2.10
70	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	2.10
	424196	AL133660	Hs.142926	Homo sapiens beta cysteine string protei	2.10
	408831	AF090114	Hs.48433	endocrine regulator	2.10
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	2.09
	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	2.09
75	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	2.09
	403532			NM_024638:Homo sapiens hypothetical prot	2.09
	432141	BE410964	Hs.272736	nuclear receptor binding protein	2.08
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.08
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	2.08
80	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	2.08
	418755	Y14443	Hs.88219	zinc finger protein 200	2.08
	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.07
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.07
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protei	2.07

5	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.07
	417230	U40998	Hs.81728	unc119 (C.elegans) homolog	2.07
	425966	NM_001761	Hs.1973	cyclin F	2.07
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	2.06
	407162	N63855	Hs.142634	zinc finger protein	2.06
	422382	D79988	Hs.115778	KIAA0166 gene product	2.06
	402677			NM_000478:Homo sapiens alkaline phosphat	2.06
10	433017	Y15067	Hs.279914	zinc finger protein 232	2.05
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	2.05
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.05
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.05
	402678			Target Exon	2.05
15	408146	R45621	Hs.81057	hypothetical protein MGC2718	2.05
	420027	AF009746	Hs.94395	ATP-binding cassette, sub-family D (ALD)	2.04
	427447	T65414	Hs.6647	Homo sapiens cDNA FLJ13088 fis, clone NT	2.04
	433219	AB040916	Hs.24106	KIAA1483 protein	2.04
	431126	AF085243	Hs.283619	zinc finger protein 236	2.04
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	2.04
20	419669	AJ007041	Hs.92236	KIAA0304 gene product	2.04
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.03
	426242	AL096727	Hs.168249	Homo sapiens mRNA; cDNA DKFZp434B104 (fr	2.02
	432185	AA221032	Hs.272838	hypothetical protein FLJ10494	2.02
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	2.02
25	408636	BE294925	Hs.46680	CGI-12 protein	2.02
	420005	AW271106	Hs.133294	ESTs	2.02
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.02
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.02
	425358	AL079658	Hs.338207	FK506 binding protein 12-rapamycin assoc	2.01
30	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.01
	438450	AI050866	Hs.65853	nodal, mouse, homolog	2.00
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	2.00
	424934	U75370	Hs.153880	polymerase (RNA) mitochondrial (DNA dire	2.00
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.00
35	414251	AL042306	Hs.97689	VASA protein	2.00

TABLE 51B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
40		
45	432666	144_7
	423458	30480_1
	418477	4172_1
50	436812	659779_1
	436899	1000797_1
	437421	978554_1
	430676	60836_2
55	427521	513212_1
60	436909	596835_1
	429228	215430_1
	435514	132288_1
	422689	874209_1
	421974	864120_1
	414136	30243_1
65	417886	1031334_1
	418235	886897_1
	414725	19377_1
70	434609	14739_1
	408065	101881_1
	412537	14066_1
75	415684	18695_18
	433641	35983_1
80	424281	892055_1

427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
418049	12052_4	AJ314647 NM_052888 BI494693 AA835065 AI634477 AI336678 AI807696 BF477887 AI701147 Z39187 R38979 F02234 AA984711 BI222234 AV731417 R42406 H04996 T98498 R12489 R12577 R42405
433023	3970_8	BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148 AI968683 AA846676 AA927355 H80424 AW973295 R88209 F29868 BE928871
418866	245947_1	T65754 AA229658 AA229857
427239	20459_2	AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF718773 BF718645 AW074866 BE857822
437834	294580_1	BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573
438243	2532601_1	AI581311 AA781682 AA781678
410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523 BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866 AW840571
430968	1237115_1	AW972830 AA489820 AA527647 AA570362
427260	11272_50	AA401424 AA400100 AA663848
433979	2076469_1	N50454 AA620999 T16375
426919	347372_1	BI917595 AI203314 AL041228 AV727959 D61361 D82004 BI753157 AA961066 AI990307 BF439651 AI453076 AI376075 AI014836 AI018308 AW183530 AA393346 AA935601 AA628633 AI150282 AI028574 AI217182 AA431478 AW087473 AW900295 H50055 AL041229 BI917726
438869	52134_1	AF075009 R63109 R63068
412389	1174403_1	AW947655 AW984020
400205	2538_1	NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355 AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205 BE090841 AW163750 BF747730 BF898637 AI206506 AV660870 AV692110 AW386830 AV656831 N84710 AW993470 BF086802 BF758454 BG960772 BF757769 BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE909924 AA708208 BG530266 BF968015 AW992930 BF888862 BG536628 AA143164 AW748953 BG498922 BF885190 BF889005 BF754781 BF800003 BM476529 AI627668 AW028126 AL046011 BF590668 AI017447 AA579936 AI367597 AA699622 BE280597 AI124620 AI082548 AW274985 AA677870 AI056767 BE551689 AA287642 H94499 AI752427 AI652365 AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813 AI092115 BF312771 BF242859 BG533616 BG533761 BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353 AU155318 BE302211 AI375022 AA085641 AU157923 H88858 AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296 AI184820 AI469178 AA782432 H92184 AA340562 BF195818 AA852821 AW576342 AA827107 AA173317 AW190014 AI918514 AA729372 AA729718 AI055958 AA331424 BE328601 AA515690 BI018896 AW628277 AA748368 AA626222 BG492636 AW380620 BF800058 AW370956 AA290909 R25857 BG952995 BF801437 AA172077 AU155890 AU149783 AI720904 AA902936 AA865727 AI470830 AV740677 AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427 BE928472 D25910 BF758439 BF968785 BE565238 AA355981 AI905607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471 BG574501 AA187596 AA361196 T95557 BG531446 BG527242 BG527513 BG611106 AA085995 BF847252 BG024608 BE540261 BG531236 AL579993 BG108733 BG483503 BG571032 BG492505
425331	1227464_1	AA427363 AW962128 AA355353
437437	6087_1	BC009352 BC014630 AU131857 AL527140 AU131768 BI769362 BI753220 AU129886 AU128771 AA314135 AU126819 AI333799 AA479336 AA258503 AL597351 AL359619 BG697218 BI254283 AI743846 AA236444 AA397533 AA247450 AI051464 AI224533 AU153442 AU151001 AU152621 AU151829 AU153069 AW269958 AU154195 AI862754 AI589780 AW273839 AI338155 AI126632 BE046048 AA976930 AI289304 AI625961 AI222288 AI280054 AA973329 AI524262 AI242371 AA296517 AI567865 AI590681 AJ346616 AW247913 AI422051 AI475352 AI689531 AW469308 AW198034 AA936939 AU151059 AU148134 AA486419 AU151953 AI830968 BI493265 BI493264 AU149861 BE268763 AV763495 AW962827 BM480300 AA226869 AL529368 BM451957 AU132714 BI871319 AA380739 BI911351 BF795906 BE548853 AW579751
430183	17316_1	AK055746 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852 BF173139 BE010038
430504	5477_6	BE219720 BF475241 AI571723 BE219848 BI789268 AI224899 AA724864 AW771467 AA480255 AW845616 AI440295 H52800 BE218790 AI681575 AW300064 AW262133 H21568 AI363015 AI884914 H86948
428612	1383189_1	AA770001 AA431112 AA432126
409670	8882_8	AI625045 AW504152 AI469086 AA905873 AW504662 AW136114 AI927270 BE041754 AI648386 AA662655 AA400052 AI143501 AI744934 AI400147 AI381657 AA676551 AA974367 AW117437 AI570383 AI242456 AI274581 AA678138 R49939 AI393926 AA345854 AW605850 AI869780 AW391171 R77044
418574	12009_2	AW955043 AI990326 AA776406 AI016250 AW451882 AA843678 BF916900 AW945895 AI979339 N23129 W70051 AA322672 N23137
409019	32320_4	BM480413 N28908 H39792 BE240826 BE882093 BE240827 AW868637 BF739795 AA700834 AA769597 AA489668 AW968806 AW085196 AI093280 AI218457 AA063138 AI632958 AW515005 AI570530 Z41724 AA748789 AI696584 AA062544 AA773643 AA490285
430935	15297_3	BC017923 AA789302 AW466994 BF513878 AI819642 AI184913 AW469044 AI220572 AW072916 AI280239 AI473611 AW841126 D60937
424677	2518_37	AA489195 N59350 AA693435 BG531204 AA484243 AW514092 U09414 NM_003438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW609708

TABLE 51C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406547	7711513	Minus	172780-174358
402145	8018280	Plus	113086-114800
402199	8576116	Minus	84187-84744
401435	8217934	Minus	54508-55233
402408	9796239	Minus	110326-110491
406367	9256126	Minus	58313-58489
402680	8113438	Plus	137634-137768,139702-139893,140475-14059
402299	6693370	Plus	23367-25175
401091	9958240	Plus	94760-94898

5	401464	6682291	Minus	170688-170834
	403969	8569909	Plus	31237-31375,32405-32506
	401837	7630990	Minus	120993-121095,121660-121729
	404068	3168621	Minus	18123-18766
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
10	402679	8113438	Plus	132079-132216
	403780	8076989	Plus	93160-93409
	404071	7210053	Minus	167354-167859,168810-168920,169000-16910
	403242	7637817	Minus	11297-12511
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
15	400587	9887626	Plus	25435-25588,25668-25747
	405770	2735037	Plus	61057-62075
	403532	8076842	Minus	81750-81901
	406137	9166422	Minus	30487-31058
	402677	8113438	Plus	22135-22309,23063-23238
	402678	8113438	Plus	37395-37514,37866-37981

20

TABLE 52A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of testicular cancer (non-seminomatous and Seminomatous) compared to normal adult testicular tissues

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
30	414438	AI879277	Hs.76136	thioredoxin	51.77
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	49.93
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	49.20
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	44.46
	438091	AW373062		nuclear receptor subfamily 1, group I, m	40.70
35	406658	AI920965	Hs.77961	major histocompatibility complex, class	39.64
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	38.70
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	38.25
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	37.50
	430542	AI557486	Hs.119122	ribosomal protein L13a	37.22
40	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	35.98
	432730	AI066520	Hs.131358	ESTs	35.25
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	31.69
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	31.33
	417088	M54915	Hs.81170	pim-1 oncogene	31.20
45	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	29.93
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	29.35
	426295	AW367283		zinc finger protein 6 (CMPX1)	29.32
	406856	AW515336	Hs.29797	ribosomal protein L10	28.93
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	27.99
50	440207	AI371978	Hs.128326	ESTs	27.75
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	26.95
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.90
	420367	AA259090	Hs.257028	ESTs	26.50
	429978	AA249027		ribosomal protein S6	26.43
55	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	26.36
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	26.23
	412636	NM_004415		desmoplakin (DPI, DPLI)	26.15
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	25.25
	446899	NM_005397	Hs.16426	podocalyxin-like	25.25
60	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	25.15
	406656	M16714	Hs.89643	major histocompatibility complex, class	25.13
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	24.78
	423961	D13666	Hs.136348	periostin(OSF-2os)	24.48
	425543	R23313	Hs.334895	ribosomal protein L10a	24.38
65	420676	AI434780	Hs.4248	vav 2 oncogene	24.18
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	23.96
	440869	NM_014297	Hs.7486	protein expressed in thyroid	23.80
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	23.56
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	23.22
70	446627	AI973016	Hs.15725	hypothetical protein SBBI48	22.93
	449571	AW016812	Hs.200266	ESTs	22.83
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	22.81
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	22.68
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	22.45
75	422714	AB018335	Hs.119387	KIAA0792 gene product	22.45
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	22.30
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.69
	406648	AA563730	Hs.277477	major histocompatibility complex, class	21.58
	448588	AI970276	Hs.156905	KIAA1676	21.23
80	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	21.19
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.70
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	20.60
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	20.57

	420754	W79431	Hs.346911	ribosomal protein L22	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	20.15
	424800	AL035588	Hs.153203	MyoD family inhibitor	20.10
5	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	20.01
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	19.89
	410143	AA188169		KIAA1191 protein	19.41
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	19.08
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.03
10	425535	AB007937	Hs.158287	KIAA0468 gene product	18.78
	411573	AB029000	Hs.70823	KIAA1077 protein	18.63
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.53
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	18.52
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	18.50
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	18.50
15	429183	AB014604	Hs.197955	KIAA0704 protein	18.48
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	18.44
	450377	AB033091		KIAA1265 protein	18.40
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.15
	440528	BE313555	Hs.7252	KIAA1224 protein	18.05
20	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	17.98
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	17.80
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	17.75
	428782	X12830	Hs.193400	interleukin 6 receptor	17.48
25	415221	W07418	Hs.78225	annexin A1	17.47
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	17.40
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	17.30
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	17.14
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	17.13
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	17.10
30	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	17.03
	425996	W67330		hypothetical protein AL110115	16.98
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	16.98
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	16.98
35	427521	AW973352		ESTs	16.93
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.93
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	16.53
	449338	H73444	Hs.394	adrenomedullin	16.36
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	16.23
40	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	16.21
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	16.15
	427691	AW194426	Hs.20726	ESTs	16.13
	406786	AW161678	Hs.111334	ferritin, light polypeptide	16.11
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	16.10
	451106	BE382701	Hs.25960	N-MYC oncogene	16.09
45	408380	AF123050	Hs.44532	diubiquitin	16.00
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	15.93
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	15.69
50	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	15.64
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	15.55
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	15.55
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	15.53
	410185	BE294068	Hs.737	immediate early protein	15.49
55	422105	AI929700	Hs.111680	endosulfine alpha	15.23
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	15.23
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	15.05
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	15.02
	426552	BE297660	Hs.170328	moesin	14.96
60	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	14.88
	436860	H12751	Hs.5327	PRO1914 protein	14.85
	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	14.84
	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	14.78
	412623	R28898	Hs.74170	metallothionein 1E (functional)	14.70
65	408989	AW361666	Hs.49500	KIAA0746 protein	14.53
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	14.48
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	14.31
	410325	AB023154	Hs.62264	KIAA0937 protein	14.23
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	14.20
70	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	14.19
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	14.18
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.13
	447211	AL161961	Hs.17767	KIAA1554 protein	14.08
	417426	NM_002291	Hs.82124	laminin, beta 1	14.08
75	414420	AA043424	Hs.76095	immediate early response 3	14.04
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.02
	454413	AI653672	Hs.40092	PNAS-123	13.93
	452651	AI218918	Hs.30209	KIAA0854 protein	13.86
	450581	AF081513	Hs.25195	TGF-beta 4	13.85
80	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.78
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.63
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.59
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	13.57
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	13.53

	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	13.43
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	13.41
	447534	AW953935	Hs.288655	ESTs	13.33
5	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	13.31
	428065	AI634046	Hs.157313	ESTs	13.30
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	13.28
	436398	H87136	Hs.5174	ribosomal protein S17	13.18
	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	12.93
10	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	12.90
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	12.90
	408437	AW957744	Hs.278469	lacrimal proline rich protein	12.90
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	12.89
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.83
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	12.79
15	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	12.78
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	12.75
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	12.73
	430630	AW269920	Hs.2621	cystatin A (stefin A)	12.68
20	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	12.65
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	12.50
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	12.48
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	12.43
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.43
25	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	12.41
	412247	AF022375	Hs.73793	vascular endothelial growth factor	12.41
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	12.40
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	12.38
	432409	AA806538	Hs.130732	KIAA1575 protein	12.33
30	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.33
	419384	AA490866	Hs.39429	ESTs	12.33
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	12.32
	432805	X94630	Hs.3107	CD97 antigen	12.32
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	12.25
35	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	12.13
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	12.12
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	12.03
	402145			Target Exon	12.01
	407179	AA206465		thymosin, beta 4, X chromosome	12.00
40	433208	AW002834	Hs.24095	ESTs	11.95
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.90
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	11.83
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	11.75
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	11.75
45	427761	AA412205	Hs.140996	ESTs	11.68
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	11.58
	436075	BE090176	Hs.179902	transporter-like protein	11.50
	440774	AI420611	Hs.153934	ESTs	11.35
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	11.25
50	419223	X60111	Hs.1244	CD9 antigen (p24)	11.08
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	11.08
	444656	AI277924	Hs.145199	ESTs	10.98
	420943	AI718702	Hs.279930	major histocompatibility complex, class	10.96
	450294	H42587	Hs.238730	hypothetical protein MGC10823	10.92
55	413686	AI469213	Hs.71404	ESTs	10.83
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	10.78
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	10.75
	407252	AA659037	Hs.163780	ESTs	10.75
	445929	AI089660	Hs.323401	dpy-30-like protein	10.70
60	451864	N20370	Hs.69547	ESTs	10.69
	429307	AU076592	Hs.198951	jun B proto-oncogene	10.64
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	10.63
	447519	U46258	Hs.339665	ESTs	10.63
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	10.59
65	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	10.55
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	10.54
	437103	AW139408	Hs.152940	ESTs	10.50
	449961	AW265634	Hs.133100	ESTs	10.50
	441244	BE612935	Hs.184052	PP1201 protein	10.49
70	450139	AK001838		serum/glucocorticoid regulated kinase	10.48
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	10.48
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rholekin, clone	10.47
	446682	AW205632	Hs.211198	ESTs	10.43
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.43
75	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	10.40
	424950	AA602917	Hs.156974	ESTs	10.40
	434442	AA737415		ESTs	10.33
	438089	W05391		nuclear receptor subfamily 1, group I, m	10.33
	432559	AW452948	Hs.257631	ESTs	10.30
80	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	10.30
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	10.28
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	10.27
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	10.27
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	10.23

	445245	AB032973	Hs.12461	LCHN protein	10.18
	446488	AB037782	Hs.15119	KIAA1361 protein	10.15
	410611	AW954134	Hs.20924	KIAA1628 protein	10.15
5	425875	AL077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	10.14
	416926	H03109	Hs.263395	HT018 protein	10.07
	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	10.05
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	10.04
	411975	AI916058	Hs.144583	ESTs	10.03
10	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	10.00
	408784	AW971350	Hs.63386	ESTs	9.95
	444795	AI193356	Hs.160316	ESTs	9.93
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.90
	400440	X83957	Hs.83870	nebulin	9.90
	414829	AA321568	Hs.77436	pleckstrin	9.88
15	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.88
	426827	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	9.85
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	9.83
	446795	AI797713	Hs.156471	ESTs	9.78
20	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	9.67
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	9.65
	419904	AA974411	Hs.18672	ESTs	9.63
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	9.63
	414405	AI362533		KIAA0306 protein	9.58
25	418840	AI821614	Hs.185831	ESTs	9.53
	453716	AA037675	Hs.152675	ESTs	9.50
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	9.50
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.45
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	9.45
30	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	9.43
	434423	NM_006769	Hs.3844	LIM domain only 4	9.43
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	9.43
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	9.42
	410397	AF217517	Hs.63042	DKFZp564J157 protein	9.37
35	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	9.37
	434524	AA635931	Hs.249716	ESTs	9.36
	422960	AW890487		cadherin 13, H-cadherin (heart)	9.35
	414774	X02419	Hs.77274	plasminogen activator, urokinase	9.32
	411960	R77776	Hs.18103	ESTs	9.30
40	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	9.28
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.28
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	9.27
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	9.27
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	9.25
45	427968	AI857607	Hs.181301	cathepsin S	9.23
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	9.23
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	9.23
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.18
	417315	AI080042	Hs.180450	ribosomal protein S24	9.18
50	421098	AI697901	Hs.192425	ESTs	9.18
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.18
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	9.17
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	9.17
	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.15
55	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	9.14
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.13
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	9.12
	420099	D80011	Hs.95140	KIAA0189 gene product	9.10
	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	9.08
60	441436	AW137772	Hs.185980	ESTs	9.08
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	9.08
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	9.08
	430556	AW967807	Hs.13797	ESTs	9.07
	450147	AW373713	Hs.146324	CGI-145 protein	9.06
65	442806	AW294522	Hs.149991	ESTs	9.05
	431187	AW971146	Hs.293187	ESTs	9.05
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	9.03
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	9.03
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	9.02
70	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	9.00
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.99
	432314	AA533447	Hs.312989	ESTs	8.98
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.95
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	8.94
75	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	8.93
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.90
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	8.90
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.89
	417228	AL134324	Hs.7312	ESTs	8.88
80	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	8.88
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	8.88
	438980	AW502384		gb:UL-HF-BR0p-aka-f-12-0-UL.r1 NIH_MGC_5	8.85
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	8.85
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	8.85

	430592	AJ224864	Hs.9688	leukocyte membrane antigen(IRC1)	8.83
	445612	N94126	Hs.12959	hypothetical protein	8.80
	427254	AL121523	Hs.97774	ESTs	8.80
5	428970	BE276891	Hs.194691	retinoic acid induced 3	8.80
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subunit	8.79
	430162	AW450843	Hs.346348	ESTs	8.75
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	8.73
	446659	AI335361	Hs.226376	ESTs	8.73
	447198	D61523	Hs.283435	ESTs	8.73
10	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	8.70
	401091			decay accelerating factor for complement	8.68
	442832	AW206560	Hs.253569	ESTs	8.68
	442495	AI184717		ESTs	8.63
15	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	8.63
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	8.61
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	8.59
	425580	L11144	Hs.1907	galanin	8.55
	449656	AA002008	Hs.188633	ESTs	8.55
	412093	BE242691	Hs.14947	ESTs	8.54
20	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.54
	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.53
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	8.51
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	8.45
25	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	8.45
	425284	AF155568		NS1-associated protein 1	8.45
	441623	AA315805		desmoglein 2	8.43
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	8.42
	441021	AW578716	Hs.7644	H1 histone family, member 2	8.40
30	446630	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	8.40
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	8.35
	433655	AL036559	Hs.3463	ribosomal protein S23	8.33
	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.32
	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1-like	8.31
35	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.30
	414662	AL036058	Hs.76807	major histocompatibility complex, class	8.30
	414601	AV660804	Hs.301417	AHNAK nucleoprotein (desmoyokin)	8.29
	406699	L06505	Hs.182979	ribosomal protein L12	8.28
	443884	N20617	Hs.194397	leptin receptor	8.28
40	442821	BE391929	Hs.8752	transmembrane protein 4	8.26
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	8.24
	435968	AW161481	Hs.111577	integral membrane protein 3	8.23
	440327	R12581	Hs.191146	ESTs	8.23
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.22
45	435684	NM_001290	Hs.4980	LIM domain binding 2	8.16
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	8.15
	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	8.14
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown (H.s	8.13
	448094	H24387	Hs.32061	ESTs, Weakly similar to I38022 hypotheti	8.10
50	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	8.09
	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	8.08
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	8.07
	423523	AW299828	Hs.193580	ESTs	8.03
	426759	AI590401	Hs.21213	ESTs	8.03
55	426780	BE242284	Hs.172199	adenylate cyclase 7	8.03
	426215	AW963419	Hs.155223	stanniocalcin 2	8.03
	435748	AA699756	Hs.117335	ESTs	8.00
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	8.00
	447500	AI381900	Hs.159212	ESTs	8.00
60	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	8.00
	428728	NM_016625	Hs.191381	hypothetical protein	8.00
	434511	R28982	Hs.18106	ESTs	7.99
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	7.98
	424875	AI187945	Hs.199310	ESTs	7.95
65	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	7.95
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	7.93
	425277	NM_001241	Hs.155478	cyclin T2	7.91
	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	7.90
70	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	7.90
	429999	AI761902	Hs.99597	ESTs	7.90
	445493	AI915771		metallothionein 1E (functional)	7.89
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.88
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	7.88
75	453485	BE620712	Hs.33026	hypothetical protein PP2447	7.87
	434159	AW135214	Hs.191828	ESTs	7.85
	432666	AW204069		ESTs, Weakly similar to unnamed protein	7.83
	430915	AA488953		gb:aa55e05.r1 NCL_CGAP_GCB1 Homo sapiens	7.83
	425913	AA365799		SEC22, vesicle trafficking protein (S. c	7.80
80	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	7.80
	438763	AI583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	7.79
	435905	AW997484	Hs.5003	KIAA0456 protein	7.78
	406663	U24683		immunoglobulin heavy constant mu	7.78
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.78



	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	7.75
	438962	BE046594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	7.75
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.73
5	422900	AA641201	Hs.222051	ESTs	7.73
	432598	AI341227	Hs.157106	ESTs	7.72
	449322	AI638616	Hs.196566	ESTs	7.71
	416987	D86957	Hs.80712	KIAA0202 protein	7.67
	410800	BE280421	Hs.94499	ESTs	7.67
10	416801	X98834	Hs.79971	sal (Drosophila)-like 2	7.67
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.65
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.65
	401466			vesicle-associated membrane protein 4	7.65
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	7.64
15	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.63
	457250	AA811987	Hs.125779	ESTs	7.63
	412949	AI471639	Hs.71913	ESTs	7.63
	406819	AA908472		gb:og82a10.s1 NCI_CGAP_Ov8 Homo sapiens	7.62
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.62
20	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	7.61
	435937	AA830893	Hs.119769	ESTs	7.60
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.60
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.60
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	7.56
25	418134	AA397769	Hs.86617	ESTs	7.55
	451812	X81889	Hs.152151	plakophilin 4	7.55
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.54
	429083	Y09397	Hs.227817	BCL2-related protein A1	7.54
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	7.52
30	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	7.52
	407784	AW139585	Hs.12708	ESTs	7.52
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	7.50
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	7.50
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	7.48
35	446013	AI360167	Hs.152774	ESTs	7.48
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.48
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.45
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	7.45
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	7.44
40	447082	T85314	Hs.54629	thioredoxin-like	7.43
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	7.43
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.43
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	7.43
	442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypothei	7.43
45	436394	AA531187	Hs.126705	ESTs	7.39
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	7.39
	446258	AI283476	Hs.263478	ESTs	7.38
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	7.37
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.36
50	435541	AA687361	Hs.221318	ESTs	7.35
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	7.35
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.35
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.35
	418336	BE179882		glutathione peroxidase 3 (plasma)	7.35
55	448877	AI583696	Hs.253313	ESTs	7.35
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.35
	444838	AV651680	Hs.208558	ESTs	7.33
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	7.31
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	7.30
60	441878	AI801869	Hs.127982	ESTs	7.29
	406542			C19000728*:gij12585552[sp]Q9Y2Q1J2257_HU	7.28
	408418	AW963897	Hs.44743	KIAA1435 protein	7.28
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	7.26
	442492	AA528489	Hs.234518	ribosomal protein L23	7.25
65	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	7.25
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	7.25
	426501	AW043782	Hs.293616	ESTs	7.25
	411251	R19774	Hs.22835	HHGP protein	7.25
	444670	H58373	Hs.332938	hypothetical protein MGC5370	7.25
70	418117	AI922013	Hs.83496	linker for activation of T cells	7.24
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	7.24
	434817	AA082118	Hs.102737	goliath protein	7.23
	419970	AW612022		ESTs	7.23
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	7.23
75	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	7.23
	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	7.21
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	7.21
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	7.20
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.20
80	441224	AU076964	Hs.7753	calumenin	7.18
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.18
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	7.15
	447341	AF106941	Hs.18142	arrestin, beta 2	7.15
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	7.14

	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	7.14
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.13
	421633	AF121860	Hs.106260	sorting nexin 10	7.10
5	410668	BE379794	Hs.159651	hypothetical protein	7.09
	435812	AA700439	Hs.188490	ESTs	7.08
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	7.08
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	7.08
10	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	7.06
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	7.06
	416401	N80139	Hs.268916	ESTs	7.05
	415799	AA653718	Hs.225841	DKFZP434D193 protein	7.05
	415995	NM_004573		phospholipase C, beta 2	7.05
	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.05
15	417535	AA203569	Hs.191482	ESTs	7.04
	449567	AI990790	Hs.188614	ESTs	7.03
	429355	AW973253	Hs.292689	ESTs	7.03
	442460	NM_014135	Hs.8345	PRO0641 protein	7.03
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	7.03
20	430280	AA361258	Hs.237868	interleukin 7 receptor	7.03
	426124	AI268389	Hs.250697	phosphatidylinositol glycan, class F	7.02
	442685	AB033017	Hs.8594	KIAA1191 protein	7.01
	433735	AA608955	Hs.109653	ESTs	7.00
	416003	X96001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.98
25	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.96
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.95
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	6.95
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.93
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	6.93
30	451653	W18193		ESTs, Moderately similar to HERC2 (H.sap	6.93
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	6.93
	451838	AW005866	Hs.193969	ESTs	6.91
	436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-U1.s1 NCL_CGAP_Su	6.90
	443749	R38828	Hs.143463	ESTs	6.90
35	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.90
	427919	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	6.90
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.90
	435655	AW105663	Hs.6947	HSPC069 protein	6.90
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	6.85
40	418259	AA215404		ESTs	6.85
	407244	M10014		fibrinogen, gamma polypeptide	6.85
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	6.83
	441321	H17182	Hs.7771	B-cell associated protein	6.80
	433162	AI025842		ESTs	6.80
45	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.80
	434372	AA631373		gb:np86c01.s1 NCL_CGAP_Thy1 Homo sapiens	6.80
	456629	AW891965		histone deacetylase 3	6.78
	430283	BE391688		RAB7, member RAS oncogene family	6.77
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	6.76
50	406858	AI865720	Hs.29797	ribosomal protein L10	6.75
	429582	AI569068	Hs.22247	ESTs	6.75
	401113			solute carrier family 22 (organic cation	6.75
	449576	AW014631	Hs.225068	ESTs	6.75
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	6.72
55	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.72
	430451	AA836472	Hs.297939	cathepsin B	6.72
	410503	AW975746	Hs.188662	KIAA1702 protein	6.70
	415682	AI347128	Hs.191870	ESTs	6.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	6.70
60	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	6.70
	457073	AA233210	Hs.179943	ribosomal protein L11	6.69
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	6.68
	436137	AI056769	Hs.133512	ESTs	6.68
	425787	AA363867	Hs.155029	ESTs	6.67
65	437802	AI475995	Hs.122910	ESTs	6.65
	432636	AA340864	Hs.278562	claudin 7	6.65
	407340	AA810168	Hs.284289	vittiligo-associated protein VIT-1	6.65
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	6.65
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	6.63
70	441355	AI822034	Hs.137097	ESTs	6.63
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	6.63
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.63
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	6.62
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	6.60
75	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	6.60
	449057	AB037784	Hs.22941	KIAA1363 protein	6.60
	446979	AI654443	Hs.197683	ESTs	6.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	6.60
	424868	AI568170	Hs.96886	ESTs	6.59
80	409485	S80990	Hs.252136	ficolin (collagen/fibrinogen domain-cont	6.58
	451603	BE379499	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H	6.58
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.58
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	6.57
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.56

5	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	6.56
	444207	AI565004		calhepsin D (lysosomal aspartyl protease	6.55
	418459	R85436	Hs.268814	ESTs	6.55
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.55
	406745	AW511970	Hs.279860	tumor protein, translationally-controlle	6.55
10	446173	BE565849	Hs.14158	copine III	6.53
	436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	6.53
	423825	NM_004402	Hs.133089	DNA fragmentation factor, 40 kD, beta po	6.53
	443441	AW291196	Hs.92195	ESTs	6.51
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	6.50
15	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smo	6.50
	450219	AI826999	Hs.224624	ESTs	6.50
	408896	AI610447	Hs.48778	niban protein	6.50
	442618	R56222	Hs.26514	ESTs	6.49
	422773	AB028962	Hs.301552	KIAA1039 protein	6.48
20	413663	BE247585	Hs.75462	BTG family, member 2	6.48
	418905	BE539674		actinin, alpha 4	6.48
	405086			NM_006662*:Homo sapiens Snf2-related CBP	6.45
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	6.45
	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.45
25	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	6.45
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	6.43
	426496	D31765	Hs.170114	KIAA0061 protein	6.43
	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	6.42
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [Hs	6.41
30	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.40
	435918	AF263538	Hs.86232	growth differentiation factor 3	6.38
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	6.38
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.38
	436716	AI433540		gb:ti69g05.x1 NCI_CGAP_Kid11 Homo sapien	6.38
35	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	6.38
	413326	H88621	Hs.19762	ESTs, Weakly similar to KIAA1140 protein	6.38
	441970	AW959918	Hs.73737	ESTs	6.38
	430835	AI240006	Hs.192326	ESTs	6.38
	414890	BE281095	Hs.77573	uridine phosphorylase	6.37
40	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.37
	414768	AW376989	Hs.259855	elongation factor-2 kinase	6.36
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	6.36
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	6.35
	432586	AA568548		ESTs	6.35
45	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	6.35
	420012	AW957965	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	6.35
	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.35
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.35
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosyl	6.35
50	437296	AA350994	Hs.20281	KIAA1700	6.35
	427747	AW411425	Hs.180655	serine/threonine kinase 12	6.33
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	6.33
	410387	AI277367	Hs.47094	ESTs	6.33
	413677	AW503116	Hs.301819	zinc finger protein 146	6.31
55	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	6.31
	443634	H73972	Hs.134460	ESTs	6.30
	409453	AI885516	Hs.95612	ESTs	6.29
	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	6.29
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.29
60	410532	T53088	Hs.155376	hemoglobin, beta	6.28
	428453	AB011110	Hs.184367	GTPase activating protein-like	6.27
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	6.26
	458965	AA010319	Hs.60389	ESTs	6.25
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	6.25
65	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	6.25
	412528	AI123478	Hs.32112	ESTs	6.25
	410079	U94362	Hs.58589	glycogenin 2	6.25
	427477	AW973119	Hs.178391	ribosomal protein L44	6.24
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.24
70	435961	BE293127	Hs.283722	GTT1 protein	6.23
	424090	X99699	Hs.139262	XIAP associated factor-1	6.23
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.23
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	6.23
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	6.23
75	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	6.22
	428773	BE256238	Hs.193163	bridging integrator 1	6.20
	436372	AW972301	Hs.310286	ESTs	6.19
	440719	AA150869	Hs.26267	ATP-dependant interferon response protei	6.18
	406685	M18728		gb:Human nonspecific crossreacting antig	6.18
80	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	6.17
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	6.16
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	6.15
	406806	AW088535		ribosomal protein, large, P0	6.15
	420151	AA255931	Hs.186704	ESTs	6.14
	413441	AI929374	Hs.75367	Src-like-adaptor	6.13
	449317	AW293413	Hs.132906	19A24 protein	6.13
	421568	W85858	Hs.99804	ESTs	6.13

435919	AI052189	Hs.114104	ESTs	6.13
417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	6.13
448946	AI652855	Hs.23363	hypothetical protein FLJ10983	6.13
432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.13
406857	AA613726	Hs.29797	ribosomal protein L10	6.11
417944	AU077196	Hs.82985	collagen, type V, alpha 2	6.11
425095	AW014160	Hs.182585	KIAA1276 protein	6.10
435756	AI418466	Hs.33665	ESTs	6.10
431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	6.10
413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	6.10
451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	6.10
450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	6.08
447832	AI433357		ESTs	6.08
434421	AI915927	Hs.34771	ESTs	6.08
437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	6.08
449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	6.08
415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	6.07
433339	AF019226	Hs.8036	glioblastoma overexpressed	6.06
435511	AA683336	Hs.189046	ESTs	6.06
423458	AI204212		ESTs	6.06
442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	6.06
457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	6.06
444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathi	6.06
455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	6.05
432925	AA878324	Hs.264750	ESTs	6.05
457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	6.05
449810	AB008681	Hs.23994	activin A receptor, type IIB	6.04
406797	AI432224		ribosomal protein L6	6.04
450157	AW961576	Hs.60178	ESTs	6.03
422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.03
407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-link	6.03
453331	AI240665		ESTs	6.03
430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	6.02
444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isom	6.01
409945	AW015935	Hs.122642	ESTs	6.00
419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	6.00
453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	6.00
430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	6.00

TABLE 52B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581 BE880923 BG390191 AW470082 AW014585 AI423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI422030 AI348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI215830 AI283836 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085455 BE551404 AA780704 AW008596 AI796964 AA917471 AI400531 AA668626 N72207 AI306482 AW440562 AI084687 AA347280 AA063536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI916336 AI350590 BF198106 AI433377 AI300638 AI672626 AI282741 AI351487 AW105544 AA973627 AW517914 AA715424 AA508454 BF334080 AI274618 AW367201 AW572619 AW469088 AA382095 AI368364 AI146934 AI357180 AI361181 BI911347 BI871044 AA136325 BF084010 BF084007 AA335788 AI920878 AA809614 BE932941 AI678261 C75308 AI148479 BE178174 W88513 BM013627 BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI918664 AW963196 C06195 AI678018 M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720095 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AI027260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723

5			AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE719915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 A190590 A1554403 A1392926 AU158477 BI467252 AU159919 A1760816 BF082516 A1439101 AA451923 A1340326 A1590975 B1791553 A1700963 A1142882 AA039975 AA946936 AA644381 BM314884 AA702424 A1417612 AW190555 A1220573 A1304772 A1270345 A1627383 AA552300 A1911702 AW166807 A1346078 W95070 AA149191 AA026864 A1830049 AW780435 A1078449 A1819984 A1858282 B1468588 A1860584 A1025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 A1927207 A1205263 BF082491 AW021347 A1568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 A1910434 BF082513 A1494069 A1270027 A1635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 B1762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 A1571075 BE067786 AV721320 A1022862 N29754 C03378 N84767 AA131077 H30146 BE714290 A1686869 A1568892 A1915596 AW105614 A1887258 A1538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 A1905927 BF992780 AW853812 BG954443 B1770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 B1089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 B1040941 AA337270 AW384371 AW847442 B1058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 A1284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 B1013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 A1948487 A1056685 BG399272 AA187835 BF821903 AV660550 AV660556 AV660502 BG564397 BE379584 BF446961 A1653056 AW973709 A1653173 BG054997 A1266043 B1054879 A1656750 A1492830 AW021142 A1472184 AW170056 A1082443 A1167921 D59940 B1492088 H74180 AW130886 A1348677 A1278577 AA761517 A1698203 AA115535 A1264790 AW205074 AA860452 AA554902 A1000715 D62102 BE544768 A1376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832 BC003047 S80794 NM_003405 X78138 AY007132 L08439 AW340648 AW131665 A1082748 A1470204 B1711078 BF350700 B1496963 A1087141 AA720684 AA862331 AA605146 BM313650 A1089749 A1359738 N69107 AW995424 A1086917 A1083995 AW340217 N99662 A1829449 A1089839 A1608761 A1342365 A1199076 AA908944 A1248943 A1160053 A1191245 A1218477 A1077943 AA864930 A1310394 AA872478 A1279782 W61343 AA565955 W46596 AA126874 AA223241 AA491574 R84813 AA491520 BG055114 A1469689 BE464590 AW664539 H67097 AL534332 C21397 A1085941 AW028427 BG939820 A1697089 A1039008 A1125315 A1655561 AW150042 L20422 X57345 A1458375 AU142852 B1666601 BE888276 AU119302 B1603754 BG705953 B1598754 BE296713 BG002538 BF951911 N29226 BE909424 AV698274 AV683116 AV708195 AA127798 A1124697 D54224 F08031 AA340253 BF923383 BM467808 B1546644 BG777200 BG705941 BG685777 AU127209 AW403970 B1597630 B1458091 AV689560 B1669267 BG506219 B1837163 B1667275 AA343750 BE783112 BF671405 BF954720 H67636 H69456 AA484894 B1869271 BF998207 N31547 BF945817 BF947918 N90630 BG980194 AA156681 B1493502 AW273118 A1473820 AA608688 A1359337 AV712091 AA084101 BF592036 H13301 A1864305 AA505883 A1423963 AW084401 A1917740 R69858 AA033631 N79982 BE885276 A1635674 AA096126 AA700018 AV707753 A1082545 A1145681 AA629032 A1421367 AA740589 AA150830 A1248541 AA988608 AA150478 W65437 BM310234 AA262704 T28031 A1811116 BM272753 H21979 T15405 AA938406 F04963 A1188296 AW152629 AA905196 BG223058 A1831016 A1766457 A1811102 AA776573 A1922133 AA775958 A1261476 AA219489 A1688035 A1872093 BE537084 AW189078 D82630 A1123121 AL583492 BE350791 R69901 W65436 BE155392 B1089081 BE155394 AL120538 AW166100 A1359620 A1174338 N20527 W47413 AA155615 A1272249 H52593 BE614558 H69864 AW383484 H78021 H11617 R56892 H23204 N21530 R82499 AW383522 AA774536 AL534331 W94127 W46459 A1866231 AA513281 AA192465 H69844 W85827 AW383642 AW383529 AA171496 AL537424 BE814866 BF823254 R82553 A1809817 A1559406 AK000357 A1571830 AA579613 AA668790 BF939495 BF196886 A1990982 BF591561 A1809189 AW410232 BF739769 A1144392 BF438721 A1707495 A1423359 N52503 BE855784 N94367 A1023931 AA563662 A1744624 A1221298 A1299523 A1299520 B1491312 A1452711 A1360730 AA622643 AW195955 AA470473 AW392767 A1218127 AA873430 AA906005 AA748160 H89523 AW020252 AW664988 AA970424 AA879079 A1581622 A1361357 AA468498 AW008694 AA903275 A1187724 A1187718 AA890505 BF092771 A1066655 BE714172 BG289028 AW080390 BE001197 BF132049
20	442562	39593_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 A1679751 A1873695 BG700891 B1553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 A1857643 A1768486 AW512118 AA479302 AW770384 AW072470 A1041596 A1049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 B1038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 A1693720 AA743364 A1915793 N48185 A1573107 AA043474 A1351615 A1969490 A1910763 R50866 A1699181 N73808 H08164 BM006551 AA367152 AW953705 A1631833 AW237429 AW027804 AA729038 BE503409 A1521935 BF739953 AA702982 AA557633 AA780065 A1218139 AW194264 D20120 A1082715 A1969980 BE857686 BE326711 AW953706 A1393749 A1383821 W67199 A1431759 A1796526 A1521794 A1796380 AW117545 A1749657 A1537634 N50122 AW973352 BF222929 AW016853 BF059130 A1651829 BE551767 AA558414 A1339359 BF059601 A1961162 A1341422 A1206248 A1206165 AA548736 AA768578 A1539081 AW025957 AA736837 N79575 AW594357 AA480892 AK055070 AK055612 AK000174 BG619806 BG108086 A1741949 A1004176 BF891936 BF378565 A197163 BE856860 BE245124 AW674411 AA490531 AW674981 AA740788 AW274758 BF512523 A1521278 AA548759 A1802431 AW051682 A1628247 A1799606 AW088103 AA236549 A1191529 AW273168 A1168451 AW073812 AW090611 AW003593 A1215845 A1799616 AW474940 AA954927 BM193740 AW662704 AW090127 AA969444 A1080438 AA552500 AW237538 AA481060 A1246378 AA565227 AA398921 AA207051 AA721378 BF438608 A1086295 A1886630 AA904112 A1864588 AW271985 AW078868 AA725342 BF326598 AA843572 A1082536 AA766664 A1453279 AA435673 A1619515 AA879080 AA234592 AA890223 AA766824 B1259822 AA393631 AW968840 BE940639 T83865 BE762742 AW897470 W05809 N41323 T87376 R68544 H88711 B1087136 AK074047 A1144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372 AA989341 A1824838 A1963970 A1637671 AW196330 BG427526 BM148789 BF893644 BF881946 BE177661 H06215 BE144709 BE144829 BE005398 AA628622 AA994155 AK001838 AU135179 AU134241 AV651702 AV650032 AV651304 AV650101 AV651263 AV651888 AV651866 AA628554 AV651355 AV651174 AV651172 AW856145 AU117599 A135386 BG254665 AA166919 BG483981 AW809606 BG494194 AA622811 A1676156 AA687804 A1701729 AU133725 AW961387 AU144387 AU151757 AA551031 BE675412 N34769 AA713483 A1890079 A1588918 A1361889 A1209020 AA668981 A1240990 AA741144 AA490899 A1200221 AW589574 W96201 BG154182 AV655159 AA328145 N36348 A1081357 N76715 AA693346 AA742488 A1269719 AA897483 A1886459 AU155873 H04255 AW243986 AA557749 A1286227 R68691 R33453 AW388097 AA947566 AA662701 AA633929 AA737415 BM475665 BE644917 AW770789 AW952971 N64863 BM263259 A1224545 A1184866 N69114 AW518902 A1440169 AA809472 AV654440 AA281642 AU185230 AW337382 A1872923 A1537113 N73882 T83378 H63731 BF671764 AW897824 A1811204 AA344646 BE009112 BG899664 H91240 R60548 N41701 BE072881 A1762181 BE072946 AL047596 AA393792 A1670731 A1037957 AW874364 A1038137 N62286 A1241379 BE501096 AW090696 A1927369 A1669226 A1369437 A1371075 AW612409 A1686711 A183289 AA477717 A1076122 AA635190 AA700984 AA781508 D81020 BF575223 A1356183 D79312 A1375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545 BF090249 AW954947 AW890487 A1305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 A1350279 AA879119 AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260 BG427950 AA826016 A1903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823 AW954733 AA315006 AW856665
25	413787	7612_1	
30			
35			
40	410143	MH1244_8	
45	450377	12109_1	
50	425996	138046_1	
55	427521	513212_1	
60	444060	6315_1	
65	409208	10117_2	
70	413497	1518002_1	
75	434280	1474904_1	
80	450139	34017_1	

438980	917280_1	AW502384 AA828822 AI982587
442495	928718_1	AI184717 AW518883 AF121173
425284	3834_5	BM476120 BE672181 AI697653 AA938187 AI280879 AW340123 AI912727 AI081775 AI089556 AI191349 AI871604 AI631607 AI890800 AI701917
5		AW771624 AA663041 AI991576 AI160622 AA771763 BE089784 BE089788 AI222942 AW18516 AA329211 AI095736 BE550294 AA738345
		BE218683 BE670548 BG149505 BF061776 D19821 BE005786 BE178892 BE005728 BF841237 BE005648 R27634
	441623	3362_1
		BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853
		AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424
10		AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448
		AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306
		AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522
		BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595
		BI094458 BE706702 BG496559 BF248373 BG494800
	445493	423456_1
	432666	144_7
15	430915	197844_1
	425913	4123_2
		AV703649 AW959818 AI582119 AI523459 AI674473 AW663543 AA825476 AI935231 BF742805 AA426156 AI253626 AA846477 AI024230
		BF221780 AI493027 AW006841 AA814699 H99650 AI088977 AA442691 AI783526 BF207915 AI752847 AA782635 AI978980 AA788634 BG119454
		BF678528 AI627829 BG993975 AV701283
20	438962	195763_1
	406870	0_0
	406819	0_0
	447197	2176805_1
	418336	58817_1
		AA075144
		AA908472
		R36075 R36167 AI366546
		AW969583 BI722505 BE179578 AI493714 AI937718 AA663709 BI868925 AW138743 AI911314 BE645538 BG911947 AI380325 AI265803 W56175
25	424677	2518_37
	419970	13569_1
		AI658779 AI675997 AW665991 AI459263 AW374413 BF898880 AW630959 BF875526 AW402206 BF818690 BF893068 AW504110 AW408049
		BG002913 AL530753 AI524064 AW769231 AA464970 AA293723 AI095051 AI953375 AI982938 BM146050 AW575804 AA962489 AI655426
		BM146046 T28538 BE241936 T89023 BI910963 AI416986 AI767111 AI422290 AW468260 BE676853 AI656771 AI961755 F04675 AA682826
		AA737606 BM194382 AA912021 AW183098 BE676682 AI962227 AI591366 AA621765 AA293724 R51642 F10194 BI909727 BF892632 AW950600
		AW950138 BG258587 BF892649 AI800647 BF892710 AA353176 BF894726 AA465038 BI040869 BI837749 BE244320 H18054 T74300 AW797026
		AA926790 F32814 AW751282 AI933994 AA578823 T78372 BF898986 BF882808 BF974969
35	451653	MH115364_1
		BG119563 AW975776 BG498478 BE245304 AW450934 BF508792 AA599489 AA599477 AI805268 AA055489 AI128758 AA761425 AA731858
		AI302271 BE219432 AA687294 AA018972 AW629429 Z45675 AW961626 T30940 R34554 T84712 BG986694
	436812	659779_1
40	412559	133853_1
		AW978773 AW298067 AA810101 AW194180 AA731645 AI906073
		BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969
		BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563
		AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317
		BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254
		W05240
45	433162	2167905_1
	434372	858779_1
	456629	207_22
		AI742311 AI025842 AA578843
		BG622121 AA631424 AA988296 AA631373
		AW891965 AW604749 BE080872 R15559 BE177623 AW883520 AW945343 AI246167 T07082 AW805679 W96278 AA135796 W32615 AW995418
		AW801688 BE003837 AW801621 AW385721 AW385742 AW385714 AW604757 W87409 AW604738 AW385757 AW580796 AW801247 BE003239
		BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW362791 AW604759 AW866589 AW604758 N44337 AI378548
		AW890438 AA077172 AI288683 AA229639 AA091945 AW945454 AA063629 AA702504 AW861938 AW894816 AW580841 AA094372 T06399
50		AW885686 BE244086 BE005035 AW861913 AA551773 AW858460 AW370926 AW754352 AW889695 AW384408 AI907428 BE067491 AW861939
		AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE067470 AW894935 BE082529 AI248911 BE179917 BE002200
		AW607506 AW392889 AW894560 AW381360 AI904206 AW863533 C00609 AW381372 BE082530 AW898120 BE075323 AW392799 AW601420
		AI695314 BE083790 AW858568 AW945550 BE177153 AW970506 BE350419 AI906919 AW360794 AI906917 AW885979 AW794240 AW945566
		AI688683 AI688694 AW009660 AW601421 AW360793 BE066524 BE083901 AW369847 AW381871 AW935435 AW664582 AW87775 AW838449
55		BE180466 AW858501 BE180464 AI371163 AA778231 AI174991 BE011720 AW877776 AW877800 AW877795 T19900 AW866365 AW989099
		BE011715 BE167842 BE011718 BE011724 AW363639 AW878658 AW878662 AW894887 BE082356 AW389211 AW804286 AW610312 AI904717
		AW610318 AW996909 AW610296 AW901923 AW880003 AI762171 AW062582 AW368713 AW062593 AW176663 AW842064 AW842089
		AW842095 AI243049 AW902074 AW062592 AW176684 AW751692 BE087703 AI907439 BE009686 BE172115 BE077030 AW608556 AW835577
		AI909628 BE077029 AW176241 BE077552 BE160370 BE160288 AW835656 AW606765 AW606770 AW835678 AW606758 AW606778 AI907484
60		BE172821 AW606768 AW99517 AW844165 BE171738 AW751683 AW610493 BE177484 BE177487 AW090510 AW844117 BE173367 AW998978
		AI124870 BE163472 AW841823 AW379762 AW893297 AI290296 BE089132 AA610287 AW176676 AW607622 BE172639 AW893232 AA329629
		BE089008 BE178350 BE178214 BE063291 AW820236 AW999653 BE089486 BE173126 BE171775 BE185787 AA558280 AI174840 AW999112
		BE218391 BE172734 BE178021 BE172738 BE173324 AW603494 AL036722 R38192 R60905 H53721 H41052 AL037917 R37795 AW998972
		AA767189 AW044272 H50689 AA768399 AA767764 AI087888 H44202 BE222792 N90597 W81396 N90615 AI935353 BE501168 F10945
65		AW118215 AI970480 AI627641 AW236081 AA574090 AI627652 AI681913 AI759983 N69591 N69276 BE467722 AW392780 BE172467 H92861
	430283	1418_1
		AI524921 F02989 Z39328 F02705 F01414 T88678 AI215165 H87220 AW374781
		BC013728 BI084032 BF090365 BE410706 N36391 W80436 BF813124 R90857 R62778 H00591 H02329 AA355285 AK008826 BC008721
		BG744004 BG479141 BG823656 BG479061 AU121103 AU138176 BG702567 BI599840 BG422775 BG700944 BE280747 AU138529 BE269929
70		BG704110 AU123329 AU122058 AU138135 BG723106 BG722291 BG831041 BG705239 BE740517 BE207133 BE252867 AU139772 BG714385
		BF568538 BE304393 BF971755 BE267965 BE272012 AU135396 AU124535 BI551682 BG700612 AI815488 BG475195 BE388273 BE391517
		BM148991 BF929247 AV653435 AW250299 AW249189 BF093150 BF093173 AW205325 BF057101 BF000551 AI341108 AL162009 AK026136
		BE907957 W73238 BI711467 BG926027 AI816428 AA837518 AI754405 BG179142 AA481485 AW023435 BE855747 AI885101 N52163 AI016096
		AI090204 BE677045 AI523320 AI126855 N26501 AA043680 AA976459 AI039590 AI937917 AI361000 W94866 AI375797 AI079801 AI168236
75		AA599882 AA084368 AI342635 AI190294 N26093 AI085234 AI298169 BF939715 AI223164 H98704 BE218925 N29394 AI918735 N41520 AI147784
		AI918796 AA854317 N22193 AA199850 AI149728 AA121263 AI051074 AA565116 AI097349 N22209 AA552917 N33151 D52422 BF477483
		AA476599 AA525787 AI279198 D53353 AA738063 AA558406 BI496334 AA999948 AA425847 BI496335 AA909624 BF197591 AW023259 AI652819
80		T311424 AA088213 T31115 AI206650 AA976796 AI948989 AW248762 AA449265 AA290687 AI682521 AA310227 Z38743 AA935369 AW119141
		BF941087 AI470657 AI349451 AW079338 D45665 N21640 T30071 AI446705 R60220 BE833481 R49680 R70049 R41223 R32402 R69984 R70111
		BM476906 BE293615 BE382443 BF155692 BE720638 BE931983 BE720594 BF085890 AA336953 BF081638 AA359915 AA384116 AA360142
		BI667664 BG823235 BE315559 BE301958 BE891114 BG826267 BE253680 BG979094 AV722757 N67629 BG997927 BI915769 BG680692 R62777
		BE251116 H56358 AW369586 BG677759 BI044604 R75787 BE770960 H69529 R69983 AA259238 R97827 AA310379 W01103 AI873384
		AL554578 BF038102 H87182 H87517 H01574 T52573 N28881 AA301397 T92375 R68401 AW800466 AI268172 BE876949 D54019 AI909769
		AW798415 BI222383 AI393171 CI5260 N26959 H17129 T53095 T52494 R68602 AI364765 BF687869 AI817035 AW105354 BE293820 H14206
		BI093066 C14063 AL534349 BE255883 BE254098 AA428399 AW579360 AW579381 N53144 D60748 D54020 BG292106 H96705 D52423 T36174

			D54161 R73016 D55021 B1857200 H83444 B1016954 D54163 R15563 B1818664 BE152207 B1048502 BF885667 BE613212 BE165773 BF149332 AW607045 BE305200 AW972830 AA489820 AA527647 AA570362 BE739425 AA514221 AA865491 A1828293 AA470456 A1276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 A1432496 A1470335 A1247243 BG533994 AA513783 A1887309 AA528036 AW972006 AW873028 A1924914 A1818810 AW152378 AW084946 A1521413 A1669583 BE932521 A1581370 BE180238 AW089750 AW771461 AW089714 A1590949 A1819148 AA731056 BF815234 BF911506 AA235803 AA485373 A1735658 AW393133 AW073080 A1707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 A1807430 A1676072 AA837010 A1452482 A1625817 AW241750 BE048616 A1290928 A1680714 AA485530 BE175687 AV648513 AW130312 A1000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 A1244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658871 BG678060 A1565004 AW819026 BE843092 AV686437 AV723049 BG616948 A1911647 A1743490 A1091096 BE857251 A1962074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE006682 BF342375 AA903144 BF338083 BF984258 AV657996 A1749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BM469076 AA533027 A1127512 A1368802 AA533141 AA700560 AW576028 A1610851 A1435361 BM129172 AW474544 BM128899 A1814292 AW502039 AA531243 BF941858 AW502037 AA702337 A1419854 AA662755 AA934364 A1300510 A1291136 AA505263 A1144527 A1076919 A1633534 A1242473 AA938561 BG055372 AA512894 A1671356 AA962403 BF808010 AA663911 AA847056 AA513301 AA369069 AA377265 BG291206 AA402298 AA885766 AW801002 AA302290 A1305842 AW800873 AA302492 AA478427 A1817291 AW801104 AW801028 AA865744 BF155979 A1374743 AA478431 A1159846 A1369757 A1800672 BF435788 AA255451 A1937707 AW006198 A1280363 BF062434 AW801115 A1919181 F28413 W04214 AW152380 AW901567 AW901570 AA886371 AA384251 A1302846 BE701902 AA931606 H42673 R33703 AW901556 AA009816 AW901568 AW352200 AA256558 H15928 B1087170 AW800530 AA369068 N98562 H28652 N34644 H97650 H00956 W70039 A1142831 AA009817 F37136 N70289 AA531347 R72374 H27488 R66605 A1433540 AA804981 AA728984 BG015794 BE158357 BE158353 BE158358 BE158360 BE158352 BE158351 BE158355 BC022881 AU150944 BG750783 AW754175 AW857737 A1911659 A1050036 AA554053 A1826259 AA568548 A1732997 AA977633 AA865818 M18728 AW088535 A1889321 AA954221 A1337552 R42581 AW194670 AA064862 AW001147 AA864374 AA630699 AW276176 AA676615 AA857965 A1625428 AA580792 AA582038 AA581668 AA658065 AA828156 AA857160 AA936103 A1149335 AA936925 AA581684 AA954198 AW238461 A1281504 A1265812 AA583267 AW236162 AA876535 AW304286 AW474334 A1559415 A1589241 A1660952 AA641137 A1431696 A1688844 AA552513 AA564954 AW090553 A1205612 A1245753 AA954883 AA947909 A1866014 AW971213 AA493925 AA493567 AA876839 AA934462 A1628543 A1433357 AW772732 B1918168 AW779760 N48674 A1375997 AA235370 BG699146 A1913631 A1498402 A1016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 A1203107 R35004 F07491 R25094 R35360 BC018070 BG702493 A1204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539 BG215094 BG198867 BG196332 BG208220 BG212418 BG216963 BG164885 BG213710 BG204771 BG193014 BG197556 BG217481 BG198185 BG183594 B1596425 AA115605 A1589156 BF439839 BG188832 A1359615 BG190473 A1024233 BF439574 AW118065 A1672797 AA610042 BG212008 A1204382 R70913 AA033534 AA781036 A1627278 AA307285 AA034218 BG482749 AW162429 B1602460 AA721969 AA476516 AA476416 AA903019 BF110864 AA307286 AA115471 AW964555 AA423826 AA115129 A1419107 A1432224 AW276890 A1499346 AA937014 AA653573 A1318525 A1246219 AA961591 A1270640 BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 B1057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 A1161014 AA099554 BG572534 A1803329 A1809932 A1808765 AA411449 A1378760 AA976929 A1378620 AA909684 R75632 A1360919 A1350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 A1204665 BF989591 B1056086 BG001590 BF107035 BE219720 BF475241 A1571723 BE219848 B1789268 A1224899 AA724864 AW771467 AA480255 AW845616 A1440295 H52800 BE218790 A1681575 AW300064 AW262133 H21568 A1363015 A1884914 H86948		
	430968	1237115_1			
5	444207	9172_3			
10					
15	418905	517_1			
20					
25	436716	2472838_1			
	413703	376077_1			
	432586	6633_1			
	440129	2607882_1			
	406685	0_0			
	406806	0_0			
30					
	431155	1235742_1			
	447832	1036795_1			
	449625	249224_1			
35					
	423458	30480_1			
	455263	26143_1			
40					
	406797	0_0			
	453331	16559_1			
45					
	430504	5477_6			
50					
	TABLE 52C				
	Pkey:	Unique number corresponding to an Eos probeset			
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.			
55	Strand:	Indicates DNA strand from which exons were predicted.			
	NL_position:	Indicates nucleotide positions of predicted exons.			
	Pkey	Ref	Strand	NL_position	
60	402474	7547175	Minus	53526-53628,55755-55920,57530-57757	
	402145	8018280	Plus	113086-114800	
	401091	9958240	Plus	94760-94898	
	401466	6682292	Plus	28748-29023	
	406542	7711499	Plus	117335-118473	
	401113	9966541	Minus	19419-19959	
65	405086	8072509	Plus	73664-73841,74081-74217,74610-74779,7492	
70					
	TABLE 53A:				
	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
75	R1:	Ratio of testicular cancer (non-seminomatous and seminomatous) compared to normal adult tissues			
	Pkey	ExAccn	UnigenelD	Unigene Title	R1
80	432666	AW204069		ESTs, Weakly similar to unnamed protein	78.20
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	75.45
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	58.80
	432730	A1066520	Hs.131358	ESTs	51.80
	450581	AF081513	Hs.25195	TGF-beta 4	48.40

	426534	U58096	Hs.2051	testis specific protein, Y-linked	44.05
	423458	AI204212		ESTs	36.60
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	34.65
	420367	AA259090	Hs.257028	ESTs	32.60
5	451106	BE382701	Hs.25960	N-MYC oncogene	30.10
	437052	AA861697	Hs.120591	ESTs	29.35
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	29.05
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	28.45
10	420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	28.25
	407710	AW022727	Hs.23616	ESTs	26.86
	448981	AI968719	Hs.195387	ESTs	26.40
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	25.55
	420528	AF130728	Hs.98586	doublesex and mab-3 related transcriptio	25.10
15	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	23.70
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.95
	454077	AC005952	Hs.37062	insulin-like 3 (Leydig cell)	21.73
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	20.15
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	19.65
	424578	AK001973	Hs.150890	hypothetical protein	19.16
20	427335	AA448542	Hs.251677	G antigen 7B	19.05
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	18.95
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	18.86
	449322	AI638616	Hs.196566	ESTs	18.30
25	430691	C14187	Hs.157208	aristless-related homeobox protein ARX	18.00
	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (	17.96
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	17.41
	418756	AA252254	Hs.226949	ESTs	17.20
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	16.20
30	447534	AW953935	Hs.288655	ESTs	16.04
	407122	H20276	Hs.31742	ESTs	15.95
	446979	AI654443	Hs.197683	ESTs	15.90
	406547			Target Exon	15.70
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.65
35	456847	AI360456	Hs.37776	ESTs	15.50
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	15.00
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	14.95
	408908	BE296227	Hs.250822	serine/threonine kinase 15	14.65
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	14.20
40	422828	AL133396		prion protein 2 (dublet)	14.08
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	14.05
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	14.05
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	13.90
	418134	AA397769	Hs.86617	ESTs	13.85
45	454438	AA224053	Hs.172405	cell division cycle 27	13.70
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	13.40
	426427	M86699	Hs.169840	TTK protein kinase	13.35
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	13.20
	419384	AA490866	Hs.39429	ESTs	13.10
50	418477	AW022983		gb:df46h12.y1 Morton Fetal Cochlea Homo	12.85
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	12.80
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.78
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	12.72
	443068	AI188710		ESTs	12.65
55	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	12.60
	420401	AK001907	Hs.97464	hypothetical protein	12.50
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	12.50
	413494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	12.45
	406937	U14622		gb:Human transketolase-like protein gene	12.25
60	439451	AF086270	Hs.278554	heterochromatin-like protein 1	12.10
	404996			Target Exon	11.86
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	11.85
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	11.60
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	11.55
65	421241	X91817	Hs.102866	transketolase-like 1	11.50
	414972	BE263782	Hs.77695	KIAA0008 gene product	11.45
	426866	U02330	Hs.172816	neuregulin 1	11.37
	433159	AB035898	Hs.150587	kinesin-like protein 2	11.35
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	11.24
70	440207	AI371978	Hs.128326	ESTs	11.12
	407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	11.10
	450142	AW207469	Hs.24485	chondroitin sulfate proteoglycan 6 (bama	11.05
	449576	AW014631	Hs.225068	ESTs	10.95
	414251	AL042306	Hs.97689	VASA protein	10.95
75	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	10.90
	436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Su	10.85
	427521	AW973352		ESTs	10.81
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	10.80
	442832	AW206560	Hs.253569	ESTs	10.62
80	436899	AA764852		ESTs	10.60
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	10.55
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	10.45
	435206	AI432364	Hs.160594	ESTs	10.15
	433975	AA971953	Hs.122055	ESTs	10.10



	446791	AI632278	Hs.195922	ESTs	10.05
	422232	D43945	Hs.113274	transcription factor EC	10.00
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	9.71
5	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	9.50
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.44
	438188	AA779975	Hs.128859	ESTs	9.30
	418973	AA233056	Hs.191518	ESTs	9.25
	413627	BE182082	Hs.246973	intron of Bicaudal D homolog 1	9.25
10	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.15
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	9.11
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	9.08
	426518	Z43039	Hs.170198	KIAA0009 gene product	9.05
	440968	N36327		gb:yx82b06.r1 Soares melanocyte 2NbHM Ho	9.05
15	440952	AI291804	Hs.118101	ESTs	9.05
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	9.05
	442618	R56222	Hs.26514	ESTs	8.96
	419423	D26488	Hs.90315	KIAA0007 protein	8.95
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	8.80
20	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	8.76
	444971	AI651116	Hs.148659	ESTs	8.75
	436513	AJ278110	Hs.125507	DEAD-box protein	8.60
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.59
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.58
25	428847	AI954833	Hs.98881	ESTs	8.57
	408465	AW196940	Hs.253277	ESTs	8.54
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	8.53
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	8.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.50
30	450480	X82125	Hs.25040	zinc finger protein 239	8.50
	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	8.42
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	8.35
	430835	AI240006	Hs.192326	ESTs	8.33
35	416859	H43437	Hs.80305	hypothetical protein MGC14258	8.30
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	8.26
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	8.25
	449260	AA741180	Hs.29879	ESTs	8.25
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	8.18
40	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	8.17
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	8.14
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.14
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.03
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	7.98
45	410420	AA224053	Hs.172405	cell division cycle 27	7.90
	453878	AW964440	Hs.19025	DC32	7.75
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	7.66
	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	7.65
	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	7.65
50	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	7.65
	451950	AW292317	Hs.213307	ESTs	7.60
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	7.59
	435514	AW592804		ESTs	7.55
	431041	AA490967	Hs.197955	KIAA0704 protein	7.55
55	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.51
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	7.38
	409421	AA199883	Hs.67624	ESTs	7.35
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	7.35
	458570	AW971698	Hs.12627	TJ6 protein	7.30
60	441287	AW293132	Hs.131373	ESTs	7.30
	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	7.25
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.25
	441425	AA933590	Hs.28937	homeobox protein from AL590526	7.25
	446293	AI420213	Hs.149722	LIM domain transcription factor LIM-1 (h	7.21
65	414136	AA812434		SMC2 (structural maintenance of chromoso	7.20
	409089	NM_014781	Hs.50421	KIAA0203 gene product	7.19
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.18
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	7.15
	452226	AA024898	Hs.157103	ESTs	7.15
	435918	AF263538	Hs.86232	growth differentiation factor 3	7.14
70	418661	NM_001949	Hs.1189	E2F transcription factor 3	7.10
	436360	AI962796	Hs.156100	ESTs	7.10
	442950	AI500417	Hs.46764	ESTs	7.00
	415684	D59356		sorbitol dehydrogenase	7.00
75	448336	R53848	Hs.44976	ESTs	7.00
	453183	AW086185	Hs.223856	ESTs	7.00
	444434	NM_004849	Hs.11171	APG5 (autophagy 5, S. cerevisiae)-like	6.95
	422665	AJ011812	Hs.119018	transcription factor NRF	6.95
	437421	AA917062		ESTs	6.95
80	428916	AF003001	Hs.194562	telomeric repeat binding factor (NIMA-in	6.94
	408045	AW138959	Hs.245123	ESTs	6.90
	448588	AI970276	Hs.156905	KIAA1676	6.89
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	6.85
	439780	AL109688		gb:Homo sapiens mRNA full length insert	6.85

	449911	AI262106	Hs.12653	ESTs	6.85
	417791	AW965339	Hs.111471	ESTs	6.80
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
5	453160	AI263307		H2B histone family, member L	6.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.75
	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.73
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	6.70
	418379	AA218940	Hs.137516	fidgetin-like 1	6.70
10	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	6.70
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	6.69
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	6.66
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	6.65
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	6.65
15	433247	AB040948	Hs.142856	KIAA1515 protein	6.65
	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	6.65
	417886	AA214584		ESTs	6.64
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	6.62
	412537	AL031778		nuclear transcription factor Y, alpha	6.61
20	426614	AA411925	Hs.301960	ESTs	6.57
	457465	AW301344	Hs.122908	DNA replication factor	6.52
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	6.50
	440801	AA906366		ESTs	6.50
	453116	AI276680	Hs.146086	ESTs	6.50
25	436909	AA907120		ESTs	6.50
	402199			Target Exon	6.50
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	6.46
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	6.41
	438494	AA908678	Hs.130183	ESTs	6.41
30	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	6.40
	408758	NM_003686	Hs.47504	exonuclease 1	6.40
	442671	AI005668	Hs.130673	EST	6.40
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.38
	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.35
35	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	6.33
	441878	AI801869	Hs.127982	ESTs	6.31
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	6.31
	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	6.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	6.30
40	421650	AA781795	Hs.122587	ESTs	6.30
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.28
	408291	AB023191	Hs.44131	KIAA0974 protein	6.26
	438180	AA808189	Hs.272151	ESTs	6.25
	412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	6.25
45	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	6.20
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	6.20
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	6.18
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	6.12
	426223	AW977812	Hs.130391	ESTs	6.10
50	445038	AI635444	Hs.143917	dJ467N11.1 protein	6.10
	419197	N48921	Hs.27441	KIAA1615 protein	6.09
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	6.05
	436902	AW247145	Hs.192729	ESTs	6.05
	429228	AI553633		ESTs	5.99
55	457065	AI476318	Hs.192480	ESTs	5.90
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	5.90
	449132	BE045641	Hs.197573	ESTs	5.90
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.89
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	5.85
60	457289	AW573204	Hs.137078	ESTs	5.85
	433849	BE465884	Hs.280728	ESTs	5.85
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	5.85
	438450	AI050866	Hs.65853	nodal, mouse, homolog	5.81
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	5.80
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	5.77
65	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.77
	408460	AA054726	Hs.285574	ESTs	5.75
	442461	AW062564	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	5.75
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
	428249	AA130914	Hs.183291	zinc finger protein 268	5.74
70	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (	5.72
	402145			Target Exon	5.71
	447178	AW594641	Hs.192417	ESTs	5.70
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	5.65
75	442980	AA857025	Hs.8878	kinesin-like 1	5.65
	419131	AA406293	Hs.109526	ESTs	5.60
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor;	5.60
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
80	440553	AA889416	Hs.344043	Homo sapiens cDNA FLJ14459 fis, clone HE	5.58
	442333	AI650877	Hs.129302	ESTs	5.58
	453941	U39817	Hs.36820	Bloom syndrome	5.57
	415799	AA653718	Hs.225841	DKFZP434D193 protein	5.57
	413623	AA825721	Hs.246973	intron of Bicaudal D homolog 1	5.55

	427147	AA398587	Hs.97414	ESTs	5.55
	451050	AW937420		ESTs	5.55
	450113	AI683098	Hs.200866	ESTs, Moderately similar to ALU7_HUMAN A	5.54
5	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	5.54
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisoqu	5.53
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransferase 3 be	5.51
	449592	AI655494	Hs.195718	ESTs	5.50
	445517	AF208855	Hs.12830	hypothetical protein	5.50
10	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ara	5.48
	430044	AA464510	Hs.152812	ESTs	5.47
	437036	AI571514	Hs.133022	ESTs	5.47
	423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	5.46
	409103	AF251237	Hs.112208	XAGE-1 protein	5.45
15	420900	AL045633	Hs.44269	ESTs	5.45
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.45
	440738	AI004650	Hs.225674	WD repeat domain 9	5.45
	412723	AA648459	Hs.335951	hypothetical protein AF301222	5.45
	441122	H56777	Hs.121084	eppin-3	5.42
20	414151	AW976468	Hs.257245	ESTs	5.40
	435663	AI023707	Hs.134273	ESTs	5.40
	448986	H42169	Hs.347310	hypothetical protein FLJ14627	5.39
	433701	AW445023	Hs.15155	ESTs	5.39
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	5.35
25	440842	AA907288	Hs.130173	ESTs	5.35
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	5.34
	401837			NM_025109:Homo sapiens hypothetical prot	5.32
	423739	AA398155	Hs.97600	ESTs	5.31
	424315	AW614850	Hs.193384	putative 28 kDa protein	5.31
30	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.30
	415717	AA167270	Hs.130435	ESTs	5.30
	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	5.26
	427119	AW880562	Hs.272525	ESTs	5.25
	432117	AL036195	Hs.2909	protamine 1	5.24
35	446837	AW273055	Hs.156598	ESTs	5.23
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	5.21
	422797	AB033064	Hs.236463	KIAA1238 protein	5.19
	446258	AI283476	Hs.263478	ESTs	5.18
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	5.17
40	445413	AA151342	Hs.12677	CGI-147 protein	5.17
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	5.16
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.15
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	5.15
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	5.15
45	448038	AW015073	Hs.232026	ESTs, Weakly similar to RO52_HUMAN 52 KD	5.15
	430272	X04898	Hs.237658	apolipoprotein A-II	5.14
	422094	AF129535	Hs.272027	F-box only protein 5	5.13
	420424	AB033036	Hs.97594	KIAA1210 protein	5.13
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	5.10
50	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	5.10
	453448	AL036710	Hs.209527	ESTs	5.10
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	5.06
	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	5.05
55	427961	AW293165	Hs.143134	ESTs	5.05
	441553	AA281219	Hs.121296	ESTs	5.05
	429999	AI761902	Hs.99597	ESTs	5.04
	426496	D31765	Hs.170114	KIAA0061 protein	5.02
	410929	H47233	Hs.30643	ESTs	5.01
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	5.01
60	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	5.00
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.00
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	5.00
	407568	AA740964	Hs.62699	ESTs	5.00
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!!	5.00
65	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	5.00
	416350	AF188625	Hs.189507	phospholipase A2, group IID	4.99
	452197	AW023595	Hs.232048	ESTs	4.98
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.97
70	403780			C4001759:gi 133250 sp P19474 RO52_HUMAN	4.97
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	4.95
	418894	W73921	Hs.50743	ESTs	4.95
	426623	AA382826	Hs.132793	ESTs	4.95
	443537	D13305	Hs.203	cholecystokinin B receptor	4.94
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.94
75	453716	AA037675	Hs.152675	ESTs	4.90
	402299			Target Exon	4.90
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	4.89
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.87
80	409066	AA062980	Hs.66960	ESTs	4.85
	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.85
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
	450375	AA009647		a disintegrin and metalloproteinase doma	4.85
	416201	AA467752	Hs.195161	ESTs	4.85
	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1126 (f	4.84

5	423198	M81933	Hs.1634	cell division cycle 25A	4.82
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.81
	418971	AA360392	Hs.87113	ESTs	4.80
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.80
	409517	X90780		troponin I, cardiac	4.80
10	424322	AL157491	Hs.145211	Homo sapiens mRNA; cDNA DKFZp434K1111 (f	4.80
	443169	AI038687	Hs.133338	ESTs	4.80
	438624	AA889055	Hs.123468	ESTs	4.79
	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	4.76
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.76
15	443715	AI583187	Hs.9700	cyclin E1	4.76
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	4.75
	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	4.71
	444431	AW513324	Hs.42280	Homo sapiens, clone MGC:9010, mRNA, comp	4.71
	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	4.71
20	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	4.70
	447175	AI365208	Hs.293606	ESTs	4.70
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.69
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	4.68
	416445	AL043004	Hs.79337	KIAA0135 protein	4.66
25	429652	AA766810	Hs.259290	ESTs	4.65
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	4.65
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	4.64
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.62
	427298	AA400495		ESTs	4.62
30	412863	AA121673	Hs.59757	zinc finger protein 281	4.62
	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	4.61
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.60
	446751	AA766998	Hs.79126	Human DNA sequence from clone RP11-16L21	4.60
	432656	NM_000246	Hs.3076	MHC class II transactivator	4.60
35	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	4.60
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 leratoca	4.60
	421830	AA789269	Hs.122509	ESTs, Weakly similar to dJ1018D12.3 [H.s	4.59
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	4.58
	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	4.58
40	431721	AB032996	Hs.268044	KIAA1170 protein	4.55
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.55
	453529	AA036729	Hs.335639	ESTs	4.55
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.55
	444386	BE065183		gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.55
45	428976	AL037824	Hs.194695	ras homolog gene family, member i	4.55
	449510	AI653154	Hs.328147	ESTs	4.55
	414725	AA769791		ring finger protein 21, interferon-respo	4.54
	424153	AA451737	Hs.141496	MAGE-like 2	4.53
	414466	AA349211	Hs.76205	cytochrome P450, subfamily XIA (choleste	4.52
50	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	458443	AV647010	Hs.27	glycine dehydrogenase (decarboxylating;	4.48
	453289	AI188161	Hs.144627	ESTs	4.48
	433641	AF080229		gb:Human endogenous retrovirus K clone 1	4.45
	440196	N72847	Hs.125221	ESTs	4.45
55	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.45
	428855	AI435901	Hs.89563	nuclear cap binding protein subunit 1, 8	4.45
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	4.45
	442240	AI791883	Hs.292719	ESTs	4.45
	421917	AB028943	Hs.109445	KIAA1020 protein	4.45
60	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	4.44
	449676	AW380579	Hs.209657	ESTs	4.43
	433183	AF231338	Hs.222024	transcription factor BMAL2	4.40
	439314	AA382413	Hs.178144	ESTs	4.40
	425312	AA354940	Hs.145958	ESTs	4.39
65	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.39
	430444	AW296421	Hs.121035	ESTs	4.35
	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.35
	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.34
	418216	AA662240	Hs.283099	AF15q14 protein	4.32
70	450351	BE547267	Hs.59791	hypothetical protein MGC13183	4.32
	454073	AW206286	Hs.116727	ESTs	4.30
	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	4.30
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.30
	448877	AI583696	Hs.253313	ESTs	4.28
75	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.27
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	4.25
	430292	AK000634	Hs.238270	hypothetical protein FLJ20627	4.25
	427778	AA412323	Hs.105323	ESTs	4.25
	418768	T39310		gb:ya04a09.r2 Stratagene lung (937210) H	4.25
80	409268	AA625304		ESTs	4.25
	442010	AI032680	Hs.132213	ESTs	4.24
	452807	AA028933	Hs.162434	ESTs	4.23
	401435			C14000397*:g[i]7499898[pir][T33295 hypoth	4.23
	447519	U46258	Hs.339665	ESTs	4.21
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.21
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	4.20
	453909	AW004045	Hs.203365	ESTs	4.20

5	431126	AF085243	Hs.283619	zinc finger protein 236	4.20
	429628	H09604	Hs.13268	ESTs	4.20
	415989	AI267700		ESTs	4.20
	421373	AA808229	Hs.46677	ESTs	4.20
	433979	AA620999		gb:ag03a08.s1 Soares_testis_NHT Homo sap	4.20
10	408321	AW405882	Hs.44205	cortistatin	4.19
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.17
	430335	D80007	Hs.239499	KIAA0185 protein	4.17
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	4.16
	438885	AI886558	Hs.184987	ESTs	4.15
15	451578	NM_016323	Hs.26663	cyclin-E binding protein 1	4.15
	432446	AA542845	Hs.294088	GAJ protein	4.13
	445076	AI206888	Hs.154131	ESTs	4.11
	420218	AW958037		ribosomal protein L4	4.10
	453628	AW243307	Hs.83937	hypothetical protein	4.10
20	418459	R85436	Hs.268814	ESTs	4.10
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.08
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	4.06
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.06
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	4.05
25	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	4.05
	449687	W68520		intermediate filament protein syncoilin	4.05
	452109	AI526873	Hs.61164	hypothetical protein FLJ14909	4.05
	401464			histone deacetylase 5	4.05
	444670	H58373	Hs.332938	hypothetical protein MGC5370	4.05
30	415884	H22966	Hs.13471	ESTs	4.05
	442066	BE502147	Hs.128418	ESTs	4.04
	402098			ENSP00000217725*:Laminin alpha-1 chain p	4.02
	404287			FGENESH predicted novel CUB-domain conta	4.01
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	4.01
35	449704	AK000733	Hs.23900	GTPase activating protein	4.00
	445685	AW779829		gb:hn88a05.x1 NCI_CGAP_Kid11 Homo sapien	4.00
	444379	N99035	Hs.30352	ESTs	4.00
	435373	AW665538	Hs.117689	ESTs	4.00
	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	4.00
40	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	4.00
	418648	AW979223	Hs.292478	ESTs	4.00
	446074	AA079799	Hs.343103	hypothetical protein FLJ11896	4.00
	447353	AI375701	Hs.25884	ESTs	4.00
	410100	AA081636	Hs.271916	ESTs, Weakly similar to S41044 chromosom	4.00
45	428856	AA436735	Hs.183171	hypothetical protein FLJ22002	4.00
	445140	AI650599	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
	406367			NM_022357:Homo sapiens putative metallop	3.99
	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	3.99
	453985	N44545	Hs.251865	ESTs	3.98
50	408446	AW450669	Hs.45068	hypothetical protein DKFZp4341143	3.97
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	3.97
	414713	BE465243	Hs.12664	ESTs	3.96
	426067	AW664691	Hs.97053	ESTs	3.96
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 utinu	3.96
55	456479	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo	3.95
	451865	H43737	Hs.33186	ESTs, Weakly similar to unknown protein	3.95
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	3.95
	445730	AI624342	Hs.179082	ESTs	3.95
	451993	AA765776	Hs.122983	ESTs	3.95
60	428819	AL135623	Hs.193914	KIAA0575 gene product	3.92
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	3.91
	420812	AA715303	Hs.107369	ESTs	3.90
	423806	AA331247	Hs.86617	ESTs	3.90
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	3.90
65	449211	AI922972	Hs.196073	ESTs	3.90
	409757	NM_001898	Hs.123114	cystatin SN	3.90
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	3.89
	432512	NM_003284	Hs.3017	transition protein 1 (during histone to	3.89
	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	3.88
70	449099	AI629041	Hs.46908	ESTs	3.88
	408092	NM_007057	Hs.42650	ZW10 interactor	3.85
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	3.85
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.84
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.83
75	433023	AW864793		thrombospondin 1	3.82
	452571	W31518	Hs.34665	ESTs	3.81
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protei	3.80
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.80
	420697	AA827705	Hs.26605	ESTs	3.80
80	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	3.80
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.80
	411856	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	3.80
	449529	AI990559	Hs.232033	ESTs	3.80
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	3.78
	444656	AI277924	Hs.145199	ESTs	3.77
	448674	W31178	Hs.154140	ovary-specific acidic protein	3.77
	415829	AW450198	Hs.163742	ESTs	3.76

	436188	AK001049	Hs.48712	hypothetical protein FLJ20736	3.75
	402178			C19001998*:gil6453813 ref NP_008926.2  b	3.75
	418179	X51630	Hs.1145	Wilms tumor 1	3.75
5	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.75
	429063	AW363845	Hs.322903	ESTs, Weakly similar to A46010 X-linked	3.75
	437440	AA846804		ESTs	3.75
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associate	3.74
	438456	AA913381	Hs.20594	ESTs	3.73
	418821	AA436002	Hs.183161	ESTs	3.73
10	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.73
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.71
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	3.70
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	3.70
	414206	AW276887	Hs.46609	ESTs	3.70
15	427761	AA412205	Hs.140996	ESTs	3.69
	428728	NM_016625	Hs.191381	hypothetical protein	3.68
	452631	AI188658	Hs.87496	ESTs	3.68
	427719	AI393122	Hs.134726	ESTs	3.68
20	431869	AA521136	Hs.190176	ESTs	3.67
	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.67
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.66
	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.66
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.65
25	456030	AA136106	Hs.184852	KIAA1553 protein	3.65
	402408			NM_030920*:Homo sapiens hypothetical pro	3.65
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	3.65
	416608	R11499	Hs.189716	ESTs	3.65
	417553	L09190		trichohyalin	3.65
30	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.65
	431077	AI669133	Hs.115660	hypothetical protein FLJ12810	3.64
	452461	N78223	Hs.108106	transcription factor	3.60
	437660	W31708	Hs.55304	ESTs	3.60
	420552	AK000492	Hs.98806	hypothetical protein	3.60
35	419926	AW900992	Hs.93796	DKFZP586D2223 protein	3.59
	420161	AI683069	Hs.120817	ESTs	3.59
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.59
	449571	AW016812	Hs.200266	ESTs	3.56
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	3.55
40	441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein	3.55
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	3.55
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.55
	437700	AA766060	Hs.301209	myeloid/lymphoid or mixed-lineage leukem	3.55
	438176	AW138970	Hs.122113	ESTs	3.55
	453062	AW207538	Hs.61603	KIAA1677	3.55
45	447064	AB002350	Hs.17262	KIAA0352 gene product	3.55
	430056	X97548	Hs.228059	KRAB-associated protein 1	3.54
	418049	AA211467		Homo sapiens, Similar to nuclear localiz	3.54
	434288	AW189075	Hs.116265	fibrillin3	3.54
50	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	3.52
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.52
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	3.52
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	3.51
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.50
55	449467	AW205006	Hs.197042	ESTs	3.50
	405935			Target Exon	3.50
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	3.50
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.50
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.49
60	429183	AB014604	Hs.197955	KIAA0704 protein	3.49
	428878	AA436884	Hs.48926	ESTs	3.49
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.49
	435068	H16262	Hs.31415	ESTs	3.48
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.48
65	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.48
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.48
	406542			C19000728*:gil12585552 sp Q9Y2Q1 Z257_HU	3.47
	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.46
	402099			ENSP00000217725*:Laminin alpha-1 chain p	3.45
70	418826	AK000375	Hs.88820	HDCMC28P protein	3.45
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	3.45
	427617	D42063	Hs.199179	RAN binding protein 2	3.45
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.45
	400288			NM_003292:Homo sapiens translocated prom	3.45
75	443596	AW026048	Hs.134124	ESTs	3.45
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	3.45
	416031	T30290	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	3.45
	435244	N77221	Hs.187824	ESTs	3.45
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.45
80	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.45
	420686	AI950339	Hs.40782	ESTs	3.44
	429467	NM_004477	Hs.203772	FSHD region gene 1	3.43
	448769	N66037	Hs.38173	ESTs	3.43
	423453	AW450737	Hs.128791	CGI-09 protein	3.41

	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.41
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.41
	404068			Target Exon	3.40
	401644			Target Exon	3.40
5	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	3.40
	452907	BE256966	Hs.31652	ESTs, Moderately similar to I54374 gene	3.40
	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.39
	452404	AW450675	Hs.212709	ESTs	3.39
10	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	3.39
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	3.39
	440606	AI828751		ESTs, Weakly similar to I38022 hypotheti	3.38
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.37
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.37
15	446214	AK001322	Hs.14347	hypothetical protein FLJ10460	3.36
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.36
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.36
	421633	AF121860	Hs.106260	sorting nexin 10	3.36
	438192	AI859065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	3.36
20	436511	AA721252	Hs.291502	ESTs	3.35
	402680			Target Exon	3.35
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.35
	449477	AI652602	Hs.197043	ESTs	3.35
	413686	AI69213	Hs.71404	ESTs	3.35
	401091			decay accelerating factor for complement	3.35
25	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.35
	433220	AI076192	Hs.131933	ESTs	3.34
	453200	AA033832	Hs.212433	ESTs	3.33
	427239	BE270447		ubiquitin carrier protein	3.33
30	418355	L42563	Hs.1165	ATPase, H <sup>+</sup> transporting, nongastric, alp	3.33
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthase	3.31
	441243	AI767056	Hs.193002	ESTs	3.30
	440716	AW105245	Hs.146509	ESTs	3.30
	400587			C10000649*.gil7296574[gb]AAF51857.1 [AE	3.30
35	401148			Target Exon	3.30
	411752	AW236047	Hs.126497	ESTs	3.30
	433252	AB040957	Hs.151343	KIAA1524 protein	3.30
	434008	AA740878	Hs.112982	ESTs	3.30
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.30
40	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.30
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.29
	452761	BE244742	Hs.30532	CGI-77 protein	3.29
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	3.29
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.28
45	432809	AA565509	Hs.131703	ESTs	3.27
	449426	T92251	Hs.198882	ESTs	3.27
	425174	D87450	Hs.154978	KIAA0261 protein	3.25
	435159	AA668879	Hs.116649	ESTs	3.25
	446597	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	3.25
50	411554	W22895	Hs.112360	prominin (mouse)-like 1	3.25
	447555	AI391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	3.25
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.25
	445093	AI207197		ESTs	3.25
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.24
55	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.24
	453293	AA382267	Hs.10653	ESTs	3.24
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.23
	430552	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	3.22
	411975	AI916058	Hs.144583	ESTs	3.22
60	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.22
	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.21
	436515	AJ278111	Hs.195292	putative tumor antigen	3.21
	456505	AA504595		ESTs	3.21
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	3.21
65	452794	AI192444	Hs.25892	ESTs, Weakly similar to I37356 epithelia	3.20
	427314	AB033024	Hs.175475	KIAA1198 protein	3.20
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.20
	452028	AK001859	Hs.27595	hypothetical protein FLJ21142	3.20
	421002	AF116030	Hs.100932	transcription factor 17	3.20
70	422225	BE245652	Hs.118281	zinc finger protein 266	3.20
	437549	AA759149	Hs.128757	gb:ah70e03.s1 Soares_testis_NHT Homo sap	3.20
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	3.20
	427642	R40761	Hs.9834	ESTs	3.20
	442765	BE567353	Hs.99480	ESTs	3.20
75	410048	W76467	Hs.343874	proline oxidase homolog	3.20
	412008	NM_001841	Hs.73037	cannabinoid receptor 2 (macrophage)	3.20
	423675	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	3.20
	453895	AA039843	Hs.61948	Homo sapiens, clone MGC:16466, mRNA, com	3.20
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.19
80	428612	AA770001		ESTs	3.19
	422805	AA436989	Hs.121017	H2A histone family, member A	3.19
	444371	BE540274	Hs.239	forkhead box M1	3.18
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.17
	451684	AF216751	Hs.26813	CDA14	3.17

5	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	3.17
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.16
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.16
	444823	BE262989	Hs.12045	putative protein	3.15
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.15
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.15
	447801	H88923	Hs.270247	Homo sapiens cDNA FLJ11977 fis, clone HE	3.15
	424188	AW954552	Hs.142634	zinc finger protein	3.15
10	436941	AA860383	Hs.292791	ESTs	3.15
	400592			Target Exon	3.15
	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.15
	450405	AI694913	Hs.279637	ESTs	3.15
	414161	AA136106	Hs.184852	KIAA1553 protein	3.15
15	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	3.14
	438538	AA832203	Hs.291955	ESTs	3.14
	441013	AI125252	Hs.126419	ESTs	3.14
	450431	AW136797	Hs.266041	ESTs	3.14
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	3.13
20	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.13
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.12
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	3.12
	412673	AL042957	Hs.31845	ESTs	3.11
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.11
25	423419	R55336	Hs.23539	ESTs	3.11
	428925	AW242474	Hs.98960	ESTs	3.11
	426108	AA622037	Hs.166468	programmed cell death 5	3.10
	439398	AA284267	Hs.221504	ESTs	3.10
	449138	AW294215	Hs.195631	ESTs	3.10
30	441795	N58115	Hs.21137	AD024 protein	3.10
	456053	S57498	Hs.76252	endothelin receptor type A	3.10
	403610			C3001199:gil7494834 pir  T15308 hypothet	3.10
	421281	AI299139	Hs.17517	ESTs	3.10
	429274	AI379772	Hs.99206	ESTs	3.10
35	438243	AI581311		ESTs	3.10
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.09
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.08
	416443	N69469	Hs.194225	ESTs	3.08
	421230	AW958439	Hs.105633	ESTs	3.07
40	427906	AA864330	Hs.166520	ESTs	3.07
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.06
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.06
	445679	AI343868	Hs.301059	hypothetical protein FLJ12488	3.06
	434456	AW452621	Hs.116832	ESTs	3.05
45	433228	F28212	Hs.14953	KIAA1491 protein	3.05
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	3.05
	415227	AW821113	Hs.72402	ESTs	3.05
	421184	NM_003616	Hs.102456	survival of motor neuron protein interac	3.05
50	438869	AF075009		gb:Homo sapiens full length insert cDNA	3.05
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	3.04
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.04
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.04
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	3.04
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	3.04
55	435726	BE535787	Hs.113170	ESTs	3.03
	426386	AA748850	Hs.125830	bladder cancer overexpressed protein	3.03
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.02
	427953	AA417944	Hs.44331	ESTs	3.01
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.01
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	3.00
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	3.00
	434776	AA648988		gb:ns41f1.1.s1 NCI_CGAP_GCB1 Homo sapiens	3.00
	414132	AI801235	Hs.48480	ESTs	3.00
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
65	433493	AA594915	Hs.155087	ESTs	3.00
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	3.00
	453416	NM_003037	Hs.32970	signaling lymphocytic activation molecu	3.00

TABLE 53B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
		BG215094 BG198867 BG196332 BG208220 BG212418
430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603
		AI352469 BE061601 BI052752 AW818206 BF887722
422828	227063_1	BE671981 BE503379 AI655440 AI337054 AI288920 AI242370 AI825182 AA758081 BF855141 BF091068
418477	4172_1	BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092
		AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
443068	18695_17	AV752763 AI032142 N30308 N22181 H95390 AW675632
436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673



5	427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892 AA764852 AA736937 AW954733 AA315006 AW856665 AI964001 AI634418 AW236545 AI824860 BF223710 AW139686 AI672051 AI655566 AW025712 N36327 BF222876 N34083 AA911045 N40303 AW835451
	436899	1000797_1	BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433
	422689	874209_1	AA301270 AA301379 AA301366
	440968	518029_1	AA683356 AW592804 AI150287 AF147390 R76593 R76594 AJ420453 AL526740 AW968449 AA459140 AA843893 AI566516 AW971760 AA430089 AI753216 AA854268 AA743075 AI864957 AA458920 AI566634 AA211796 BG615512 BE169275 BF983253 BF969462 AA766261 AI769894 AA135833 AI831542 N63376 AA214392 AU154486 AW605017 AW450072 AA446459 BE881875 AI061423 AA598549 AW439151 AA426273 Z40087 AA812434 AA135965 H04812 BF666746 D59356 BG678312 N56640 AA166861 AA917062 AA757369 AW592218 AL109688 R23665 R26578 BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336 AA210987 D57294 AA214584 AA207006 D56572 AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114 AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364 BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793 AA382556 AW235763 AA927051 AI862075 BE886691 BE619282 AA906366 AA938956 AI910938 AW102570 AA907150 AA907120 AA737188 AI248890 AW977353 BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633 BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 BE072634 BE072653 AA830615 AA214736 AA331718 AA218925 AW962081 AA354237 BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758 NM_000363 X54163 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI657074 C03333 AI193911 C05024 C03193 AI950215 C05070 C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255 T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339 AK056685 BG399272 AA187835 BF821903 AV660550 AV660556 AV660502 BG564397 BE379584 BF446961 AI653056 AW973709 AI653173 BG054997 AI266043 BI054879 AI656750 AI492830 AW021142 AI472184 AW170056 AI082443 AI167921 D59940 BI492088 H74180 AW130886 AI348677 AI278577 AA761517 AI698203 AA115535 AI264790 AW205074 AA860452 AA554902 AI000715 D62102 BE544768 AI376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832 BI015205 AI761324 AW880937 AW880941 AA338252 AA338213 AK055746 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852 BF173139 BE010038 AA933717 BF061897 AW628327 AA641788 AA400495 BE065183 AI144398 BE065367 BF377924 NM_058166 AF220030 AL043894 AW974257 AA625445 AU153502 AI650537 AW612116 AI672377 AW772451 BE892241 BE501740 AA718936 AI650276 AI654206 BE503226 AI651327 AW873562 AW271269 AW271565 AI873518 AI207150 AI338826 AI650258 AI628362 AA227117 AI207149 AW052076 AI470776 AA588100 AW235852 AA769791 AI701653 AK027664 AI984770 AU153469 BE222316 AA609539 BE220093 AA609112 BI054316 AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594 AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614951 N29986 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611 AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833 AA207155 BI004756 AA206262 AI365204 H77608 AW590511 T39328 T39310 T39303 T39284 BE893356 AA625304 AI765607 AI624898 R76060 AA069651 BG988885 R35783 BF086499 AA428755 AI245055 BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236 N50454 AA620999 T16375 AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727 T65754 AA229658 AA229857 AK056550 AK056356 AI928212 AI742073 AW300558 BG058755 AA058343 AI554842 AW207438 BF059981 BF444954 AW026234 AI620104 AA973460 AI370934 N63066 AA493129 AW590888 AI682952 AI167202 AA631394 AI421915 AI222883 BF477519 AI208777 AA765849 AI675076 AI370922 AI339579 AA486224 AA453524 AW771805 AI492842 H54679 AA961022 AW023555 H06192 AA910222 AI660021 AI032525 AI375480 AI361860 AI032919 AA833599 BG057928 AA553913 AW235737 AA002124 AA913636 F04607 AI867699 AA648100 BE091446 AA486378 BE002022 H84627 BI059837 BF917659 BF917100 BF917043 BF917104 BF916878 BG290981 AW954251 AA757126 H11545 AA353384 N48448 AA379845 AA004943 AA379928 AA002123 BM470118 AL598847 AL598830 BG899239 R57470 BF939179 AI650642 AI758851 BF352505 W68422 W35297 H11435 AA937499 AI783996 R12500 AI619557 N39093 Z41619 H22849 AA004942 R09436 R02403 T90942 T85823 BG029683 AI248120 BI850480 AW779829 N22494 BE155042 BE155040 BE154987 BE155012 BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573 AW813110 BF771370 BF771371 AW813113 AW003381 BI862319 AA204955 BF240507 BG212143 AW205739 BI760647 BM129481 BI760482 AW300025 AI288591 AW236114 AI302852 AI038548 AI797207 AA534496 BG188194 AA921877 BG191846 BG182959 BE620243 BF217428 BC009514 BM463015 AI529077 BM051874 BG773269 BM314351 BM314660 AW629666 AA316207 AI623431 AA504153 AA314700 BG195449 BG614101 BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148 AI968683 AA846676 AA927355 H80424 AW973295 R88209 F29868 BE928871 AA846804 AA757581 AI050950 AI092024 AA838807
10	427486	684159_1	
	421974	864120_1	
	435514	132288_1	
	434609	14739_1	
15	414136	30243_1	
	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
20	453160	6028_5	
	417886	1031334_1	
	412537	14066_1	
25	440801	2635916_1	
	436909	596835_1	
	429228	215430_1	
30	451050	11847_4	
	418235	886897_1	
	418378	1227421_1	
	450375	16559_3	
35	409517	4537_1	
	442562	39593_1	
40	451105	1145037_1	
	424281	892055_1	
	430183	17316_1	
45	427298	115241_1	
	444386	1490237_1	
	414725	19377_1	
50	433641	35983_1	
55	418768	2293204_1	
	409268	109625_1	
	415989	10194_1	
60	433979	2076469_1	
	420218	191547_1	
65	418866	245947_1	
	449687	25369_2	
70	445685	381678_1	
	413646	1525656_1	
	437834	294580_1	
75	454679	174325_1	
	440840	29686_1	
80	433023	3970_8	
	437440	2497201_1	

417553	258857_1	AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204699 W60115 N56751 N30878 AI769345 R71250 AI363766 R22777 R17009 R27985 R28243
408065	101881_1	BI603077 AW954272 BI598724 AI003154 AA059300 AA046911 BI669907 BI600966 BI669987
418049	12052_4	AJ314647 NM_052888 BI494693 AA835065 AI634477 AI336678 AI807696 BF477887 AI701147 Z39187 R38979 F02234 AA984711 BI222234
430968	1237115_1	AV731417 R42406 H04996 T98498 R12489 R12577 R42405
400268	840_4	AW972830 AA489820 AA527647 AA570362
		U69668 AA448366 X63105 BC016514 BE694436 AI655840 AW235355 BG427984 AA612862 AA448223 BM145813 BM194565 AI870824 BE973573
		BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687
		BF908518 BF907890 R11490 AL536642 BF109180 AA953881 AI783716 BE622908 AI621005 AW148784 AI690114 AW275000 AI765790 BF222859
		AW167268 AI990460 AW300443 AA779660 AI620568 BF115024 BE504703 AW628332 AI922851 BE006636 AU158376 AI168279 AA809916
		AI469757 AA830828 AA830388 N64324 AI049683 AA970275 BF477364 BG261301 AA326388 AU150565 AU158374 AA687967 N58510 AI650450
		AL549572 BF349280 BF349269 BM463016 AW836798 AL120958 AW836891 AW385525 BE175733 BE175727 BE175723 BF092430 BI061782
		AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW847833 AL536643 AW366516 AW391532
		BE934857 BF925057 AW438446 R86246 AW179270 BE087782 BI832144
		BC017350 BC021031 AI220219 AI828751 AW134498 BE139642 AA894554 AI278594 AV747315 BE561749 BI085890 T80117 H69682 N70904
		AV741999 H70098
		AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881
		AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478
		AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839
		AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420
		AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260
		AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427
		BF718773 BF718645 AW074866 BE857822
		AI207197 BF773544 AW196462
		BC017965 AW969075 AA279982 AA504511 AI219979 AA504595 AI245579 AA278181 BG485019 BI049312
		AA770001 AA431112 AA432126
		AL079309 AA281819
		AI732997 AA977633 AA865818
		AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
		BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
		AW840571
		AI581311 AA781682 AA781678
		AF075009 R63109 R63068
		AW974599 AA648988 R98760

TABLE 53C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
406547	7711513	Minus	172780-174358
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
402199	8576116	Minus	84187-84744
402145	8018280	Plus	113086-114800
401837	7630990	Minus	120993-121095,121660-121729
403780	8076989	Plus	93160-93409
402299	6693370	Plus	23367-25175
401435	8217934	Minus	54508-55233
401464	6682291	Minus	170688-170834
402098	8117697	Minus	44186-44330
404287	2326514	Plus	53134-53281
406367	9256126	Minus	58313-58489
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
402178	8575912	Plus	391138-391711
403433	9719611	Minus	72225-72437
402408	9796239	Minus	110326-110491
405935	6758795	Minus	163112-163652
406542	7711499	Plus	117335-118473
402099	8117697	Plus	121553-121742,123265-123423
404068	3168621	Minus	18123-18766
401644	8576138	Plus	82655-83959
402680	8113438	Plus	137634-137768,139702-139893,140475-14059
401091	9958240	Plus	94760-94898
400587	9887626	Plus	25435-25588,25668-25747
401148	2547238	Minus	22521-23053
403432	9719611	Minus	68204-68392
400592	9887642	Minus	24642-24815
403610	8308266	Plus	157705-157860

TABLE 54A:

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of normal testis to normal adult tissues  
 R2: Ratio of "average" normal testis to "average" testicular cancer

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
------	--------	-----------	---------------	----	----

	401979		C17000767:gil11990770[emb]CAC19651.1  (A	10.08	43.3
	421825	AA298758	Hs.183747	ESTs, Moderately similar to CALB_HUMAN C	10.35
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.74
5	417128	AI797395	Hs.169797	Homo sapiens BOULE (BOULE) mRNA, complet	10.54
	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	4.86
	415211	R64730	Hs.155986	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	6.93
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	4.94
	449108	AI140683	Hs.98328	hypothetical protein MGC13040	7.94
	420437	AA992768	Hs.97633	A kinase (PRKA) anchor protein 4	16.75
10	436632	AA724299	Hs.304020	ESTs, Weakly similar to CRTC_HUMAN CALRE	6.51
	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	4.96
	406409			Target Exon	3.98
	427060	AW378993	Hs.90286	ESTs	3.56
15	427310	AI613480	Hs.47152	teklin 3	4.50
	427166	AA431576	Hs.99154	ESTs	4.28
	427178	AA398866	Hs.97542	Homo sapiens testis-development related	10.19
	410694	AL137538	Hs.65500	Homo sapiens mRNA; cDNA DKFZp434N2019 (f	5.76
	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.24
20	427441	AA412605	Hs.343879	SPANX family, member C	10.45
	438057	AW294544	Hs.125785	ESTs, Weakly similar to CORB MOUSE CORNI	18.57
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	5.18
	427293	AA705799	Hs.183714	ESTs	10.79
	444963	AI916973	Hs.213603	ESTs	3.18
25	428608	AI699329	Hs.99168	ESTs, Weakly similar to AF132972 1 CGI-3	15.40
	453178	AA496086	Hs.61648	ESTs	4.13
	428618	AA885360		Target CAT	7.53
	401741			Target Exon	10.41
	422086	AW182930	Hs.250182	ESTs	4.39
30	426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	7.04
	442373	AI377758	Hs.164799	testes development-related NYD-SP17	8.23
	427455	AF173081	Hs.178215	Vertebrate LIN7 homolog 1, Tax interacti	3.03
	437248	AW449340	Hs.93090	ESTs	9.06
	426608	AA444162	Hs.99344	hypothetical protein PRTD-NY3	3.68
35	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	9.70
	422358	AL133030	Hs.115429	Homo sapiens mRNA for KIAA1666 protein,	11.85
	451610	AW118604	Hs.207126	ESTs	5.63
	410630	BE044562	Hs.266847	ESTs, Weakly similar to KIAA1214 protein	4.38
	426677	AW949856	Hs.97165	ESTs	6.58
40	437558	AI126471	Hs.124112	ESTs, Moderately similar to HSJ2_HUMAN D	4.47
	423088	NM_006687	Hs.123530	actin-like 7A	15.07
	426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	18.55
	421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	13.93
	429877	W37337	Hs.103014	ESTs	6.97
45	413114	AI825838	Hs.75206	protein phosphatase 3 (formerly 2B), cat	3.78
	412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	22.03
	411844	AI807681	Hs.144658	ESTs, Weakly similar to T17257 hypotheti	7.34
	436868	AA974253	Hs.120319	Homo sapiens autoimmune infertility-rela	4.16
	426599	AW183574		ESTs	6.29
50	426683	AI073430	Hs.146775	ESTs, Weakly similar to T30993 hypotheti	10.89
	426930	AA393442		ESTs	5.06
	427836	AA416642	Hs.116176	ESTs	4.79
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	5.11
55	430822	AI005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	21.26
	434150	BE047007	Hs.116116	testis specific, 10	4.85
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	10.29
	422116	H64205	Hs.111850	mitochondrial capsule selenoprotein	9.12
	433724	AI827749	Hs.144924	serine/threonine protein kinase SSTK	22.24
	410187	AA860341	Hs.104680	ESTs	3.03
60	419584	AF053356	Hs.283764	F-box only protein 24	6.43
	458182	AI147996	Hs.155833	ESTs, Weakly similar to spliceosomal pro	9.90
	418665	T19204	Hs.195685	ESTs	7.14
	426646	AA382787	Hs.122713	ESTs	7.03
	420349	NM_016611	Hs.97174	potassium inwardly-rectifying channel, s	14.90
65	428624	AI125222	Hs.98712	hypothetical protein DKFZp434H0311	3.71
	420710	NM_007009	Hs.99875	zona pellucida binding protein	20.78
	434317	AI674095		ESTs	3.98
	443432	AI056863	Hs.339871	ESTs	3.46
	425709	AA383076	Hs.159274	outer dense fibre of sperm tails 1	23.21
70	426670	AA383047	Hs.310210	ESTs	6.92
	408613	AW242086	Hs.253967	ESTs	5.77
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	9.23
	434133	AI655275	Hs.236635	ESTs, Weakly similar to ATHUB actin beta	7.46
	427294	AA412594	Hs.125902	ESTs	3.44
75	427262	AA448509	Hs.128652	ESTs	5.66
	429851	AA459835	Hs.120573	hypothetical protein DKFZp434K1172	9.01
	406378			NM_021247*:Homo sapiens protamine 3 (PRM	3.96
	425865	AA393491	Hs.183740	ESTs	9.15
	428665	NM_017481	Hs.189184	ubiquitin 3	11.07
80	439379	AA835002	Hs.125611	ESTs	5.06
	427520	BE467881	Hs.97489	ESTs, Weakly similar to B28096 line-1 pr	9.29
	458940	BE149824	Hs.132888	KIAA1674	3.11
	426620	AW450252		ESTs	12.27
	429516	AI653299	Hs.99354	ESTs, Weakly similar to hyperpolarizatio	9.15

	426736	AA431615	Hs.130722	ESTs	3.58	6.1
	427843	AC005622	Hs.180943	hypothetical protein R30953_1	6.34	6.1
	426639	AI799059	Hs.112807	ESTs	6.93	6.0
5	438637	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein	3.04	6.0
	433795	AI216683	Hs.122599	ESTs, Weakly similar to ALU7_HUMAN ALU S	10.45	5.9
	441232	AI656050	Hs.7086	hypothetical protein MGC12435	4.27	5.9
	433943	AA992805	Hs.44865	lymphoid enhancer-binding factor 1	6.87	5.8
	426955	AA393669	Hs.238094	ESTs	4.75	5.8
10	428918	AL036967	Hs.2324	protamine 2	38.40	5.8
	427851	AA846543	Hs.98257	ESTs	15.87	5.8
	428208	AA442327	Hs.104854	ESTs	6.34	5.7
	422207	AI828862	Hs.10964	ESTs	6.43	5.7
	431153	AW972342	Hs.77823	hypothetical protein FLJ21343	9.24	5.7
	419350	AC005328		Homo sapiens chromosome 19, cosmid R2666	14.94	5.6
15	427107	AA889586	Hs.180346	ESTs	6.25	5.6
	429461	AI188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	3.92	5.6
	432512	NM_003284	Hs.3017	transition protein 1 (during histone to	22.03	5.6
	434451	AW445179	Hs.121438	ESTs	7.89	5.5
20	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1126 (f	11.26	5.5
	427214	AA442240	Hs.178213	ESTs	8.41	5.5
	458658	AI301117	Hs.122055	ESTs	4.35	5.5
	457034	AA398061	Hs.296587	Homo sapiens chromosome 21 segment HS21C	11.29	5.4
	423120	AW160551	Hs.124021	soggy-1 gene	8.88	5.4
25	438983	AF085884	Hs.20029	proacrosin binding protein sp32 precursor	22.69	5.4
	426619	AI357194	Hs.119284	ESTs	7.07	5.4
	440822	AI554897		Homo sapiens clone 191B7 placenta expres	3.60	5.4
	416205	AA176396	Hs.169624	ESTs	10.26	5.4
	426712	AW173177	Hs.197755	hypothetical protein MGC5356	8.17	5.3
30	427840	AI216654	Hs.98251	ESTs	6.44	5.3
	439314	AA382413	Hs.178144	ESTs	8.35	5.3
	426943	BE551631	Hs.20969	ESTs	6.31	5.2
	409209	AA460160	Hs.73217	ESTs	7.85	5.2
	441710	AI187883	Hs.127510	ESTs, Weakly similar to ENC1_HUMAN ECTOD	7.73	5.1
35	420571	AA442366	Hs.98952	Human DNA sequence from clone RP1-39G22	9.39	5.1
	428563	AA431616	Hs.98660	ESTs	14.94	5.1
	433994	AL042483	Hs.335499	ESTs	6.84	5.0
	441856	AI674774	Hs.128014	ESTs	3.74	5.0
	427789	AA412428	Hs.48642	hypothetical protein FLJ23093	4.29	5.0
40	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	4.14	4.9
	430232	AA469940	Hs.105324	ESTs, Moderately similar to FRHUH ferrit	10.66	4.9
	421850	AW274576	Hs.121021	ESTs	12.27	4.9
	449436	AA860329	Hs.279307	hypothetical protein DKFZp434I2117	4.50	4.9
	426699	AA383337	Hs.121269	ESTs	5.67	4.9
45	426627	AF012359	Hs.195685	ESTs	20.66	4.9
	427285	AA401664	Hs.97784	ESTs	4.72	4.8
	423693	AL133633	Hs.131779	Homo sapiens mRNA; cDNA DKFZp434E2118 (f	6.03	4.8
	457019	AA421844	Hs.12830	hypothetical protein	3.87	4.8
	405264			NM_030813*:Homo sapiens suppressor of po	4.48	4.8
50	450606	AI668605	Hs.60380	ESTs, Moderately similar to ALU6_HUMAN A	3.76	4.8
	421378	L77564	Hs.103978	serine/threonine kinase 22B (spermio gene	7.35	4.8
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	8.66	4.7
	427423	BE267041	Hs.177926	exonuclease NEF-sp	19.27	4.7
	438756	AW081754	Hs.303923	hypothetical protein DKFZp434L1717	12.05	4.7
55	424197	AF096834	Hs.142989	germ cell specific Y-box binding protein	17.70	4.7
	423284	AC005764	Hs.126496	Homo sapiens chromosome 19, cosmid R3134	7.50	4.7
	432117	AL036195	Hs.2909	protamine 1	55.33	4.7
	424426	AI476416	Hs.132888	KIAA1674	5.41	4.6
	437387	AI198874	Hs.28847	AD026 protein	5.04	4.6
60	420718	NM_002301	Hs.99881	lactate dehydrogenase C	9.18	4.6
	420768	AI468780	Hs.292503	ESTs, Weakly similar to T47142 hypotheti	5.70	4.6
	423677	M86808	Hs.131361	pyruvate dehydrogenase (lipoamide) alpha	10.93	4.5
	436661	AI125270	Hs.128069	ESTs, Weakly similar to T19142 hypotheti	3.82	4.5
	427749	BE045979	Hs.98095	Homo sapiens cDNA: FLJ23052 fis, clone L	6.45	4.5
65	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	11.29	4.5
	427877	AW138725	Hs.178067	ESTs	4.09	4.5
	426623	AA382826	Hs.132793	ESTs	26.62	4.5
	429965	AL040379	Hs.99551	Homo sapiens cDNA FLJ11789 fis, clone HE	13.25	4.5
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.88	4.4
70	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosom	3.46	4.4
	421938	AA405951		gb:zu66c01.r1 Soares_testis_NHT Homo sap	4.69	4.4
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	19.15	4.4
	426710	BE041517	Hs.143893	ESTs	5.57	4.4
	428710	AI890919	Hs.126780	ESTs, Weakly similar to T12519 hypotheti	11.86	4.4
75	438641	AW138484	Hs.190653	ESTs	6.19	4.4
	420614	AL110291	Hs.99364	putative transmembrane protein	6.86	4.4
	422705	NM_006686	Hs.119287	actin-like 7B	9.73	4.4
	421805	AL042716	Hs.130947	hypothetical protein DKFZp434N1415	5.89	4.4
	448963	AA459796	Hs.331247	Homo sapiens, clone IMAGE:3610712, mRNA,	6.77	4.3
80	426738	AA421097	Hs.291902	ESTs	3.49	4.3
	440403	AW665135	Hs.130531	ESTs	6.97	4.3
	456085	AI184560	Hs.130352	ESTs, Weakly similar to A47582 B-cell gr	6.30	4.3
	439594	AI245026	Hs.111099	hypothetical protein MGC10974	7.85	4.3
	428909	AI190714	Hs.98945	ESTs	7.79	4.3

	426735	T78716	Hs.120446	ESTs	5.10	4.3
	438653	AW188099	Hs.131813	ESTs	5.29	4.3
	443038	AI968058	Hs.209206	ESTs, Weakly similar to S38782 actin bet	7.29	4.2
5	428677	AI657119	Hs.120036	troponin I, cardiac	10.73	4.2
	424220	AK000869	Hs.143251	hypothetical protein	9.13	4.2
	426299	H93373	Hs.169222	acrosomal vesicle protein 1	4.87	4.2
	428871	AA913840	Hs.98903	ESTs	3.76	4.2
	410163	AF151977	Hs.59260	NTT5 protein	7.29	4.2
10	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.29	4.2
	427757	AI142295	Hs.129794	ESTs	3.57	4.1
	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	11.13	4.1
	401692			C16000122:gi 5689527 dbj BAA83047.1  (A	6.37	4.1
	403783			NM_031956:Homo sapiens NYD-SP14 protein	3.74	4.0
15	421611	AA459841	Hs.97309	ESTs	11.51	4.0
	404271			ENSP00000244792*:Phosphoglycerate kinase	4.02	4.0
	441800	AW027571	Hs.7973	hypothetical protein DKFZp434G156; KIAA1	8.86	4.0
	423000	AF049615	Hs.122959	Huntingtin interacting protein M	3.60	4.0
	423118	AL035460	Hs.124009	Human DNA sequence from clone RP5-860F19	4.84	4.0
20	420419	AA397796	Hs.11614	HSPC065 protein	4.07	3.9
	435897	AF269223	Hs.128322	I-complex 11 (a murine tcp homolog)	23.29	3.9
	428516	R38137	Hs.156469	ESTs, Moderately similar to KIAA0940 pro	5.28	3.9
	427179	AA400590	Hs.97543	ESTs	6.18	3.9
	426609	AL040604	Hs.99344	hypothetical protein PRTD-NY3	10.07	3.9
25	452579	AA131657	Hs.23830	ESTs	5.24	3.9
	441443	BE465999	Hs.129293	ESTs	4.60	3.9
	427709	AI631811	Hs.180403	STRIN protein	3.82	3.9
	435484	AA682756	Hs.88051	ESTs	5.10	3.9
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	4.61	3.8
30	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	7.14	3.8
	421620	AA446183	Hs.91885	ESTs, Weakly similar to I55214 salivary	5.20	3.8
	427086	AA436131	Hs.188781	ESTs	5.76	3.8
	420475	AW408407	Hs.187018	ESTs	3.99	3.8
	441357	AI240184	Hs.343487	ESTs	4.63	3.8
35	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	8.04	3.8
	441806	AI024442	Hs.346385	ESTs	5.48	3.8
	413209	AW083791	Hs.21263	suppressor of potassium transport defect	9.02	3.8
	414544	AA149285	Hs.115659	hypothetical protein MGC5521	10.15	3.8
	427251	AI026844	Hs.98843	ESTs, Highly similar to GRA2_HUMAN GLYCI	7.69	3.8
40	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekti	3.46	3.7
	442589	BE409869		protein kinase, cAMP-dependent, regulato	4.50	3.7
	425841	BE262951	Hs.99052	ESTs	8.26	3.7
	410350	AA446395	Hs.62595	chromosome 9 open reading frame 9	7.64	3.7
45	440487	AI203685	Hs.135763	ESTs	5.90	3.7
	419455	AW172570	Hs.14600	ESTs	4.23	3.7
	436588	AA759233		ESTs	5.04	3.7
	421610	AA393168	Hs.90034	hypothetical protein FLJ21916	5.53	3.7
	441982	AI216902	Hs.48802	ESTs	4.79	3.6
	427288	AI139000	Hs.97792	hypothetical protein DKFZp434I099	5.17	3.6
50	414439	W45387	Hs.100007	regulatory factor X, 2 (influences HLA c	4.43	3.6
	401798			Target Exon	4.83	3.6
	433395	AF039442	Hs.160881	Homo sapiens colon cancer antigen NY-CO-	3.17	3.6
	438064	AI476330	Hs.234934	ESTs	3.56	3.6
	426658	AA397912	Hs.115366	Human DNA sequence from clone RP4-803K15	7.26	3.6
55	431986	AA536130		Novel human gene mapping to chromosome 20	6.13	3.6
	427872	AA835058	Hs.9622	Human DNA sequence from clone RP1-261G23	4.04	3.6
	437896	AA813689	Hs.123436	ESTs, Weakly similar to KIAA1205 protein	4.69	3.6
	420431	AB007131		Homo sapiens cDNA FLJ12825 fis, clone NT	4.24	3.5
	409467	Z22780	Hs.307358	cylicin, basic protein of sperm head cyt	5.13	3.5
60	422770	AL117544	Hs.120021	DKFZP434I092 protein	8.02	3.5
	437399	AI808626	Hs.121188	ESTs, Weakly similar to T29922 hypotheti	5.03	3.5
	428448	AA625766	Hs.98609	ESTs, Weakly similar to A Chain A, Coagu	4.30	3.5
	426705	AL042749	Hs.97714	ESTs	10.45	3.5
	427312	AA400657	Hs.135283	ESTs	4.47	3.5
65	423329	AF054910	Hs.127111	tektin 2 (testicular)	4.40	3.5
	439290	AI638094	Hs.236896	ESTs	3.29	3.4
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	6.18	3.4
	420500	AC005261	Hs.98338	serine/threonine kinase 13 (aurora)/PL1-	6.24	3.4
	441168	AI198850	Hs.131654	DMRT-like family B with proline-rich C-t	10.39	3.4
70	420482	X57655	Hs.98243	serine protease inhibitor, Kazal type, 2	20.38	3.4
	426988	AI208684	Hs.163960	Homo sapiens heat shock transcription fa	5.02	3.4
	444968	AW628609	Hs.148653	ESTs	5.10	3.4
	429210	AA448011	Hs.131918	ESTs	4.22	3.4
	442970	R28215	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	4.20	3.4
75	422782	AL133054	Hs.120369	hypothetical protein DKFZp434H2215	4.72	3.4
	436601	AA969884		ESTs	4.84	3.4
	421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	7.83	3.4
	415705	U06632	Hs.966	collin	6.30	3.4
	435587	AF215924	Hs.97899	putative allantoicase	3.48	3.3
80	427572	AA417291	Hs.97978	hypothetical protein MGC4766 similar to	3.54	3.3
	427541	AI798983	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.33	3.3
	429404	NM_005738	Hs.201672	ADP-ribosylation factor-like 4	3.57	3.3
	415014	AW954064	Hs.24951	ESTs	4.03	3.3
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	10.76	3.3

	412092	H43229	Hs.125201	ESTs, Weakly similar to I38022 hypotheti	5.27	3.3
	441579	AW468847	Hs.127194	ESTs	7.13	3.3
	420619	AF130255	Hs.99430	testis zinc finger protein	5.19	3.3
5	425368	AB014595	Hs.155976	cullin 4B	3.07	3.3
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.52	3.3
	429938	BE296804	Hs.226377	phosphate cytidyltransferase 2, ethano	3.03	3.3
	453017	R84301	Hs.31387	DKFZP564J0123 protein	3.30	3.3
	424466	AL040420	Hs.148250	Homo sapiens mRNA; cDNA DKFZp434N1535 (f	4.81	3.3
10	442084	H81173	Hs.34596	ESTs	4.78	3.3
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	4.63	3.3
	434183	AW104257	Hs.123426	ESTs, Weakly similar to SN1L_HUMAN PROBA	5.73	3.3
	428093	AW594506	Hs.104830	ESTs	6.95	3.3
	433982	AA724720	Hs.112941	ESTs	5.11	3.2
15	429821	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (fr	4.04	3.2
	408415	AW418788	Hs.123426	ESTs, Weakly similar to S43569 R01H10.6	3.49	3.2
	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.77	3.2
	402857			Target Exon	3.19	3.2
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	3.69	3.2
20	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	14.29	3.2
	427748	AA421041		ESTs	4.57	3.2
	422794	AJ011733	Hs.120857	synaptogyrin 4	4.23	3.2
	417488	AL046052	Hs.321046	hypothetical protein FLJ11743	3.57	3.2
	440115	R41808		ESTs, Weakly similar to B Chain B, Solut	4.67	3.2
25	437143	AW204056	Hs.8917	ESTs	4.16	3.2
	417473	M55268	Hs.82201	casein kinase 2, alpha prime polypeptide	4.02	3.2
	426594	AA884317	Hs.97130	ESTs	3.45	3.2
	428733	AA346824	Hs.191996	Homo sapiens organic cation transporter	6.29	3.2
	440864	AI382142	Hs.132104	ESTs	8.48	3.2
30	427141	AW628007	Hs.97643	testis-specific protein TSP-NY	5.60	3.2
	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp434F0919 (f	5.10	3.2
	438670	AI275803	Hs.123428	ESTs	4.08	3.2
	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	4.26	3.2
	452251	R37132	Hs.65009	ESTs	4.01	3.1
35	444141	AW629475	Hs.8977	ESTs, Weakly similar to RED1_HUMAN DOUBL	4.89	3.1
	428254	AK000542	Hs.183362	hypothetical protein FLJ20535	5.23	3.1
	421621	AL045589	Hs.180197	ESTs	7.09	3.1
	451017	BE391847	Hs.181173	hypothetical protein MGC10771	3.57	3.1
	457138	AW140059	Hs.98579	ESTs	13.17	3.1
40	428524	AA429772		ESTs	4.40	3.1
	428726	AA432195	Hs.98694	ESTs	6.47	3.1
	431310	AW327889	Hs.252433	Homo sapiens cDNA FLJ13794 fis, clone TH	4.07	3.1
	428076	AA420979	Hs.234895	ESTs, Weakly similar to Lysozyme [H.sapi	5.97	3.1
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.45	3.1
45	424450	AL137526	Hs.147472	dynein intermediate chain 2	6.01	3.1
	433953	AI218808	Hs.187778	ESTs	5.68	3.1
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.20	3.1
	440933	AI208217		ESTs	3.44	3.1
	441854	AA215990	Hs.99841	ESTs, Weakly similar to dJ1108D11.1 [H.s	4.03	3.1
50	423313	NM_014269	Hs.126838	a disintegrin and metalloproteinase doma	6.36	3.1
	428630	AA431270	Hs.140646	ESTs	3.59	3.1
	448813	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	5.63	3.0
	434720	AI208541	Hs.189160	ESTs, Weakly similar to cytochrome c-lik	6.04	3.0
	436328	AI201145	Hs.122042	Human DNA sequence from clone RP4-576H24	7.10	3.0
55	429293	AI767879	Hs.99214	ESTs	5.69	3.0
	427255	AA400082	Hs.343593	ESTs, Weakly similar to TD54_HUMAN TUMOR	5.37	3.0
	440713	AA904448	Hs.126368	ESTs	6.28	3.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	7.88	3.0
	423218	NM_015896	Hs.167380	BLu protein	6.68	3.0
60	444644	AW070634	Hs.144794	ESTs	5.00	3.0
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.75	3.0
	427829	AI188225		ESTs	7.36	3.0
	426879	AI969340	Hs.115437	hypothetical protein MGC3048	7.24	3.0
	427362	AA625582	Hs.97752	EST	4.38	3.0
65	441973	T60072	Hs.10688	ESTs, Weakly similar to HRIHFB2157 [H.sa	4.06	2.9
	428989	AF104260	Hs.194712	piwi (Drosophila)-like 1	4.45	2.9
	438735	M76676		ESTs	3.81	2.9
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	11.37	2.9
	427586	AA609661	Hs.190592	ESTs, Moderately similar to WASP-family	6.26	2.9
70	427306	AI476743	Hs.229275	ESTs	3.00	2.9
	418725	AL117637	Hs.306094	DKFZP434I225 protein	7.13	2.9
	456748	AW137749	Hs.125902	ubiquitin specific protease 2	3.48	2.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.60	2.9
	433836	AA610065	Hs.179646	ESTs	3.33	2.9
75	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.22	2.9
	437426	AW136558	Hs.125246	ESTs	4.49	2.9
	405528			C2002647:gi 4507721 ref NP_003310.1  tit	6.03	2.9
	442977	AW291731	Hs.144090	ESTs	4.23	2.9
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	13.24	2.8
80	424275	AW673173	Hs.144505	DKFZP566F0546 protein	5.60	2.8
	426667	AA770016	Hs.121192	ESTs	3.64	2.8
	410202	AB023213	Hs.60177	KIAA0996 protein	3.00	2.8
	428080	AI198656	Hs.98330	ESTs	4.09	2.8
	427252	AA400069	Hs.97757	hypothetical protein FLJ13031	4.34	2.8

	458255	AW140126	Hs.132357	ESTs	3.23	2.8
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.95	2.8
	440582	AA993337	Hs.129082	ESTs	5.29	2.8
5	435566	AI457958	Hs.80464	hepatitis B virus x-interacting protein	3.28	2.8
	433771	AI028794	Hs.112684	ESTs	3.36	2.8
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	5.30	2.8
	426703	AI221893	Hs.121549	ESTs	3.93	2.8
	430251	AA609246	Hs.181451	ESTs	4.04	2.8
10	427184	AI969361	Hs.180471	ESTs	6.78	2.8
	439909	AW450062	Hs.187134	ESTs, Moderately similar to AF263742 1 g	3.65	2.8
	448885	AW003686	Hs.30325	ESTs, Highly similar to AF200923 1 tesli	3.34	2.7
	450340	AA442322	Hs.60288	ESTs	5.39	2.7
	428100	AW665592	Hs.190413	ESTs	5.32	2.7
15	449333	AI203021		ESTs	4.35	2.7
	429861	AI989571	Hs.99510	ESTs	3.28	2.7
	426622	AL044400	Hs.25371	ESTs, Weakly similar to A37232 mucin, tr	5.38	2.7
	427256	AL042436	Hs.97723	ESTs	4.08	2.7
	408407	AF214680	Hs.44685	C3HC4-like zinc finger protein	3.27	2.7
20	403328			Target Exon	4.26	2.7
	436264	AA707457	Hs.120014	ESTs	3.58	2.7
	427104	AA398187	Hs.104682	ESTs, Weakly similar to mitochondrial ci	3.68	2.7
	426640	AI200961	Hs.98104	ESTs	4.60	2.7
	428789	AW296167	Hs.91930	ESTs	4.23	2.7
25	435274	AA887547	Hs.150905	ESTs	4.25	2.7
	426612	AA922067	Hs.184185	ESTs	7.17	2.7
	435110	N42688	Hs.81001	F-box only protein 25	4.85	2.7
	433792	AA778661		ESTs	4.06	2.7
	423278	AL117627	Hs.126289	Homo sapiens mRNA; cDNA DKFZp434B115 (fr	3.04	2.7
30	427284	AA400298	Hs.144696	ESTs	5.81	2.6
	423375	Z94277	Hs.127689	type 1 protein phosphatase inhibitor	3.36	2.6
	422362	Z46967	Hs.115460	calicin	4.72	2.6
	439993	T18864	Hs.144924	serine/threonine protein kinase SSTK	5.03	2.6
	409364	AI480252	Hs.137368	ESTs	7.22	2.6
35	419224	NM_012189	Hs.314452	fibrousheathin II	13.86	2.6
	428915	AI041278	Hs.87908	Snf2-related CBP activator protein	4.73	2.6
	427181	AI183653	Hs.27888	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.21	2.6
	442122	AI932330		ESTs	3.07	2.6
	424812	AF059252	Hs.153299	DOM-3 (C. elegans) homolog Z	3.80	2.6
40	430956	AI183529	Hs.2706	glutathione peroxidase 4 (phospholipid h	3.19	2.6
	427234	AA399667	Hs.104675	ESTs	3.43	2.6
	423005	AL080148	Hs.123004	DKFZP434B204 protein	3.53	2.6
	428214	AA936282	Hs.120397	ESTs	4.14	2.6
	452613	AA461599	Hs.23459	ESTs	7.78	2.6
45	410380	AL133068	Hs.62880	novel protein similar to mouse MOV10	3.45	2.6
	452537	AW247390	Hs.77735	hypothetical protein FLJ11618	3.43	2.6
	401712			Target Exon	4.51	2.6
	429186	BE503443	Hs.112095	hypothetical protein DKFZp434F1819	5.90	2.6
	438124	AA778610	Hs.122045	ESTs	3.43	2.6
50	422937	U03270	Hs.122511	centrin, EF-hand protein, 1	3.60	2.6
	410279	BE271977	Hs.61809	hypothetical protein FLJ14117	4.36	2.6
	428625	W87565	Hs.18566	ESTs	5.29	2.6
	433439	AA431176	Hs.133230	ribosomal protein S15	3.50	2.5
	433760	AW592321		ESTs	3.26	2.5
55	431219	AI190773	Hs.127204	ESTs, Weakly similar to similar to CR16,	5.10	2.5
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	8.07	2.5
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.56	2.5
	445158	AI992108	Hs.127206	ESTs	3.60	2.5
	440860	R10482	Hs.132876	ESTs	4.26	2.5
60	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.95	2.5
	433281	N48673	Hs.146037	hypothetical protein DKFZp434C135	5.68	2.5
	429369	AI269514	Hs.129802	ESTs	3.49	2.5
	433949	AI674766	Hs.112877	ESTs	5.15	2.5
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	10.46	2.5
65	414708	AA393379	Hs.97415	ESTs, Weakly similar to T33068 hypotheti	3.87	2.5
	408485	AW274294	Hs.144092	ESTs, Weakly similar to A Chain A, Sacch	6.10	2.4
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	5.64	2.4
	426956	AA393673		ESTs, Weakly similar to ALU5_HUMAN ALU S	4.68	2.4
	429152	AA447209	Hs.99099	Homo sapiens NYD-SP28 mRNA, complete cds	4.34	2.4
70	426247	U92992	Hs.98834	ESTs	5.40	2.4
	427589	T19219	Hs.97978	hypothetical protein MGC4766 similar to	3.40	2.4
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2 (testis)	5.85	2.4
	453353	U33055	Hs.32959	G protein-coupled receptor kinase 2 (Dro	4.82	2.4
	413372	H55532		tubulin, alpha 2	9.32	2.4
75	411737	AW160339	Hs.71791	hypothetical protein	5.26	2.4
	453868	NM_014433	Hs.35984	rhabdoid tumor deletion region protein 1	3.05	2.4
	427098	AA398161	Hs.97602	ESTs	3.21	2.4
	427165	AA429709	Hs.99336	ESTs, Weakly similar to T15446 hypotheti	4.27	2.4
	425808	AA364109	Hs.177990	ESTs	7.80	2.4
80	444790	AB030506	Hs.11955	B9 protein	3.32	2.4
	426718	AA383555	Hs.126413	ESTs	4.20	2.4
	411441	AL042355	Hs.70202	WD repeat domain 10	6.14	2.4
	450852	AI983354	Hs.7740	oxysterol binding protein-like 1	4.97	2.3
	427054	AA421240	Hs.97570	ESTs	3.10	2.3

5	438633	AI653327	Hs.123501	ESTs	3.46	2.3
	427199	AW015836	Hs.292919	ESTs	4.31	2.3
	440182	AA868919	Hs.250110	ESTs	3.03	2.3
	435517	AA926626	Hs.130177	ESTs	3.64	2.3
	446309	BE044261	Hs.149774	ESTs	3.52	2.3
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	4.23	2.3
	433829	AI190715	Hs.102021	ESTs	6.08	2.3
	429485	AW197086	Hs.99338	ESTs	3.14	2.3
10	423058	AW964568	Hs.111591	ESTs	3.36	2.3
	433822	AI218609	Hs.112772	ESTs	3.83	2.3
	442268	BE278064	Hs.8179	hypothetical protein, clone 2746033	3.00	2.3
	434298	AA860090	Hs.116290	ESTs	3.71	2.3
	440720	AW662776	Hs.336943	Human DNA sequence from clone RP11-60H7	3.08	2.3
15	427554	AW246578	Hs.179615	hypothetical protein FLJ10058	3.39	2.3
	414251	AL042306	Hs.97689	VASA protein	11.25	2.3
	430254	AI809520		ESTs	3.27	2.3
	437418	AI478954	Hs.59459	ESTs	3.43	2.2
	437522	AA983844	Hs.121383	ESTs	4.15	2.2
20	422808	AA449014	Hs.121025	chromosome 11 open reading frame 5	3.09	2.2
	436695	AA725655	Hs.120480	ESTs	5.26	2.2
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	6.78	2.2
	421625	AA405386	Hs.178004	ESTs	3.22	2.2
	434807	AA364183	Hs.323443	hypothetical protein FLJ11806	5.51	2.2
25	428174	AA913321	Hs.126778	ESTs	3.09	2.2
	409735	AL035295	Hs.56175	H.sapiens gene from PAC 106H8, similar t	3.11	2.2
	444467	AI150368		ESTs	3.81	2.2
	433832	AA918018	Hs.172516	ESTs	6.94	2.2
	440036	AW593295	Hs.210956	ESTs	5.87	2.2
30	415240	AA161411	Hs.58668	chromosome 21 open reading frame 57	3.66	2.2
	432538	BE258332	Hs.278362	male-enhanced antigen	3.58	2.1
	440882	AI205777	Hs.129538	ESTs	3.83	2.1
	436605	AI187742		ESTs	3.41	2.1
	422990	AF035620	Hs.122764	BRCA1 associated protein	5.66	2.1
35	432174	AW590264	Hs.132806	ESTs	3.05	2.1
	409267	NM_012453	Hs.52515	transducin (beta)-like 2	5.46	2.1
	423021	AL036111	Hs.292767	ESTs	3.87	2.1
	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	5.25	2.1
	433812	AA725026	Hs.97165	ESTs, Weakly similar to T31611 hypotheti	3.62	2.1
40	456924	AI631510	Hs.196956	ESTs, Highly similar to match to EST AA3	4.38	2.1
	437249	AA432202	Hs.103147	hypothetical protein FLJ21347	3.38	2.1
	426038	AA368101	Hs.99052	ESTs	3.03	2.1
	427065	AA397903	Hs.236635	gb:zl89f12.r1 Soares_testis_NHT Homo sap	3.23	2.1
	428824	W23624	Hs.173059	ESTs	3.07	2.1
45	428224	X54017	Hs.183088	acrosin	3.18	2.1
	436954	AA740151	Hs.130425	ESTs	3.20	2.1
	444470	AA412195	Hs.13740	ESTs	4.27	2.1
	457579	AB030816	Hs.36761	HRAS-like suppressor	5.30	2.1
	427886	AA417083	Hs.104789	ESTs	3.49	2.1
50	439273	AW139099	Hs.269701	ESTs	3.83	2.1
	434318	AW207552	Hs.116328	ESTs, Weakly similar to A39564 transcrip	4.01	2.1
	427015	AA397520		ESTs	4.28	2.1
	421598	AW630942	Hs.106061	RD RNA-binding protein	3.30	2.1
	427236	AA399859	Hs.148271	ESTs	3.07	2.1
55	434520	AA205273	Hs.177011	hypothetical protein	3.19	2.0
	456051	T85626	Hs.76239	hypothetical protein FLJ20608	3.11	2.0
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	8.41	2.0
	451807	W52854		hypothetical protein FLJ23293 similar to	3.52	2.0
	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	4.73	2.0
60	420484	W32963	Hs.98289	VRK3 for vaccinia related kinase 3	3.86	2.0
	414181	AK000476	Hs.75798	hypothetical protein	3.33	2.0
	424558	AF038847	Hs.150490	FK506-binding protein 6 (36kD)	7.70	2.0

TABLE 54B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

70	Pkey	CAT Number	Accession
	428618	2668_1	BC017998 BI826643 BG715794 BG722697 BI460787 BG773459 H52859 AI652853 AI990773 AW665193 AW340601 AA913806 AI337099 BE045942 AW572790 AW515652 H15004 AA909115 BI465310 BI462024 BI561578 BI463075 BG722527 R86003 BG623286 H15003 BI562131 BG435272
	426599	10110_1	BE736800 BM471423 AL557221 BG763302 BF742196 BF991016 BG200112 BF920027 BG576409 BG332214 BI830957 AI827504 AW183574 AI805171 AI126491 AA448257 AI090641 AW183329 AA994873 AI203663 BE041513 AA382260 AA382261 AL554887 BE273483
75	426930	1310779_1	AI809889 AA393442 AI150574 AI200886 AI221692 AA608977 AA813213
	434317	599587_1	AI209094 AI377740 AW117382 AW182289 AI674095 AW188019 AA897352 AA931314 AA923336 AW665317 AA629314 AA776691 AA906846 AA974625 AA884357 AI808590
	426620	142987_1	AL042392 AI147451 AA758821 AW450252 AA399310 AI656343 AI636668 AW515660 AI190733 AI025812 AA723645 AA709253 AA725709 AA398244 AA382463 AI139837
80	419350	13086_1	AI218809 BC014609 BG724383 AI024359 AA904573 AI138595 AA868685 AI768931 BI828436 BG717350 BG719800 AW182303 AA448181 BI826670 BI827131 BI830254 BI824155 BI831745 T19190 BI830415
	440822	532606_1	BG207562 BG192113 AA977616 AW274024 AI554897 AI221379 AA969158 AA906867 AI873494 AI015039
	421938	863689_1	AA412383 AA300675 BG773248 AA412243 AA405951



	442589	33097_2	NM_004157 X14968 BG480488 BE409869 BG723898 BG476313 AU121626 BE386516 AI969297 AW172340 AA889668 R23436 AI015037 BE250558 BF590945 AW385993 BF983000 AA070235 AL556082 M78388 AW504473 AW370139 BG913697 BE899096 BG827945 BE741233 AI015465 AW370169 BE297350 AA093249 AI122828 AA909991 AA759233 AI591713 BF197609 AI985094 AW448916 AI243277 AL449630 AL449629 AW241405 AW205071 AI671586 AI652354 AI638465 AW590359 AW662771 AW594067 BE502532 AI218894 BE466416 BF056295 AI247366 AI990484 AI917746 AW665925 AI216456 AW182169 AA969884 AA723888 AI018419 BI602176 BI603138 BI459895 BI755030 AW418788 AA883999 AA724858 AI480311 AW196355 AI004813 AI651117 BE814363 AW589856 AA448124 AA447982 BI461166 AA405629 AI208966 AA421041 AA815377 AA411954 BF980396 R51074 BF979883 AI539370 BM128735 AA993397 AI611039 AW593985 R41808 AI208080 AA442862 AA429772 AI125404 AW593312 AI247364 AI208217 AA910021 AI915307 AI190292 AI188225 AA416673 AA416596 AA952888 AA972172 AA906874 MF6676 NM_022571 BG772522 BF516449 AI537485 AW517245 BF762536 AA634446 AW196331 AI203035 BG722281 AK056320 AL522040 BI793043 AW071691 AI433682 AA865414 AA702684 BI792794 H96879 R52351 AA211126 AA442875 N25725 AA482563 N33446 N25222 Z41110 N26507 N73447 N24077 N20492 AW275550 H99619 AL518306 AL522041 AW959849 AL518307 AA725907 AI655113 AI309906 F10184 BM451081 BE257595 BG721625 BI828509 BG700470 F12568 Z45396 BI829288 AA364618 AA364851 AA421448 T74231 R52350 AA482415 AI203021 T88948 AI565842 AI024286 AA769898 AA778661 AA868972 AA609524 AI932330 AI190707 AI376782 AA976847 AA609179 AW592321 AA758282 AI214437 AW072537 AA781937 BI831486 AW190479 AI472793 AA460217 AA459937 BF082576 AA393673 AA398702 NM_006001 L11645 AI205604 AI207994 AI187362 AA709190 BI462421 BG772170 BG		
--	--------	---------	--	--	--

	406856	AW515336	Hs.29797	ribosomal protein L10	23.66
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	23.60
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (ig),	23.60
5	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	22.35
	417426	NM_002291	Hs.82124	laminin, beta 1	21.60
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	21.55
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	21.50
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	21.50
10	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	20.90
	412636	NM_004415		desmoplakin (DPI, DP11)	20.90
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	20.30
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	19.45
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	19.30
15	406648	AA563730	Hs.277477	major histocompatibility complex, class	19.10
	412247	AF022375	Hs.73793	vascular endothelial growth factor	17.45
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	17.40
	424800	AL035588	Hs.153203	MyoD family inhibitor	17.20
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	16.90
20	415314	N88802	Hs.5422	glycoprotein M6B	16.80
	406656	M16714	Hs.89643	major histocompatibility complex, class	16.75
	426295	AW367283		zinc finger protein 6 (CMPX1)	16.25
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	16.00
25	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	15.85
	417088	M54915	Hs.81170	p1m-1 oncogene	15.60
	449338	H73444	Hs.394	adrenomedullin	15.51
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	15.33
	414420	AA043424	Hs.76095	immediate early response 3	15.30
	425543	R23313	Hs.334895	ribosomal protein L10a	15.10
30	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	15.00
	420754	W79431	Hs.346911	ribosomal protein L22	14.92
	410397	AF217517	Hs.63042	DKFZp564J157 protein	14.86
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	14.70
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	14.60
35	406786	AW161678	Hs.111334	ferritin, light polypeptide	14.57
	422105	AI929700	Hs.111680	endosulfine alpha	14.57
	422714	AB018335	Hs.119387	KIAA0792 gene product	14.25
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.05
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.00
40	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	14.00
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	13.95
	410185	BE294068	Hs.737	immediate early protein	13.85
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	13.60
	410611	AW954134	Hs.20924	KIAA1628 protein	13.60
45	448588	AI970276	Hs.156905	KIAA1676	13.40
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	13.10
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.00
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	13.00
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	13.00
50	454413	AI653672	Hs.40092	PNAS-123	12.90
	415221	W07418	Hs.78225	annexin A1	12.89
	425535	AB007937	Hs.158287	KIAA0468 gene product	12.48
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	12.45
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.40
55	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	12.19
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	12.12
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	12.07
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	11.90
	408437	AW957744	Hs.278469	lacrimal proline rich protein	11.80
60	430542	AI557486	Hs.119122	ribosomal protein L13a	11.51
	424670	W61215	Hs.116651	epithelial V-like antigen 1	11.50
	432409	AA806538	Hs.130732	KIAA1575 protein	11.50
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	11.44
	425996	W67330		hypothetical protein AL110115	11.40
65	449961	AW265634	Hs.133100	ESTs	11.40
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	11.25
	407179	AA206465		thymosin, beta 4, X chromosome	11.21
	412623	R28898	Hs.74170	metallothionein 1E (functional)	11.10
	429978	AA249027		ribosomal protein S6	11.10
70	450377	AB033091		KIAA1265 protein	11.10
	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	11.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	11.00
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	11.00
	451106	BE382701	Hs.25960	N-MYC oncogene	10.93
75	426552	BE297660	Hs.170328	moesin	10.91
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	10.90
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	10.80
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	10.80
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rhotekin, clone	10.75
80	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.70
	435056	AW023337	Hs.5422	glycoprotein M6B	10.70
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	10.70
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	10.65
	420676	AI434780	Hs.4248	vav 2 oncogene	10.60

	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	10.60
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	10.50
	436075	BE090176	Hs.179902	transporter-like protein	10.30
5	450139	AK001838		serum/glucocorticoid regulated kinase	10.30
	427691	AW194426	Hs.20726	ESTs	10.26
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	10.15
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	10.10
	440528	BE313555	Hs.7252	KIAA1224 protein	10.06
10	423184	NM_004428	Hs.1624	ephrin-A1	10.05
	450847	NM_003155	Hs.25590	stanniocalcin 1	9.90
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.90
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), miloc	9.90
	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	9.89
15	435918	AF263538	Hs.86232	growth differentiation factor 3	9.89
	411251	R19774	Hs.22835	HHGP protein	9.80
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	9.75
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	9.75
	425580	L11144	Hs.1907	galanin	9.60
20	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	9.60
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	9.60
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.60
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	9.53
	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	9.51
25	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	9.42
	416926	H03109	Hs.263395	HT018 protein	9.41
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	9.40
	428065	AI634046	Hs.157313	ESTs	9.40
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	9.39
30	410325	AB023154	Hs.62264	KIAA0937 protein	9.30
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.30
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	9.29
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	9.24
	447211	AL161961	Hs.17767	KIAA1554 protein	9.22
35	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	9.20
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	8.93
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	8.90
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.90
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	8.90
40	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.84
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	8.80
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	8.70
	426215	AW963419	Hs.155223	stanniocalcin 2	8.70
	446627	AI973016	Hs.15725	hypothetical protein SBB148	8.60
45	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	8.60
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	8.60
	445245	AB032973	Hs.12461	LCHN protein	8.50
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.40
50	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	8.35
	410143	AA188169		KIAA1191 protein	8.35
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.30
	433208	AW002834	Hs.24095	ESTs	8.30
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.25
55	432559	AW452948	Hs.257631	ESTs	8.20
	450581	AF081513	Hs.25195	TGF-beta 4	8.10
	450157	AW961576	Hs.60178	ESTs	8.10
	444795	AI193356	Hs.160316	ESTs	8.10
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	8.05
60	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	8.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	8.00
	419970	AW612022		ESTs	8.00
	411975	AI916058	Hs.144583	ESTs	7.95
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	7.90
65	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	437103	AW139408	Hs.152940	ESTs	7.90
	432636	AA340864	Hs.278562	claudin 7	7.87
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	7.84
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	7.80
70	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.80
	450147	AW373713	Hs.146324	CGI-145 protein	7.75
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.70
	449571	AW016812	Hs.200266	ESTs	7.70
	429355	AW973253	Hs.292689	ESTs	7.70
75	446488	AB037782	Hs.15119	KIAA1361 protein	7.70
	414774	X02419	Hs.77274	plasminogen activator, urokinase	7.69
	422424	AI186431	Hs.296638	prostate differentiation factor	7.67
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	7.65
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	7.65
	451812	X81889	Hs.152151	plakophilin 4	7.65
80	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	7.60
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	7.60
	422746	NM_004484	Hs.119651	glypican 3	7.60
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	7.57

5	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.57
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	7.55
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	7.53
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	7.50
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	7.50
10	419223	X60111	Hs.1244	CD9 antigen (p24)	7.47
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.44
	401466			vesicle-associated membrane protein 4	7.43
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	7.40
	413686	AI469213	Hs.71404	ESTs	7.40
15	408605	AF025374	Hs.46465	T-cell, immune regulator 1	7.40
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.30
	444838	AV651680	Hs.208558	ESTs	7.30
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	7.28
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	7.20
20	452924	AW580939	Hs.97199	complement component C1q receptor	7.15
	436398	H87136	Hs.5174	ribosomal protein S17	7.15
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.10
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.10
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	7.10
25	401192			Target Exon	7.08
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	7.08
	420474			NM_004079: Homo sapiens cathepsin S (CTSS	7.00
	449567	AI990790	Hs.188614	ESTs	7.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to t38022 hypot	7.00
30	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	7.00
	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor Nb:HOT H	7.00
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	6.90
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	6.87
	442492	AA528489	Hs.234518	ribosomal protein L23	6.84
35	417365	D50683	Hs.82028	transforming growth factor, beta recepto	6.80
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	6.80
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	6.80
	435684	NM_001290	Hs.4980	LIM domain binding 2	6.80
	442685	AB033017	Hs.8594	KIAA1191 protein	6.79
40	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	6.77
	411789	AF245505	Hs.72157	Adiclan	6.76
	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	6.75
	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	6.74
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.72
45	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	6.70
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	6.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.70
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	6.70
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	6.70
50	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	6.70
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	6.66
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	6.65
	406858	AI865720	Hs.29797	ribosomal protein L10	6.65
	435748	AA699756	Hs.117335	ESTs	6.63
55	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	6.62
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	6.62
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.61
	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.60
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	6.55
60	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	6.50
	450294	H42587	Hs.238730	hypothetical protein MGC10823	6.45
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	6.45
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	6.43
	402145			Target Exon	6.43
65	414662	AL036058	Hs.76807	major histocompatibility complex, class	6.42
	436860	H12751	Hs.5327	PRO1914 protein	6.40
	438962	BE046594		gb:hn41c11.x1 NCL_CGAP_RDF2 Homo sapiens	6.40
	435937	AA830893	Hs.119769	ESTs	6.40
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	6.40
70	446173	BE565849	Hs.14158	copine III	6.39
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	6.36
	412093	BE242691	Hs.14947	ESTs	6.34
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.30
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.30
75	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.30
	447519	U46258	Hs.339665	ESTs	6.30
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	6.30
	434423	NM_006769	Hs.3844	LIM domain only 4	6.30
	434524	AA635931	Hs.249716	ESTs	6.30
80	441970	AW959918	Hs.73737	ESTs	6.30
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	6.30
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	6.25
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	6.23
	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.20
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.20
	447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f	6.20
	417315	AI080042	Hs.180450	ribosomal protein S24	6.20

	418840	AI821614	Hs.185831	ESTs	6.20
	410668	BE379794	Hs.159651	hypothetical protein	6.16
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.13
5	413840	AI301558		RNA binding motif protein, X chromosome	6.13
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	6.12
	450944	AA554989		sudD (suppressor of bimD6, Aspergillus n	6.10
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	6.10
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.10
10	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	6.10
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.10
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	6.10
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.09
	435812	AA700439	Hs.188490	ESTs	6.06
	432805	X94630	Hs.3107	CD97 antigen	6.06
15	441283	AA927670	Hs.131704	ESTs	6.06
	417632	R20855	Hs.5422	glycoprotein M6B	6.00
	435905	AW997484	Hs.5003	KIAA0456 protein	6.00
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	5.99
	429083	Y09397	Hs.227817	BCL2-related protein A1	5.95
20	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	5.95
	425291	AA354572		gb:EST62857 Jurkat T-cells V Homo sapien	5.95
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	5.93
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	5.90
25	447217	BE465754	Hs.17778	neuropilin 2	5.90
	417228	AL134324	Hs.7312	ESTs	5.86
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.86
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.84
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.84
	414483	R25513	Hs.10683	ESTs	5.82
30	428570	AA430321	Hs.293945	ESTs	5.81
	443194	AI954968		matrix Gla protein	5.80
	429582	AI569068	Hs.22247	ESTs	5.80
	414405	AI362533		KIAA0306 protein	5.80
35	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	5.80
	437739	AW579216	Hs.264610	ESTs, Moderately similar to lbd1 [H.sapi	5.80
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	5.80
	442821	BE391929	Hs.8752	transmembrane protein 4	5.77
	434511	R28982	Hs.18106	ESTs	5.76
40	406745	AW511970	Hs.279860	tumor protein, translationally-controlle	5.70
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	5.70
	453115	AW772041	Hs.18439	ESTs, Moderately similar to JC5238 galac	5.70
	406857	AA613726	Hs.29797	ribosomal protein L10	5.69
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	5.68
45	444273	AI903474	Hs.230	fibromodulin	5.65
	441623	AA315805		desmoglein 2	5.63
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	5.63
	440099	AL080058	Hs.6909	DKFZP564G202 protein	5.60
50	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	5.60
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associated	5.60
	422610	AF153820	Hs.1547	potassium inwardly-rectifying channel, s	5.60
	438278	BE409248	Hs.57988	hypothetical protein FLJ22357 similar to	5.58
	430451	AA836472	Hs.297939	cathepsin B	5.57
	406699	L06505	Hs.182979	ribosomal protein L12	5.53
55	458965	AA010319	Hs.60389	ESTs	5.50
	430592	AJ224864	Hs.9688	leukocyte membrane antigen(IRC1)	5.50
	433655	AL036559	Hs.3463	ribosomal protein S23	5.50
	428471	X57348	Hs.184510	stratifin	5.42
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	5.40
60	417849	AW291587	Hs.82733	nidogen 2	5.40
	408989	AW361666	Hs.49500	KIAA0746 protein	5.40
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	5.40
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	5.40
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	5.40
65	406819	AA908472		gb:og82a10.s1 NCL_CGAP_Ov8 Homo sapiens	5.39
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.36
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.34
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.34
	427968	AI857607	Hs.181301	cathepsin S	5.32
70	429307	AU076592	Hs.198951	jun B proto-oncogene	5.30
	424950	AA602917	Hs.156974	ESTs	5.30
	410619	BE512730	Hs.65114	keratin 18	5.30
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.27
	425430	BE185921	Hs.98073	ESTs, Moderately similar to Z195_HUMAN Z	5.27
75	411165	NM_000169	Hs.69089	galactosidase, alpha	5.26
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	5.26
	435631	BE254086	Hs.29647	uncharacterized hematopoietic stem/proge	5.24
	418905	BE539674		actinin, alpha 4	5.23
	449303	AK001495	Hs.23467	hypothetical protein FLJ10633	5.22
80	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	5.20
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	5.20
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	5.20
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	5.20

	409604	AW444448	Hs.49124	ESTs	5.20
	432581	AU076465	Hs.278441	KIAA0015 gene product	5.16
	430556	AW967807	Hs.13797	ESTs	5.16
5	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5.16
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subunit	5.15
	454227	AW963897	Hs.44743	KIAA1435 protein	5.15
	429367	AB007867	Hs.278311	plexin B1	5.12
	452191	AU076408	Hs.28309	UDP-glucose dehydrogenase	5.11
10	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis, clone NT	5.11
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	5.10
	443030	R68048	Hs.9238	hypothetical protein FLJ23516	5.10
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	5.10
	424875	AI187945	Hs.199310	ESTs	5.10
	427641	AI270591	Hs.146116	ESTs	5.10
15	442806	AW294522	Hs.149991	ESTs	5.10
	442495	AI184717		ESTs	5.10
	439941	AI392640	Hs.18272	amino acid transporter system A1	5.10
	444981	AW855398	Hs.12210	hypothetical protein FLJ13732 similar to	5.09
20	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.07
	418117	AI922013	Hs.83496	linker for activation of T cells	5.06
	431824	AW972842		gb:EST384937 MAGE resequences, MAGL Homo	5.06
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	5.06
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	5.03
	431805	NM_014053	Hs.270594	FLVCR protein	5.00
25	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	5.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	5.00
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	5.00
	443634	H73972	Hs.134460	ESTs	5.00
30	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	5.00
	444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathi	4.97
	422200	AA080895	Hs.347969	cytochrome c oxidase subunit IV	4.95
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	4.94
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	4.94
35	452063	R53185	Hs.32366	ESTs, Weakly similar to TWST_HUMAN TWIST	4.93
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.93
	429558	AI391454	Hs.207251	nucleolar autoantigen (55kD) similar to	4.92
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	4.92
	433162	AI025842		ESTs	4.92
40	406797	AI432224		ribosomal protein L6	4.91
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	4.90
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	4.90
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	4.90
	447832	AI433357		ESTs	4.90
45	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697 hypotheti	4.90
	413593	AA205248		gb:zq78c12.r1 Stratagene hNT neuron (937	4.90
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	4.90
	441224	AU076964	Hs.7753	calumenin	4.90
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	4.90
50	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.90
	417308	H60720	Hs.81892	KIAA0101 gene product	4.90
	438763	AI583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	4.89
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.89
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	4.88
55	421748	NM_014718	Hs.107809	KIAA0726 gene product	4.87
	427486	AA974433		fibroblast growth factor 4 (heparin secr	4.86
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	4.82
	406867	AA157857	Hs.182265	keratin 19	4.81
	449378	AW664026	Hs.59892	ESTs	4.81
60	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	4.80
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	4.80
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.80
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	4.79
65	441321	H17182	Hs.7771	B-cell associated protein	4.75
	448896	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFzP762M127 (fr	4.75
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	4.73
	449317	AW293413	Hs.132906	19A24 protein	4.73
	436372	AW972301	Hs.310286	ESTs	4.71
70	422082	AA016188	Hs.111244	hypothetical protein	4.70
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	4.70
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	4.70
	446659	AI335361	Hs.226376	ESTs	4.70
	414829	AA321568	Hs.77436	pleckstrin	4.70
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	4.70
75	417677	NM_016055	Hs.82389	CGI-118 protein	4.70
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.70
	423766	AA303799	Hs.300141	ribosomal protein L39	4.70
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	4.69
	453485	BE620712	Hs.33026	hypothetical protein PP2447	4.67
80	452973	H88409	Hs.40527	ESTs	4.67
	427816	AA159248	Hs.180909	peroxiredoxin 1	4.67
	406794	AI890243		ribosomal protein L6	4.66
	449475	AI348027	Hs.108557	hypothetical protein PP1057	4.65

	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.64
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	4.62
	407874	AI766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	4.61
	417535	AA203569	Hs.191482	ESTs	4.61
5	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	4.61
	408491	AI088063	Hs.7882	ESTs	4.60
	428398	AI249368	Hs.98558	ESTs	4.60
	410295	AA741357		nidogen (enactin)	4.60
10	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.60
	440327	R12581	Hs.191146	ESTs	4.60
	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.60
	426141	C05886	Hs.293972	ESTs	4.60
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	4.59
15	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.58
	416987	D86957	Hs.80712	KIAA0202 protein	4.57
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.57
	416581	H66276	Hs.108288	ESTs	4.56
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	4.56
20	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	4.56
	413663	BE247585	Hs.75462	BTG family, member 2	4.55
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, rec	4.54
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	4.53
	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	4.52
25	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	4.51
	440774	AI420611	Hs.153934	ESTs	4.51
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	4.51
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	4.51
	449267	AI638640	Hs.220624	ESTs	4.51
30	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.50
	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	4.50
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypothe	4.50
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	4.50
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	4.50
35	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	406623	X69392	Hs.91379	ribosomal protein L26	4.49
	456642	AW451623	Hs.109752	putative c-Myc-responsive	4.47
	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.47
	408307	AI761786	Hs.204674	ESTs	4.46
40	428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito	4.46
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.45
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	4.45
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	4.45
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.44
45	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	4.44
	428773	BE256238	Hs.193163	bridging integrator 1	4.43
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	4.43
	437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	4.43
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	4.43
50	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	4.42
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	4.41
	424868	AI568170	Hs.96886	ESTs	4.41
	408380	AF123050	Hs.44532	diubiquitin	4.40
	411960	R77776	Hs.18103	ESTs	4.40
55	428782	X12830	Hs.193400	interleukin 6 receptor	4.40
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	4.40
	456629	AW891965		histone deacetylase 3	4.40
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	4.40
	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypothe	4.39
60	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	4.39
	427779	AA906997	Hs.180780	TERA protein	4.38
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.37
	413276	Z24725	Hs.75260	mitogen inducible 2	4.36
	452651	AI218918	Hs.30209	KIAA0854 protein	4.35
65	453467	AI535997	Hs.30089	ESTs	4.35
	435961	BE293127	Hs.283722	GTT1 protein	4.35
	415691	AW963979	Hs.24723	ESTs	4.34
	435968	AW161481	Hs.111577	integral membrane protein 3	4.34
	420099	D80011	Hs.95140	KIAA0189 gene product	4.33
70	421522	R48881	Hs.102991	hypothetical protein FLJ13956	4.33
	457073	AA233210	Hs.179943	ribosomal protein L11	4.31
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.31
	420732	AA789133	Hs.63525	ESTs	4.30
	432731	R31178	Hs.287820	fibronectin 1	4.30
75	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.30
	408784	AW971350	Hs.63386	ESTs	4.30
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	4.30
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.30
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	4.30
80	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.30
	413677	AW503116	Hs.301819	zinc finger protein 146	4.29
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.28
	408896	AI610447	Hs.48778	niban protein	4.26
	433550	AA989061	Hs.177376	ESTs	4.26

	406230		Target Exon	4.25
	435655	AW105663	Hs.6947 HSPC069 protein	4.25
	448717	R67419	Hs.21851 Homo sapiens cDNA FLJ12900 fis, clone NT	4.24
5	437386	W52452	ribosomal protein L10	4.24
	416759	AK000978	Hs.79741 hypothetical protein FLJ10116	4.23
	447341	AF106941	Hs.18142 arrestin, beta 2	4.22
	410423	AW402432	Hs.63489 protein tyrosine phosphatase, non-recept	4.22
	409453	AI885516	Hs.95612 ESTs	4.22
10	428453	AB011110	Hs.184367 GTPase activating protein-like	4.22
	444681	AJ243937	Hs.288316 chromosome 6 open reading frame 9	4.21
	416072	AL110370	Hs.79000 growth associated protein 43	4.20
	450937	R49131	Hs.26267 ATP-dependant interferon response protei	4.20
	447595	AW379130	Hs.18953 phosphodiesterase 9A	4.20
15	418452	BE379749	Hs.85201 C-type (calcium dependent, carbohydrate-	4.20
	430594	AK000790	Hs.246885 hypothetical protein FLJ20783	4.20
	425259	AL049280	Hs.155397 Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.20
	431560	BE244135	Hs.260238 hypothetical protein FLJ10842	4.20
20	439403	BE265745	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.20
	409245	AA361037	IRNA isopentenylpyrophosphate transferas	4.18
	437296	AA350994	Hs.20281 KIAA1700	4.17
	406877	AA226392	Hs.179943 ribosomal protein L11	4.17
	419652	AL157485	Hs.91973 hypothetical protein	4.15
	406661	X66975	Hs.172550 polypyrimidine tract binding protein (ha	4.15
25	452432	AW206008	Hs.283378 Homo sapiens cDNA: FLJ21778 fis, clone H	4.14
	448782	AL050295	KIAA0758 protein	4.14
	407110	AA018042	Hs.252085 Prader-Willi/Angelman syndrome-5	4.14
	422960	AW890487	cadherin 13, H-cadherin (heart)	4.13
30	432841	M93425	Hs.62 protein tyrosine phosphatase, non-recept	4.12
	415857	AA866115	Hs.127797 Homo sapiens cDNA FLJ11381 fis, clone HE	4.11
	420298	AI199510	Hs.267912 ESTs, Weakly similar to ALU7_HUMAN ALU S	4.11
	419726	U50330	Hs.1274 bone morphogenetic protein 1	4.11
	426075	AW513691	Hs.270149 ESTs, Weakly similar to 2109260A B cell	4.10
	430255	AK000703	Hs.323822 Homo sapiens mRNA for KIAA1551 protein,	4.10
35	418699	BE539639	Hs.173030 ESTs, Weakly similar to ALU8_HUMAN ALU S	4.10
	443035	Z45822	Hs.8906 Homo sapiens clone 24889 mRNA sequence	4.10
	457415	AK000010	Hs.258798 hypothetical protein FLJ20003	4.10
	412220	BE350058	Hs.36787 chromodomain helicase DNA binding protei	4.10
	427509	M62505	Hs.2161 complement component 5 receptor 1 (C5a l	4.10
40	444633	AF111713	Hs.286218 junctional adhesion molecule 1	4.10
	441384	AA447849	Hs.288660 Homo sapiens cDNA: FLJ22182 fis, clone H	4.09
	431958	X63629	Hs.2877 cadherin 3, type 1, P-cadherin (placenta	4.09
	422310	AA316622	Hs.98370 cytochrome P450, subfamily IIS, polypept	4.08
	439815	AA206079	Hs.6693 hypothetical protein FLJ20420	4.07
45	417930	H81136	Hs.334604 Homo sapiens mRNA for KIAA1870 protein,	4.06
	418458	AA332941	Hs.85226 lipase A, lysosomal acid, cholesterol es	4.06
	424464	R68537	Hs.17962 ESTs	4.06
	417035	AA192455	Hs.22968 Homo sapiens clone IMAGE:451939, mRNA se	4.06
	412627	BE391959	Hs.74276 chloride intracellular channel 1	4.06
50	414890	BE281095	Hs.77573 uridine phosphorylase	4.05
	452248	AA093668	Hs.28578 muscleblind (Drosophila)-like	4.05
	450887	AA011518	Hs.271778 ESTs, Weakly similar to I38022 hypotheti	4.05
	444224	AV648599	Hs.199438 ESTs	4.05
	451351	AW058261	Hs.321435 ESTs, Weakly similar to ALU1_HUMAN ALU S	4.04
55	407792	AI077715	Hs.39384 putative secreted ligand homologous to f	4.04
	439864	AI720078	Hs.291997 ESTs, Weakly similar to A47582 B-cell gr	4.04
	408745	AW936356	Hs.300925 ESTs, Weakly similar to A46010 X-linked	4.03
	409132	AJ224538	Hs.50732 protein kinase, AMP-activated, beta 2 no	4.01
	410597	W16518	Hs.279518 amyloid beta (A4) precursor-like protein	4.01
60	409485	S80990	Hs.252136 ficolin (collagen/fibrinogen domain-cont	4.01
	426398	BE256390	Hs.169718 calponin 2	4.01
	417777	AI823763	Hs.7055 ESTs, Weakly similar to I78885 serine/th	4.01
	446979	AI654443	Hs.197683 ESTs	4.00
	416000	R82342	Hs.79856 ESTs, Weakly similar to S65657 alpha-1C-	4.00
65	426647	AA243464	Hs.294101 pre-B-cell leukemia transcription factor	4.00
	436394	AA531187	Hs.126705 ESTs	4.00
	409956	AW103364	Hs.727 inhibin, beta A (activin A, activin AB a	4.00
	414602	AW630088	Hs.76550 Homo sapiens mRNA; cDNA DKFZp564B1264 (f	4.00
	446013	AI360167	Hs.152774 ESTs	4.00
70	452404	AW450675	Hs.212709 ESTs	4.00
	444736	AA533491	Hs.23317 hypothetical protein FLJ14681	4.00
	438590	AA811465	Hs.123375 ESTs	4.00
	451838	AW005866	Hs.193969 ESTs	4.00
	449832	AA694264	Hs.60049 ESTs	4.00

TABLE 55B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
------	------------	-----------







5

413703 376077\_1  
406870 0\_0  
456629 207\_22

10

15

20

25

30

437386 5541\_2

35

439403 4937\_10  
409245 3199\_2

40

45

448782 34980\_1

50

422960 11862\_2

55

TABLE 55C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

65

Pkey	Ref	Strand	Nt_position
401466	6682292	Plus	28748-29023
401192	9719502	Minus	69559-70101
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402145	8018280	Plus	113086-114800
406230	4760409	Plus	71716-72515

70

75

TABLE 56A:

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UnigenelD: Unigene number  
Unigene Title: Unigene gene title  
R1: Ratio of seminomatous testicular cancer compared to normal adult testicular tissues

80

Pkey	ExAccn	UnigenelD	Unigene Title	R1
414438	AI879277	Hs.76136	thioredoxin	47.30

AI336371 AI989381 AI131425 AI147483 AI311537 AW338638 AI141649 AA709414 AI187177 AA780884 AI333805 AA045312 AI623918 AI349421  
W63753 W70299 AA557276 AA299007 N98212 W74064 N24823 T54892 AA054724 W73059 AI869152 N93462 N71889 AI537432 R71628  
AA303089 AI498550 T60941 AV706417 AW067848 AI150677 AW338118 AI336313 AA826256 AI139518 AA662948 AA902723 AI970175 W68682  
AI089380 AI148372 H99951 AW183001 AI270317 AA532767 AA044727 AA931652 R82469 AA150261 W67788 H67495 R80715 AW149812 N78914  
AI862034 W61122 AW023118 W69375 T88917 T47984 N21531 R35646 AA055544 H15534 AA688295 AA090586 AA044764 BF994641 R79547  
N21313 BF674610 H02874 AW975323 R16904 AA328030 AA054671 R79546 BF832310 AI249109  
BG015794 BE158357 BE158353 BE158358 BE158360 BE158352 BE158351 BE158355  
AA075144  
AW891965 AW604749 BE080872 R15559 BE177623 AW883520 AW945343 AI246167 T07082 AW805679 W96278 AA135796 W32615 AW995418  
AW801688 BE003837 AW801621 AW385721 AW385742 AW385714 AW604757 W87409 AW604738 AW385757 AW580796 AW801247 BE003239  
BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW362791 AW604759 AW866589 AW604758 N44337 AI378548  
AW890438 AA077172 AI288683 AA229639 AA091945 AW945454 AA063629 AA702504 AW861938 AW894816 AW580841 AA094372 T06399  
AW885686 BE244086 BE005035 AW861913 AA551773 AW858460 AW370926 AW754352 AW889695 AW384408 AI907428 BE067491 AW861939  
AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE067470 AW894935 BE082529 AI248811 BE179917 BE002200  
AW607506 AW392889 AW894560 AW381360 AI904206 AW863533 C00609 AW381372 BE082530 AW898120 BE075323 AW392799 AW601420  
AI695314 BE083790 AW858568 AW945550 BE177153 AW970506 BE350419 AI906919 AW360794 AI906917 AW885979 AW794240 AW945566  
AI688683 AI688694 AW009660 AW601421 AW360793 BE066524 BE083901 AW369847 AW361871 AW935435 AW664582 AW877775 AW838449  
BE180466 AW858501 BE180464 AI371163 AA778231 AI174991 BE011720 AW877776 AW877800 AW877795 T19900 AW866365 AW898099  
BE011715 BE167842 BE011718 BE011724 AW363639 AW878658 AW878662 AW894887 BE082356 AW389211 AW804286 AW610312 AI904717  
AW610318 AW996909 AW610296 AW901923 AW880003 AI762171 AW062582 AW368713 AW062593 AW176663 AW842064 AW842089  
AW842095 AI243049 AW902074 AW062592 AW176664 AW751692 BE087703 AI907439 BE009686 BE172115 BE077030 AW608556 AW835577  
AI909628 BE077029 AW176241 BE077552 BE160370 BE160288 AW835656 AW606765 AW606770 AW835678 AW606758 AW606778 AI907484  
BE172821 AW606768 AW999517 AW844165 BE171738 AW751683 AW610493 BE177484 BE177487 AA090510 AW841117 BE173367 AW999878  
AI124870 BE163472 AW841823 AW379762 AW893297 AI290296 BE089132 AA610287 AW176676 AW607622 BE172639 AW893232 AA329629  
BE089008 BE178350 BE178214 BE063291 AW820236 AW999653 BE089486 BE173126 BE171775 BE185787 AA58280 AI174840 AW999912  
BE218391 BE172734 BE178021 BE172738 BE173324 AW603494 AL036722 R38192 R60905 H53721 H41052 AL037917 R37795 AW998972  
AA767189 AW044272 H50689 AA768399 AA767764 AI087888 H44202 BE222792 N90597 W81396 N90615 AI935353 BE501168 F10945  
AW118215 AI970480 AI627641 AW236081 AA574090 AI627652 AI681913 AI759983 N69591 N69276 BE467722 AW392780 BE172467 H92861  
AI524921 F02989 Z39328 F02705 F01414 T88678 AI215165 H87220 AW374781  
BM476605 BI545004 BI834636 BG112453 BI199049 BG112759 AA149846 H97925 AA306121 AA313204 W52451 AI734997 AA931168 AA429766  
N47913 AA584321 BF940241 AI083648 AI089410 AI347705 AI343661 AI186232 AI889031 N98464 AI820039 AI459034 AV652512 AA622990  
BE857200 AA932998 AA740573 AI826264 AA865683 AI344550 AI027349 AI056087 AA442777 AA603724 AA873347 AI056717 AI092185 AI032895  
AA535689 BF806025 BF806061 BF805985 BF746099 BF746097 AI309259 AI597603 BF806066 AI090653 AI129205 AI248410 H72993 AW615341  
BF805990 BF805982 AA993819 T34373 T35604 H56242 AA648145 T35907 BF808691 N94015 AV703438 BG774276 H82341 R76371  
AK056692 AF086220 AI375066 AA284293 W32566 AW797961 AA960897 AA504145  
AF030234 BC017465 BG008526 AW505550 BM450141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857  
AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R66856 H01374 BI257369 BI259830  
AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024  
BF093291 AW021929 H22650 AA459715 BG496341 BE697763 BI254209 BG499543 H42946 BI059780 BI086741 H87896 H87599 BF691752  
BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF909744 AW966003 AV714014 BI492868 BI495144 AA921845  
AI693426 AI652147 AI435449 N47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897  
AW665247 AW340077 N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AI080245  
AA884954 AI125702 AI382934 AA931835 AI358631 AW439905 AI027833 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI768667  
AA948472 AI819214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AW42769 D56771 AA095911 BE222062  
D56772 AW372265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI492848  
H16217 H21980 H22651 H88179 H87354 H44052 H25165 H44128  
AB018301 AL050295 BF513128 AW385080 AL551708 AI352542 AI829703 AI819388 AW629019 AW073189 AW273857 AW118768 AI453845  
AI452494 AA886341 AI057144 AA904647 AI423547 AW263913 AI094774 AI434419 AI039546 AI002491 AI240412 Z25099 AA995178 AW050649  
AW026140 AI796309 AI584012 BE166666 AI767591 AI309041 AA724059 AI695284 AI245095 T63971 Z40627 BE166681 BG570071 BF921915  
BI562702 BG506502 AV658066 R48378 AA121543 AI096938 AA618131 H40993 R48277 AI352281 BG540263 BG538901 N95226 AI356752  
AI221152 Z28777 R16574 AW966449 AA044116 AW797518 BI010405 AA044288 AI093508 BE140169 T64039 BG433106 AW130367 AW130361  
N73937 AA127680 AW044037 AI096437 AA384077 BF941499 T93764 BG003285  
BF090249 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119  
AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260

5	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	44.80
	438091	AW373062		nuclear receptor subfamily 1, group I, m	40.10
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	34.90
	417088	M54915	Hs.81170	p1m-1 oncogene	31.10
	430542	AI557486	Hs.119122	ribosomal protein L13a	29.60
10	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	29.10
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	28.15
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	28.13
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	28.10
	406658	AI920965	Hs.77961	major histocompatibility complex, class	27.85
15	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	27.70
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	27.20
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.30
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	25.80
	429978	AA249027		ribosomal protein S6	25.40
20	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	24.60
	440207	AI371978	Hs.128326	ESTs	24.50
	425543	R23313	Hs.334895	ribosomal protein L10a	24.30
	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	24.10
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	24.05
25	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	24.00
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	22.90
	420367	AA259090	Hs.257028	ESTs	22.90
	406856	AW515336	Hs.29797	ribosomal protein L10	22.77
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	22.75
30	412636	NM_004415		desmoplakin (DPI, DPII)	22.40
	420676	AI434780	Hs.4248	vav 2 oncogene	22.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	21.40
	446627	AI973016	Hs.15725	hypothetical protein SBBI48	21.20
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	21.10
35	420754	W79431	Hs.346911	ribosomal protein L22	20.98
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	20.90
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	20.80
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	19.50
40	422714	AB018335	Hs.119387	KIAA0792 gene product	19.15
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.00
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	18.50
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.50
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.00
45	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	17.90
	448588	AI970276	Hs.156905	KIAA1676	17.70
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	17.50
	428782	X12830	Hs.193400	interleukin 6 receptor	17.40
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIb	17.20
50	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	17.15
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	17.10
	440528	BE313555	Hs.7252	KIAA1224 protein	17.06
	410143	AA188169		KIAA1191 protein	17.05
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.90
55	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	16.70
	429183	AB014604	Hs.197955	KIAA0704 protein	16.70
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	16.60
	449571	AW016812	Hs.200266	ESTs	16.50
	432730	AI066520	Hs.131358	ESTs	16.20
60	426295	AW367283		zinc finger protein 6 (CMPX1)	16.15
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	15.90
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	15.80
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	15.80
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
65	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	15.50
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	14.90
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	14.90
	406656	M16714	Hs.89643	major histocompatibility complex, class	14.85
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	14.71
70	450377	AB033091		KIAA1265 protein	14.70
	425996	W67330		hypothetical protein AL110115	14.60
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	14.60
	427691	AW194426	Hs.20726	ESTs	14.42
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	14.35
75	451106	BE382701	Hs.25960	N-MYC oncogene	14.21
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	14.13
	436860	H12751	Hs.5327	PRO1914 protein	13.90
	446899	NM_005397	Hs.16426	podocalyxin-like	13.90
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	13.75
80	408380	AF123050	Hs.44532	diubiquitin	13.70
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	13.40
	427521	AW973352		ESTs	13.30
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.25
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	13.23
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	13.23
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	12.70
	426552	BE297660	Hs.170328	moesin	12.69

5	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.55
	436398	H87136	Hs.5174	ribosomal protein S17	12.50
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.30
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.30
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	12.28
10	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	12.25
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	12.25
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	12.20
	419384	AA490866	Hs.39429	ESTs	12.20
	410185	BE294068	Hs.737	immediate early protein	12.15
15	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	12.05
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.00
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	11.90
	408989	AW361666	Hs.49500	KIAA0746 protein	11.80
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	11.80
20	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.80
	410325	AB023154	Hs.62264	KIAA0937 protein	11.70
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	11.70
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	11.61
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	11.60
25	454413	AI653672	Hs.40092	PNAS-123	11.60
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	11.40
	428065	AI634046	Hs.157313	ESTs	11.40
	432805	X94630	Hs.3107	CD97 antigen	11.36
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.35
30	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	11.30
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	11.30
	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	11.11
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	11.00
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.00
35	406786	AW161678	Hs.111334	ferritin, light polypeptide	10.95
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	10.90
	444656	AI277924	Hs.145199	ESTs	10.90
	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	10.85
	440774	AI420611	Hs.153934	ESTs	10.82
40	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	10.80
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	10.80
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.80
	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	10.70
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	10.65
45	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	10.60
	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	10.43
	424800	AL035588	Hs.153203	MyoD family inhibitor	10.40
	446682	AW205632	Hs.211198	ESTs	10.40
	447211	AL161961	Hs.17767	KIAA1554 protein	10.31
50	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	10.30
	422105	AI929700	Hs.111680	endosulfine alpha	10.21
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	10.20
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	10.20
	452651	AI218918	Hs.30209	KIAA0854 protein	10.15
55	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	10.11
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	10.10
	427761	AA412205	Hs.140996	ESTs	10.10
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	9.90
	402145			Target Exon	9.82
60	413686	AI469213	Hs.71404	ESTs	9.80
	446488	AB037782	Hs.15119	KIAA1361 protein	9.80
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	9.80
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	9.80
	407179	AA206465		thymosin, beta 4, X chromosome	9.72
65	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	9.70
	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	9.70
	446795	AI797713	Hs.156471	ESTs	9.70
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	9.65
	451864	N20370	Hs.69547	ESTs	9.65
70	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	9.60
	419904	AA974411	Hs.18672	ESTs	9.60
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.60
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	9.52
	424950	AA602917	Hs.156974	ESTs	9.50
75	447534	AW953935	Hs.288655	ESTs	9.50
	419223	X60111	Hs.1244	CD9 antigen (p24)	9.41
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.40
	422960	AW890487		cadherin 13, H-cadherin (heart)	9.33
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	9.32
80	408784	AW971350	Hs.63386	ESTs	9.30
	417407	AA923278	Hs.290905	ESTs, Weakly similar to prolease [H.sapi	9.30
	432409	AA806538	Hs.130732	KIAA1575 protein	9.30
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	9.30
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.22
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.20
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.20
	434524	AA635931	Hs.249716	ESTs	9.20

	450294	H42587	Hs.238730	hypothetical protein MGC10823	9.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.10
	434442	AA737415		ESTs	9.10
5	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.03
	447519	U46258	Hs.339665	ESTs	9.00
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	8.98
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	8.90
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypothe	8.90
10	442806	AW294522	Hs.149991	ESTs	8.90
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	8.89
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	8.81
	408437	AW957744	Hs.278469	lacrimal proline rich protein	8.80
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	8.80
15	431187	AW971146	Hs.293187	ESTs	8.80
	421098	AI697901	Hs.192425	ESTs	8.70
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	8.70
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	8.70
	401091			decay accelerating factor for complement	8.62
20	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	438089	W05391		nuclear receptor subfamily 1, group I, m	8.60
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	8.60
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	8.59
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	8.56
	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.50
25	414829	AA321568	Hs.77436	pleckstrin	8.50
	430162	AW450843	Hs.346348	ESTs	8.50
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	8.50
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.45
	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.43
30	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	8.40
	433208	AW002834	Hs.24095	ESTs	8.40
	428970	BE276891	Hs.194691	retinoic acid induced 3	8.38
	425284	AF155568		NS1-associated protein 1	8.33
35	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.33
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	8.30
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	8.30
	453716	AA037675	Hs.152675	ESTs	8.30
	418840	AI821614	Hs.185831	ESTs	8.20
40	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	8.20
	449656	AA002008	Hs.188633	ESTs	8.20
	425535	AB007937	Hs.158287	KIAA0468 gene product	8.17
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.13
	432559	AW452948	Hs.257631	ESTs	8.10
45	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.10
	420099	D80011	Hs.95140	KIAA0189 gene product	8.01
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	8.00
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.00
	434423	NM_006769	Hs.3844	LIM domain only 4	8.00
50	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	8.00
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	7.92
	433655	AL036559	Hs.3463	ribosomal protein S23	7.89
	435968	AW161481	Hs.111577	integral membrane protein 3	7.89
	434511	R28982	Hs.18106	ESTs	7.88
55	423523	AW299828	Hs.193580	ESTs	7.86
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	7.84
	411960	R77776	Hs.18103	ESTs	7.80
	434159	AW135214	Hs.191828	ESTs	7.80
	447500	AI381900	Hs.159212	ESTs	7.80
60	406699	L06505	Hs.182979	ribosomal protein L12	7.75
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	7.68
	426759	AI590401	Hs.21213	ESTs	7.66
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.62
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	7.60
65	444795	AI193356	Hs.160316	ESTs	7.60
	406663	U24683		immunoglobulin heavy constant mu	7.59
	442821	BE391929	Hs.8752	transmembrane protein 4	7.56
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.52
	407252	AA659037	Hs.163780	ESTs	7.50
70	414405	AI362533		KIAA0306 protein	7.50
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.50
	429999	AI761902	Hs.99597	ESTs	7.50
	441436	AW137772	Hs.185980	ESTs	7.50
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	7.50
75	420943	AI718702	Hs.279930	major histocompatibility complex, class	7.46
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.43
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.42
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	7.41
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	7.40
80	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	7.40
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	7.40
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	7.40
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	7.40
	432598	AI341227	Hs.157106	ESTs	7.38

	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.34
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.30
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.30
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.30
5	437103	AW139408	Hs.152940	ESTs	7.30
	442495	AI184717		ESTs	7.30
	445929	AI089660	Hs.323401	dpy-30-like protein	7.30
	446013	AI360167	Hs.152774	ESTs	7.30
10	436075	BE090176	Hs.179902	transporter-like protein	7.20
	450139	AK001838		serum/glucocorticoid regulated kinase	7.20
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	7.17
	406819	AA908472		gb:og82a10.s1 NCI_CGAP_Ov8 Homo sapiens	7.16
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.12
15	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	7.10
	413886	AW958264	Hs.103832	similar to yeast Upt3, variant B	7.10
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	7.10
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	7.10
	427254	AL121523	Hs.97774	ESTs	7.10
20	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.10
	438980	AW502384		gb:U1-HF-BR0p-aka-f-12-0-U1.r1 NIH_MGC_5	7.10
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	7.10
	441878	AI801869	Hs.127982	ESTs	7.09
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.04
25	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	7.00
	417315	AI090042	Hs.180450	ribosomal protein S24	7.00
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.00
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.00
	445245	AB032973	Hs.12461	LCHN protein	7.00
30	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.00
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	6.97
	410397	AF217517	Hs.63042	DKFZp564J157 protein	6.96
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	6.96
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	6.95
35	418134	AA397769	Hs.86617	ESTs	6.90
	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	6.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	6.90
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheri	6.89
	451838	AW005866	Hs.193969	ESTs	6.88
40	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	6.87
	453485	BE620712	Hs.33026	hypothetical protein PP2447	6.85
	401466			vesicle-associated membrane protein 4	6.84
	457073	AA233210	Hs.179943	ribosomal protein L11	6.83
	412093	BE242691	Hs.14947	ESTs	6.83
45	442492	AA528489	Hs.234518	ribosomal protein L23	6.83
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	6.83
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	6.82
	416401	N80139	Hs.268916	ESTs	6.80
	426501	AW043782	Hs.293616	ESTs	6.80
50	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	6.80
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	6.80
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.80
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.79
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	6.77
55	425277	NM_001241	Hs.155478	cyclin T2	6.72
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	6.70
	428728	NM_016625	Hs.191381	hypothetical protein	6.70
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	6.70
	433735	AA608955	Hs.109653	ESTs	6.70
60	430556	AW967807	Hs.13797	ESTs	6.69
	417535	AA203569	Hs.191482	ESTs	6.69
	418117	AI922013	Hs.83496	linker for activation of T cells	6.67
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.65
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	6.62
65	447341	AF106941	Hs.18142	arrestin, beta 2	6.61
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	6.60
	442460	NM_014135	Hs.8345	PRO0641 protein	6.60
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	6.59
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.57
70	415221	W07418	Hs.78225	annexin A1	6.56
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.54
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	6.51
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	6.50
	441224	AU076964	Hs.7753	calumenin	6.50
75	443749	R38828	Hs.143463	ESTs	6.50
	448094	H24387	Hs.32061	ESTs, Weakly similar to I38022 hypotheri	6.50
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	6.40
	418259	AA215404		ESTs	6.40
	421633	AF121860	Hs.106260	sorting nexin 10	6.40
80	435937	AA830893	Hs.119769	ESTs	6.40
	445612	N94126	Hs.12969	hypothetical protein	6.40
	451653	W18193		ESTs, Moderately similar to HERC2 [H.sap	6.40
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.40
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	6.39

5	434817	AA082118	Hs.102737	goliath protein	6.38
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	6.35
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.34
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.33
	435812	AA700439	Hs.188490	ESTs	6.31
	401113			solute carrier family 22 (organic cation	6.30
	408418	AW963897	Hs.44743	KIAA1435 protein	6.30
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.30
10	426780	BE242284	Hs.172199	adenylate cyclase 7	6.30
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	6.30
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	6.30
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	6.30
	449576	AW014631	Hs.225068	ESTs	6.30
15	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	6.30
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.27
	411975	AI916058	Hs.144583	ESTs	6.26
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	6.25
	433162	AI025842		ESTs	6.23
20	449322	AI638616	Hs.196566	ESTs	6.22
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	6.20
	440327	R12581	Hs.191146	ESTs	6.20
	442832	AW206560	Hs.253569	ESTs	6.20
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	6.20
25	427968	AI857607	Hs.181301	cathepsin S	6.18
	414662	AI036058	Hs.76807	major histocompatibility complex, class	6.16
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.16
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	6.15
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.15
30	445493	AI915771		metallothionein 1E (functional)	6.15
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.14
	427477	AW973119	Hs.178391	ribosomal protein L44	6.14
	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypotheti	6.13
	443441	AW291196	Hs.92195	ESTs	6.12
35	413677	AW503116	Hs.301819	zinc finger protein 146	6.11
	406797	AI432224		ribosomal protein L6	6.10
	406857	AA613726	Hs.29797	ribosomal protein L10	6.10
	410387	AI277367	Hs.47094	ESTs	6.10
	410503	AW975746	Hs.188662	KIAA1702 protein	6.10
40	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	6.10
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.08
	406877	AA226392	Hs.179943	ribosomal protein L11	6.07
	407784	AW139585	Hs.12708	ESTs	6.05
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.05
45	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	6.01
	412949	AI471639	Hs.71913	ESTs	6.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	6.00
	435756	AI418466	Hs.33665	ESTs	6.00
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.00
50	441623	AA315805		desmoglein 2	5.98
	416926	H03109	Hs.263395	HT018 protein	5.96
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subuni	5.95
	441244	BE612935	Hs.184052	PP1201 protein	5.95
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.95
55	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	5.94
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	5.92
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	5.91
	433891	AA613792		gb:nc097h03.s1 NCI_CGAP_Pr2 Homo sapiens	5.90
	406542			C19000728*:gij12585552sp Q9Y2Q1 Z257_HU	5.90
60	406858	AI865720	Hs.29797	ribosomal protein L10	5.90
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.90
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	5.90
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	5.90
	455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	5.90
65	441321	H17182	Hs.7771	B-cell associated protein	5.88
	429083	Y09397	Hs.227817	BCL2-related protein A1	5.87
	406806	AW088535		ribosomal protein, large, P0	5.87
	416987	D86957	Hs.80712	KIAA0202 protein	5.86
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	5.83
70	428773	BE256238	Hs.193163	bridging integrator 1	5.83
	406794	AI890243		ribosomal protein L6	5.82
	457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	5.82
	435511	AA683336	Hs.189046	ESTs	5.81
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.80
75	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	5.80
	412528	AI123478	Hs.32112	ESTs	5.80
	424875	AI187945	Hs.199310	ESTs	5.80
	426981	AL044675	Hs.173081	KIAA0530 protein	5.80
	447711	AI459554	Hs.161286	ESTs	5.80
80	449961	AW265634	Hs.133100	ESTs	5.80
	416759	AK000978	Hs.79741	hypothetical protein FLJ10116	5.80
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	5.79
	422773	AB028962	Hs.301552	KIAA1039 protein	5.78
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	5.78



	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.77
	449317	AW293413	Hs.132906	19A24 protein	5.75
	425787	AA363867	Hs.155029	ESTs	5.73
5	414890	BE281095	Hs.77573	uridine phosphorylase	5.72
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	5.71
	435961	BE293127	Hs.283722	GTT1 protein	5.71
	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	5.70
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	5.70
10	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	5.70
	446659	AI335361	Hs.226376	ESTs	5.70
	457250	AA811987	Hs.125779	ESTs	5.70
	414150	AA136026		gb:zn88d07.r1 Stratagene lung carcinoma	5.68
	439924	AI985897	Hs.125293	ESTs	5.67
15	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.66
	451812	X81889	Hs.152151	plakophilin 4	5.65
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	5.63
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	5.63
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	5.60
20	431770	BE221880	Hs.268555	5'-3' exoribonuclease 2	5.60
	436511	AA721252	Hs.291502	ESTs	5.60
	446630	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	5.60
	406623	X69392	Hs.91379	ribosomal protein L26	5.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.57
25	416047	BE439894	Hs.78991	DNA segment, numerous copies, expressed	5.56
	437296	AA350994	Hs.20281	KIAA1700	5.56
	453985	N44545	Hs.251865	ESTs	5.56
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	5.55
	448877	AI583696	Hs.253313	ESTs	5.53
30	435748	AA699756	Hs.117335	ESTs	5.52
	420732	AA789133	Hs.63525	ESTs	5.51
	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	5.50
	430915	AA488953		gb:aa55e05.r1 NCI_CGAP_GCB1 Homo sapiens	5.50
	436716	AI433540		gb:ti69g05.x1 NCI_CGAP_Kid11 Homo sapien	5.50
35	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	5.50
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	5.50
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	5.50
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associa	5.50
	433701	AW445023	Hs.15155	ESTs	5.49
40	427640	AF058293	Hs.180015	D-dopachrome tautomerase	5.47
	420552	AK000492	Hs.98806	hypothetical protein	5.45
	449338	H73444	Hs.394	adrenomedullin	5.42
	427176	AW381569	Hs.40334	ESTs	5.42
	409945	AW015935	Hs.122642	ESTs	5.40
45	421568	W85858	Hs.99804	ESTs	5.40
	423961	D13666	Hs.136348	periostin(OSF-2os)	5.40
	440719	AA150869	Hs.26267	ATP-dependant interferon response protei	5.40
	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	5.40
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	5.40
50	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	5.40
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	5.39
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	5.38
	439815	AA206079	Hs.6693	hypothetical protein FLJ20420	5.37
	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	5.37
55	457465	AW301344	Hs.122908	DNA replication factor	5.37
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.36
	409485	S80990	Hs.252136	ficollin (collagen/fibrinogen domain-cont	5.35
	430283	BE391688		RAB7, member RAS oncogene family	5.33
	406814	AA642947	Hs.119122	ribosomal protein L13a	5.33
60	409019	AW385412		myosin regulatory light chain 2, smooth	5.30
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	5.30
	412623	R28898	Hs.74170	metallothionein 1E (functional)	5.30
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	5.30
	418702	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	5.30
65	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.30
	422900	AA641201	Hs.222051	ESTs	5.30
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	5.30
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.30
	427774	AA278583	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA	5.30
70	430177	AW969233	Hs.302746	MSTP028 protein	5.30
	430835	AI240006	Hs.192326	ESTs	5.30
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	5.30
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	5.30
	447082	T85314	Hs.54629	thioredoxin-like	5.30
75	415995	NM_004573		phospholipase C, beta 2	5.29
	424578	AK001973	Hs.150890	hypothetical protein	5.27
	441303	AW293081	Hs.241801	ESTs	5.27
	427816	AA159248	Hs.180909	peroxiredoxin 1	5.27
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.26
80	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	5.24
	444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isome	5.23
	415121	D60971	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	5.21
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.21
	405086			NM_006662*:Homo sapiens Snf2-related CBP	5.20

	413401	AI361861	Hs.118659	ESTs	5.20
	418459	R85436	Hs.268814	ESTs	5.20
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.20
	426496	D31765	Hs.170114	KIAA0061 protein	5.20
5	431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp564F133 (fr	5.20
	434372	AA631373		gb:np86c01.s1 NCI_CGAP_Thy1 Homo sapiens	5.20
	436812	AW298067		gb:UL-H-BW0-ajp-g-09-0-UL.s1 NCI_CGAP_Su	5.20
	441390	AI692560	Hs.131175	ESTs	5.20
	449419	R34910	Hs.119172	ESTs	5.20
10	453127	AI696671	Hs.294110	ESTs	5.20
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	5.20
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	5.19
	451814	AA847992	Hs.137003	ESTs	5.18
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	5.18
15	406799	AA908548		gb:og83g12.s1 NCI_CGAP_Ov8 Homo sapiens	5.16
	413963	R84282	Hs.75643	nuclear factor (erythroid-derived 2), 45	5.15
	422293	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	5.14
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	5.12
	414768	AW376989	Hs.259855	elongation factor-2 kinase	5.12
20	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	5.12
	430478	NM_014349	Hs.241535	apolipoprotein L, 3	5.11
	420151	AA255931	Hs.186704	ESTs	5.11
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	5.10
	419317	AA236282	Hs.172318	ESTs	5.10
25	424699	AW206227	Hs.287727	hypothetical protein FLJ23132	5.10
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	5.10
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	5.10
	431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	5.10
	436137	AI056769	Hs.133512	ESTs	5.10
30	440948	AW188311	Hs.128619	ESTs	5.10
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	5.09
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.09
	417228	AL134324	Hs.7312	ESTs	5.09
	424868	AI568170	Hs.96886	ESTs	5.08
35	418905	BE539674		actinin, alpha 4	5.08
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.07
	442618	R56222	Hs.26514	ESTs	5.06
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.06
40	406813	AW276131		ribosomal protein L13a	5.06
	454128	AL031259	Hs.41639	programmed cell death 2	5.05
	440709	AW797724	Hs.130350	ESTs	5.05
	436372	AW972301	Hs.310286	ESTs	5.05
	446173	BE565849	Hs.14158	copine III	5.05
45	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	5.04
	418876	AA740616		gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens	5.03
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	5.00
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	5.00
	410800	BE280421	Hs.94499	ESTs	5.00
50	431451	AA761378	Hs.192013	ESTs	5.00
	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.00
	435655	AW105663	Hs.6947	HSPC069 protein	5.00
	435919	AI052189	Hs.114104	ESTs	5.00
	436394	AA531187	Hs.126705	ESTs	5.00
55	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	5.00
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	5.00
	442685	AB033017	Hs.8594	KIAA1191 protein	5.00
	444454	BE018316	Hs.11183	sorting nexin 2	5.00
	444670	H58373	Hs.332938	hypothetical protein MGC5370	5.00
60	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.00
	450113	AI683098	Hs.200866	ESTs, Moderately similar to ALU7_HUMAN A	5.00
	450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	5.00
	450887	AA011518	Hs.271778	ESTs, Weakly similar to I38022 hypothei	5.00
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	5.00
65	457068	X69391		ribosomal protein L6	5.00
	406793	AW264291	Hs.5662	guanine nucleotide binding protein (G pr	4.97
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	4.95
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.94
	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	4.92
70	400281			Eos Control	4.91
	414420	AA043424	Hs.76095	immediate early response 3	4.90
	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.90
	434666	AF151103	Hs.112259	T cell receptor gamma locus	4.90
	449057	AB037784	Hs.22941	KIAA1363 protein	4.90
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.90
75	451598	N29102	Hs.118078	ESTs	4.90
	409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	4.88
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	4.88
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.86
80	447150	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r	4.86
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.85
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	4.85
	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	4.84
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	4.84

	406781	AA639388		gb:nq88b06.s1 NCI_CGAP_Co9 Homo sapiens	4.83
	449810	AB008681	Hs.23994	activin A receptor, type IIB	4.82
	410323	AI241708	Hs.296322	Homo sapiens cDNA: FLJ22844 fis, clone K	4.81
5	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	4.81
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.81
	400424	AJ276316	Hs.287374	zinc finger protein 304	4.80
	411573	AB029000	Hs.70823	KIAA1077 protein	4.80
	421045	BE144608	Hs.55533	ESTs	4.80
10	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.80
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.80
	438590	AA811465	Hs.123375	ESTs	4.80
	442071	BE048433	Hs.276043	ESTs	4.80
	449567	AI990790	Hs.188614	ESTs	4.80
15	453213	AA082650	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	4.80
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	4.78
	437802	AI475995	Hs.122910	ESTs	4.77
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.77
	421932	W51778	Hs.323949	kangai 1 (suppression of tumorigenicity	4.74
20	428453	AB011110	Hs.184367	GTPase activating protein-like	4.74
	413441	AI929374	Hs.75367	Src-like-adaptor	4.74
	446560	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	4.73
	435541	AA687361	Hs.221318	ESTs	4.71
	410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	4.70
25	412766	BE544475	Hs.54347	ESTs	4.70
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.70
	418973	AA233056	Hs.191518	ESTs	4.70
	421433	AI829192	Hs.22380	ESTs	4.70
	432925	AA878324	Hs.264750	ESTs	4.70
30	438869	AF075009		gb:Homo sapiens full length insert cDNA	4.70
	442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypotheti	4.70
	447198	D61523	Hs.283435	ESTs	4.70
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	4.70
	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	4.66
35	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	4.66
	447817	BE620775	Hs.4866	Homo sapiens cDNA FLJ14387 fis, clone HE	4.65
	416062	AA724811	Hs.334791	Homo sapiens cDNA FLJ14609 fis, clone NT	4.65
	406661	X66975	Hs.172550	polypyrimidine tract binding protein (he	4.64
	424582	AF026849	Hs.150922	BCS1 (yeast homolog)-like	4.64
40	411165	NM_000169	Hs.69089	galactosidase, alpha	4.63
	435905	AW997484	Hs.5003	KIAA0456 protein	4.63
	445776	NM_001310	Hs.13313	cAMP responsive element binding protein-	4.62
	424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	4.62
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	4.62
45	410668	BE379794	Hs.159651	hypothetical protein	4.61
	406774	AW518383	Hs.177592	ribosomal protein, large, P1	4.60
	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.60
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	4.60
	415682	AI347128	Hs.191870	ESTs	4.60
50	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	4.60
	419970	AW612022		ESTs	4.60
	420012	AW957965	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	4.60
	431574	AW572659	Hs.261373	hypothetical protein dJ434014.3	4.60
	432586	AA568548		ESTs	4.60
55	437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	4.60
	441355	AI822034	Hs.137097	ESTs	4.60
	444539	AI955765	Hs.146907	ESTs, Weakly similar to 2004399A chromos	4.60
	458965	AA010319	Hs.60389	ESTs	4.60
	406655	M21533	Hs.277477	major histocompatibility complex, class	4.60
60	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	4.60
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.59
	423766	AA303799	Hs.300141	ribosomal protein L39	4.59
	451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
	450043	AA885699	Hs.24332	CGI-26 protein	4.56
65	447742	AF113925	Hs.19405	caspase recruitment domain 4	4.54
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.54
	426395	BE151985		hypothetical protein FLJ23316	4.53
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	4.53
	423799	AW026300	Hs.132906	19A24 protein	4.53
70	445093	AI207197		ESTs	4.52
	428044	AA093322	Hs.301404	RNA binding motif protein 3	4.52
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	4.51
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	4.50
	427747	AW411425	Hs.180655	serine/threonine kinase 12	4.50
75	406745	AW511970	Hs.279860	tumor protein, translationally-controlle	4.50
	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	4.50
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	4.50
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	4.50
	429687	AI675749	Hs.211608	nucleoporin 153kD	4.50
80	436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	4.50
	437634	AW293046	Hs.255158	ESTs	4.50
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	4.50
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	4.50
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	4.50

	450497	H64159	Hs.15328	ESTs	4.50
	417497	AW402482	Hs.82212	CD53 antigen	4.50
	447667	AL117611	Hs.19150	Homo sapiens mRNA; cDNA DKFZp564A2164 (f	4.49
5	413856	D13639	Hs.75586	cyclin D2	4.49
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	4.49
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.48
	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.48
	446021	BE389213	Hs.286	ribosomal protein L4	4.47
10	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.46
	412819	T25829	Hs.24048	FK506 binding protein precursor	4.46
	448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.45
	401846			NM_000988*:Homo sapiens ribosomal protei	4.44
	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	4.43
15	442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	4.43
	436623	AI417073	Hs.107265	ESTs	4.42
	412146	M92444	Hs.73722	APEX nuclease (multifunctional DNA repai	4.42
	437042	AK000702	Hs.5420	hypothetical protein FLJ20695	4.42
	416754	H07145	Hs.6799	ESTs, Weakly similar to T12483 hypotheti	4.41
20	436671	AW137159	Hs.183291	ESTs	4.40
	410079	U94362	Hs.58589	glycogenin 2	4.40
	420150	AA648712	Hs.29798	KIAA1712 protein	4.40
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	4.40
	428931	AA994979	Hs.98967	ATPase, H(-)-transporting, lysosomal, non	4.40
25	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	4.40
	430280	AA361258	Hs.237868	interleukin 7 receptor	4.40
	438330	AW450572	Hs.257316	ESTs	4.40
	438962	BE046594		gb:hn41c11.x1 NCL_CGAP_RDF2 Homo sapiens	4.40
	444794	AI419991	Hs.145225	ESTs	4.40
30	445100	AW188205	Hs.12311	Homo sapiens clone 23570 mRNA sequence	4.40
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	4.40
	449832	AA694264	Hs.60049	ESTs	4.40
	452404	AW450675	Hs.212709	ESTs	4.40
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.39
35	425097	NM_014247		PDZ domain containing guanine nucleotide	4.37
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.37
	406742	AI468091	Hs.279860	tumor protein, translationally-controlle	4.35
	425095	AW014160	Hs.182585	KIAA1276 protein	4.34
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, rec	4.34
40	442333	AI650877	Hs.129302	ESTs	4.33
	424971	AA479005	Hs.154036	tumor suppressing subtransferable cand'id	4.32
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.32
	437386	W52452		ribosomal protein L10	4.31
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	4.30
45	408875	NM_015434	Hs.48604	DKFZP434B168 protein	4.30
	409604	AW444448	Hs.49124	ESTs	4.30
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.30
	419423	D26488	Hs.90315	KIAA0007 protein	4.30
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	4.30
50	422797	AB033064	Hs.236463	KIAA1238 protein	4.30
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.30
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	4.30
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	4.30
	436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	4.30
55	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	4.30
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	4.30
	452994	AW962597	Hs.31305	KIAA1547 protein	4.30
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.30
	437250	BE257342	Hs.94576	hypothetical protein MGC3062	4.29
60	440910	H97875	Hs.117974	ESTs	4.29
	406853	AA614553	Hs.252259	hypothetical protein FLJ23059	4.28
	432295	BE091049	Hs.343665	ribosomal protein S15a	4.28
	400244			Eos Control	4.28
	413518	BE149455	Hs.75415	beta-2-microglobulin	4.28
65	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.27
	406746	AA580395	Hs.279860	tumor protein, translationally-controlle	4.26
	400395	AF111167		v-fos FBJ murine osteosarcoma viral onco	4.26
	443229	AI057129	Hs.133396	ESTs	4.26
	450201	T97838	Hs.25722	ESTs	4.25
70	409636	AA305729	Hs.18272	amino acid transporter system A1	4.25
	422082	AA016188	Hs.111244	hypothetical protein	4.24
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	4.24
	453902	BE502341	Hs.3402	ESTs	4.24
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	4.22
75	404854			Target Exon	4.21
	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.20
	400440	X83957	Hs.83870	nebulin	4.20
	415049	N67334	Hs.50158	ESTs	4.20
	418304	AA215702		gb:zr97g10.r1 NCL_CGAP_GCB1 Homo sapiens	4.20
80	423180	AF068302	Hs.125031	choline/ethanolaminephosphotransferase	4.20
	424684	AW752714	Hs.5174	ribosomal protein S17	4.20
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	4.20
	438141	AW946871		gb:RC2-ET0022-080500-012-d02 ET0022 Homo	4.20
	438607	AW080237	Hs.252884	ESTs	4.20

	451952	AL120173	Hs.301663	ESTs	4.20
	455397	AW936332		gb:QV4-DT0021-281299-070-g01 DT0021 Homo	4.20
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287 similar to	4.19
	453247	T80198	Hs.111806	ESTs	4.19
5	430451	AA836472	Hs.297939	cathepsin B	4.19
	414283	AW960011	Hs.154993	ESTs	4.18
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.18
	450746	D82673	Hs.278589	general transcription factor II, i	4.16
10	444797	AB018333	Hs.12002	KIAA0790 protein	4.16
	445718	H79791	Hs.15227	ESTs	4.15
	425783	AI026740	Hs.1948	ribosomal protein S21	4.15
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 family, member	4.15
	406710	AI708347	Hs.184014	ribosomal protein L31	4.15
	424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	4.14
15	422343	AI628633	Hs.346823	gb:ty77d05.x1 NCL_CGAP_Kid11 Homo sapien	4.13
	416207	NM_014745	Hs.79077	Homo sapiens, clone MGC:2908, mRNA, comp	4.13
	406724	C14071	Hs.234518	ribosomal protein L23	4.12
	449475	AI348027	Hs.108557	hypothetical protein PP1057	4.12
	413828	L19067		v-rel avian reticuloendotheliosis viral	4.11
20	416819	U77735	Hs.80205	pim-2 oncogene	4.11
	436674	AA725002	Hs.272018	low molecular mass ubiquinone-binding pr	4.11
	405266			Target Exon	4.10
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	4.10
25	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	4.10
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.10
	423096	AA732684	Hs.278428	progesterone induced protein	4.10
	428328	AA426080	Hs.292812	ESTs, Weakly similar to I38022 hypothi	4.10
	429355	AW973253	Hs.292689	ESTs	4.10
30	433308	AA582718	Hs.291650	ESTs	4.10
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.10
	450850	AA648886	Hs.151999	ESTs	4.10
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	4.10
	406854	AA613705	Hs.252259	ribosomal protein S3	4.10
35	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	4.09
	419612	AI498267	Hs.110613	KIAA0421 protein	4.09
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.08
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	4.08
	441374	AA043696	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564C1216 (f	4.08
40	443415	AI056523	Hs.133472	ESTs	4.08
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	4.07
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.07
	400233			Eos Control	4.06
	421959	AW751497	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.06
45	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	4.06
	424795	AW102850	Hs.153177	ribosomal protein S28	4.05
	446231	NM_002163	Hs.14453	interferon consensus sequence binding pr	4.05
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	4.05
	427681	AB018263	Hs.180338	tumor necrosis factor receptor superfam	4.05
50	409061	AI204994	Hs.7874	Homo sapiens cDNA: FLJ21435 fis, clone C	4.03
	413891	BE271020		tumor suppressor deleted in oral cancer-	4.03
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	4.02
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.02
	410584	AB011112		KIAA0540 protein	4.01
55	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.00
	423645	AI215632	Hs.147487	ESTs	4.00
	430048	T65054	Hs.73605	ESTs	4.00
	431113	AK000673	Hs.274337	hypothetical protein FLJ20666	4.00
	434170	AA626509	Hs.122329	ESTs	4.00
60	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	4.00
	435391	AA704588	Hs.58934	ESTs	4.00
	446768	AV660305	Hs.110286	ESTs	4.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	4.00
	451831	NM_001674	Hs.460	activating transcription factor 3	4.00

## TABLE 56B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI555133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552



			AA969444 AI080438 AA552500 AW237538 AA481060 AI246378 AA565227 AA398921 AA207051 AA721378 BF438608 AI086295 AI886630 AA904112 AI864588 AW271985 AW078868 AA725342 BF326598 AA843572 AI082536 AA766664 AI453279 AA435673 AI619515 AA879080 AA234592 AA890223 AA766824 BI259822 AA393631 AW968840 BE940639 T83865 BE762742 AW897470 W05809 N41323 T87376 R68544 H88711 BI087136 BE177661 H06215 BE144709 BE144829 AA947566 AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372 AA989341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF881946 BF090249 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119 AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260 BE005398 AA628622 AA994155 AA662701 AA633929 AA737415 BG427950 AA826016 AI903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823 BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701 BM476120 BE672181 AI697653 AA938187 AI280879 AW340123 AI912727 AI081775 AI089556 AI191349 AI871604 AI631607 AI890800 AI701917 AW771624 AA663041 AI991576 AI160622 AA771763 BE089784 BE089788 BE089788 AI222942 AW18516 AA329211 AI095736 BE550294 AA738345 BE218683 BE670548 BG149505 BF061776 D19821 BE005786 BE178892 BE005728 BF841237 BE005648 R27634 AW954733 AA315006 AW856665 AL047596 AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090696 AI927369 AI669226 AI369437 AI371075 AW612409 AI866711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 D81020 BF575223 AI356183 D79312 AI375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545 AI184717 AW518883 AF121173 AK001838 AU135179 AU134241 AV651702 AV650032 AV651304 AV650101 AV651263 AV651888 AV651866 AA628554 AV651355 AV651174 AV651172 AW856145 AU117599 AU135386 BG254665 AA166919 BG483981 AW809606 BG494194 AA622811 AI676156 AA687804 AI701729 AU133725 AW961387 AU144387 AU151757 AA551031 BE675412 N34769 AA713483 AI890079 AI588918 AI361889 AI209020 AA668981 AI240990 AA741144 AA490899 AI200221 AW589574 W96201 BG154182 AV655159 AI328145 N36348 AI081357 N76715 AA693346 AA742488 AI269719 AA897483 AI886459 AU155873 H04255 AW243986 AA557749 AI286227 R68691 R33453 AW388057 AA908472 U09414 NM_003438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW609708 AW502384 AA828822 AI982587 BE072881 AI762181 BE072946 AA558585 AA565499 AI360576 AW204069 AA991648 AA864939 BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240 BG119563 AW975776 BG498478 BE245304 AW450934 BF508792 AA599489 AA599477 AI805268 AA055489 AI128758 AA761425 AA731858 AI302271 BE219432 AA687294 AA018972 AW629429 Z45675 AW961626 T30940 R34554 T84712 BG986694 AI742311 AI025842 AA578843 AA075144 AV711317 AI809938 AI808768 AI240593 AI915771 AI432224 AW276890 AI499346 AA937014 AA653573 AI318525 AI246219 AA961591 AI270640 BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424 AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448 AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE706702 BG496559 BF248373 BG494800 BE219720 BF475241 AI571723 BE219848 BI789268 AI224899 AW724864 AW771467 AA480255 AW845616 AI440295 H52800 BE218790 AI681575 AW300064 AW262133 H21568 AI363015 AI884914 H86948 AW182329 AA613792 T05304 AW858385 BG216963 BG164885 BG213710 BG204771 BG193014 BG197556 BG217481 BG198185 BG183594 BI596425 AA115605 AI589156 BF439839 BG188832 AI359615 BG190473 AI024233 BF439574 AW118065 AI672797 AA610042 BG212008 AI204382 R70913 AA033534 AA781036 AI627278 AA307285 AA034218 BG482749 AW162429 BI602460 AA721969 AA476516 AA476416 AA903019 BF110864 AA307286 AA115471 AW964555 AA423826 AA115129 AI419107 AW088535 AI889321 AA954221 AI337552 R42581 AW194670 AA064862 AW001147 AA864374 AA630699 AW276176 AA676615 AA857965 AI625428 AA580792 AA582038 AA581668 AA658065 AA828156 AA857160 AA936103 AI149335 AA936925 AA581684 AA954198 AW238461 AI281504 AI265812 AA583267 AW236162 AA876535 AW304286 AW474334 AI559415 AI589241 AI660952 AA641137 AI431696 AI688844 AA552513 AA564954 AW090553 AI205612 AI245753 AA954883 AA947909 AI866014 AI890243 AW971213 AA493925 AA493567 AA876839 AA934462 T40644 AA136139 AA136026 BG425760 BF997600 N48516 W73454 BF816344 BF997601 AA488953 AI433540 AA804981 AA728984 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360 BC013728 BI084032 BF090365 BE410706 N36391 W80436 BF813124 R90857 R62778 H00591 H02329 AA355285 AK000826 BC008721 BG744004 BG479141 BG823656 BG479061 AU121103 AU138176 BG702567 BI599840 BG422775 BG700944 BE280747 AU138529 BE269929 BG704110 AU123329 AU122058 AU138135 BG723106 BG722291 BG831041 BG705239 BE740517 BE207133 BE252867 AU139772 BG714385 BF568538 BE304393 BF971755 BE267965 BE272012 AU135396 AU124535 BI551682 BG700612 AI815488 BG475195 BE388273 BE391517 BM148991 BF929247 AV653435 AW250299 AW249189 BF093150 BF093173 AW205325 BF057101 BF000551 AI341108 AI162009 AK026136 BE907957 W73238 BI711467 BG926027 AI816428 AA837518 AI754405 BG179142 AA481485 AW023435 BE855747 AI885101 N52163 AI016096 AI090204 BE677045 AI523320 AI126855 N26501 AA043680 AA976459 AI039590 AI937917 AI361000 W94866 AI375797 AI079801 AI168236 AA599882 AA084368 AI342635 AI190294 N26093 AI085234 AI298169 BF939715 AI223164 H98704 BE218925 N29394 AI918735 N41520 AI147784 AI918796 AA854317 N22193 AA199850 AI149728 AA121263 AI051074 AA565116 AI097349 N22209 AA552917 N33151 D52422 BF477483 AA476599 AA525787 AI279198 D53353 AA738063 AA558406 BI496334 AA999948 AA425847 BI496335 AA909624 BF197591 AW023259 AI652819 T31424 AA088213 T31115 AI206650 AA976796 AI948989 AW248762 AA449265 AA290687 AI682521 AA310227 Z38743 AA935369 AW119141 BF941087 AI470657 AI349451 AW079338 D45665 N21640 T30071 AI446705 R60220 BE833481 R49680 R70049 R41223 R32402 R69984 R70111 BM476906 BE293615 BE382443 BF155692 BE720638 BE931983 BE720594 BF085890 AA336953 BF081638 AA359915 AA384116 AA360142
5	413497 430068 409208	1518002_1 1177709_2 10117_2	
10	422960 434280 434442 410730 438089	11862_2 1474904_1 111738_1 114639_1 22448_4	
15	425284	3834_5	
20	422689 414405	874209_1 112689_1	
25	442495 450139	928718_1 34017_1	
30	406819 424677 438980 451129 432666 418259	0_0 2518_37 917280_1 1495511_1 144_7 133853_1	
35			
40	451653	MH115364_1	
45	433162 406870 445493 406797 441623	2167905_1 0_0 423456_1 0_0 3362_1	
50			
55	430504 433891 455263	5477_6 647290_1 26143_1	
60	406806	0_0	
65	406794 431155 414150 430915 436716 449625	0_0 1235742_1 2305332_1 197844_1 2472838_1 249224_1	
70	430283	1418_1	
75			
80			

5			BI667664 BG823235 BE315559 BE301958 BE891114 BG826267 BE253680 BG979094 AV722757 N67629 BG997927 BI915769 BG680692 R62777 BE251116 H56358 AW369586 BG677759 BI044604 R75787 BE770960 H69529 R69983 AA259238 R97827 AA310379 W01103 AI873384 AL554578 BF038102 H87182 H87517 H01574 T52573 N28881 AA301397 T92375 R68401 AW800466 AI268172 BE876949 D54019 AI909769 AW798415 BI222383 AI393171 C15260 N26959 H17129 T53095 T52494 R68602 AI364765 BF687869 AI817035 AW105354 BE293820 H14206 BI093066 C14063 AL534349 BE255883 BE254088 AA428399 AW579360 AW579381 N53144 D60748 D54020 BG292106 H96705 D52423 T36174 D54161 R73016 D55021 BI857200 H83444 BI016954 D54163 R15563 BI818664 BE152207 BI048502 BF885667 BE613212 BE165773 BF149332 AW607045 BE305200
	409019	32320_4	BM480413 N28908 H39792 BE240826 BE882093 BE240827 AW868637 BF739795 AA700834 AA769597 AA489668 AW968806 AW085196 AI093280 AI218457 AA063138 AI632958 AW515005 AI570530 Z41724 AA748789 AI696584 AA062544 AA773643 AA490285 AA761668 AA573621 R09670 R92814 M95678 NM_D04573 AL530754 AI439623 AW374413 BF898880 AW630959 BF875526 AW402206 BF818690 BF893068 AW504110 AW408049 BG002913 AL530753 AI524064 AW769231 AA64970 AA293723 AI095051 AI953375 AI982938 BM146050 AW575804 AA962489 AI655426 BM146046 T28538 BE241936 T89023 BI910963 AI416986 AI767111 AI422290 AW468260 BE676853 AI656771 AI961755 F04675 AA682826 AW376066 BM194382 AA912021 AW183098 BE676682 AI962227 AI591366 AA621765 AA293724 R51642 F10194 BI909727 BF892632 AW950600 AW950138 BG258587 BF892649 AI800647 BF892710 AA353176 BF894726 AA465038 BI040869 BI837749 BE244320 H18054 T74300 AW797026 AA926790 F32814 AW751282 AI933994 AA578823 T78372 BF899896 BF882808 BF974969 BG622121 AA631424 AA988296 AA631373 AW978773 AW298067 AA810101 AW194180 AA731645 AI690673 AA908548 AW972830 AA489820 AA527647 AA570362 BM469076 AA533027 AI127512 AI368802 AA533141 AA700560 AW576028 AI610851 AI435361 BM129172 AW474544 BM128899 AI814292 AW502039 AA531243 BF941858 AW502037 AA702337 AI419854 AA662755 AA934364 AI300510 AI291136 AA505263 AI144527 AI076919 AI633534 AI242473 AA938561 BG055372 AA512894 AA962403 BF808010 AA663911 AA487056 AA513301 AA369069 AA377265 BG291206 AA402298 AA885766 AW801002 AA302290 AI305842 AW800873 AA302492 AA478427 AI817291 AW801104 AW801028 AA865744 BF155979 AI374743 AA478431 AI159846 AI369757 AI800672 BF435788 AA255451 AI937707 AW006198 AI280363 BF062434 AW801115 AI919181 T28413 W04214 AW152380 AW901567 AW901570 AA886371 AA384251 AI302846 BE701902 AA931606 H42673 R33703 AW901556 AA009816 AW901568 AW352200 AA256558 H15928 BI087170 AW800530 AA369068 N98562 H28652 N34644 H97650 H00956 W70039 AI142831 AA009817 F37136 N70289 AA531347 R27374 H27488 R66605 AW276131 AA740616 AA654854 AA229923 R36075 R36167 AI366546 BC022444 BC004138 NM_000970 BC020679 X69391 D17554 BC013863 BG779630 BG574189 BG571986 BG494603 BG575713 AV702244 AU145720 AI568177 BE350654 BG943995 AA730918 AA634024 AV744673 AI611573 AI613381 AI613403 AI250148 AW301759 AI312307 AI376488 BE139682 AV743357 AI371951 AI613376 AI613570 AI345719 AI312458 AI612697 AI334453 AW268747 AW268318 AI343026 AI335454 AI313096 AI308011 AW075176 AI348782 AI334479 AW268332 AI611433 AI371906 AI312459 AI371647 AI370051 AI335217 AI312262 AI610971 AI348798 AI613378 AI612698 AI348772 AI345434 AI345283 AI312292 AA775853 AI611363 AI345286 AI318305 BF054854 AI613384 AI348808 AI802857 AI609452 AI583301 AI349258 AI345645 AI345011 AI340442 AI335410 AI310907 BF055880 BF055774 BF055754 BF054712 AI583261 AI309664 BF054905 AI370092 AI349212 AI345583 AI334554 AI312242 BF055856 AI612686 AI611382 AI610952 AI345301 AI312235 AI610936 AI609836 AI340650 AI312472 BF054840 AI802838 AI345448 AI336508 AI313098 AI312293 AI312277 AI254912 AW302091 AW074788 AI611968 AI611948 AI583362 AI583284 AI583245 AI379398 AI371935 AI340564 AW301840 AI862239 AI612025 AI611869 AI609852 AI345449 AI312375 AI312318 AI311993 AI310895 BF057960 BE178604 AI802860 AI612115 AI611886 AI370059 AI313286 AI802856 AI611438 AI311987 AI802821 AI312997 BF054711 AI611889 AI376483 AI252445 AI611577 AI349139 BF054925 AI802840 AI583286 AI340739 AI345196 BF054833 AI308909 AI611883 AI313275 BF477097 AI609466 AI348792 AI340468 BG944254 BG941457 AW302007 BG944413 BG941475 D58042 AA328428 BG429596 BE395392 BM424161 BF663310 AV727364 BM473884 BG531178 AA307591 BF965435 BG009500 AI376551 AA897445 T87714 BE564506 Z47727 BF028489 BI597545 AA152273 AA730753 W07504 AA406507 AA316220 AA424683 N35844 N72473 AA442109 W01788 AA747605 AA235894 N41438 AA382786 AI906934 AI906935 BF091197 N85572 N75678 AV758098 BE719745 BE719744 BE719735 AA639388 AA584945 AA776364 AA776365 AA865528 AI732997 AA977633 AA865818 AF075009 R63109 R63068 AK055270 BE348291 AI190289 AW612022 AI269506 AI266578 AI269675 AW271406 BE879851 BF574163 BI497126 AW903775 BI917368 AW150900 BF244813 H79201 BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548 AK057067 BF111915 AW249706 AI222199 AI887251 AI818753 AI244687 AW135782 BF476693 BF060935 AI197928 AW251092 AI685636 AI685630 BE673458 AA932894 AW205200 AA720784 BG236866 AI583152 BE677464 AW149338 AI926439 BG031285 BF915924 BG982583 BI060025 BG991393 BE830027 BE151985 BE152208 BE152002 BE818337 BE717581 BE818354 BE830030 AA377477 T51255 BF920761 BG170636 N90052 AI207197 BF773544 AW196462 AI207343 BF813684 BF928775 AA828585 AF070570 BF439282 BF109960 AI480268 AI038060 AW082339 BF516290 BE218214 AI469956 AA039955 BE644674 AI861871 AA766231 AA845840 W85716 AA676253 AI087188 AA022908 AW953178 T33195 BF594711 AA488969 R55652 D81245 D80778 D81560 AW960933 BF930897 BE698103 AA040024 BF515960 BE168475 AA453247 AI267601 R60894 R44223 T33194 AA114936 W31640 W38829 W39109 AA004849 H41952 W88634 BF031932 BM423354 AL041825 H29654 AI908178 W85754 AI905762 AA309860 C04540 AA340246 H84669 BM476605 BI545004 BI834636 BG112453 BI199049 BG112759 AA149846 H97925 AA306121 AA313204 W52451 AI734997 AA931168 AA429766 N47913 AA584321 BF940241 AI083648 AI089410 AI347705 AI343661 AI186232 AI889031 N98464 AI820039 AI459034 AW652512 AA622990 BE857200 AA932998 AA740573 AI826264 AA865683 AI344550 AI027349 AI056087 AA442777 AA603724 AA873347 AI056717 AI092185 AI032895 AA535689 BF806025 BF806061 BF805985 BF746099 BF746097 AI309259 AI597603 BF806066 AI090653 AI129205 AI248410 H72993 AW615341 BF805990 BF805982 AA993819 T34373 T35604 H56242 AA648145 T35907 BF808691 N94015 AV703438 BG774276 H82341 R76371 T65754 AA229658 AA229857 X79449 BC017853 AL121035 BF196384 AW119044 AI028023 AW451110 AI971911 AW015069 AI079170 AI376367 AI264113 AA829646 AA737579 AA449679 AA740864 NM_001111 U18121 AL567297 BG773801 BF973874 AV687104 AA527579 AA843525 BE706355 AI074589 AI523475 BE880249 AW406263 BE074258 AV729485 BF809610 BG058619 AA677244 BE179838 AA622264 AI460106 AA740411 AI499168 AI078223 AI682923 BE696559 AW375385 AA788739 BG984978 Z40874 T17054 F09669 AW844043 U10439 BI711870 AW245957 AU158567 AA679305 AA679316 W72510 AI346029 BG059762 AW251062 AA132373 AI925621 AI860230 AI340172 AW192891 AI707990 AI094937 AI042115 AI200901 BE328452 AA644678 AA551209 BE351065 AA970761 N68609 AW002028 AA160826 AI422774 AW873114 AW073597 AW664481 AI218710 AW020550 AW190607 AI984545 AI871921 AI333970 AI452887 AI818335 AA398655 AI554424 AI274187 BE465703 AW512940 AW241366 AI923954 AA576649 AW168294 AA813181 AA912168 AI049738 AW514073 AA548255 AI569630 BE710031 AA244182 AI341697 AA563904 AI537990 AW517908 AW172943 Z39498 AI750294 AW150414 AI253293 BE825720 T31860 AW150775 D20310 AA150892 AU133933 BE781148 AL038957 BF910979 AA352297 BG988142 AW372175 BF229106 AW866705 BE093482 BG990396 AI499917 AA054452 H05484 AI828502 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418 BF998473 T92021 BI021048 BM047873 AW501366 AW501342 AW501549 BE939021 BE707147 BE160974 BE305207 N49011 AA947119 AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 BI919250 BI253018 AW130996 BE074249 BE895428 BI034862 BE083277 BF952166 BE883520 BI057842 AA215702 AA215703 AA368006 BE006876 BE006655
10	433009	2142268_1	
	415995	2117_1	
15			
	434372	858779_1	
20	436812	659779_1	
	406799	0_0	
25	430968	1237115_1	
	418905	517_1	
30	406813	0_0	
	418876	121279_1	
35	447197	2176805_1	
	457068	1196_1	
40			
45	440638	371165_1	
	400281	9758_4	
50	406781	0_0	
	440129	2607882_1	
55	438869	52134_1	
	419970	13569_1	
60	432586	6633_1	
	426395	22291_3	
65	445093	175963_1	
	438962	195763_1	
70	425097	23175_2	
	437386	5541_2	
75	418866	245947_1	
	400244	12188_1	
80			
	418304	1093209_1	



438141 1173217\_1 AA778849 AW946871 AW946782 AW946955  
 455397 1163608\_1 AW936332 AW936341  
 413828 9453\_1 BC011603 BG479117 AU124990 BG829759 AU143705 BG701663 BG699781 AU131718 BE515064 AU121812 BG898850 AL558461 BM151887  
 AU128758 BM263692 AU099013 AI241350 U88316 AW058398 AW469340 BF683967 AI470140 AU150993 AA633376 AW150821 AA536142  
 AU148749 AI620647 AU151769 AU153404 AW070666 AI457758 AU153077 N99966 AW050940 BG055674 AA506657 AW301529 AI918646  
 AI611235 AI266081 AI334542 AW071277 AI312434 AW303114 AI436544 AI436466 R22972 AI472987 N77886 AW072883 AA318683 D19761  
 AW050566 AI312433 AA328444 R72435 AA430721 AI142599 AA582290 AU148896 AA721233 AW628132 R93935 AA100710 BI520773 AI934172  
 BG222461 H85359 AW074639 AA017117 BI026412 AL582142 AA443547 AA586793 AA777535 AA693844 AI018661 AA577422 AA522800  
 BF054818 AA102378 AA757993 AA687769 R55540 AA505784 BI820705 BI767939  
 AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523  
 BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866  
 AW840571  
 410704 1054673\_1 BC004324 NM\_001020 BC007977 M60854 BM050628 BG829809 BE385504 BG744451 BI826914 BE440007 BI260656 BE395117 BE389334  
 BE255792 BI194169 BI668218 BI194376 BG716213 BG714408 BE392513 AV722219 AW328077 BM424171 BI828267 AW958606 BG831252  
 BE392943 BE394033 BI858915 BI668334 BE621019 BG706995 BE791985 BF967484 BI193635 BG761859 BM466537 BG747165 BG827488  
 AI133550 BM011511 BI227282 BG489212 BG478388 BE727769 BI160880 BG831707 BG324692 BM470427 BI083889 BG831605 BG754114  
 BG420536 BF308210 BE384213 BG832271 BG828032 BG481641 BF205675 BE899041 BE271558 BI193807 BI159866 BG473786 BG397178  
 BI194428 BI117210 BG768326 BG759507 BF975645 BF343657 BM020598 BG831082 BG829943 BG829501 BF306557 BE562511 BM050145  
 BM017978 BI193934 BI160764 BI160371 BG754991 BF973348 BF663234 BF032537 BE388168 BM009051 BI192794 BG831002 BG830459  
 BG764737 BG761808 BG481705 BG104314 BM464565 BI261500 BG831857 BG831684 BG829852 BG765030 BG760419 BG760268 BG749762  
 BG480900 BG419627 BG248771 BF975542 BM042233 BI161149 BG831302 BG830033 BG829626 BM050064 BI193014 BI161360 BG822729  
 BG110091 BG106500 BI258369 BG831982 BM458301 BM019513 BI161350 BI114178 BG481969 BG474870 BF974048 BF971122 BE741405  
 BE395269 BG832027 BG831469 BG490895 BM413638 BG943529 BG831012 BG829471 BG686284 BG337575 BG336551 BF206677 BI258301  
 BI160946 BG105893 BF183072 BM459542 BI193881 BG832043 BG831323 BI194545 BI160968 BG755930 BG706018 BE743865 BM465145  
 BG831227 BG774290 BF683451 BE907161 BM045391 BI194396 BI161269 BG747091 BG546643 BF984863 BI160206 BI226402 BI226336  
 AW328236 BG339458 BF972634 BE909808 BI160988 BI160251 BG828764 BG826860 BG758360 BF568228 BI818282 BI457127 BG831491  
 BG759864 AI830010 BF568381 BE907238 BI161172 BI116773 BG827153 BG825088 BG335419 BG109404 AI929068 BE906354 BE408564  
 BM045000 BG339617 BG282794 BG335767 BE907263 BF568921 BG829961 BG479305 BG260397 AI922228 BE301975 AW516055 BG480919  
 BG480626 AW196817 BG336261 BE906157 BE395717 BE391427 BI192954 BG829757 BG476379 BE301536 BE394727 BE257695 BE905344  
 AI433577 BE894416 BE886992 BE409223 BF034756 BE904077 BG830886 BE909153 BE907998 BE395767 AI871751 BE744523 BI192663  
 BG831669 AI000225 BE743836 BE272515 AA628078 BM463802 BE393375 BE393033 AW170187 BE730961 BE395410 BE744572 BE392297  
 BE391448 BE390780 BE388821 BE258477 BE905970 BE901567 BE898833 BE880326 BF726889 BE910504 BE390753 BE390131 AA650542  
 BE744156 BE394125 BE742207 BE395265 BE392942 BE894336 BE378222 BE906926 BE904650 BE393704 BE620999 BE515162 BE378753  
 BE272370 BE907458 BE612801 BE392484 BE907636 BE907353 BE910491 BE909796 BE905331 AW248173 AI683576 BE908826 BE620180  
 BF037570 BE908312 BE615015 BE256977 BE746875 BE394133 BE391478 BE910068 BE907185 BE742109 AA995746 BE561195 BE908825  
 BE906472 BE906509 BE906017 BE910442 BE514657 BI261969 BE741707 BE392216 BM042793 BF570283 BI262119 BE395707 BE378298  
 AW327827 BE394422 BF569178 BE263240 AI700512 BG830290 BF569308 BF569156 BI194587 BE390831 BG745096 AI681675 BE395674  
 AA136372 BE279892 AA442822 BE384898 AA313519 AI878866 AA305904 F33366 BE394852 F29153 F33618 AI133637 AA300009 F34063  
 F29455 AU099691 AI905085 AI906656 AA343249 BE388691 AW404280 AA379888 F29022 BF089981 F31013 F24305  
 BE271020 AI925430 AI806151 AW129911 AA828002 AW003539 BE042625 AI287859 AW778973 AI621173 AI991000 AA846016 AW150029  
 AW169748 AA649945 AI358496 AI470921 BF434211 AW513748 AW451232 AI953739 AI249448 AI040580 AI655280 AI637976 AW194345  
 AW611997 AI367197 BF064039 F29558 AI537342 BF593207 AW879538 AA973211 AI674328 AW879559 BF061961 AA481914 AA426532  
 AA426653 AA480106 AW243290 BF513102 BF346057 AI763358 AW003726 AI139045 AI570748 AW237602 T57492 BE887212 AI969311  
 AA133045 F23464 AA576416 T15590 AI650891 AI950958 AI983931 AW515101 AI650820 H81989 AA508473  
 BF828833 AI968217 BI651409 AI760574 AI147562 AW001418 AI146791 AI650589 AI952939 AI432373 AI964094 AI963870 AI420438 AI336803  
 AA809634 BF590826 AA741075 BI712639 AL134637 BM264338 AA527993 AI867208 AI439038 AI684987 AI631696 AI587126 AI637622 AI651931  
 AI867525 AI783674 AI638281 AI825752 AI339197 AI653411 AI341372 AI673213 AI673191 AW779768 AI627934 AI921836 AI741634 AI382284  
 AI741624 AI401569 AW190430 AW196390 AI829182 AI523816 AI760522 BE505014 AI917343 BG818909 AW009307 AA927544 AA825621  
 AA829400 AA527307 AI887999 AI865022 AA885063 AA653458 AA483816 AA836167 AA505879 AA421004 AA252626 AI380678 AW196980  
 AA649133 AI742276 AW015700 AA595019 AA877835 AI701658 AA729793 AA535004 AA926792 AA505113 AA603726 W68390 N90130 AA489461  
 AA830462

TABLE 56C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402145	8018280	Plus	113086-114800
401091	9958240	Plus	94760-94898
401466	6682292	Plus	28748-29023
401113	9966541	Minus	19419-19959
406542	7711499	Plus	117335-118473
405086	8072509	Plus	73664-73841,74081-74217,74610-74779,7492
401846	7712190	Minus	82775-82823,82912-83022
404854	7143420	Plus	14260-14537
405266	4156171	Minus	63337-63552

TABLE 57A: 703 genes upregulated in testicular cancer relative to normal body tissues

Table 57A lists about 703 genes upregulated in testicular cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix HuO3 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar accession number, GenBank accession number  
 UniGeneID: UniGene number  
 5 Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).  
 UniGene Title: UniGene gene title  
 R1 95th percentile of testicular cancer Als divided by the 50th percentile of normal tissues Als, where the 10th percentile of all normal tissue Als was subtracted from both the numerator and denominator

10 Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prod.Domains; R1

424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase); matrix metalloproteinase 9 (gelatinase B; 31.23  
 440119; AA865455; Hs.125331; ESTs, Moderately similar to unknown [H.sapiens]; ESTs, Moderately similar to unknown [H.s; 27.37  
 421241; X91817; Hs.102866; transketolase-like 1; transketolase-like 1; 26.89  
 15 431840; AA534908; Hs.2860; POU domain, class 5, transcription factor 1; POU domain, class 5, transcription facto; 25.03  
 435918; AF263538; Hs.86232; growth differentiation factor 3; growth differentiation factor 3; 19.88  
 432666; AWW204069; Hs.351118; ESTs, Weakly similar to unnamed protein product [H.sapiens]; ESTs, Weakly similar to unnamed protein; 17.74  
 419556; U29615; Hs.91093; chitinase 1 (chitotriosidase); chitinase 1 (chitotriosidase); 17.64  
 452838; U65011; Hs.30743; preferentially expressed antigen in melanoma; preferentially expressed antigen in mela; 17.06  
 20 417886; AA214584; ; ESTs; ESTs; 15.95  
 412265; AA101325; Hs.86154; hypothetical protein FLJ12457; hypothetical protein FLJ12457; 15.93  
 425572; AB011076; Hs.158307; undifferentiated embryonic cell transcription factor 1; undifferentiated embryonic cell transcri; 15.82  
 423905; AW579960; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 15.11  
 25 419741; NM\_007019; Hs.93002; ubiquitin carrier protein E2-C; ubiquitin carrier protein E2-C; 15.08  
 427584; BE410293; Hs.179718; v-myb avian myeloblastosis viral oncogene homolog-like 2; v-myb avian myeloblastosis viral oncogen; 14.17  
 418696; AWW59433; Hs.326290; hypothetical protein FLJ12581; hypothetical protein FLJ12581; 13.58  
 416819; U77735; Hs.80205; pim-2 oncogene; pim-2 oncogene; 13.20  
 414034; U89277; Hs.305985; early development regulator 1 (homolog of polyhomeotic 1); early development regulator 1 (homolog o; 12.93  
 454077; AC005952; Hs.37062; insulin-like 3 (Leydig cell); insulin-like 3 (Leydig cell); 12.90  
 30 432730; AI066520; Hs.131358; ESTs; ESTs; 12.84  
 446293; AI420213; Hs.149722; LIM domain transcription factor LIM-1 (hLIM-1) mRNA; LIM domain transcription factor LIM-1 (h; 12.74  
 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; calcium channel, voltage-dependent, alph; 12.46  
 450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta 4; 12.42  
 35 450719; AI096837; Hs.21349; ESTs, Weakly similar to RB8B\_HUMAN RAS-RELATED PROTEIN RAB-8B [H.sapiens]; ESTs, Weakly similar to RB8B\_HUMAN RAS-R; 12.26  
 431462; AWW583672; Hs.256311; granin-like neuroendocrine peptide precursor; granin-like neuroendocrine peptide precu; 11.96  
 431354; BE046956; Hs.251673; DNA (cytosine-5)-methyltransferase 3 beta; DNA (cytosine-5)-methyltransferase 3 be; 11.91  
 402199; ; Target Exon; Target Exon; 11.85  
 424578; AK001973; Hs.150890; hypothetical protein; hypothetical protein; 11.81  
 416350; AF188625; Hs.189507; phospholipase A2, group IID; phospholipase A2, group IID; 11.67  
 40 439979; AWW600291; Hs.6823; hypothetical protein FLJ10430; hypothetical protein FLJ10430; 11.57  
 410048; W76467; Hs.343874; proline oxidase homolog; proline oxidase homolog; 11.42  
 442573; H93366; Hs.7567; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 11.42  
 414812; X72755; Hs.77367; monokine induced by gamma interferon; monokine induced by gamma interferon; 11.38  
 45 421917; AB028943; Hs.109445; KIAA1020 protein; KIAA1020 protein; 11.15  
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-like; NALP2 protein; PYRIN-Containing APAF1-li; 10.92  
 414683; S78296; Hs.76888; hypothetical protein MGC12702; hypothetical protein MGC12702; 10.91  
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage elastase); matrix metalloproteinase 12 (macrophage ; 10.74  
 433800; AI034361; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 10.68  
 429120; AK001673; Hs.196530; hypothetical protein FLJ10811; hypothetical protein FLJ10811; 10.48  
 50 444371; BE540274; Hs.239; forkhead box M1; forkhead box M1; 10.46  
 441553; AA281219; Hs.121296; ESTs; ESTs; 10.37  
 426534; U58096; Hs.2051; testis specific protein, Y-linked; testis specific protein, Y-linked; 10.28  
 441878; AI801869; Hs.127982; ESTs; ESTs; 10.06  
 55 432117; AL036195; Hs.2909; protamine 1; protamine 1; 10.01  
 425427; AI652662; Hs.317432; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 9.97  
 416201; AA467752; Hs.195161; ESTs; ESTs; 9.97  
 410929; H47233; Hs.30643; ESTs; ESTs; 9.91  
 427486; AA974433; Hs.362432; fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene); fibroblast growth factor 4 (heparin secr; 9.81  
 60 427239; BE270447; Hs.356512; ubiquitin carrier protein; ubiquitin carrier protein; 9.68  
 402680; ; Target Exon; Target Exon; 9.68  
 409208; Y00093; Hs.172631; integrin, alpha X (antigen CD11C (p150), alpha polypeptide); integrin, alpha X (antigen CD11C (p150); 9.46  
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; chromosome 20 open reading frame 1; 9.42  
 440207; AI371978; Hs.128326; ESTs; ESTs; 9.41  
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; clone HQ0310 PRO0310p1; 9.41  
 65 447534; AWW53935; Hs.288655; ESTs; ESTs; 9.33  
 442333; AI650877; Hs.129302; ESTs; ESTs; 9.28  
 421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp434B0425 (from clone DKFZp434B0425); Homo sapiens mRNA; cDNA DKFZp434B0425 (f; 9.24  
 423458; AI204212; Hs.351113; ESTs; ESTs; 9.23  
 70 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placental); cadherin 3, type 1, P-cadherin (placenta); 9.23  
 422938; NM\_001809; Hs.1594; centromere protein A (17kD); centromere protein A (17kD); 9.21  
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 9.21  
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); topoisomerase (DNA) II alpha (170kD); 9.18  
 428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosophila)-like; similar to SALL1 (sal (Drosophila)-like; 9.17  
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabotropic glutamate family GPCR; retinoic acid induced 3 (RAIG1); metabo; 9.11  
 75 447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient, yeast, homolog)-like 2; MAD2 (mitotic arrest deficient, yeast, h; 9.11  
 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 9.10  
 449722; BE280074; Hs.23960; cyclin B1; cyclin B1; 8.86  
 441580; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 8.86  
 440983; M20681; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; solute carrier family 2 (facilitated glu; 8.86  
 80 409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; BRCA1 associated RING domain 1; 8.83  
 420367; AA259090; Hs.257028; ESTs; ESTs; 8.82  
 415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1); mutS (E. coli) homolog 2 (colon cancer, ; 8.73  
 418613; AA744529; Hs.85575; mitogen-activated protein kinase kinase kinase kinase 1; mitogen-activated protein kinase kinase ; 8.71

- 417407; AA923278; Hs.290905; ESTs, Weakly similar to protease [H.sapiens]; ESTs, Weakly similar to protease [H.sapi]; 8.64  
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor; ; 8.58  
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-conjugating enzyme; HSPC150 protein similar to ubiquitin-con; 8.55  
 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like (rabkinesin 6); RAB6 interacting, kinesin-like (rabkines); 8.52  
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, m; 8.51  
 424800; AL035588; Hs.153203; MyoD family inhibitor; MyoD family inhibitor; 8.45  
 447188; H65423; Hs.17631; hypothetical protein DKFZp434E2135; hypothetical protein DKFZp434E2135; 8.45  
 430056; X97548; Hs.228059; KRAB-associated protein 1; KRAB-associated protein 1; 8.42  
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor 2); midkine (neurite growth-promoting factor); 8.40  
 430676; AF084866; Hs.372585; gb:Homo sapiens envelope protein RIC-3 (env) gene, complete cd; gb:Homo sapiens envelope protein RIC-3 (; 8.38  
 420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.38  
 406621; X57809; Hs.181125; immunoglobulin lambda locus; immunoglobulin lambda locus; 8.37  
 453914; NM\_000507; Hs.574; fructose-1,6-bisphosphatase 1; fructose-1,6-bisphosphatase 1; 8.25  
 423198; M81933; Hs.1634; cell division cycle 25A; cell division cycle 25A; 8.19  
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin, beta 2 (antigen CD18 (p95), ly; 8.17  
 453968; AA847843; Hs.62711; High mobility group (nonhistone chromosomal) protein 4; High mobility group (nonhistone chromoso; 8.16  
 453985; N44545; Hs.251865; ESTs; ESTs; 8.14  
 451108; BE382701; Hs.25960; N-MYC oncogene; N-MYC oncogene; 8.10  
 420347; AL033539; Hs.97124; Human DNA sequence from clone RP1-309H15 on chromosome 6p22.1-22.3 Contains a gene similar to HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)), ESTs, STSs, GSSs and a CpG Is; Human DNA sequence from clone RP1-309H15; 8.03  
 415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.02  
 425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; GSK-3 binding protein FRAT2; 7.90  
 421016; AA504583; Hs.101047; transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47); transcription factor 3 (E2A immunoglobul; 7.89  
 432407; AA221036; ; gb:z03f12.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL\_BAEVM P10272 POL POLYPROTEIN ; mRNA sequence; gb:z03f12.r1 Stratagene NT2 neuronal pr; 7.83  
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); neutrophil cytosolic factor 1 (47kD, chr; 7.80  
 433228; F28212; Hs.14953; KIAA1491 protein; KIAA1491 protein; 7.73  
 446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); nucleolar protein 1 (120kD); 7.71  
 447350; AI375572; Hs.172634; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 7.71  
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; nudix (nucleoside diphosphate linked moi; 7.71  
 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; hypothetical protein FLJ10652; 7.70  
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1); ectonucleotide pyrophosphatase/phosphodi; 7.62  
 443537; D13305; Hs.203; cholecystokinin B receptor; cholecystokinin B receptor; 7.57  
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; interferon, gamma-inducible protein 30; 7.55  
 410006; AW732308; Hs.57783; eukaryotic translation initiation factor 3, subunit 9 (eta, 118kD); eukaryotic translation initiation factor; 7.53  
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551 protein, partial cds; Homo sapiens mRNA for KIAA1551 protein; ; 7.52  
 411975; AI916058; Hs.144583; 3'UTR of: dead ringer (Drosophila)-like 1; 3'UTR of: dead ringer (Drosophila)-like ; 7.50  
 439864; AI720078; Hs.291997; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 7.47  
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN cDNA 2700083B06 gene, clone MGC:4669, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 2700; 7.47  
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; hypothetical protein FLJ14541; 7.47  
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; protein tyrosine phosphatase, receptor t; 7.47  
 407710; AW022727; Hs.23616; ESTs; ESTs; 7.45  
 445093; AI207197; Hs.374149; ESTs; ESTs; 7.41  
 418113; AI272141; Hs.83484; SRY (sex determining region Y)-box 4; SRY (sex determining region Y)-box 4; 7.39  
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevisiae, homolog); CDC20 (cell division cycle 20, S. cerevi; 7.37  
 429469; M64590; Hs.111801; glycine dehydrogenase (decarboxylating); glycine decarboxylase, glycine cleavage system protein P; glycine dehydrogenase (decarboxylating; ; 7.33  
 422726; U11690; Hs.1572; faciogenital dysplasia (Aarskog-Scott syndrome); faciogenital dysplasia (Aarskog-Scott sy; 7.33  
 430504; H52761; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 7.32  
 448981; AI968719; Hs.195387; ESTs; ESTs; 7.28  
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); FK506-binding protein 4 (59kD); 7.26  
 435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; Homo sapiens mRNA; cDNA DKFZp761E13121 (; 7.25  
 434414; AI798376; ; gb:tr34b07.x1 NCI\_CGAP\_Ov23 Homo sapiens cDNA clone 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ; mRNA sequence; gb:tr34b07.x1 NCI\_CGAP\_Ov23 Homo sapiens; 7.24  
 428977; AK001404; Hs.194698; cyclin B2; cyclin B2; 7.19  
 434274; AA628539; Hs.57783; ESTs, Moderately similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Moderately similar to ALU1\_HUMAN A; 7.19  
 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc f; Human DNA sequence from clone RP11-145L2; 7.16  
 420524; AB010575; Hs.98547; amiloride-sensitive cation channel 3, testis; amiloride-sensitive cation channel 3, te; 7.15  
 439053; BE244588; Hs.6456; chaperonin containing TCP1, subunit 2 (beta); chaperonin containing TCP1, subunit 2 (b; 7.14  
 445076; AI206888; Hs.154131; ESTs; ESTs; 7.14  
 448588; AI970276; Hs.156905; KIAA1676; KIAA1676; 7.13  
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; hypothetical protein FLJ10339; 7.10  
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E. coli RecA homolog); RAD51 (S. cerevisiae) homolog (E. coli Re; 7.04  
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homolog (PIF1) mRNA, partial cds; Homo sapiens DNA helicase homolog (PIF1); 7.02  
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; interferon-stimulated protein, 15 kDa; 7.02  
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840937, mRNA, partial cds; Homo sapiens, clone IMAGE:3840937, mRNA; ; 6.96  
 416658; U03272; Hs.79432; fibrillin 2 (congenital contractural arachnodactyly); fibrillin 2 (congenital contractural ara; 6.92  
 438450; AI050866; Hs.65853; nodal, mouse, homolog; nodal, mouse, homolog; 6.90  
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); neutrophil cytosolic factor 2 (65kD, chr; 6.90  
 444381; BE387335; Hs.283713; hypothetical protein BC014245; hypothetical protein BC014245; 6.89  
 447582; BE293520; Hs.18910; prostate cancer overexpressed gene 1; prostate cancer overexpressed gene 1; 6.89  
 424779; AL046851; Hs.153053; CD37 antigen; CD37 antigen; 6.89  
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding protein; TYRO protein tyrosine kinase binding pro; 6.84  
 427298; AA400495; ; ESTs; ESTs; 6.82  
 414732; AW410976; Hs.77152; minichromosome maintenance deficient (S. cerevisiae) 7; minichromosome maintenance deficient (S.; 6.81  
 424959; NM\_005781; Hs.153937; activated p21cdc42Hs kinase; activated p21cdc42Hs kinase; 6.81  
 426866; U02330; Hs.172816; neuregulin 1; neuregulin 1; 6.80  
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CDC28 protein kinase 2; 6.80  
 427521; AW973352; ; ESTs; ESTs; 6.75  
 430397; AI924533; Hs.105607; bicarbonate transporter related protein 1; bicarbonate transporter related protein ; 6.75  
 427719; AI393122; Hs.134726; ESTs; ESTs; 6.74

- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; thyroid hormone receptor interactor 13; 6.72  
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; hypothetical protein FLJ12438; 6.71  
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083 protein, partial cds; Homo sapiens mRNA for FLJ00083 protein, ; 6.70  
 445363; NM\_005993; Hs.12570; tubulin-specific chaperone d; tubulin-specific chaperone d; 6.70  
 433701; AW445023; Hs.15155; ESTs; ESTs; 6.69  
 418054; NM\_002318; Hs.83354; lysyl oxidase-like 2; lysyl oxidase-like 2; 6.63  
 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen, B beta polypeptide; 6.62  
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 6.59  
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); protein kinase Chk2 (CHEK2); 6.58  
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Fc fragment of IgG, high affinity Ia, re; 6.58  
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; acid phosphatase 5, tartrate resistant; 6.57  
 414161; AA136106; Hs.184852; KIAA1553 protein; KIAA1553 protein; 6.57  
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L0311; hypothetical protein DKFZp762L0311; 6.55  
 425769; UT2513; Hs.159486; Human RPL13-2 pseudogene mRNA, complete cds; Human RPL13-2 pseudogene mRNA, complete ; 6.55  
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; Homo sapiens, Similar to complement comp; 6.55  
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); baculoviral IAP repeat-containing 5 (sur; 6.51  
 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin); minichromosome maintenance deficient (S.; 6.50  
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; CD2 antigen (p50), sheep red blood cell ; 6.49  
 417911; AA333387; Hs.82916; chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing TCP1, subunit 6A ; 6.44  
 427747; AW411425; Hs.180655; serine/threonine kinase 12; serine/threonine kinase 12; 6.43  
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; SMC4 (structural maintenance of chromoso; 6.42  
 430280; AA361258; Hs.237868; interleukin 7 receptor; interleukin 7 receptor; 6.42  
 432938; T27013; Hs.3132; steroidogenic acute regulatory protein; steroidogenic acute regulatory protein; 6.42  
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; hypothetical protein FLJ10549; 6.40  
 427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3\_HUMAN TUBBY RELATED PROTEIN 3 [H.sapiens]; ESTs, Highly similar to TUL3\_HUMAN TUBBY; 6.40  
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; small nuclear ribonucleoprotein polypept; 6.39  
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cys-X-Cys), member 10; small inducible cytokine subfamily B (Cy; 6.39  
 441384; AA447849; Hs.288660; retinoic acid induced 3; retinoic acid induced 3; 6.38  
 438915; AA280174; Hs.285681; Williams-Beuren syndrome chromosome region 14; Williams-Beuren syndrome chromosome regi; 6.34  
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; hypothetical protein FLJ20333; 6.34  
 451999; AW176401; Hs.27424; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase); DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; 6.31  
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like 2 (bright and dead ringer); dead ringer (Drosophila)-like 2 (bright ; 6.31  
 425274; BE281191; Hs.155462; minichromosome maintenance deficient (mis5, S. pombe) 6; minichromosome maintenance deficient (mi; 6.31  
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350 transcription repressor protein YY1 [H.sapiens]; ESTs, Highly similar to A40350 transcript; 6.30  
 420507; AF093408; Hs.98397; A kinase (PRKA) anchor protein 3; A kinase (PRKA) anchor protein 3; 6.30  
 415829; AW450198; Hs.163742; ESTs; ESTs; 6.28  
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; Fc fragment of IgE, high affinity I, rec; 6.26  
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil related protein; mitotic spindle coiled-coil related prot; 6.25  
 457465; AW301344; Hs.122908; DNA replication factor; DNA replication factor; 6.25  
 428918; AL036967; Hs.2324; protamine 2; protamine 2; 6.24  
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; hypothetical protein FLJ10713; 6.19  
 424415; NM\_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase 2, (gamma, neuronal); 6.19  
 407245; X90568; Hs.172004; titin; titin; 6.18  
 458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (SOX17); SRY (sex determining region Y)-box 17 (S; 6.18  
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cys-X-Cys), member 11; small inducible cytokine subfamily B (Cy; 6.16  
 435099; AC004770; Hs.4756; flap structure-specific endonuclease 1; flap structure-specific endonuclease 1; 6.13  
 424308; AW975531; Hs.154443; minichromosome maintenance deficient (S. cerevisiae) 4; minichromosome maintenance deficient (S.; 6.12  
 430521; NM\_016383; Hs.242183; HOM-TES-85 tumor antigen; HOM-TES-85 tumor antigen; 6.10  
 444823; BE262989; Hs.12045; putative protein; putative protein; 6.10  
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; solute carrier family 7 (cationic amino ; 6.09  
 402260; ; NM\_001436; Homo sapiens fibrillarin (FBL), mRNA. transcript (F8A), mRNA.; NM\_001436; Homo sapiens fibrillarin (FBL); 6.09  
 441321; H17182; Hs.7771; B-cell associated protein; B-cell associated protein; 6.05  
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like; CDC45 (cell division cycle 45, S.cerevis; 6.04  
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); interferon, alpha-inducible protein (clo; 6.04  
 402678; ; Target Exon; Target Exon; 6.03  
 453884; AA355925; Hs.36232; KIAA0186 gene product; KIAA0186 gene product; 6.01  
 439753; BE262233; Hs.7423; hypothetical protein from EUROIMAGE 2168212; hypothetical protein from EUROIMAGE 2168; 6.01  
 420596; NM\_002692; Hs.99185; polymerase (DNA directed), epsilon 2; polymerase (DNA directed), epsilon 2; 6.01  
 420676; AI434780; Hs.4248; vav 2 oncogene; vav 2 oncogene; 6.00  
 418756; AA252254; Hs.226949; ESTs; ESTs; 5.99  
 454438; AA224053; Hs.172405; cell division cycle 27; cell division cycle 27; 5.98  
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; jumonji (mouse) homolog; 5.98  
 413313; NM\_002047; Hs.293885; glycyl-tRNA synthetase; glycyl-tRNA synthetase; 5.96  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lysozyme (renal amyloidosis); 5.95  
 417777; AI823763; Hs.7055; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; ESTs, Weakly similar to I78885 serine/th; 5.94  
 449569; AI656634; Hs.195389; ESTs; ESTs; 5.92  
 436576; AI458213; Hs.77542; ESTs; ESTs; 5.90  
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; Human melanoma-associated antigen p97 (m; 5.89  
 420005; AW271106; Hs.133294; ESTs; ESTs; 5.89  
 417208; S67773; Hs.81665; v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog; v-kit Hardy-Zuckerman 4 feline sarcoma v; 5.88  
 403171; ; C2001472; gi5809678[gb]AAB41848.2 [U64675] sperm membrane protein BS-63 [Homo sapiens]||; C2001472; gi5809678[gb]AAB41848.2 [U64; 5.87  
 448730; AB032983; Hs.21894; KIAA1157 protein; KIAA1157 protein; 5.87  
 406137; ; NM\_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA. VERSION NM\_000178.1 GI; NM\_000179; Homo sapiens mutS (E. coli) h; 5.85  
 423787; AJ295745; Hs.236204; nuclear pore complex protein; nuclear pore complex protein; 5.85  
 425126; N32759; Hs.172944; chorionic gonadotropin, beta polypeptide; chorionic gonadotropin, beta polypeptide; 5.84  
 452796; AB011100; Hs.30656; KIAA0528 gene product; KIAA0528 gene product; 5.84  
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); cyclin-dependent kinase inhibitor 3 (CDK; 5.80  
 447359; NM\_012093; Hs.18268; adenylate kinase 5; adenylate kinase 5; 5.79  
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; putative G protein-coupled receptor; 5.78  
 420297; AI628272; Hs.128757; ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU1\_HUMAN ALU S; 5.75  
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila) homolog 2; enhancer of zeste (Drosophila) homolog 2; 5.75

- 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5\_HUMAN LEUKEMIA ASSOCIATED PROTEIN 5 [H.sapiens]; ESTs, Weakly similar to LEU5\_HUMAN LEUKE; 5.74  
 436251; BE515065; Hs.296585; nucleolar protein (KKE/D repeat); nucleolar protein (KKE/D repeat); 5.73  
 421535; AB002359; Hs.105478; phosphoribosylformylglycinamide synthase (FGAR amidotransferase); phosphoribosylformylglycinamide synthase; 5.71  
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CDC28 protein kinase 1; 5.69  
 425159; NM\_004341; Hs.154868; carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; carbamoyl-phosphate synthetase 2, aspartate; 5.69  
 401704; ; NM\_021195; Homo sapiens claudin 6 (CLDN6), mRNA, VERSION NM\_020982.1 GI; NM\_021195; Homo sapiens claudin 6 (CLDN6); 5.66  
 425358; AL079658; Hs.338207; FK506 binding protein 12-rapamycin associated protein 1; FK506 binding protein 12-rapamycin associated protein 1; 5.65  
 402677; ; NM\_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA, alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM\_000478; Homo sapiens alkaline phosphatase; 5.64  
 409264; NM\_014937; Hs.52463; KIAA0966 protein; KIAA0966 protein; 5.63  
 432185; AA221032; Hs.272838; hypothetical protein FLJ10494; hypothetical protein FLJ10494; 5.63  
 409012; AL117435; Hs.49725; DKFZP434I216 protein; DKFZP434I216 protein; 5.63  
 430252; AL638774; Hs.105328; testes development-related NYD-SP20; testes development-related NYD-SP20; 5.61  
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeast homolog)-like; chromosome segregation 1 (yeast homolog); 5.61  
 452816; AA131789; Hs.61509; ESTs; ESTs; 5.60  
 402679; ; NM\_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA, alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM\_000478; Homo sapiens alkaline phosphatase; 5.59  
 414291; AL289619; Hs.13040; G protein-coupled receptor 86; G protein-coupled receptor 86; 5.58  
 453028; AB006532; Hs.31442; RecQ protein-like 4; RecQ protein-like 4; 5.58  
 453905; NM\_002314; Hs.36566; LIM domain kinase 1; LIM domain kinase 1; 5.56  
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin-like 6 (mitotic centromere-associated); 5.55  
 419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; solute carrier family 7 (cationic amino acid transporter, y system), member 7; 5.55  
 446979; AL654443; Hs.197683; ESTs; ESTs; 5.54  
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; lymphocyte-specific protein tyrosine kinase; 5.53  
 418962; AA714835; Hs.271863; ESTs; ESTs; 5.53  
 447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, complete cds; 5.52  
 427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180)), lymphocyte function-associated antigen 1; alpha polypeptide; integrin, alpha L (antigen CD11A (p180)); 5.52  
 449322; AL638616; Hs.196566; ESTs; ESTs; 5.51  
 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KIAA0175 gene product; 5.51  
 415141; AA189099; Hs.268171; ESTs, Weakly similar to ALU7\_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU7\_HUMAN ALU S; 5.48  
 454048; H05626; Hs.6921; ESTs; ESTs; 5.46  
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; interleukin 1 receptor antagonist; 5.45  
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 f1s, clone HEMBB1001304; Homo sapiens cDNA FLJ11980 f1s, clone HE; 5.44  
 414334; AA824298; Hs.21331; hypothetical protein FLJ10036; hypothetical protein FLJ10036; 5.44  
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; 5.44  
 438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; major histocompatibility complex, class II, DQ alpha 1; 5.44  
 427668; AA298760; Hs.180191; hypothetical protein FLJ14904; hypothetical protein FLJ14904; 5.43  
 449437; AL702038; Hs.100057; Homo sapiens cDNA: FLJ22902 f1s, clone KAT05581; Homo sapiens cDNA: FLJ22902 f1s, clone K; 5.41  
 453633; AA357001; Hs.34045; hypothetical protein FLJ20764; hypothetical protein FLJ20764; 5.40  
 450746; D82673; Hs.278589; general transcription factor II, i; general transcription factor II, i; 5.40  
 425966; NM\_001761; Hs.1973; cyclin F; cyclin F; 5.39  
 418134; AA397769; Hs.86617; ESTs; ESTs; 5.38  
 432141; BE410964; Hs.272736; nuclear receptor binding protein; nuclear receptor binding protein; 5.37  
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, member 3; nuclear receptor subfamily 1, group H, member 3; 5.36  
 428329; AA426091; Hs.98453; ESTs, Moderately similar to R27328 2 [H.sapiens]; ESTs, Moderately similar to R27328 2 [H.sapiens]; 5.35  
 406811; U82979; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; 5.34  
 415819; AU077330; Hs.360791; transcription elongation factor A (SII), 1; transcription elongation factor A (SII), 1; 5.33  
 448133; AA723157; Hs.73769; folate receptor 1 (adult); folate receptor 1 (adult); 5.33  
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor 4 gamma, 2; eukaryotic translation initiation factor 4 gamma, 2; 5.32  
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypeptide 1; 5.32  
 429271; AF039850; Hs.198515; dead ringer (Drosophila)-like 1; dead ringer (Drosophila)-like 1; 5.32  
 456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); 5.30  
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; polo (Drosophila)-like kinase; 5.30  
 422997; BE018212; Hs.122908; DNA replication factor; DNA replication factor; 5.29  
 440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; 5.28  
 418399; AF131781; Hs.84753; hypothetical protein FLJ12442; hypothetical protein FLJ12442; 5.26  
 416178; AL080527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; serologically defined breast cancer antigen NY-BR-81; 5.21  
 450377; AB033091; Hs.355925; KIAA1265 protein; KIAA1265 protein; 5.20  
 409670; AL368109; Hs.375604; KIAA1856 protein; KIAA1856 protein; 5.20  
 429083; Y09397; Hs.227817; BCL2-related protein A1; BCL2-related protein A1; 5.20  
 449523; NM\_000579; Hs.54443; chemokine (C-C motif) receptor 5; chemokine (C-C motif) receptor 5; 5.20  
 408908; BE296227; Hs.250822; serine/threonine kinase 15; serine/threonine kinase 15; 5.19  
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); 5.19  
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, member 3; 5.16  
 437623; D63880; Hs.5719; chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-associated protein 1; 5.15  
 448181; AF272833; Hs.279763; hypothetical protein FLJ10504; hypothetical protein FLJ10504; 5.15  
 436540; BE397032; Hs.14468; hypothetical protein MGC14226; hypothetical protein MGC14226; 5.14  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; protein tyrosine phosphatase, receptor type, C; 5.14  
 426752; X69490; Hs.172004; titin; titin; 5.13  
 415007; BE244332; Hs.77770; adaptor-related protein complex 3, mu 2 subunit; adaptor-related protein complex 3, mu 2 subunit; 5.13  
 400263; ; Hs.75309; Eos Control; Eos Control; 5.13  
 437099; N77793; Hs.48659; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; 5.12  
 427209; H06509; Hs.92423; KIAA1566 protein; KIAA1566 protein; 5.10  
 407347; AA829847; ; gb:od40d07.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1370413 3' similar to contains Alu repetitive element, mRNA sequence.; gb:od40d07.s1 NCI\_CGAP\_GCB1 Homo sapiens; 5.10  
 458933; AL638429; Hs.24763; RAN binding protein 1; RAN binding protein 1; 5.10  
 450431; AW136797; Hs.266041; ESTs; ESTs; 5.09  
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 5.08  
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; protein tyrosine phosphatase, non-receptor type 6; 5.08  
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Human T-cell receptor active alpha-chain; 5.05  
 412723; AA648459; Hs.335951; hypothetical protein AF301222; hypothetical protein AF301222; 5.05

- 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 5.03  
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; collagen, type XI, alpha 1; 5.03  
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; Musashi (Drosophila) homolog 1; 5.02  
 433592; NM\_004642; Hs.3436; deleted in oral cancer (mouse, homolog) 1; deleted in oral cancer (mouse, homolog) ; 5.02  
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); karyopherin alpha 2 (RAG cohort 1, importin alpha 1); 5.00  
 425237; U07695; Hs.155227; EphB4; EphB4; 5.00  
 414809; A1434699; Hs.77356; transferrin receptor (p90, CD71); transferrin receptor (p90, CD71); 4.99  
 402145; ; Target Exon; Target Exon; 4.99  
 432126; AA865239; Hs.37196; ESTs; ESTs; 4.99  
 408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 4.98  
 419525; T79257; Hs.1259; asialoglycoprotein receptor 2; asialoglycoprotein receptor 2; 4.97  
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; ligase I, DNA, ATP-dependent; 4.97  
 427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis, clone NT2RP1000112; Homo sapiens cDNA FLJ10417 fis, clone NT; 4.96  
 457313; AF047002; Hs.241520; transcriptional coactivator; transcriptional coactivator; 4.96  
 448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; signal transducer and activator of trans; 4.94  
 426427; M86699; Hs.169840; TTK protein kinase; TTK protein kinase; 4.91  
 440129; AA865818; Hs.369523; ESTs, Weakly similar to S71886 Ste20-like protein kinase [H.sapiens]; ESTs, Weakly similar to S71886 Ste20-lik; 4.91  
 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; budding uninhibited by benzimidazoles 1 ; 4.90  
 435602; AF217515; Hs.283532; uncharacterized bone marrow protein BM039; uncharacterized bone marrow protein BM03; 4.89  
 452698; NM\_001295; Hs.301921; chemokine (C-C motif) receptor 1; chemokine (C-C motif) receptor 1; 4.88  
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; hypothetical protein FLJ12538 similar to; 4.88  
 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; thyroid hormone receptor coactivating pr; 4.87  
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIG51) mRNA, complete cds; Homo sapiens cysteine knot protein (ZSIG; 4.87  
 421350; AW301608; Hs.278188; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene; 4.87  
 409093; BE243834; Hs.50441; CGI-04 protein; CGI-04 protein; 4.86  
 424304; NM\_001395; Hs.144879; dual specificity phosphatase 9; dual specificity phosphatase 9; 4.86  
 437696; Z83844; Hs.5790; hypothetical protein dJ37E16.5; hypothetical protein dJ37E16.5; 4.86  
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; solute carrier family 23 (nucleobase tra; 4.84  
 416445; AL043004; Hs.79337; KIAA0135 protein; KIAA0135 protein; 4.83  
 448939; BE267795; Hs.22595; hypothetical protein FLJ10637; hypothetical protein FLJ10637; 4.82  
 413566; AW604451; Hs.285814; sprouty (Drosophila) homolog 4; sprouty (Drosophila) homolog 4; 4.82  
 424081; NM\_006413; Hs.139120; ribonuclease P (30kD); ribonuclease P (30kD); 4.81  
 425474; Z48054; Hs.158084; peroxisome receptor 1; peroxisome receptor 1; 4.81  
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); macrophage migration inhibitory factor (; 4.81  
 422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapiens cDNA, mRNA sequence; gb:RC3-CT0297-290100-013-d03 CT0297 Homo; 4.80  
 409101; NM\_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide binding protein (G pr; 4.79  
 412760; AW379030; Hs.41324; ESTs; ESTs; 4.79  
 447250; A1878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; protein phosphatase 1G (formerly 2C), ma; 4.79  
 429345; R11141; Hs.199695; hypothetical protein; hypothetical protein; 4.78  
 448950; AF288687; Hs.9275; CGI-152 protein; CGI-152 protein; 4.78  
 412926; A1879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; macrophage myristoylated alanine-rich C ; 4.78  
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; heat shock 90kD protein 1, beta; 4.76  
 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 4.76  
 421905; A1660247; Hs.32699; ESTs, Weakly similar to LIV-1 protein [H.sapiens]; ESTs, Weakly similar to LIV-1 protein [H]; 4.75  
 413880; A1660842; Hs.110915; interleukin 22 receptor; interleukin 22 receptor; 4.75  
 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2 (NEK2); NIMA (never in mitosis gene a)-related k; 4.74  
 418355; L42563; Hs.1165; ATPase, H<sup>+</sup> transporting, nongastric, alpha polypeptide; ATPase, H<sup>+</sup> transporting, nongastric, alp; 4.74  
 435905; AW997484; Hs.5003; KIAA0456 protein; KIAA0456 protein; 4.74  
 428024; Z29067; Hs.2236; NIMA (never in mitosis gene a)-related kinase 3; NIMA (never in mitosis gene a)-related k; 4.74  
 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; protein kinase C substrate 80K-H; 4.72  
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ryanodine receptor 1 (skeletal); 4.72  
 437296; AA350936; Hs.20281; KIAA1700; KIAA1700; 4.70  
 450142; AW207469; Hs.24485; chondroitin sulfate proteoglycan 6 (bamacan); chondroitin sulfate proteoglycan 6 (bama; 4.70  
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism); fibroblast growth factor receptor 3 (ach; 4.69  
 449475; A1348027; Hs.129826; hypothetical protein PP1057; hypothetical protein PP1057; 4.69  
 420062; AW411096; Hs.94785; TGF(beta)-induced transcription factor 2; TGF(beta)-induced transcription factor 2; 4.69  
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1; cytochrome P450, subfamily XXVIIIB (25-hy; 4.69  
 436856; A1469355; Hs.127310; ESTs; ESTs; 4.68  
 406937; U14622; ; gb:Human transketolase-like protein gene, partial cds.; gb:Human transketolase-like protein gene; 4.67  
 411296; BE207307; Hs.10114; growth suppressor 1; growth suppressor 1; 4.67  
 426726; AA488915; Hs.171955; trophinin associated protein (tastin); trophinin associated protein (tastin); 4.67  
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; protein kinase, AMP-activated, beta 2 no; 4.67  
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; melanoma cell adhesion molecule; 4.66  
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; hypothetical protein FLJ20371; 4.65  
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; complement component 1, q subcomponent, ; 4.65  
 441595; AW206035; Hs.356457; ESTs; ESTs; 4.64  
 423419; R55336; Hs.23539; ESTs; ESTs; 4.64  
 415724; NM\_003580; Hs.78687; neutral sphingomyelinase (N-SMase) activation associated factor; neutral sphingomyelinase (N-SMase) activ; 4.63  
 435045; BE297155; Hs.143698; ESTs; ESTs; 4.62  
 424441; X14850; Hs.147097; H2A histone family, member X; H2A histone family, member X; 4.62  
 414972; BE263782; Hs.77695; KIAA0008 gene product; KIAA0008 gene product; 4.62  
 436685; W28661; Hs.5288; Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245); Homo sapiens mRNA; cDNA DKFZp434M245 (fr; 4.62  
 449515; A1653378; Hs.302012; ESTs; ESTs; 4.61  
 425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; fibroblast growth factor receptor 4; 4.61  
 420027; AF009746; Hs.94395; ATP-binding cassette, sub-family D (ALD), member 4; ATP-binding cassette, sub-family D (ALD); 4.61  
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; Down syndrome critical region gene 2; 4.61  
 413441; A1929374; Hs.75367; Src-like-adaptor; Src-like-adaptor; 4.60  
 456847; A1360456; Hs.86088; ESTs; ESTs; 4.58  
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; thymidine kinase 1, soluble; 4.57  
 426935; NM\_000088; Hs.172928; collagen, type I, alpha 1; collagen, type I, alpha 1; 4.57  
 428782; X12830; Hs.193400; interleukin 6 receptor; interleukin 6 receptor; 4.56  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; splicing factor, arginine/serine-rich 5; 4.56  
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; similar to vaccinia virus HindIII K4L ORF; 4.55

- 443068; AI188710; Hs.374480; ESTs; ESTs; 4.55  
 441607; NM\_005010; Hs.7912; neuronal cell adhesion molecule; neuronal cell adhesion molecule; 4.54  
 453227; AW135862; Hs.243991; ESTs; ESTs; 4.52  
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; Homo sapiens cDNA FLJ13655 fis, clone PL; 4.51  
 422565; BE259035; Hs.118400; singed (Drosophila)-like (sea urchin fascin homolog like); singed (Drosophila)-like (sea urchin fas); 4.51  
 453613; F06838; Hs.374476; ESTs; ESTs; 4.50  
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); stress-induced-phosphoprotein 1 (Hsp70/H; 4.50  
 412507; L36645; Hs.73964; EphA4; EphA4; 4.50  
 419034; NM\_002110; Hs.89555; hemopoietic cell kinase; hemopoietic cell kinase; 4.49  
 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); ubiquitin-conjugating enzyme E2N (homolo; 4.49  
 406547; ; Target Exon; Target Exon; 4.49  
 443216; W80487; Hs.324521; hypothetical protein DC50; hypothetical protein DC50; 4.48  
 417497; AW402482; Hs.82212; CD53 antigen; CD53 antigen; 4.47  
 448595; AB014544; Hs.21572; KIAA0644 gene product; KIAA0644 gene product; 4.47  
 445350; AF052112; Hs.12540; lysophospholipase I; lysophospholipase I; 4.46  
 446236; NM\_006293; Hs.301; TYRO3 protein tyrosine kinase; TYRO3 protein tyrosine kinase; 4.46  
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; smoothened (Drosophila) homolog; 4.46  
 420340; NM\_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TIT3 complex); CD3Z antigen, zeta polypeptide (TIT3 com; 4.46  
 413426; U88837; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; GCN1 (general control of amino-acid synt; 4.44  
 421819; NM\_013403; Hs.108665; zinedin; zinedin; 4.44  
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; melanoma differentiation associated prot; 4.44  
 428995; AW004975; Hs.194716; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; MAD (mothers against decapentaplegic, Dr; 4.43  
 434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; ESTs, Highly similar to A35661 DNA excis; 4.43  
 418295; AW970043; Hs.238039; hypothetical protein FLJ11090; hypothetical protein FLJ11090; 4.42  
 409243; AB037761; Hs.51743; KIAA1340 protein; KIAA1340 protein; 4.42  
 437103; AW139408; Hs.152940; ESTs; ESTs; 4.42  
 413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic acid transporters), member 1; solute carrier family 16 (monocarboxylic; 4.42  
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 4.40  
 424078; AB006625; Hs.139033; paternally expressed 3; paternally expressed 3; 4.39  
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; HMT1 (hnRNP methyltransferase, S. cerevi; 4.37  
 410134; U68140; Hs.58927; nuclear VCP-like; nuclear VCP-like; 4.36  
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; membrane-spanning 4-domains, subfamily A; 4.35  
 400440; X83957; Hs.83870; nebulin; nebulin; 4.35  
 437218; AL117497; Hs.58185; ESTs, Weakly similar to T42727 proliferation potential-related protein - mouse [M.musculus]; ESTs, Weakly similar to T42727 prolifera; 4.34  
 430478; NM\_014349; Hs.241535; apolipoprotein L, 3; apolipoprotein L, 3; 4.34  
 432744; AA988835; Hs.38664; ESTs; ESTs; 4.33  
 423173; AA442655; Hs.124942; protein phosphatase 2A 48 kDa regulatory subunit; protein phosphatase 2A 48 kDa regulatory; 4.33  
 415995; NM\_004573; Hs.355888; phospholipase C, beta 2; phospholipase C, beta 2; 4.33  
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; hypothetical protein FLJ13912; 4.30  
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A (sperm receptor); zona pellucida glycoprotein 3A (sperm re; 4.30  
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; tumor necrosis factor receptor superfami; 4.29  
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; Human proteinase activated receptor-2 mR; 4.29  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); Fc fragment of IgG, low affinity IIb, r; 4.29  
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; pyruvate dehydrogenase phosphatase; 4.29  
 412314; AA825247; Hs.356084; downstream of: G protein-coupled receptor 27 (GPR27) (SREB1); downstream of: G protein-coupled recepto; 4.28  
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; protein tyrosine phosphatase, receptor t; 4.28  
 426108; AA622037; Hs.166468; programmed cell death 5; programmed cell death 5; 4.28  
 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); integrin, alpha M (complement component : 4.27  
 437908; AI082424; Hs.351043; ESTs; ESTs; 4.27  
 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; map kinase phosphatase-like protein MK-S; 4.27  
 429002; AW248439; Hs.2340; junction plakoglobin; junction plakoglobin; 4.26  
 439334; AI148976; Hs.112062; ESTs; ESTs; 4.26  
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan receptor 2; receptor tyrosine kinase-like orphan rec; 4.25  
 413869; NM\_000878; Hs.75596; interleukin 2 receptor, beta; interleukin 2 receptor, beta; 4.25  
 453648; W21493; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 4.24  
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 4.24  
 447528; AI612027; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 4.23  
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; solute carrier family 37 (glycerol-3-pho; 4.22  
 449810; AB008681; Hs.23994; activin A receptor, type IIB; activin A receptor, type IIB; 4.22  
 447198; D61523; Hs.283435; ESTs; ESTs; 4.22  
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); CD79A antigen (immunoglobulin-associated; 4.22  
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 145kD; inositol polyphosphate-5-phosphatase, 14; 4.22  
 422605; H16646; Hs.118666; hypothetical protein PP591; hypothetical protein PP591; 4.21  
 444535; AF011466; Hs.122575; EDG-4 (endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4); EDG-4(endothelial differentiation, lys; 4.21  
 417088; M54915; Hs.81170; pim-1 oncogene; pim-1 oncogene; 4.20  
 421707; NM\_014921; Hs.107054; lectomedin-2; lectomedin-2; 4.20  
 408717; AF045458; Hs.47061; unc-51 (C. elegans)-like kinase 1; unc-51 (C. elegans)-like kinase 1; 4.20  
 438485; W57578; Hs.378718; RAB7, member RAS oncogene family; RAB7, member RAS oncogene family; 4.19  
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; PTK7 protein tyrosine kinase 7; 4.18  
 418755; Y14443; Hs.88219; zinc finger protein 200; zinc finger protein 200; 4.18  
 417212; AW952823; Hs.351547; NS1-binding protein; NS1-binding protein; 4.17  
 413686; AI469213; Hs.71404; ESTs; ESTs; 4.17  
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); diacylglycerol kinase, zeta (104kD); 4.16  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); chemokine (C-X-C motif), receptor 4 (fus; 4.16  
 408482; NM\_000676; Hs.45743; adenosine A2b receptor; adenosine A2b receptor; 4.16  
 422391; D63479; Hs.115907; diacylglycerol kinase, delta (130kD); diacylglycerol kinase, delta (130kD); 4.15  
 409421; AA199883; Hs.67624; ESTs; ESTs; 4.15  
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; A kinase (PRKA) anchor protein 1; 4.14  
 415198; AW009480; Hs.943; natural killer cell transcript 4; natural killer cell transcript 4; 4.14  
 424685; W21223; Hs.151734; nuclear transport factor 2 (placental protein 15); nuclear transport factor 2 (placental pr; 4.13



428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; cell division cycle 2, G1 to S and G2 to; 4.13  
 423728; AW891294; Hs.132136; solute carrier family 4, sodium bicarbonate cotransporter, member 8; solute carrier family 4, sodium bicarbon; 4.13  
 433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; Ts translation elongation factor, mitocho; 4.13  
 420253; A1656055; Hs.96200; neighbor of A-kinase anchoring protein 95; neighbor of A-kinase anchoring protein 9; 4.12  
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; DNA segment on chromosome 12 (unique) 24; 4.12  
 400205; ; Hs.81848; NM\_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA. (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; NM\_006265; Homo sapiens RAD21 (S. pombe); 4.12  
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; protein kinase, DNA-activated, catalytic; 4.11  
 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Homo sapiens clone 23783 mRNA sequence; 4.10  
 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothetical protein Y50E8A.g - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31611 hypotheti; 4.10  
 432512; NM\_003284; Hs.3017; transition protein 1 (during histone to protamine replacement); transition protein 1 (during histone to; 4.10  
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; DNA segment on chromosome 19 (unique) 11; 4.09  
 423804; AW403448; Hs.1706; interferon-stimulated transcription factor 3, gamma (48kD); interferon-stimulated transcription fact; 4.09  
 413745; AW247252; Hs.75514; nucleoside phosphorylase; nucleoside phosphorylase; 4.09  
 442091; AW770493; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; guanine nucleotide binding protein (G pr; 4.09  
 425003; AF119046; Hs.154149; apurinic/aprimidinic endonuclease(APEX nuclease)-like 2 protein; apurinic/aprimidinic endonuclease(APEX; 4.08  
 421859; AA356620; Hs.108947; KIAA0050 gene product; KIAA0050 gene product; 4.08  
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-receptor type 12; protein tyrosine phosphatase, non-recept; 4.08  
 452059; AB028949; Hs.183994; KIAA1026 protein; KIAA1026 protein; 4.08  
 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; potassium voltage-gated channel, shaker; 4.07  
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; solute carrier family 16 (monocarboxylic; 4.07  
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; Homo sapiens cDNA FLJ12169 fis, clone MA; 4.07  
 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe combined immunodeficiency); interleukin 2 receptor, gamma (severe co; 4.06  
 446791; A1632278; Hs.195922; ESTs; ESTs; 4.06  
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; protein phosphatase 4 (formerly X), cata; 4.06  
 431194; D43704; Hs.250712; calcium channel, voltage-dependent, beta 3 subunit; calcium channel, voltage-dependent, beta; 4.06  
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); phosphoinositide-3-kinase, regulatory su; 4.06  
 425923; NM\_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, delta polypeptide; phosphoinositide-3-kinase, catalytic, de; 4.05  
 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; dipeptidylpeptidase VI; 4.04  
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; hematopoietic cell-specific Lyn substrat; 4.04  
 439176; A1446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; ESTs, Weakly similar to B28096 line-1 pr; 4.04  
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); selectin L (lymphocyte adhesion molecule; 4.04  
 410068; A1633888; Hs.58435; FYN-binding protein (FYB-120/130); FYN-binding protein (FYB-120/130); 4.03  
 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; hypothetical protein FLJ20596; 4.03  
 427716; L38951; Hs.180446; karyopherin (importin) beta 1; karyopherin (importin) beta 1; 4.03  
 451050; AW937420; Hs.351869; ESTs; ESTs; 4.02  
 449667; AB023227; Hs.23860; KIAA1010 protein; KIAA1010 protein; 4.02  
 448499; BE613280; Hs.77550; p53-regulated DDA3; p53-regulated DDA3; 4.01  
 437527; A1241019; Hs.145644; ESTs; ESTs; 4.01  
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase; methylene tetrahydrofolate dehydrogenase; 4.00  
 451931; AK000208; Hs.27267; Homo sapiens cDNA FLJ20201 fis, clone COLF1210; Homo sapiens cDNA FLJ20201 fis, clone CO; 4.00  
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor 1 gamma; eukaryotic translation elongation factor; 4.00  
 409581; U66243; Hs.55039; mitogen-activated protein kinase 12; mitogen-activated protein kinase 12; 3.99  
 433577; AW007080; Hs.284192; ESTs; ESTs; 3.99  
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); platelet-activating factor acetylhydrola; 3.99  
 418629; BE247550; Hs.88659; growth factor receptor-bound protein 7; growth factor receptor-bound protein 7; 3.99  
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin, gamma 1; 3.98  
 402398; ; ; C19000263.gi|3108023|gb|AAC15755.1| (AC004659) BC62940\_2 [Homo sapiens] |66335; C19000263.gi|3108023|gb|AAC15755.1| (AC0; 3.97  
 408414; A1114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell; 3.97  
 415012; NM\_004383; Hs.77793; c-src tyrosine kinase; c-src tyrosine kinase; 3.97  
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kinase); deoxythymidylate kinase (thymidylate kin; 3.95  
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; solute carrier family 25 (mitochondrial; 3.95  
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine protease; caspase 8, apoptosis-related cysteine pr; 3.95  
 430770; AA765694; Hs.123296; ESTs; ESTs; 3.94  
 442994; A1026718; Hs.16954; ESTs; ESTs; 3.94  
 420333; AJ001383; Hs.97084; lymphocyte antigen 94 (mouse) homolog (activating NK-receptor; NK-p46); lymphocyte antigen 94 (mouse) homolog (a; 3.94  
 438456; AA913381; Hs.279763; ESTs; ESTs; 3.94  
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; non-metastatic cells 1, protein (NM23A); 3.93  
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; cyclin-dependent kinase 4; 3.93  
 424829; NM\_002507; Hs.1827; nerve growth factor receptor (TNFR superfamily, member 16); nerve growth factor receptor (TNFR super; 3.93  
 447574; AF162666; Hs.18895; tousel-like kinase 1; tousel-like kinase 1; 3.93  
 425797; AF002986; Hs.159545; platelet activating receptor homolog; platelet activating receptor homolog; 3.93  
 412910; NM\_014586; Hs.109437; hormonally upregulated neu tumor-associated kinase; hormonally upregulated neu tumor-associa; 3.92  
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; IMP (inosine monophosphate) dehydrogenas; 3.92  
 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis, clone NT2RP4002075; Homo sapiens cDNA FLJ13221 fis, clone NT; 3.92  
 400262; ; Hs.75309; Eos Control; Eos Control; 3.90  
 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 3.90  
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; phosphoserine phosphatase-like; 3.90  
 435206; A1432364; Hs.160594; ESTs; ESTs; 3.90  
 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; paired immunoglobulin-like receptor beta; 3.90  
 413627; BE182082; Hs.246973; intron of Bicaudal D homolog 1; intron of Bicaudal D homolog 1; 3.90  
 426265; AA421069; Hs.97896; ESTs; ESTs; 3.89  
 451063; AW163702; Hs.25911; HLA-B associated transcript-2; HLA-B associated transcript-2; 3.89  
 407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial cds; gb:Human nebulin mRNA, partial cds; 3.89  
 437239; AW503395; Hs.5541; ATPase, Ca transporting, ubiquitous; ATPase, Ca transporting, ubiquitous; 3.88  
 400261; ; Hs.1802; Eos Control; Eos Control; 3.88  
 450447; AF212223; Hs.25010; hypothetical protein P15-2; hypothetical protein P15-2; 3.88  
 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamyl gamma-semialdehyde synthetase); pyrroline-5-carboxylate synthetase (glut; 3.87  
 414251; AL042306; Hs.97689; VASA protein; VASA protein; 3.87  
 417767; BE242241; Hs.82542; acylxyacyl hydrolase (neutrophil); acylxyacyl hydrolase (neutrophil); 3.87  
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor, beta polypeptide; platelet-derived growth factor receptor; 3.87



- 444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; solute carrier family 7 (cationic amino ; 3.86  
 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; MKP-1 like protein tyrosine phosphatase; 3.86  
 427022; AW245839; Hs.173255; small nuclear ribonucleoprotein polypeptide A; small nuclear ribonucleoprotein polypept; 3.86  
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.86  
 408056; AA312329; Hs.42331; ephrin-A4; ephrin-A4; 3.86  
 410552; X66945; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 3.85  
 450778; U81375; Hs.25450; solute carrier family 29 (nucleoside transporters), member 1; solute carrier family 29 (nucleoside tra; 3.85  
 418978; T85295; Hs.268606; ESTs; ESTs; 3.84  
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); cyclin-dependent kinase 5, regulatory su; 3.84  
 442980; AA857025; Hs.8878; kinesin-like 1; kinesin-like 1; 3.84  
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; interleukin 10 receptor, alpha; 3.84  
 434689; AF154115; Hs.4076; CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1; CTD (carboxy-terminal domain, RNA polyme; 3.83  
 432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; karyopherin beta 2b, transportin; 3.83  
 415684; D59356; Hs.374480; sorbitol dehydrogenase; sorbitol dehydrogenase; 3.83  
 451598; N29102; Hs.79658; ESTs; ESTs; 3.82  
 449433; AI672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-binding protein 5 [H.sapiens]; ESTs, Weakly similar to S26650 DNA-bind; 3.82  
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.81  
 435160; AB002374; Hs.4791; KIAA0376 protein; KIAA0376 protein; 3.80  
 443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, Williams-Beuren syndrome); elastin (supravalvular aortic stenosis, ; 3.80  
 422753; AI928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); small nuclear ribonucleoprotein D3 polyp; 3.79  
 421508; NM\_004833; Hs.105115; absent in melanoma 2; absent in melanoma 2; 3.79  
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; phosphatidylserine synthase 1; 3.79  
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone LNG15735; Homo sapiens cDNA: FLJ23602 fis, clone L; 3.79  
 421654; AW163267; Hs.106466; suppressor of var1 (S.cerevisiae) 3-like 1; suppressor of var1 (S.cerevisiae) 3-like; 3.79  
 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; frizzled (Drosophila) homolog 8; 3.79  
 411125; AA151647; Hs.88877; cytochrome b-245, alpha polypeptide; cytochrome b-245, alpha polypeptide; 3.78  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; dual specificity phosphatase 4; 3.78  
 425354; U62027; Hs.155935; complement component 3a receptor 1; complement component 3a receptor 1; 3.78  
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, member 6; immunoglobulin superfamily, member 6; 3.78  
 429687; AI675749; Hs.211608; nucleoporin 153kD; nucleoporin 153kD; 3.77  
 414177; AI351355; Hs.356303; uncharacterized hypothalamus protein HARP11; uncharacterized hypothalamus protein HAR; 3.77  
 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; dual specificity phosphatase 5; 3.77  
 445817; NM\_003642; Hs.13340; histone acetyltransferase 1; histone acetyltransferase 1; 3.77  
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, complete cds; Homo sapiens, clone MGC:15203, mRNA, com; 3.76  
 412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); APEX nuclease (multifunctional DNA repai; 3.76  
 413011; AW068115; Hs.821; biglycan; biglycan; 3.76  
 428157; AI738719; Hs.198427; hexokinase 2; hexokinase 2; 3.76  
 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor, alpha polypeptide); integrin, alpha 5 (fibronectin receptor,; 3.75  
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; melanoma antigen, family D, 1; 3.75  
 405484; ; C3002124\*.gi|12737280|ref|XP\_006682.2| keratin 18 [Homo sapiens]; C3002124\*.gi|12737280|ref|XP\_006682.2| k; 3.75  
 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; splicing factor 3b, subunit 4, 49kD; 3.75  
 432460; H12912; Hs.274691; adenylate kinase 3; adenylate kinase 3; 3.75  
 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; ATP-binding cassette, sub-family C (CFTR; 3.74  
 431884; AA521246; Hs.210792; ESTs, Weakly similar to ALU8\_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar  
 45 to ALU8\_HUMAN ALU S; 3.74  
 453329; T97205; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell ; 3.74  
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; solute carrier family 2 (facilitated glu; 3.74  
 438330; AW450572; Hs.257316; ESTs; ESTs; 3.74  
 419911; L15301; Hs.1276; BN51 (BHK21) temperature sensitivity complementing; BN51 (BHK21) temperature sensitivity com; 3.74  
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; mitogen-activated protein kinase-activat; 3.73  
 442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; ESTs, Weakly similar to I38022 hypotheti; 3.73  
 451295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene ; 3.73  
 410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Homo sapiens clone 24675 mRNA sequence; 3.73  
 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; intercellular adhesion molecule 1 (CD54); 3.72  
 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; solute carrier family 31 (copper transpo; 3.71  
 423523; AW299828; Hs.193580; ESTs; ESTs; 3.71  
 413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like 1; inositol polyphosphate phosphatase-like ; 3.71  
 448336; R53848; Hs.44976; ESTs; ESTs; 3.70  
 422083; NM\_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; arachidonate 15-lipoxygenase, second typ; 3.70  
 416087; AF045184; Hs.79008; SKI-INTERACTING PROTEIN; SKI-INTERACTING PROTEIN; 3.70  
 442200; AW590572; Hs.235768; ESTs; ESTs; 3.70  
 414280; BE410769; Hs.75873; zyxin; zyxin; 3.69  
 409354; N68188; Hs.159472; Homo sapiens cDNA: FLJ22224 fis, clone HRC01703; Homo sapiens cDNA: FLJ22224 fis, clone H; 3.69  
 415276; U88666; Hs.78353; SFRS protein kinase 2; SFRS protein kinase 2; 3.69  
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA; leucine-rich repeat-containing G protein; 3.69  
 446522; NM\_003876; Hs.15196; putative receptor protein; putative receptor protein; 3.69  
 422785; AI824114; Hs.289088; heat shock 90kD protein 1, alpha; heat shock 90kD protein 1, alpha; 3.68  
 401083; ; NM\_016582\*.Homo sapiens peptide transporter 3 (LOC51296), mRNA. VERSION NM\_016579.1 GI; NM\_016582\*.Homo sapiens peptide transpo; 3.68  
 413048; M93221; Hs.75182; mannose receptor, C type 1; mannose receptor, C type 1; 3.68  
 452690; AI536070; Hs.15085; ESTs; ESTs; 3.68  
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2\_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar  
 45 to ALU2\_HUMAN ALU S; 3.68  
 415010; NM\_004203; Hs.77783; membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase; membrane-associated tyrosine- and threon; 3.68  
 428579; NM\_005756; Hs.184942; G protein-coupled receptor 64; G protein-coupled receptor 64; 3.68  
 446430; AA346837; Hs.15075; hypothetical protein DKFZp434E2216; hypothetical protein DKFZp434E2216; 3.66  
 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains the NIFS gene for  
 cysteine desulfurase, two genes for novel proteins and the gene for the; Human DNA sequence from clone RP11-353C1; 3.66  
 416602; NM\_006159; Hs.367895; Protein kinase C-binding protein NELL2; Protein kinase C-binding protein NELL2; 3.65  
 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 0610;  
 3.65  
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; wee1 (S. pombe) homolog; 3.65  
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; ESTs, Weakly similar to S65657 alpha-1C-; 3.65  
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN20), member 2; ATP-binding cassette, sub-family F (GCN2; 3.65

451558; NM\_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ATP-binding cassette, sub-family A (ABC1); 3.65  
 414774; X02419; Hs.77274; plasminogen activator, urokinase; plasminogen activator, urokinase; 3.65  
 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin, beta 1; 3.65  
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; hepatocyte growth factor-regulated tyrosine kinase substrate; 3.64  
 437669; AI358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA667999 [H.sapiens]; ESTs, Weakly similar to match to ESTs AA; 3.64  
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); mannose-6-phosphate receptor (cation dep); 3.64  
 444388; AB033058; Hs.11101; KIAA1232 protein; KIAA1232 protein; 3.64  
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; CCAAT-box-binding transcription factor; 3.63  
 451484; AV648896; Hs.283771; hypothetical protein; hypothetical protein; 3.63  
 444613; H29627; Hs.79092; hypothetical protein FLJ14427; hypothetical protein FLJ14427; 3.63  
 447495; AV401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); programmed cell death 8 (apoptosis-induc); 3.62  
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; CDC2-related protein kinase 7; 3.62  
 424732; D80001; Hs.152629; KIAA0179 protein; KIAA0179 protein; 3.62  
 411165; NM\_000169; Hs.69089; galactosidase, alpha; galactosidase, alpha; 3.62  
 422112; BE540240; Hs.111783; Lsm1 protein; Lsm1 protein; 3.62  
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); Homo sapiens mRNA; cDNA DKFZp434M229 (fr; 3.61  
 438795; AA825792; Hs.377119; gb:od84b11.s1 NCI\_CGAP\_Ov2 Homo sapiens cDNA clone, mRNA sequence; gb:od84b11.s1 NCI\_CGAP\_Ov2 Homo sapiens; 3.61  
 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; Homo sapiens, clone IMAGE:3457003, mRNA; 3.61  
 407797; AK000524; Hs.39850; hypothetical protein FLJ20517; hypothetical protein FLJ20517; 3.60  
 423217; NM\_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); collagen, type VII, alpha 1 (epidermolys; 3.60  
 444985; AI677737; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 3.60  
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM\_023929); zinc finger protein RINZF (NM\_023929); 3.59  
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; hypothetical protein FLJ22865; 3.59  
 415020; BE249915; Hs.293533; Human DNA sequence from clone RP11-127L20 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains the gene for a novel  
 glutathione-S-transferase and five novel genes; Human DNA sequence from clone RP11-127L2; 3.59  
 415149; X12451; Hs.78056; cathepsin L; cathepsin L; 3.57  
 458715; AK000973; Hs.1706; hypothetical protein FLJ10111; hypothetical protein FLJ10111; 3.57  
 423576; NM\_000383; Hs.129829; autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy); autoimmune regulator (autoimmune polyen; 3.57  
 440270; NM\_015986; Hs.7120; cytokine receptor-like molecule 9; cytokine receptor-like molecule 9; 3.57  
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; hypothetical protein MGC12959; 3.57  
 404976; ; NM\_014323\*; Homo sapiens zinc finger protein 278 (ZNF278), transcript variant 1, mRNA; NM\_014323\*; Homo sapiens zinc finger prot; 3.57  
 449656; AA002008; Hs.188633; ESTs; ESTs; 3.56  
 413795; AL040178; Hs.142003; ESTs; ESTs; 3.56  
 406859; AI581134; Hs.181357; laminin receptor 1 (67kD, ribosomal protein SA); laminin receptor 1 (67kD, ribosomal prot; 3.56  
 411030; BE387193; Hs.67896; 7-60 protein; 7-60 protein; 3.56  
 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; ESTs, Weakly similar to dJ963K23.2 [H.sa; 3.56  
 424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs)  
 syndrome, spastic paraplegia 1); L1 cell adhesion molecule (hydrocephalus; 3.55  
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; solute carrier family 1 (glial high affi; 3.55  
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible IkappaB kinase; IKK-related kinase epsilon; inducible Ik; 3.55  
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); uridine monophosphate synthetase (orotat; 3.55  
 450931; N25156; Hs.25648; tumor necrosis factor receptor superfamily, member 5; tumor necrosis factor receptor superfam; 3.55  
 425836; AW955696; Hs.90960; ESTs; ESTs; 3.54  
 441054; AA913591; Hs.126480; ESTs; ESTs; 3.54  
 440592; AL137268; Hs.7285; KIAA0759 protein; KIAA0759 protein; 3.54  
 458946; AA009716; Hs.42311; ESTs; ESTs; 3.53  
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; dipeptidylpeptidase III; 3.53  
 421662; NM\_014141; Hs.106552; cell recognition molecule Caspr2; cell recognition molecule Caspr2; 3.53  
 422732; AA577455; Hs.24937; transformer-2 alpha (htra-2 alpha); transformer-2 alpha (htra-2 alpha); 3.53  
 424870; T15545; Hs.244624; ESTs; ESTs; 3.52  
 442794; AI744130; Hs.356753; hypothetical protein MGC2975; hypothetical protein MGC2975; 3.52  
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); protein C receptor, endothelial (EPCR); 3.51  
 419971; AA400027; Hs.296234; ESTs, Weakly similar to T31613 hypothetical protein Y50E8A.1 - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31613 hypotheti; 3.51  
 410257; BE244044; Hs.61469; hypothetical protein; hypothetical protein; 3.51  
 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerevisiae ARD1; N-acetyltransferase, homolog of S. cerev; 3.51  
 421921; H83363; Hs.355993; translocase of inner mitochondrial membrane 10 (yeast) homolog; translocase of inner mitochondrial membr; 3.50  
 454128; AL031259; Hs.367900; programmed cell death 2; programmed cell death 2; 3.50  
 434049; AA501430; Hs.5771; amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2; amyotrophic lateral sclerosis 2 (juvenil; 3.50  
 453641; AA444140; Hs.90960; ESTs; ESTs; 3.50  
 429592; AB029041; Hs.209646; KIAA1118 protein; KIAA1118 protein; 3.49  
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211\_HUMAN ZINC FINGER PROTEIN 211 [H.sapiens]; ESTs, Weakly similar to Z211\_HUMAN ZINC; 3.47  
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; RAD54 (S.cerevisiae)-like; 3.44  
 413372; H55532; Hs.349695; tubulin, alpha 2; tubulin, alpha 2; 3.07  
 437224; AL117628; Hs.97808; ESTs; ESTs; 2.77  
 430439; AL133561; ; DKFZP434B061 protein; DKFZP434B061 protein; 2.76  
 435897; AF269223; Hs.128322; t-complex 11 (a murine tcp homolog); t-complex 11 (a murine tcp homolog); 2.53  
 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383 chromosome segregation protein smc1 [H.sapiens]; ESTs, Weakly similar to I54383 chromosom; 2.46  
 412026; AA383618; Hs.73073; testis-specific ankyrin motif containing protein; testis-specific ankyrin motif containing; 2.35  
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; hypothetical protein FLJ10251; 2.33  
 426627; AF012359; Hs.195685; ESTs; ESTs; 2.12  
 438983; AF085884; Hs.20029; proacrosin binding protein sp32 precursor; proacrosin binding protein sp32 precursor; 2.07  
 425709; AA383076; Hs.159274; outer dense fibre of sperm tails 1; outer dense fibre of sperm tails 1; 1.99  
 433724; AI827749; Hs.144924; serine/threonine protein kinase SSTK; serine/threonine protein kinase SSTK; 1.68  
 420710; NM\_007009; Hs.99875; zona pellucida binding protein; zona pellucida binding protein; 1.54

TABLE 57B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
------	------------	-----------

417886 1031334\_1 AA210987 D57294 AA214584 AA207006 D56572  
 432407 MH1429\_12 BG036675 BF772005 BF771866 BG960386 BG960381 NM\_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104  
 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279  
 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849  
 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859  
 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928  
 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592  
 434414 35978\_1 AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422  
 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298  
 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175  
 BF854337  
 427298 115241\_1 AA933717 BF061897 AW628327 AA641788 AA400495  
 427521 513212\_1 AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165  
 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892  
 407347 810943\_1 T23514 AI655785  
 430439 6750\_2 AL133561 AL117481 AL122069 AW439292 AI968826 AL041090

TABLE 57C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA  
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402199	8576116	Minus	84187-84744
402680	8113438	Plus	137634-137768, 139702-139893, 140475-14059
402260	3399665	Minus	113765-113910, 115653-115765, 116808-11694
402678	8113438	Plus	37395-37514, 37866-37981
403171	9838164	Minus	74502-74703
406137	9166422	Minus	30487-31058
401704	3097841	Plus	24712-25374
402677	8113438	Plus	22135-22309, 23063-23238
402679	8113438	Plus	132079-132216
402145	8018280	Plus	113086-114800
406547	7711513	Minus	172780-174358
402398	4092817	Minus	24019-24973
405484	5922025	Plus	199214-199579, 199672-199920, 200262-20049
401083	3242744	Plus	33192-33360
404976	3419864	Minus	139625-140632

TABLE 58A: 434 genes upregulated in bladder cancer relative to normal body tissues

Table 58A lists about 434 genes upregulated in bladder cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar accession number, GenBank accession number  
 UniGeneID: UniGene number  
 Pred.Prot.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).  
 UniGene Title: UniGene gene title  
 R1: 90th percentile of bladder tumor AIs divided by the 50th percentile of normal tissue AIs

Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prot.Domains; R1

430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M;; 35.25  
 422282; AF019225; Hs.114309; apolipoprotein L; MotA\_ExcB;TM=Y;SS=M; 33.25  
 414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets, ; phoslip;TM=M;SS=Y; 31.68  
 415192; D17793; Hs.78183; aldo-keto reductase family 1, member C3 ; aldo\_ket\_red;TM=M;; 31.04  
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 28.50  
 439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep\_L\_domain, Furin-like, pkinase, Recep\_L\_domain, Peptidase\_M24; 27.43  
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;SS=M; 25.98  
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM\_PNT,none; 25.38  
 418818; AA228899; Hs.101307; Homo sapiens HUT11 protein mRNA, partial; UT,none; 25.28  
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA\_gyraseB,DNA\_topoisolv,HATPase\_c;SS=M; 23.58  
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; ig, pkinase;TM=Y;SS=M; 21.24  
 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm\_1;TM=Y;SS=M; 20.45  
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 19.78  
 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M; 18.90  
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M;; 18.75  
 410687; U24389; Hs.65436; lysyl oxidase-like 1; LysylOxidase;SS=M; 18.63  
 444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypotheti; Collagen;TM=M;SS=M; 18.60  
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhabd\_glycop;TM=Y;SS=M; 18.55  
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M;; 18.25

- 413132; NM\_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic); PKI;SS=M; 17.73  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig;TM=Y;SS=M; 17.68  
 450746; D82673; Hs.278589; general transcription factor II, i; none;SH3,PX; 17.12  
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M; 16.88  
 420981; L40904; Hs.100724; peroxisome proliferative activated recep; hormone\_rec,zf-C4;TM=M; 16.78  
 439941; A1392640; Hs.18272; amino acid transporter system A1; Aa\_trans;TM=Y; 16.75  
 431846; BE019924; Hs.271580; uropod 1B; transmembrane4;TM=Y;SS=M; 16.56  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,ig,FAD\_Synth,ldh,ich\_C,kinase;SS=M; 16.43  
 414883; AA926960; ; CDC28 protein kinase 1; CKS; 16.20  
 438091; AW373062; ; nuclear receptor subfamily 1, group I, m; hormone\_rec,zf-C4,none; 15.80  
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH,lb,Lipase\_GDSL;TM=M; 15.70  
 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KA1,kinase;TM=M; 15.63  
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm\_2;TM=Y;SS=M; 15.45  
 434293; NM\_004445; Hs.3796; EphB6; EPH\_lbd,fn3,kinase,SAM;TM=Y;SS=M; 15.43  
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule); EGF,lectin\_c,sushi;TM=M;SS=M; 15.28  
 443991; NM\_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK\_channel,ion\_trans;TM=Y;SS=M; 15.10  
 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; ig;TM=Y;SS=M; 14.90  
 432306; Y18207; Hs.303090; protein phosphatase 1, regulatory (inhib); CBM\_21;TM=M; 14.80  
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M; 14.73  
 429345; R11141; Hs.199695; hypothetical protein; K\_tetra,SAM; 14.58  
 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; ig,Isodh,Ribosomal\_L6,F-box;TM=Y;SS=M; 14.55  
 421508; NM\_004833; Hs.105115; absent in melanoma 2; PAAD\_DAPIN,HIN;TM=M; 14.53  
 446006; NM\_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 14.35  
 429556; AW139399; Hs.98988; ESTs; none;TM=M; 14.18  
 416224; NM\_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand;SS=M; 14.13  
 429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-recept; Y\_phosphatase,Band\_41,PDZ;SS=M; 13.90  
 426657; NM\_015865; Hs.171731; solute carrier family 14 (urea transport; UT;TM=Y; 13.83  
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 13.80  
 400843; ; NM\_003105\*;Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 13.78  
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC\_tran,CoaE;TM=M; 13.38  
 432314; AA533447; Hs.312989; ESTs; Xlink,none; 13.25  
 413109; AW389845; Hs.110855; ESTs; PHO4,none; 13.15  
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,pkinase;TM=M; 13.13  
 426490; NM\_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M; 12.93  
 426158; NM\_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,kinase,Recep\_L\_domain,Furin-like,kinase,Recep\_L\_domain,Peptidase\_M24; 12.43  
 440249; A1246590; Hs.249175; ESTs; TatD\_DNase,pkinase,death,none; 12.38  
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 12.38  
 404942; U30825; ; splicing factor, arginine/serine-rich 9; CD36;TM=Y;SS=M; 12.03  
 439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR\_c6,granulin,CUB,Keratin\_B2,TIL;TM=M;SS=M; 11.93  
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fis, clone NT; Aa\_trans,none; 11.88  
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose\_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,ldh\_C,CH,AlP3;TM=M; 11.88  
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 4; rrm,hormone\_rec,zf-C4,sugar\_tr; 11.85  
 433470; AW960564; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.80  
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb\_DNA-binding,THF\_DHG\_C,THF\_DHG\_C,THF\_DHG\_C,CAP\_GLY,AAA,LON,Peptidase\_C9,bZIP,M,xan\_ur\_permease,HCO3\_cotransp;TM=M; 11.69  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm\_1,7tm\_2;TM=Y;SS=M; 11.50  
 426761; A1015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp58612022 (f; none;TM=Y;SS=M; 11.48  
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH\_C,IMPDH\_N,CBS,integrin\_B,Ricin\_B\_lectin; 11.38  
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 11.23  
 436729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.18  
 409960; BE261944; Hs.339673; hexokinase 1; none,none; 11.02  
 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3,PDZ,Guanylate\_kin;TM=M; 10.78  
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofillin\_ADF;SS=M; 10.63  
 427654; AA410183; Hs.137475; ESTs; ion\_trans,vwc,IGFBP,isp\_1; 10.58  
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 10.53  
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (f; SH3,PH,RhoGEF;TM=M; 10.53  
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone K; none,none; 10.52  
 436856; A1469355; Hs.127310; ESTs; pkinase,rrm;TM=M; 10.48  
 451035; AU076785; Hs.430; plastin 1 (I isoform); efhand,CH,Adaptin\_N;SS=M; 10.38  
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin\_B,EGF,PSI;TM=Y;SS=M; 10.35  
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,integrin\_A,FG-GAP;TM=Y;SS=M; 10.34  
 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD\_DAPIN;NA; 10.25  
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf\_5;TM=Y;SS=M; 10.18  
 437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365012.1 [H.s.a; GPS; 7tm\_2;TM=Y; 10.13  
 400752; ; NM\_003105\*;Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 10.08  
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPc;TM=M; 10.05  
 426728; NM\_007118; Hs.171957; triple functional domain (PTPRF interact; SH3,ig,kinase,PH,spectrin,RhoGEF;TM=M; 10.05  
 400496; ; ENSP00000224716\*;GTP-binding protein SAR; none;TM=Y; 10.01  
 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3,PDZ,Guanylate\_kin;TM=M; 10.00  
 404568; ; NM\_022071\*;Homo sapiens hypothetical pro; SH2;TM=M; 10.00  
 444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 9.93  
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand,kazal,arf,ras,7tm\_1;TM=M; 9.90  
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2,SH3;TM=M; 9.90  
 424954; NM\_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,WD40,IRK;TM=M; 9.88  
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; pkinase;TM=M; 9.85  
 439223; AW238299; Hs.260618; UL16 binding protein 2; ldl\_recept\_a,PKD,MHC,I;TM=M;SS=Y; 9.83  
 429238; NM\_002849; Hs.198288; protein tyrosine phosphatase, receptor t; Y\_phosphatase;TM=Y;SS=M; 9.80  
 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y\_phosphatase;TM=M; 9.73  
 452239; AW379378; Hs.170121; protein tyrosine phosphatase, receptor t; none,none; 9.73  
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y\_phosphatase,DSPc;TM=M; 9.72  
 403912; ; C5000394\*;gij12737280ref[XP\_006682.2] k; none;TM=M; 9.70  
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 9.70

- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xc; pkinase;TM=M;; 9.68  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y\_phosphatase;TM=M;; 9.63  
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;; 9.63  
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3\_P14\_kinase,FAT,FATC;TM=M;; 9.55  
 430259; BE550182; Hs.127826; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 9.50  
 428520; AA331901; Hs.184736; hypothetical protein FLJ10097; none;TM=M;; 9.50  
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;; 9.50  
 448913; AA194422; Hs.22564; myosin VI; rrm,zf-RanBP,kinase,GST\_C,Ets,SAM\_PNT,ABC2\_membrane,myosin\_head,IQ,Myosin\_N,bZIP,zf-  
 C2H2,PHD,BTB,TFIIS,AT\_hook,SAM;TM=M;; 9.50  
 414911; NM\_000107; Hs.77602; damage-specific DNA binding protein 2 (4; WD40,homeobox,LIM;TM=M;; 9.48  
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene ; pkinase,DAG\_PE-bind,kinase\_C,OPR,none; 9.45  
 402328; ; Target Exon; pkinase;TM=M;; 9.44  
 443710; A1928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha,none; 9.42  
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M;; 9.42  
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS\_kinase,ATP-sulfurylase,PRK,Thymidylate\_kin;SS=M; 9.40  
 418827; BE327311; Hs.47166; HT021; none;TM=M;; 9.40  
 440675; AW005054; Hs.47883; ESTs, Weakly similar to KCC1\_HUMAN CALCI; pkinase,none; 9.35  
 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE\_p10,ICE\_p20;SS=M; 9.28  
 410668; BE379794; Hs.65403; hypothetical protein; death,TNFR\_c6;TM=Y;SS=M; 9.25  
 430024; A1808780; Hs.227730; integrin, alpha 6; integrin\_A,FG-GAP;TM=Y;SS=M; 9.23  
 452696; A1826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate\_kin,PDZ,SH3; 9.13  
 434263; N34895; Hs.44648; ESTs; ig,none; 9.13  
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell ; Ribosomal\_S14,ank,kinase,death,none; 9.10  
 429332; AF030403; Hs.199263; Ste-20 related kinase; pkinase,metalthio;TM=M;SS=M; 9.08  
 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin\_EGF,laminin\_Nterm,integrin\_B;SS=M; 9.08  
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22\_Claudin,none; 9.07  
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE;; 8.98  
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;; 8.93  
 438000; A1825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M;; 8.90  
 446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.90  
 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.88  
 437056; A1147051; ; gb:ok33a11.s1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S; none,spectrin,SH3,PH,CH; 8.78  
 445496; AB007860; Hs.12802; development and differentiation enhancin; SH3,ank,PH,ArfGap;TM=M;; 8.78  
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 8.75  
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M;; 8.70  
 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank;; 8.68  
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 8.65  
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept; Y\_phosphatase;SS=M; 8.65  
 430397; A1924533; Hs.105607; bicarbonate transporter related protein ; HCO3\_cotransp;TM=Y;; 8.64  
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M;; 8.60  
 442994; A1026718; Hs.16954; ESTs; ank,kinase,death,Ribosomal\_S14; 8.60  
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M;; 8.60  
 455439; AW945484; Hs.184252; ESTs, Weakly similar to ALU8\_HUMAN ALU S; none,7tm\_1; 8.55  
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 ; TIMP,kinase,DAG\_PE-bind,RBD; 8.43  
 417035; AA192455; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA se; none,none; 8.40  
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank;; 8.39  
 448209; AW160489; Hs.20709; tetraspan 5; transmembrane4;TM=Y;SS=M; 8.33  
 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none,none; 8.33  
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase\_2;TM=M;; 8.31  
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm\_1;TM=Y;SS=M; 8.30  
 445633; A1453386; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK,none; 8.28  
 446719; W39500; Hs.301872; hypothetical protein MGC4840; AAA,SKI;TM=M;; 8.23  
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none,none; 8.20  
 427274; NM\_005211; Hs.174142; colony stimulating factor 1 receptor, fo; ig,kinase;TM=Y;SS=M; 8.18  
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none,none; 8.15  
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS,zf-C2H2,SET; 8.15  
 417386; AL037228; Hs.82043; D123 gene product; NUDIX,secY,E1\_dehydrog,transket\_pyr;TM=Y;SS=M; 8.13  
 431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 8.10  
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none;TM=M;SS=M; 8.09  
 425424; NM\_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M;; 8.08  
 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin receptor; FG-GAP,integrin\_A,none; 8.05  
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo\_seg;TM=M;SS=M; 8.03  
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase;SS=M; 8.03  
 404891; ; Target Exon; none,none; 7.95  
 414278; AA330116; Hs.77273; Human glucose transporter pseudogene; none,none; 7.93  
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 7.93  
 433211; H11850; Hs.12808; MARK; pkinase,UBA,KA1;SS=M; 7.91  
 438485; W57578; Hs.237955; RAB7, member RAS oncogene family; pkinase,ABC1,none; 7.90  
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR\_c6,Acyl-CoA\_hydro; 7.90  
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase tra; xan\_ur\_permease,RA; 7.88  
 427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase (c-erb-b2; Furin-like,kinase,Recep\_L\_domain,YLP;TM=Y;SS=M; 7.86  
 405036; ; NM\_021628; Homo sapiens arachidonate lip; lipoxigenase,complex1\_49Kd,PLAT;TM=M;; 7.83  
 418529; AW005695; Hs.250897; TRK-fused gene; Band\_41,ERM,kinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M;; 7.83  
 431912; A1660552; Hs.76549; ESTs, Weakly similar to A56154 Abl subst; none,Acyl-CoA\_dh,Acyl-CoA\_dh\_M,Acyl-CoA\_dh\_N; 7.80  
 432981; NM\_002733; Hs.3136; protein kinase, AMP-activated, gamma 1 n; CBS,Aa\_trans;TM=M;; 7.78  
 422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo; Sec7,PH,ANF\_receptor,lig\_chan,WD40,IRK; 7.78  
 446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonin; CNH,DAG\_PE-bind,PH,Involucrin,M;TM=M;; 7.78  
 431183; NM\_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER\_lumen\_recept;TM=M;SS=M; 7.78  
 400845; ; NM\_003105; Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 7.73  
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC\_tran,M,SMC\_N,SMC\_C,DUF164,none; 7.73  
 437192; AW975786; Hs.75355; ubiquitin-conjugating enzyme E2N (homolo; UQ\_con,Y\_phosphatase,SH2; 7.70  
 403212; ; NM\_019595; Homo sapiens intersectin 2 (IT; SH3,efhand,C2,PH,RhoGEF;TM=M;; 7.70  
 441190; H09073; Hs.25046; ESTs; E1-E2\_ATPase,Cation\_ATPase\_C,Cation\_ATPase\_N,Hydrolase,none; 7.68

409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm\_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rve,zf-B\_box;TM=Y;SS=M; 7.68  
 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene; SH2,SH3,kinase;SS=M; 7.65  
 447898; AW969638; Hs.112318; 6.2 kd protein; none,none; 7.65  
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD\_DAPIN,HIN;SS=M; 7.63  
 401927; ; C17000914;gi8394367[ref]NP\_058549.1; s; none; 7.60  
 407347; AA829847; ; gb:od40d07.s1 NCL\_CGAP\_GCB1 Homo sapiens; RhoGAP,SH2,kinase,POLO\_box,none; 7.58  
 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3,none; 7.57  
 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; kinase,ubiquitin,Enterotoxin\_A,PHO4,kinase,ubiquitin; 7.55  
 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, ty; none,none; 7.55  
 421489; A1922821; Hs.32433; ESTs; none,PI-PLC-X,PI-PLC-Y,C2; 7.53  
 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 7.53  
 431605; AW972407; Hs.124370; gb:EST384498 MAGE resequences, MAGL Homo; adenylatekinase,SRP54;TM=M; 7.50  
 430570; A1417881; Hs.292464; ESTs; 7tm\_2,Fz,Frizzled,none; 7.50  
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 7.48  
 420676; A1434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG\_PE-bind,none; 7.48  
 444252; R21135; Hs.54985; ESTs; none,none; 7.47  
 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3\_P14\_kinase;TM=M; 7.47  
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M; 7.45  
 418546; AA224827; ; gb:nc32g04.s1 NCL\_CGAP\_Pr2 Homo sapiens ; vwa,integrin\_A,FG-GAP,none; 7.45  
 437860; AA333063; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 7.43  
 452007; AA426234; Hs.34906; ESTs, Weakly similar to T17210 hypotheti; none,kinase; 7.40  
 432407; AA221036; ; gb:zr0311.2.r1 Stratagene NT2 neuronal pr; DEAD,helicase\_C,rrm,Ndr,Cys\_knot,TIL,vwa,vwc,vwd,IQ,Rila,abhydrolase,TGF-beta,DUF139,TPR,DSPC,isp\_1,Ribosomal\_S21,rvp;TM=M; 7.40  
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,kinase,death,SPRY,SAP,Ribosomal\_L24e,SRP54,dDENN,DENN,uDENN;TM=M; 7.40  
 421429; NM\_014922; Hs.104305; death effector filament-forming Ced-4-lj; LRR,PAAD\_DAPIN,AAA,CARD,NB-ARC;NA;NA; 7.38  
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone\_rec,zf-C4;SS=M; 7.38  
 430016; NM\_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y; 7.38  
 422813; AV656571; Hs.121068; transmembrane 4 superfamily member 6; transmembrane4;TM=Y;SS=M; 7.32  
 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 ( ; none,spectrin,SH3,PH,CH; 7.25  
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,kinase;TM=M; 7.24  
 444745; AF117754; Hs.11861; thyroid hormone receptor-associated prot; none;TM=M; 7.23  
 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; kinase,PBD;TM=M; 7.19  
 407591; NM\_000910; Hs.37125; neuropeptide Y receptor Y2; 7tm\_1;TM=Y; 7.18  
 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 7.18  
 450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M; 7.18  
 403344; ; NM\_000341;Homo sapiens solute carrier fa; alpha-amylase;TM=Y; 7.15  
 427268; X78520; Hs.174139; chloride channel 3; CBS,voltage\_CLC;TM=Y; 7.14  
 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glu; sugar\_tr;TM=Y;SS=M; 7.14  
 404875; ; NM\_022819\*Homo sapiens phospholipase A2; phoslip;SS=M; 7.11  
 433618; AA602539; Hs.345494; ESTs; G-alpha\_A\_deaminase; 7.10  
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate\_transp,STAS,HMG\_box; 7.08  
 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9;TM=M;SS=M; 7.05  
 426655; AL049589; Hs.171723; neuronal cell death-related protein; TFIID-31;TM=M; 7.05  
 423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7tm\_2,HRM,CSD;TM=Y;SS=M; 7.03  
 400211; ; NM\_003899\*Homo sapiens PAK-interacting ; SH3,PH,RhoGEF,Terpene\_synth;TM=M; 7.03  
 438150; AA037534; Hs.342874; transforming growth factor, beta recepto; zona\_pellucida,none; 6.93  
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit,; proteasome;TM=M; 6.93  
 405275; AB028989; ; mitogen-activated protein kinase 8 inter; Cys\_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 6.93  
 415392; Z44067; Hs.10957; ESTs; PIP5K,none; 6.89  
 429355; AW973253; Hs.292689; ESTs; kinase,bZIP,Armadillo\_seg,none; 6.88  
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic; ; C2,PLA2\_B;TM=M; 6.85  
 427832; AF038362; Hs.180930; TBP-associated factor 172; SNF2\_N,helicase\_C,Armadillo\_seg,HEAT;TM=M; 6.83  
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE\_p10,ICE\_p20,DED;TM=M; 6.80  
 400158; ; ENSP00000244302\*CDNA FLJ11591 fis, clone; Sm;SS=M; 6.78  
 401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT\_bind,STAT\_prot,ion\_trans,PAC,PAS,none; 6.78  
 400844; ; NM\_003105\*Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_L,ldl\_recept\_L,granulin,BNR;TM=Y;SS=M; 6.73  
 457238; U07358; Hs.211601; mitogen-activated protein kinase kinase ; kinase; 6.73  
 404440; ; NM\_021048;Homo sapiens melanoma antigen,; MAGE;TM=M; 6.73  
 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kina; Ets,SAM\_PNT;TM=M; 6.70  
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Priboyltran,OMPdecase;TM=M; 6.70  
 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 6.65  
 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate\_kin;SS=M; 6.64  
 408638; AW451353; Hs.173328; ESTs; B56,none; 6.63  
 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 6.61  
 401057; BE563196; ; eukaryotic translation elongation factor; ion\_trans,IQ;TM=Y; 6.60  
 446526; H89616; Hs.296290; Homo sapiens cDNA FLJ13357 fis, clone PL; none,none; 6.60  
 400528; ; NM\_020975\*Homo sapiens ret proto-oncoge; cadherin,kinase;TM=Y;SS=M; 6.58  
 418562; R60659; Hs.124831; CGI-67 protein; none,Skp1,AAA; 6.57  
 453826; AL138129; ; gb:DKFZp547F152\_r1 547 (synonym: hibr1) ; PK,PK\_C,none; 6.55  
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC\_tran,GTP\_EFTU,ABC\_membrane,none; 6.54  
 415088; A1077288; Hs.296323; serum/glucocorticoid regulated kinase; none,none; 6.50  
 453489; AA300067; Hs.33032; hypothetical protein DKFZp434N185; F5\_F8\_type\_C,kinase,Ets,F5\_F8\_type\_C,kinase,Ets; 6.47  
 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm,NTF2;TM=M; 6.46  
 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M; 6.46  
 441712; AW391927; Hs.7946; KIAA1288 protein; AIP3;TM=M; 6.44  
 414557; AA340111; Hs.100009; acyl-Coenzyme A oxidase 1, palmitoyl; kinase,7tm\_1; 6.43  
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY\_C;TM=M; 6.43  
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 6.40  
 438941; AF075047; Hs.31864; ESTs; Ca\_channel\_B,SH3,arf,none; 6.40  
 441466; AW673081; Hs.54828; ESTs; kinase,zf-C2H2,KRAB,none; 6.33  
 438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypotheti; lipoxigenase,PLAT,none; 6.33  
 433255; A1274270; Hs.96840; KIAA1527 protein; MHCK\_EF2\_kinase;TM=M;SS=M; 6.33  
 427801; AW979155; Hs.298275; amino acid transporter 2; Aa\_trans;TM=M;SS=M; 6.32

- 407970; AW403814; Hs.41714; BCL2-associated athanogene; ubiquitin,BAG,Tropomyosin;; 6.30  
 438464; AA669735; Hs.324743; protein phosphatase 4 regulatory subunit; none,none; 6.30  
 453977; AA886006; Hs.250427; ESTs; pkinase,P2X\_receptor,E1-E2\_ATPase,Hydrolase; 6.30  
 412491; W31589; Hs.73957; RAB5A, member RAS oncogene family; ras,arf,PP2C;TM=M;; 6.30  
 413235; BE243445; Hs.75248; topoisomerase (DNA) II beta (180kD); DNA\_gyraseB,DNA\_topoisolV,HATPase\_c,DNA\_gyraseB,DNA\_topoisolV,HATPase\_c; 6.29  
 404342;; C7002192\*.gil7299207[gblAAAF54404.1] (AE0; none;TM=M;; 6.27  
 409274; NM\_003930; Hs.52644; SKAP55 homologue; SH3,PH;SS=M; 6.25  
 419693; AA133749; Hs.301350; FXYD domain-containing ion transport reg; ATP1G1\_PLM\_MAT8;TM=Y;SS=M; 6.23  
 405429;; Target Exon; Y\_phosphatase,none; 6.23  
 404975; AL042279;; uncharacterized hypothalamus protein HT0; kringle;TM=Y;SS=M; 6.20  
 452929; AW954938; Hs.172816; neuregulin 1; Neuregulin,EGF,ig,Neuregulin,EGF,ig; 6.18  
 446883; AW452756; Hs.16364; hypothetical protein FLJ10955; DEAD,helicase\_C,rm,Ndr,Cys\_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPc,Lsp\_1,Ribosomal\_S21,rvp;TM=M;; 6.18  
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M;; 6.15  
 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y;; 6.15  
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none,none; 6.14  
 447727; AI421079;; tumor necrosis factor receptor superfam; none,synaptobrevin; 6.13  
 401536;; NM\_002530\*.Homo sapiens neurotrophic tyr; ig,pkinase,LRR,LRRNT,LRRCT;TM=M;SS=M; 6.11  
 444317; A1140566; Hs.143436; ESTs, Weakly similar to PLHU plasmin [H.; PAN,kringle,trypsin,PI-PLC-X,C2,SH2,PH,SH3,PI-PLC-Y,PAN; 6.10  
 427557; NM\_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR\_LY6,ET,PLA2\_inh;SS=M; 6.08  
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;; 6.08  
 450107; AI873287; Hs.257812; ESTs; ICE\_p20,DED;TM=M;; 6.05  
 418175; AW967054; Hs.206312; ESTs, Weakly similar to I38022 hypotheti; zf-C2H2,BTB,K\_tetra,Syntaxin,none; 6.05  
 408983; NM\_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC\_tran,ABC\_membrane,PRK,Bac\_export\_3;TM=Y;; 6.05  
 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema,PSI,integrin\_B;TM=Y;; 6.03  
 427625; AF008216; Hs.285013; putative human HLA class II associated p; none,none; 6.03  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.03  
 446650; AB016625; Hs.15813; solute carrier family 22 (organic cation; sugar\_tr;TM=Y;SS=M; 6.03  
 405102;; C15001220\*.gil4469558[gblAAD21311.1] (AF; DAG\_PE-bind,PH,RhoGEF,DC1;SS=M; 6.03  
 400121;; Eos Control; SH3,PH,RhoGEF,Terpene\_synth;TM=M;; 6.03  
 415327; H22769;; gb:ym54c02.r1 Soares infant brain 1NIB H; SH3,PDZ,Guanylate\_kin;SS=M; 6.03  
 404148;; NM\_002944\*.Homo sapiens v-ros avian UR2; fn3,pkinase,DUF139;TM=Y;SS=M; 6.03  
 405531;; Target Exon; PDZ,CARD,Guanylate\_kin;TM=M;; 6.00  
 433363; AA584829; Hs.275163; non-metastatic cells 2, protein (NM23B); NDK,none; 6.00  
 427270; H47921; Hs.174139; chloride channel 3; voltage\_CLC,CBS,none; 5.99  
 423774; L39064; Hs.1702; interleukin 9 receptor; none;TM=M;SS=M; 5.98  
 424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked; pkinase,TBC; 5.98  
 411040; AF007393; Hs.177574; protein-kinase, interferon-inducible dou; HLH;TM=M;; 5.95  
 423422; AC005175; Hs.128425; NY-REN-24 antigen; Sulfotransfer,7tm\_1,none; 5.88  
 453902; BE502341; Hs.3402; ESTs; none,none; 5.88  
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa\_trans;TM=Y;; 5.86  
 436154; AA764950; Hs.119898; ESTs; ehband,DAG\_PE-bind,DAGKa,PHD,DAGKc,PSI,none; 5.85  
 455358; AW902641;; gb:QV3-NN1024-100500-181-d08 NN1024 Homo; Sulfatase,Somatomedin\_B,Phosphodiester,none; 5.83  
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol\_BP,pkinase;TM=M;; 5.82  
 452547; AA335295; Hs.74120; adipose specific 2; LEA;TM=M;; 5.82  
 415204; T27434;; gb:hbc2294 Human pancreatic islet Homo s; Na\_Ca\_Ex,Calx-beta,none; 5.80  
 435563; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar\_tr;TM=Y;; 5.78  
 456097; C15702; Hs.288028; ESTs, Moderately similar to I54374 gene; dsrm,FKBP; 5.78  
 422445; M23114; Hs.1526; ATPase, Ca transporting, cardiac muscle; E1-E2\_ATPase,Cation\_ATPase\_C,Cation\_ATPase\_N,Hydrolase;TM=Y;; 5.77  
 436246; AW450963; Hs.119991; ESTs; none,DNA\_gyraseB,DNA\_topoisolV,HATPase\_c; 5.75  
 422953; AA488860; Hs.245043; hypothetical protein FLJ14297; ABC\_tran,PRK;TM=Y;SS=M; 5.75  
 425854; AA749190;; ESTs; RhoGAP,SH2,pkinase,POLO\_box,none; 5.74  
 424160; T74062;; gb:yc81f01.r1 Soares Infant brain 1NIB H; ROK,none; 5.70  
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN\_MK;TM=M;SS=Y; 5.69  
 437613; R19892; Hs.10267; MIL1 protein; none,none; 5.68  
 410820; BE391493; Hs.16475; Human DNA sequence from clone RP5-852M4; TBC;SS=M; 5.68  
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD;TM=M;; 5.66  
 426500; NM\_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M;; 5.63  
 406930; U04691;; gb:Human olfactory receptor (OR17-219) g; none;TM=Y;SS=M; 5.60  
 401044;; Target Exon; none,ICE\_p20,ICE\_p10,CARD,Peptidase\_M1; 5.56  
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE\_p10,ICE\_p20;TM=M;SS=M; 5.55  
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RR;  
 aa\_permeases,pyridoxal\_deC,bromodomain,PHD,MBD,AT\_hook,DDT,PI3\_Pi4\_kinase,FAT,FATC,Bola,RUN;TM=M;; 5.53  
 426248; T18988; Hs.293668; ESTs; pkinase,none; 5.50  
 418426; NM\_003804; Hs.296327; receptor (TNFRSF)-interacting serine-thr; pkinase,death;TM=M;; 5.43  
 417086; AA194446;; ESTs, Weakly similar to S55024 nebulin; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 5.43  
 447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupl; 7tm\_1,SH2;TM=Y;SS=M; 5.40  
 412247; AF022375; Hs.73793; vascular endothelial growth factor; PDGF;SS=M; 5.40  
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, com; pkinase,TBC,Rhodanese;TM=M;; 5.38  
 419355; AA428520; Hs.90061; progesterone binding protein; heme\_1;TM=Y;SS=M; 5.35  
 411188; BE161168;; gb:PM0-HT0425-170100-002-a10 HT0425 Homo; adenylatekinase,none; 5.35  
 422461; NM\_003417; Hs.117077; zinc finger protein 264; zf-C2H2,KRAB,TFIIS;TM=M;; 5.28  
 426348; BE466586; Hs.17433; hypothetical protein FLJ20967; none,none; 5.25  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y\_phosphatase,Ribosomal\_S3\_N;TM=M;; 5.23  
 429592; AB029041; Hs.209646; KIAA1118 protein; Troponin,Exo\_endo\_phos,IQ;TM=M;; 5.22  
 434821; AA159111; Hs.284281; Human putative ribosomal protein S1 mRNA; ER\_lumen\_recept,Ribosomal\_L11,Ribosomal\_L11\_N;TM=Y;SS=M; 5.21  
 434368; AW519020; Hs.73893; dopamine receptor D2; pkinase,SH3,none; 5.15  
 405586;; NM\_000299.Homo sapiens plakophilin 1 (ec; Armadillo\_seg;TM=M;; 5.13  
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylatekinase,none; 5.12  
 407443; AF227138;; gb:Homo sapiens candidate taste receptor; none;TM=Y;SS=M; 5.11  
 416817; AA398045; Hs.104679; ESTs; Furin-like,pkinase,Recep\_L\_domain,fn3,none; 5.10  
 401886;; NM\_021783.Homo sapiens XEDAR (XEDAR), mR; TNFR\_c6;TM=M;SS=M; 5.08  
 410314; AW860708; Hs.18851; hypothetical protein FLJ10875; myb\_DNA-binding,PAH,BAH,bromodomain,PHD,SET;TM=M;; 5.08



- 401579; AL031447; ; Homo sapiens, clone IMAGE:4053044, mRNA; ; Neur\_chan\_LBD, Neur\_chan\_memb, none; 5.05  
 445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-I; PABP,rm, pkinase, 14-3-3; 5.05  
 417529; AA203634; ; gb:zx58b09.r1 Soares\_fetal\_liver\_spleen\_; pkinase,UBA,KA1,none; 5.03  
 417527; AA203524; ; gb:zx56e10.r1 Soares\_fetal\_liver\_spleen\_; SH3;SS=M; 4.98  
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinas; pfb;TM=M; 4.96  
 431321; AW136372; Hs.1852; acid phosphatase, prostate; acid\_phosphat,none; 4.93  
 404298; ; C6001238\*gi|121715|sp|P26697|GTA3\_CHICK; none,GST\_C,GST\_N,pkinase; 4.85  
 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299322, mRNA; ; none;TM=M; 4.82  
 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC\_tran,ABC\_membrane;TM=Y; 4.73  
 422366; T83882; Hs.97927; ESTs; pkinase,none; 4.64  
 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase;TM=M; 4.48  
 426925; NM\_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fis, clone H; Esterase,enolase,Peptidase\_S9;TM=M; 4.45  
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm\_1;TM=Y;SS=M; 4.40  
 400749; ; NM\_003105; Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 4.38  
 425721; AC002115; Hs.159309; uroplakin 1A; transmembrane4;TM=Y;SS=M; 4.33  
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ldl\_recept\_a,PKD,MHC\_J;TM=M;SS=Y; 4.31  
 400751; ; NM\_003105; Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 4.18  
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;SS=M; 3.90  
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc transport; none,none; 3.88  
 458760; AI498631; Hs.111334; ferritin, light polypeptide; cystatin,ferritin,histone,HCO3\_cotransp,SH3,RhoGAP,xan\_ur\_permease,FCH;SS=M; 3.85  
 441218; BE327561; Hs.202345; ESTs; none,WD40,E1-E2\_ATPase,Cation\_ATPase\_C,Cation\_ATPase\_N,Hydrolase; 3.78  
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death,ZU5;SS=M; 3.76  
 451385; AA017656; ; gb:ze39h01.r1 Soares retina N2b4HR Homo; Atrophin-1,enolase,Atrophin-1,Y\_phosphatase,SH2,fibrinogen\_C,TIM; 3.60  
 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase,DAG\_PE-bind,pkinase\_C,OPR;TM=M; 3.30  
 409582; R27430; Hs.271565; ESTs; none,Neur\_chan\_LBD,Neur\_chan\_memb; 3.28  
 441155; AW161008; Hs.7719; GABA(A) receptor-associated protein; MAP1\_LC3;SS=M; 3.23  
 436740; AW975133; ; gb:EST387239 MAGE resequences, MAGN Homo; none,EPH\_lbd,fn3,pkinase,SAM; 3.20  
 418319; AW611703; Hs.190173; ESTs, Weakly similar to A46010 X-linked ; none,IRK; 3.20  
 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (f; none;NA;NA; 3.13  
 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit; none,none; 3.10  
 400846; ; sortilin-related receptor, L(DLR class) ; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 3.09  
 422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (fr; none,Na\_H\_Exchange; 3.03  
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar\_tr;TM=Y;SS=M; 3.02  
 424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK,none; 2.98  
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member; death,TNFR\_c6;TM=Y;SS=M; 2.93  
 401279; ; C13000351\*gi|2494033|sp|Q64398|KGDG\_MES; none,none; 2.88  
 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth fa; Sema,pkinase,TIG,PSI,none; 2.83  
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, s; IRK;TM=Y; 2.80  
 453619; H87648; Hs.33922; Homo sapiens, clone MGC:9084, mRNA, comp; pkinase;TM=M; 2.75  
 441699; AW511126; Hs.127572; ESTs; none,Aa\_trans; 2.73  
 458781; AI444821; Hs.63085; ESTs, Weakly similar to MPP3\_HUMAN MAGUK; SH3,PDZ,Guanylate\_kin,L27;TM=M; 2.73  
 446913; AA430650; Hs.16529; transmembrane 4 superfamily member (tet; transmembrane4;TM=Y;SS=M; 2.70  
 453487; R31770; Hs.56562; ESTs; 7tm\_1,none; 2.68  
 421279; AW664878; Hs.106645; ESTs; pkinase,none; 2.68  
 419720; AA249131; Hs.337778; hypothetical protein FLJ11068; none,none; 2.65  
 452345; AA293279; Hs.29173; hypothetical protein FLJ20515; DSPc;TM=M; 2.63  
 422247; U18244; Hs.113602; solute carrier family 1 (high affinity a; SDF;TM=Y; 2.62  
 425212; AW962253; Hs.171618; ESTs; pkinase,none; 2.60  
 427344; NM\_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor; Neur\_chan\_LBD,Neur\_chan\_memb;TM=Y;SS=M; 2.58  
 423629; AW021173; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone H; voltage\_CLC,CBS,none; 2.55  
 456737; BE247203; Hs.124831; CGI-67 protein; abhydrolase\_2;TM=M;SS=M; 2.53  
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm\_1;TM=Y;SS=M; 2.53  
 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fis, clone Y7; none,none; 2.50  
 448324; AI571356; Hs.34174; ESTs, Moderately similar to ALU8\_HUMAN A; ICE\_p20,CARD,ICE\_p10,none; 2.50  
 402256; ; Target Exon; pkinase,UBA,none; 2.43  
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HE; GDI,7tm\_1,none; 2.40  
 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypotheti; none,spectrin,SH3,PH,CH; 2.40  
 420634; S42457; Hs.1323; cyclic nucleotide gated channel alpha 1; cNMP\_binding,ion\_trans;TM=Y; 2.35  
 419630; W57756; ; gb:zd20g10.r1 Soares\_fetal\_heart\_NbHH19W; zf-C3HC4,none; 2.35  
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm\_1;TM=Y;SS=M; 2.35  
 400704; ; Target Exon; lig\_chan,SBP\_bac\_3,ANF\_receptor;TM=Y;SS=M; 2.33  
 400149; ; Eos Control; acid\_phosphat;TM=Y;SS=M; 2.30  
 459327; AW149706; Hs.7859; gb:xf41d02.x1 NCL\_CGAP\_Brn50 Homo sapien; PHD,PWWP,SET,pkinase,ig; 2.30  
 452220; BE158006; Hs.212296; ESTs; integrin\_A,FG-GAP,none; 2.25  
 416690; H84078; Hs.108551; ESTs; pkinase,none; 2.23  
 408354; AI382803; Hs.159235; ESTs; none,none; 2.23  
 452203; X57522; ; transporter 1, ATP-binding cassette, sub; ABC\_tran,ABC\_membrane,SRP54,Thymidylate\_kin;TM=Y;SS=M; 2.21  
 405093; ; C12001101\*gi|7522643|pir|T32733 AMPA g; none,none; 2.20  
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M; 2.20  
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none,none; 2.18  
 417185; NM\_002484; Hs.81469; nucleotide binding protein 1 (E.coli Min; ParA,fer4\_NiH,ArsA\_ATPase;TM=M; 2.18  
 433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none,PHO4; 2.18  
 413627; BE182082; Hs.246973; ESTs; Armadillo\_seg,IBB;TM=M; 2.18  
 407415; AF073328; ; gb:Homo sapiens tetracycline transporter-; none,none; 2.15  
 450592; AI701555; Hs.202562; ESTs; pkinase,none; 2.15  
 428767; AI421972; Hs.98802; ESTs, Moderately similar to T14342 NSD1 ; none,pkinase,ig; 2.15  
 429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm,BAG;SS=M; 2.15  
 419122; AI401360; Hs.44410; ESTs; ABC\_tran,ABC\_membrane,none; 2.10  
 446420; AW015693; Hs.135614; ESTs; ion\_trans,none; 2.05  
 420076; AA827860; Hs.293717; ESTs; DUF59,pkinase; 2.05  
 409416; AW388359; Hs.10667; ESTs; transmembrane4;TM=Y;SS=M; 2.03  
 428766; AA477989; Hs.98800; ESTs; TPR,7tm\_1; 2.03  
 427001; NM\_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphoryl; pkinase;TM=M; 2.03



453709; AL119133; ; protein kinase C substrate 80K-H; none,histone; 2.03  
 423341; AW242394; Hs.108660; ESTs; none,none; 2.00  
 456772; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.88  
 427786; BE407863; Hs.256871; ESTs; none,FG-GAP,7tm\_1; 1.65  
 423508; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.00  
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00

TABLE 58B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI368880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA459292 AI494230 BF507531 AI492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE395919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA040570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BF702221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BI790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
436729	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA040570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895



452203 2630\_1 BF093671 AA053070 T28548 AL570460 BI006862 BI007207 AA373620 W95069 AA629136 AA708164 AI014886 AW168697 D51623 AA577168  
 AI094208 AA028946 AA975078 R16815 BG151132 AI276297 D51676  
 BC014081 NM\_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519  
 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470  
 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429  
 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404  
 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220  
 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184  
 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619  
 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256  
 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601  
 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586  
 AK057669 AK054977 AL519747 BE893744 BM313248 BG913430 H80793 BF813504 N36311 N39276 H95973 BF791919 BE739392 BE144239  
 AA074615 AI291059 AI681053 AA702355 BF439899 AW055166 AI096957 BF223853 AL119659 AI692209 BM312961 AI869297 BE466252 AI292024  
 AA402764 AI214620 AA765312 BF380770 AA442682 AL519746 AW295039 AI037878 AW473433 AI499437 AI401618 AI130831 AA427406 AI042138  
 BG272488 AI828769 AI828764 AI189390 W84635 AA398496 AA761672 AA699520 AI200406 N68093 AI143913 AA993133 AA613306 AI050971  
 AA661905 AA722687 AI749977 AA829345 BG057324 BF001339 AA910169 AA765133 AI360722 AI701849 AI365083 H95974 AI830377 AI312866  
 AI370491 BE858907 N62185 AA705746 BE379632 W93803 AI440333 AW367670 AW367640 N77131 BF993216 AI858263 W52329 N68106 R83113  
 R85153 BE380058 AA082537 AA729731 W23495 W31190 BF995236 BF968827 BF355168 N24508 AA215711 BF170735 AA280395 BE738851  
 AW367707 AA630879 AA428420 R76236 BG567847 N25931 AA173568 AI073567 AA004957 AI539585 N95093 H99798 H95072 H96853 AA215712  
 AA034214 R85096 H82051 H80794 R44954 AA278972 H68352 H68346 R94750 R89010 R67951 H65817 N24891 AA173731 AI693577 BE181027  
 AA709461 BE181002 W60239 BF987598 BF995279 H17483 R76237 AL119133 BF964815 AW663315 H65903 H17591 R20167 AA310039 R58734  
 R58506

TABLE 58C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA  
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807
404942	7382153	Plus	92095-92252
400752	7331445	Minus	36215-36461
400496	9743564	Plus	41515-41695
404568	9966995	Minus	92893-93116
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
402328	4464283	Minus	13758-13922,14558-14752
404891	7329392	Plus	84974-85125
405036	7543748	Minus	121957-122129
400845	9188605	Plus	34428-34612
403212	7630897	Minus	156037-156210
401927	3873185	Minus	112000-112137

Table 59A lists about 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03  
 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 8.2. The "average" prostate cancer level was set to the  
 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 50<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific  
 background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the  
 ratio was evaluated.

TABLE 59A: ABOUT 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	108.1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	102.5
420923	AF097021	Hs.273321	differentially expressed in hematopoietic	90.5
416854	H40164	Hs.80296	Purkinje cell protein 4	79.8
425075	AA506324	Hs.1852	acid phosphatase, prostate	71.6
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	70.6
434666	AF151103	Hs.112259	T cell receptor gamma locus	69.1
419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	66.4
413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	66.4
420154	AI093155	Hs.95420	JM27 protein	63.9
428336	AA503115	Hs.183752	microseminoprotein, beta-	61.4
400287	S39329	Hs.181350	kallikrein 2, prostatic	59.7
416602	NM_006159	Hs.79389	nel (chicken)-like 2	54.6
428398	AI249368	Hs.98558	ESTs	54.6
432441	AW292425	Hs.163484	ESTs	54.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	54.2
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	54.2
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	53.7

	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	49.6
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	48.0
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	46.8
5	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	45.0
	427674	NM_003528	Hs.2178	H2B histone family, member Q	44.9
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	44.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	44.5
	415314	N88802	Hs.5422	glycoprotein M6B	43.2
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	41.9
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	41.1
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	40.5
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	39.5
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	39.3
15	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	39.0
	447726	AL137638	Hs.19368	matrilin 2	38.6
	426174	AA547959	Hs.115838	ESTs	38.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	38.0
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	37.5
20	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	37.0
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	35.5
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	35.1
	453096	AW294631	Hs.11325	ESTs	35.1
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	34.9
25	427665	AF134803	Hs.180141	cofilin 2 (muscle)	34.9
	415539	AI733881	Hs.72472	BMP-R1B	34.9
	428411	AW291464	Hs.10338	ESTs	34.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	34.3
	401424			NM_001172:Homo sapiens arginase, type II	34.0
30	452114	N22687	Hs.8236	ESTs	34.0
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	33.8
	448045	AJ297436	Hs.20166	prostate stem cell antigen	33.1
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	32.9
	432101	AI918950	Hs.123642	EphA3	32.7
35	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	32.4
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg),	32.4
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	32.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	32.3
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	31.9
40	408380	AF123050	Hs.44532	diubiquitin	31.6
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	31.4
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.3
	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	31.2
	408001	AA046458	Hs.95296	ESTs	30.8
45	440274	R24595	Hs.7122	scrapie responsive protein 1	30.7
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	30.3
	442993	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1	30.2
	433404	T32982	Hs.102720	ESTs	29.6
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	29.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	29.3
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	29.2
	418827	BE327311	Hs.47166	HT021	29.0
	410330	AW023630	Hs.46786	ESTs	28.6
	450377	AB033091	Hs.74313	KIAA1265 protein	28.6
55	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	28.5
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	28.2
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	27.7
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	27.7
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	27.6
60	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.4
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	27.4
	407202	N58172	Hs.109370	ESTs	27.4
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	27.4
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	27.3
65	403047			NM_005656*:Homo sapiens transmembrane pr	27.2
	407709	AA456135	Hs.23023	ESTs	27.0
	433444	AW975324	Hs.129816	ESTs	26.8
	415989	AI267700	Hs.317584	ESTs	26.8
	430539	AK001489	Hs.242894	ADP-ribosylation factor-like 1	26.5
70	408221	AA912183	Hs.47447	ESTs	26.5
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	26.4
	437179	AA393508	Hs.300642	serologically defined colon cancer antig	26.4
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	26.2
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	26.2
75	400292	AA250737	Hs.72472	BMP-R1B	26.0
	433647	AA603367	Hs.222294	ESTs	26.0
	429220	AW207206	Hs.136319	ESTs	25.8
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	25.6
	448106	AI800470	Hs.171941	ESTs	25.5
80	415992	C05837	Hs.145807	hypothetical protein FLJ13593	25.5
	452792	AB037765	Hs.30652	KIAA1344 protein	25.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	25.2
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	24.9
	418961	AW967646	Hs.23023	ESTs	24.8

	451027	AW519204	Hs.40808	ESTs	24.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	24.5
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	24.4
5	418396	AI765805	Hs.26691	ESTs	24.1
	412088	AI689496	Hs.108932	ESTs	24.1
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	24.0
	411644	H92064	Hs.278626	Arg/Abl-interacting protein ArgBP2	24.0
10	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	23.9
	433466	AA508353	Hs.105314	relaxin 1 (H1)	23.7
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	23.6
	440995	T57773	Hs.10263	ESTs	23.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	23.2
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	23.1
15	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	22.9
	440260	AI972867	Hs.7130	copine IV	22.5
	443622	AI911527	Hs.11805	ESTs	22.2
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	22.0
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	21.9
20	450642	R39773	Hs.7130	copine IV	21.9
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	21.8
	435981	H74319	Hs.188620	ESTs	21.8
	450693	AW450461	Hs.203965	ESTs	21.7
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.7
25	423242	AL039402	Hs.125783	DEME-6 protein	21.7
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	21.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	21.5
	404210			NM_005936:Homo sapiens myeloid/lymphoid	21.5
	417622	AW298163	Hs.82318	WAS protein family, member 3	21.5
30	419526	AI821895	Hs.193481	ESTs	21.5
	442799	AI564739	Hs.68505	ESTs	21.4
	424846	AU077324	Hs.1832	neuropeptide Y	21.3
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	21.3
	429922	Z97630	Hs.226117	H1 histone family, member 0	21.3
35	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	21.3
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	21.2
	431474	AL133990	Hs.190642	ESTs	21.2
	430887	N66801	Hs.260287	KIAA1841 protein	21.1
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	21.1
40	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	21.1
	445133	AW157646	Hs.153506	ESTs	21.0
	421513	X00949	Hs.105314	relaxin 1 (H1)	21.0
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	20.8
	446795	AI797713	Hs.156471	ESTs	20.7
45	440774	AI420611	Hs.127832	ESTs	20.7
	407168	R45175	Hs.117183	ESTs	20.6
	417511	AL049176	Hs.82223	chordin-like	20.6
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	20.6
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	20.6
50	411800	N39342	Hs.103042	microtubule-associated protein 1B	20.5
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	20.5
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.5
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	20.5
	424897	D63216	Hs.153684	frizzled-related protein	20.5
55	430280	AA361258	Hs.237868	interleukin 7 receptor	20.4
	401197			ENSP00000229263*:HSPC213.	20.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	20.3
	429918	AW873986	Hs.119383	ESTs	20.2
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	20.2
60	453469	AB014533	Hs.33010	KIAA0633 protein	20.2
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	20.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	20.0
	419440	AB020689	Hs.90419	KIAA0882 protein	20.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.9
65	441690	R81733	Hs.33106	ESTs	19.9
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	19.8
	423044	AA320829	Hs.97266	protocadherin 18	19.8
	410929	H47233	Hs.30643	ESTs	19.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	19.7
70	431556	AF016028	Hs.183428	sarcospan (Kras oncogene-associated gene	19.6
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	19.6
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	19.6
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	19.5
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	19.4
75	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	19.4
	430187	AI799909	Hs.158989	ESTs	19.3
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	19.3
	434423	NM_006769	Hs.3844	LIM domain only 4	19.2
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	19.1
80	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	19.0
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	18.9
	436032	AA150797	Hs.109276	latexin protein	18.9
	431548	AI834273	Hs.9711	novel protein	18.9
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	18.9

	445929	AI089660	Hs.323401	dpy-30-like protein	18.8
	453160	AI263307	Hs.239884	H2B histone family, member L	18.8
	439897	NM_015310	Hs.6763	KIAA0942 protein	18.8
5	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	18.8
	434987	AW975114	Hs.293273	ESTs	18.7
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	18.7
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	18.7
	418819	AA228776	Hs.191721	ESTs	18.7
10	450831	R37974	Hs.25255	ESTs	18.7
	415691	AW963979	Hs.24723	ESTs	18.7
	417124	BE122762	Hs.25338	ESTs	18.7
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	18.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	18.5
15	410099	AA081630	Hs.169387	KIAA0036 gene product	18.5
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	18.5
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	18.5
	436420	AA443966	Hs.31595	ESTs	18.4
20	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	18.4
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	18.3
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	18.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	18.2
	437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	18.2
	439569	AW602166	Hs.222399	CEGP1 protein	18.1
25	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	18.1
	424682	AW604804	Hs.151717	KIAA0437 protein	18.0
	432435	BE218886	Hs.282070	ESTs	17.9
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	17.8
	431121	AW971157		gb:EST383245 MAGE resequences, MAGL Homo	17.8
30	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	17.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	17.7
	440703	AI137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	17.7
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	17.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	17.6
35	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	17.5
	430487	D87742	Hs.241552	KIAA0268 protein	17.4
	419355	AA428520	Hs.90061	progesterone binding protein	17.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	17.3
	423943	AF163570	Hs.135756	polymerase (DNA directed) kappa	17.3
40	434217	AW014795	Hs.23349	ESTs	17.3
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	17.2
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	17.2
	430177	AW969233	Hs.302746	MSTP028 protein	17.2
	432473	AI202703	Hs.152414	ESTs	17.1
45	421823	N40850	Hs.28625	ESTs	17.1
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	17.0
	420092	AA814043	Hs.88045	ESTs	17.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	17.0
	417426	NM_002291	Hs.82124	laminin, beta 1	17.0
50	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	17.0
	401747			Homo sapiens keratin 17 (KRT17)	17.0
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	17.0
	442369	AI565071	Hs.159983	ESTs	16.9
55	432966	AA650114	Hs.325198	ESTs	16.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	16.8
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	16.8
	443745	AB039670	Hs.9728	ALEX1 protein	16.8
	438899	AF085833	Hs.135624	ESTs	16.8
60	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	16.8
	442064	AI422867	Hs.88594	ESTs	16.8
	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	16.5
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	16.4
	443801	AW206942	Hs.253594	ESTs	16.3
	437536	X91221	Hs.144465	ESTs	16.3
65	409196	NM_001874	Hs.334873	carboxypeptidase M	16.3
	438337	AK002058	Hs.6166	hypothetical protein FLJ11196	16.3
	416239	AL038450	Hs.48948	ESTs	16.3
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	16.2
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	16.2
70	409060	AI815867	Hs.50130	necdin (mouse) homolog	16.1
	442571	C06338	Hs.165464	ESTs	16.1
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	16.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	16.0
	450164	AI239923	Hs.30098	ESTs	16.0
75	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	16.0
	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	16.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	16.0
	436024	AI800041	Hs.190555	ESTs	16.0
	412652	AI801777	Hs.6774	ESTs	16.0
80	456516	BE172704	Hs.222746	KIAA1610 protein	16.0
	452576	AB023177	Hs.29900	KIAA0960 protein	15.9
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	15.9
	434792	AA649253	Hs.132458	ESTs	15.9
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	15.9

	442787	W93048	Hs.250723	hypothetical protein MGC2747	15.9
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	15.9
	402812			NM_004930*:Homo sapiens capping protein	15.8
5	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	15.8
	413597	AW302885	Hs.117183	ESTs	15.7
	439677	R82331	Hs.164599	ESTs	15.7
	432527	AW975028	Hs.102754	ESTs	15.7
	413654	AA331881	Hs.75454	peroxiredoxin 3	15.7
10	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	15.7
	426501	AW043782	Hs.293616	ESTs	15.7
	435056	AW023337	Hs.5422	glycoprotein M6B	15.7
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	15.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	15.6
15	434988	AI418055	Hs.161160	ESTs	15.6
	435380	AA679001	Hs.192221	ESTs	15.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	15.6
	446377	AW014022	Hs.170953	ESTs	15.5
20	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	15.5
	415672	N53097	Hs.193579	ESTs	15.5
	450325	AI935962	Hs.26289	ESTs	15.5
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	15.4
	443674	AI081330	Hs.145008	ESTs	15.4
25	415263	AA948033	Hs.130853	ESTs	15.4
	442081	AA401863	Hs.22380	ESTs	15.3
	415788	AW628686	Hs.78851	KIAA0217 protein	15.3
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	15.3
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	15.3
30	418693	AI750878	Hs.87409	thrombospondin 1	15.3
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	15.3
	443180	R15875	Hs.258576	claudin 12	15.2
	432437	W07088	Hs.293685	ESTs	15.2
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	15.2
35	446091	AW022192	Hs.200197	ESTs	15.2
	409341	AI963376	Hs.12532	chromosome 1 open reading frame 21	15.2
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	15.1
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	15.1
	453698	AA037615	Hs.42746	ESTs	15.1
40	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	15.1
	427707	NM_005578	Hs.180398	LIM domain-containing preferred transloc	15.1
	453308	AW959731	Hs.323099	ESTs	15.1
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	15.1
	433927	AI557019	Hs.116467	small nuclear protein PRAC	15.0
45	443162	T49951	Hs.9029	DKFZP434G032 protein	15.0
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	15.0
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	15.0
	443912	R37257	Hs.184780	ESTs	15.0
	410297	AA148710	Hs.79914	lumican	15.0
50	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	14.9
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	14.9
	451652	AA018968	Hs.133536	ESTs	14.9
	406038	Y14443	Hs.88219	zinc finger protein 200	14.8
	408784	AW971350	Hs.63386	ESTs	14.8
55	453510	AI699482	Hs.42151	ESTs	14.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	14.8
	433908	AW298141	Hs.157975	ESTs	14.8
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	14.8
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	14.8
60	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	14.7
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	14.7
	447752	M73700	Hs.105938	lactotransferrin	14.7
	426044	AA502490	Hs.336895	ESTs	14.7
	403362			NM_001615*:Homo sapiens actin, gamma 2,	14.7
65	427982	NM_016156	Hs.181326	KIAA1073 protein	14.7
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	14.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	14.7
	433226	AW503733	Hs.9414	KIAA1488 protein	14.6
	427472	AA522539	Hs.131250	transposon-derived Busler3 transposase-I	14.6
70	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	14.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.6
	409264	NM_014937	Hs.52463	KIAA0966 protein	14.6
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	14.5
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proli	14.5
75	410339	AI916499	Hs.298258	ESTs	14.5
	431992	NM_002742	Hs.2891	protein kinase C, mu	14.5
	424432	AB037821	Hs.146858	protocadherin 10	14.5
	431933	AI187057	Hs.132554	ESTs	14.5
	440749	W22335	Hs.7392	hypothetical protein MGC3199	14.5
80	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	14.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	14.5
	407021	U52077		gb:Human mariner1 transposase gene, comp	14.5
	413786	AW613780	Hs.13500	ESTs	14.5
	437866	AA156781	Hs.74170	metallothionein 1E (functional)	14.5

	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	14.4
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	14.4
	443280	AA299688	Hs.24183	ESTs	14.4
5	416836	D54745	Hs.80247	cholecystokinin	14.4
	436860	H12751	Hs.5327	PRO1914 protein	14.3
	425174	D87450	Hs.154978	KIAA0261 protein	14.3
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	14.3
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	14.3
10	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule)	14.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	14.2
	437718	AI927288	Hs.196779	ESTs	14.2
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeldt-Jakob)	14.2
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta)	14.2
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	14.2
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl)	14.2
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	14.1
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	14.1
20	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	14.0
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	14.0
	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	14.0
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	14.0
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	13.9
	418848	AI820961	Hs.193465	ESTs	13.9
25	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	13.9
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	13.9
	443967	AW294013	Hs.200942	ESTs	13.9
	424775	AB014540	Hs.153026	SWAP-70 protein	13.9
	411190	AA306342	Hs.69171	protein kinase C-like 2	13.9
30	447384	AI377221	Hs.40528	ESTs	13.9
	444880	AW118683	Hs.154150	ESTs	13.9
	433409	AI278802	Hs.25661	ESTs	13.9
	423201	NM_000163	Hs.125180	growth hormone receptor	13.9
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	13.9
35	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	13.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	13.8
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	13.8
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	13.8
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	13.8
40	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	13.8
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	13.8
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR)	13.8
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	13.8
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	13.7
45	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	13.7
	428054	AI948688	Hs.266619	ESTs	13.7
	444636	T96667	Hs.17877	ESTs	13.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	13.7
50	452260	AA453208	Hs.28726	RAB9, member RAS oncogene family	13.7
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	13.7
	450316	W84446	Hs.226434	hypothetical protein MGC4643	13.7
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	13.7
	443634	H73972	Hs.134460	ESTs	13.7
55	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	13.7
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	13.7
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	13.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	13.6
	416795	AI497778	Hs.20509	HBV pX associated protein-8	13.6
60	410001	AB041036	Hs.57771	kallikrein 11	13.6
	452242	R50956	Hs.159993	glycosyltransferase	13.6
	413231	D87461	Hs.75244	BCL2-like 2	13.6
	404641			NM_021965*:Homo sapiens phosphoglucomuta	13.6
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfami	13.6
65	414279	AW021691	Hs.101067	GCN5 (general control of amino-acid synt	13.6
	411573	AB029000	Hs.70823	KIAA1077 protein	13.5
	417632	R20855	Hs.5422	glycoprotein M6B	13.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	13.5
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	13.5
70	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	13.5
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!!	13.5
	418663	AK001100	Hs.41690	desmocollin 3	13.5
	452277	AL049013	Hs.28783	KIAA1223 protein	13.5
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	13.5
75	447082	T85314	Hs.42644	thioredoxin-like	13.5
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	13.4
	415443	T07353	Hs.7948	ESTs	13.4
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.4
	442113	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypotheti	13.3
80	433517	AW022133	Hs.189838	ESTs	13.3
	430829	AW451999	Hs.194024	ESTs	13.3
	453111	AB014598	Hs.31720	hephaestin	13.3
	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (	13.3
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	13.3



5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	13.3
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	13.3
	437323	AA371145	Hs.226627	leptin receptor	13.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.2
	433037	NM_014158	Hs.279938	HSPC067 protein	13.2
10	407938	AA905097	Hs.85050	phospholamban	13.2
	400860			Target Exon	13.2
	411031	W37943	Hs.34892	KIAA1323 protein	13.2
	436797	AA731491	Hs.336454	hypothetical protein MGC14879	13.2
	409277	T05558	Hs.156880	ESTs	13.2
15	434036	AI659131	Hs.197733	hypothetical protein MGC2849	13.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.2
	450755	AA010984	Hs.159464	ESTs	13.1
	450649	NM_001429	Hs.25272	E1A binding protein p300	13.1
	408495	W68796	Hs.237731	ESTs	13.1
20	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	13.1
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	13.1
	416987	D86957	Hs.80712	KIAA0202 protein	13.0
	453006	AI362575	Hs.167133	ESTs	13.0
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	13.0
25	415752	BE314524	Hs.78776	putative transmembrane protein	13.0
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	13.0
	417318	AW953937	Hs.12891	ESTs	13.0
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	12.9
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	12.9
30	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	12.9
	428218	AA424266	Hs.123642	EphA3	12.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	12.9
	448779	BE042877	Hs.177135	ESTs	12.8
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	12.8
35	417315	AI080042	Hs.336901	ribosomal protein S24	12.8
	429697	AW296451	Hs.24605	ESTs	12.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	12.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	12.8
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	12.8
40	424806	AA382523	Hs.105689	MSTP031 protein	12.7
	442343	AA992480	Hs.129874	ESTs	12.7
	432244	AI669973	Hs.200574	ESTs	12.7
	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	12.7
	452512	AW363486	Hs.337635	ESTs	12.7
45	415079	R43179	Hs.22895	hypothetical protein FLJ23548	12.7
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	12.7
	411067	AI681006	Hs.71721	ESTs	12.7
	442501	AA315267	Hs.23128	ESTs	12.7
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	12.7
50	437052	AA861697	Hs.120591	ESTs	12.7
	433234	AB040928	Hs.65366	KIAA1495 protein	12.6
	453830	AA534296	Hs.20953	ESTs	12.6
	409995	AW960597	Hs.30164	ESTs	12.6
	414290	AI568801	Hs.71721	ESTs	12.6
55	417248	AA329449	Hs.247302	twisted gastrulation	12.6
	418624	AI734080	Hs.104211	ESTs	12.6
	412654	AI093480	Hs.29263	hypothetical protein FLJ11896	12.6
	450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp434D0215 (f	12.6
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.5
60	427078	AI676062	Hs.111902	ESTs	12.5
	420838	AW118210	Hs.5244	ESTs	12.5
	449784	AW161319	Hs.12915	ESTs	12.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	12.5
	415276	U88666	Hs.78353	SFRS protein kinase 2	12.5
65	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	12.5
	400301	X03635	Hs.1657	estrogen receptor 1	12.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	12.5
	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced transl	12.5
	420345	AW295230	Hs.25231	ESTs	12.4
70	432205	AI806583	Hs.125291	ESTs	12.4
	451893	AW192083	Hs.290855	ESTs	12.4
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	12.4
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	12.4
	404642			NM_021965*:Homo sapiens phosphoglucomuta	12.4
75	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	12.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	12.4
	420871	AA702972	Hs.65300	ESTs	12.4
	448072	AI459306	Hs.24908	ESTs	12.4
	441269	AW015206	Hs.178784	ESTs	12.3
80	427761	AA412205	Hs.140996	ESTs	12.3
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	12.3
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	12.3
	436521	AW203986	Hs.213003	ESTs	12.3
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	12.3
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	12.2
	453994	BE180964	Hs.165590	ribosomal protein S13	12.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	12.2

	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	12.2
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	12.2
	400880			NM_000611*:Homo sapiens CD59 antigen p18	12.2
5	425920	AL049977	Hs.162209	claudin 8	12.2
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	12.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	12.1
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	12.1
	452994	AW962597	Hs.31305	KIAA1547 protein	12.1
10	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	12.1
	437124	AA554458	Hs.197751	KIAA0666 protein	12.1
	411450	H49619	Hs.127301	ESTs	12.1
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	12.1
	449625	NM_014253	Hs.23796	odx (odd Oz/ten-m, Drosophila) homolog 1	12.1
15	419459	AW291128	Hs.278422	DKFZP586G1122 protein	12.1
	426252	BE176980	Hs.28917	ESTs	12.1
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	12.1
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	12.0
	435047	AA454985	Hs.54973	cadherin-like protein VR20	12.0
20	417625	U59305	Hs.44708	Ser-Thr protein kinase related to the my	12.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	12.0
	443646	AI085198	Hs.164226	ESTs	12.0
	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	12.0
	443837	AI984625	Hs.9884	spindle pole body protein	12.0
25	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	12.0
	424232	AB015982	Hs.143460	protein kinase C, nu	11.9
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	11.9
	446874	AW968304	Hs.56156	ESTs	11.9
	454119	BE549773	Hs.40510	uncoupling protein 4	11.9
30	436746	AA730045	Hs.187866	ESTs	11.9
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	11.9
	416508	R39769	Hs.206088	ESTs, Moderately similar to ALU8_HUMAN A	11.8
	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	11.8
	413991	H44725	Hs.42683	ESTs	11.8
35	431645	AF078849	Hs.266483	dynein light chain-A	11.8
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.8
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	11.8
	412977	AA125910	Hs.191461	ESTs	11.8
40	426981	AL044675	Hs.173081	KIAA0530 protein	11.8
	410853	H04588	Hs.30469	ESTs	11.7
	444670	H58373	Hs.332938	hypothetical protein MGC5370	11.7
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	11.7
	434398	AA121098	Hs.3838	serum-inducible kinase	11.7
45	438032	BE045624	Hs.152992	ESTs	11.7
	433212	BE218049	Hs.121820	ESTs	11.6
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	11.6
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	11.6
	430929	AA489166	Hs.156933	ESTs	11.6
50	423782	AI472209	Hs.323117	ESTs	11.6
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.6
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	11.6
	430200	BE613337	Hs.234896	geminin	11.5
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.5
55	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	11.5
	422805	AA436989	Hs.121017	H2A histone family, member A	11.5
	422538	NM_006441	Hs.118131	5,10-methylnetetrahydrofolate synthetase	11.5
	412677	AW029608	Hs.17384	ESTs	11.5
	421896	N62293	Hs.45107	ESTs	11.5
60	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	11.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	11.5
	415293	R49462	Hs.106541	ESTs	11.5
	443161	AI038316		gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_	11.5
	420185	AL044056	Hs.158047	ESTs	11.5
65	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	11.5
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp556B213 (fr	11.5
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	11.5
	449919	AI674685	Hs.200141	ESTs	11.5
	414844	AA296874	Hs.77494	deoxyguanosine kinase	11.5
70	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	11.4
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	11.4
	407786	AA687538	Hs.38972	tetraspan 1	11.4
	414407	AA147026	Hs.76704	ESTs	11.4
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	11.4
	456804	AI421645	Hs.139851	caveolin 2	11.4
75	422546	AB007969	Hs.301478	KIAA0500 protein	11.4
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	11.4
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	11.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.4
80	433577	AW007080	Hs.8817	ESTs	11.4
	453935	AI633770	Hs.42572	ESTs	11.4
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	11.4
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.3
	448766	AI473827	Hs.31793	ESTs	11.3

5	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	11.3
	410108	AA081659	Hs.318775	OSBP-related protein 6	11.3
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	11.3
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	11.3
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	11.3
10	414212	AA136569	Hs.10848	KIAA0187 gene product	11.3
	401519			C15000476*:gil12737279[ref]XP_012163.1	11.3
	458509	AA654650	Hs.282906	ESTs	11.2
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	11.2
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.2
15	436758	AW977167	Hs.155272	ESTs	11.2
	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	11.2
	434715	BE005346	Hs.116410	ESTs	11.2
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	11.2
	428342	AI739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	11.2
20	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	11.2
	430519	AF129534	Hs.49210	F-box only protein 4	11.2
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	11.1
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	11.1
	434158	T86534	Hs.14372	ESTs	11.1
25	414341	D80004	Hs.75909	KIAA0182 protein	11.1
	414650	AA150435	Hs.72063	ESTs	11.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	11.1
	437575	AW954355	Hs.36529	hypothetical protein MGC11242	11.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	11.1
30	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	11.1
	452598	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	11.0
	438379	N23018	Hs.171391	C-terminal binding protein 2	11.0
	433230	AW136134	Hs.220277	ESTs	11.0
35	412622	AW664708	Hs.171959	ESTs	11.0
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	11.0
	434349	NM_015678	Hs.3821	neurobeachin	11.0
	430261	AA305127	Hs.237225	hypothetical protein HT023	11.0
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	11.0
40	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	11.0
	442082	R41823	Hs.7413	ESTs	11.0
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	11.0
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	11.0
	450244	AA007534	Hs.125062	ESTs	11.0
45	417169	R13550	Hs.246773	ESTs	11.0
	421481	AW391972	Hs.104696	KIAA1324 protein	10.9
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	10.9
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	10.9
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.9
50	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	10.9
	433658	L03678	Hs.156110	immunoglobulin kappa constant	10.9
	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	10.9
	441540	C01367	Hs.127128	ESTs	10.9
	431154	AW971228	Hs.290259	ESTs, Weakly similar to I38022 hypoteti	10.9
55	416777	AF146760	Hs.79844	DKFZP564M1416 protein	10.9
	439556	AI623752	Hs.163603	ESTs	10.9
	428280	H05541	Hs.183428	sarcospan (Kras oncogene-associated gene	10.8
	453942	AW190920	Hs.19928	hypothetical protein SP329	10.8
	447982	H22953	Hs.137551	ESTs	10.8
60	422779	AA317036	Hs.118787	transforming growth factor, beta-induced	10.8
	447595	AW379130	Hs.18953	phosphodiesterase 9A	10.8
	427115	AW972853	Hs.112237	ESTs	10.8
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	10.8
	419326	W94915	Hs.42419	ESTs	10.8
65	435163	AA668884	Hs.19155	ESTs	10.8
	417578	T91443	Hs.193963	ESTs	10.8
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	10.8
	450206	AI796450	Hs.201600	ESTs	10.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	10.8
70	421977	W94197	Hs.110165	ribosomal protein L26 homolog	10.8
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	10.8
	408243	Y00787	Hs.624	interleukin 8	10.8
	439492	AF086310	Hs.103159	ESTs	10.8
	413492	D87470	Hs.75400	KIAA0280 protein	10.8
75	436962	AW377314	Hs.5364	DKFZP564I052 protein	10.8
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	10.8
	422583	AA410506	Hs.27973	KIAA0874 protein	10.8
	417665	AW852858	Hs.22862	ESTs	10.7
	433285	AW975944	Hs.237396	ESTs	10.7
80	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	10.7
	424878	H57111	Hs.221132	ESTs	10.7
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	10.7
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	10.7
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	10.7
	452241	AI050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	10.7
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	10.7
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	10.7

	433923	AI823453	Hs.146625	ESTs	10.7
	418196	AI745649	Hs.26549	KIAA1708 protein	10.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	10.7
5	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	10.7
	429350	AI754634	Hs.131987	ESTs	10.7
	418601	AA279490	Hs.86368	calmegin	10.6
	437267	AW511443	Hs.258110	ESTs	10.6
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	10.6
10	421982	AF206019	Hs.110347	REV1 (yeast homolog)- like	10.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	10.6
	418662	AI801098	Hs.151500	ESTs	10.6
	449685	AW296669	Hs.66095	ESTs	10.6
	441111	AI806867	Hs.126594	ESTs	10.6
15	436671	AW137159	Hs.146151	ESTs	10.6
	447974	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	10.6
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.6
	424562	AI420859	Hs.150557	basic transcription element binding prot	10.6
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	10.6
20	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.6
	439584	AA838114	Hs.221612	ESTs	10.6
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	10.6
	420929	AI694143	Hs.296251	programmed cell death 4	10.6
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.6
25	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	10.6
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	10.6
	424433	H04607	Hs.9218	ESTs	10.6
	420230	AL034344	Hs.284186	forkhead box C1	10.6
	419441	AW023731	Hs.274368	MSTP032 protein	10.6
30	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	10.6
	451900	AB023199	Hs.27207	KIAA0982 protein	10.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	10.6
	439999	AA115811	Hs.6838	ras homolog gene family, member E	10.5
	424368	AB037766	Hs.146085	KIAA1345 protein	10.5
35	402076			C5002020*:gij1082876[pir]S55467 tropomy	10.5
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.5
	445041	T64183	Hs.282982	solute carrier	10.5
	428927	AA441837	Hs.90250	ESTs	10.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulaio	10.5
40	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	10.5
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	10.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	10.5
	438913	AI380429	Hs.172445	ESTs	10.5
	443684	AI681307	Hs.55098	ESTs	10.5
45	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	10.5
	421040	AA715026	Hs.135280	ESTs	10.5
	425277	NM_001241	Hs.155478	cyclin T2	10.5
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	10.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.5
50	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	10.5
	419972	AL041465	Hs.182982	golgin-87	10.5
	416182	NM_004354	Hs.79069	cyclin G2	10.4
	418365	AW014345	Hs.161690	ESTs	10.4
	452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	10.4
55	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	10.4
	446716	AA436575	Hs.16602	ESTs	10.4
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	10.4
	433023	AW864793	Hs.87409	thrombospondin 1	10.4
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	10.4
60	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	10.4
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	10.4
	443228	W24781	Hs.293798	KIAA1710 protein	10.4
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	10.4
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	10.4
65	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	10.4
	428728	NM_016625	Hs.191381	hypothetical protein	10.4
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	10.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	10.3
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	10.3
70	411359	H86088	Hs.22635	ESTs	10.3
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	10.3
	412262	W26406	Hs.295923	seven in absentia (Drosophila) homolog 1	10.3
	419875	AA853410	Hs.93557	proenkephalin	10.3
	414422	AA147224	Hs.337232	Homeo box A13	10.3
	426581	AB040956	Hs.135890	KIAA1523 protein	10.3
75	424649	BE242035	Hs.151461	embryonic ectoderm development	10.3
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	10.3
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	10.3
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	10.3
80	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	10.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	10.3
	451593	AF151879	Hs.26706	CGI-121 protein	10.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	10.3
	438157	AW137011	Hs.49576	ESTs	10.3

	443181	AI039201	Hs.283316	ESTs	10.3
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	10.2
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	10.2
5	446553	AB021179	Hs.15299	HMBa-inducible	10.2
	418278	AI088489	Hs.83937	hypothetical protein	10.2
	419791	AI579909	Hs.105104	ESTs	10.2
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	10.2
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	10.2
10	445564	AB028957	Hs.12896	KIAA1034 protein	10.2
	435021	AA922192	Hs.54709	ESTs	10.2
	457498	AI732230	Hs.191737	ESTs	10.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	10.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	10.2
15	446162	AI631319	Hs.63841	hypothetical protein DKFZp434E2318	10.2
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	10.2
	427393	AB029018	Hs.177635	KIAA1095 protein	10.1
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	10.1
	437743	AI383497	Hs.131811	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
20	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	10.1
	448172	N75276	Hs.135904	ESTs	10.1
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	10.1
	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATI	10.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	10.1
25	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.1
	410150	AW382942	Hs.6774	ESTs	10.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	10.1
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	10.1
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	10.1
30	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	10.1
	423681	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	10.1
	450205	AI219748	Hs.11356	ESTs	10.1
	408374	AW025430	Hs.155591	forkhead box F1	10.0
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	10.0
35	432589	AL135725	Hs.131708	ESTs	10.0
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	10.0
	411997	AW673478	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	10.0
	419672	AA465113	Hs.23853	ESTs, Weakly similar to A34615 profilagg	10.0
	444564	AI167877	Hs.143716	ESTs	10.0
40	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	10.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	10.0
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	10.0
	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	10.0
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	10.0
45	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	10.0
	442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.0
	418884	AA230228	Hs.59197	ESTs	10.0
	444821	AA053564	Hs.12040	STE20-like kinase	9.9
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	9.9
50	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	9.9
	453127	AI696671	Hs.294110	ESTs	9.9
	435706	W31254	Hs.7045	GL004 protein	9.9
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	9.9
55	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	9.9
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	9.9
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	9.9
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9.9
	432887	AI926047	Hs.162859	ESTs	9.9
	430291	AV660345	Hs.238126	CGI-49 protein	9.9
60	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	9.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	9.9
	428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	9.9
	441054	AA913591	Hs.126480	ESTs	9.9
	415875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	9.9
65	453078	AF053551	Hs.31584	metaxin 2	9.8
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	9.8
	446720	AI439136	Hs.140546	ESTs	9.8
	418475	AI858732	Hs.30443	sentrin/SUMO-specific protease	9.8
	417708	N74392	Hs.50495	ESTs	9.8
70	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	9.8
	420568	F09247	Hs.247735	protocadherin alpha 10	9.8
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	9.8
	453548	AL079983	Hs.116774	integrin, alpha 1	9.8
	427308	D26067	Hs.174905	KIAA0033 protein	9.8
75	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	9.8
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	9.8
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	9.8
	413174	AA723564	Hs.191343	ESTs	9.8
	443250	AI041530	Hs.132107	ESTs	9.8
80	451957	AF796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	9.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	9.8
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	9.8
	427635	BE397988	Hs.179982	tumor protein p53-binding protein	9.8
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	9.8

	439091	AA830144	Hs.135613	ESTs, Moderately similar to I38022 hypot	9.8
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	9.7
	432426	AW973152	Hs.31050	ESTs	9.7
	404571			NM_015902*:Homo sapiens progesteron induce	9.7
5	444427	H25094	Hs.293663	ESTs, Moderately similar to I38022 hypot	9.7
	439183	AW970600	Hs.303261	ESTs	9.7
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	9.7
	432689	AB018320	Hs.278626	Arg/Abl-interacting protein ArgBP2	9.7
10	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.7
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	9.7
	412324	AW978439	Hs.69504	ESTs	9.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	9.7
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	9.7
	417171	BE613486	Hs.81412	lipin 1	9.7
15	421709	AA159394	Hs.107056	CED-6 protein	9.7
	415156	X84908	Hs.78060	phosphorylase kinase, beta	9.7
	436446	AW016809	Hs.323795	ESTs	9.7
	447482	AB033059	Hs.18705	KIAA1233 protein	9.7
20	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	9.7
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	9.7
	409190	AU076536	Hs.50984	sarcoma amplified sequence	9.6
	419111	AA234172	Hs.137418	ESTs	9.6
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	9.6
25	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class III), chi	9.6
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.6
	419241	AA523939	Hs.165258	ESTs	9.6
	409752	AW963990		gb:EST376063 MAGE resequences, MAGH Homo	9.6
	453894	AW937825	Hs.56847	Homo sapiens cDNA FLJ12874 fis, clone NT	9.6
30	439671	AW162840	Hs.6641	kinesin family member 5C	9.6
	407230	AA157857	Hs.182265	keratin 19	9.6
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	9.6
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	9.6
	434263	N34895	Hs.44648	ESTs	9.6
35	412766	BE544475	Hs.54347	ESTs	9.6
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	9.6
	443970	AI280341	Hs.166571	ESTs	9.6
	424534	D87682	Hs.150275	KIAA0241 protein	9.6
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.6
40	447889	AW469180	Hs.170651	ESTs	9.5
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	9.5
	433165	AA578904	Hs.292437	ESTs	9.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	9.5
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	9.5
45	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	9.5
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	9.5
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	9.5
	432682	AI376400	Hs.159588	ESTs	9.5
	435803	Z44194	Hs.4994	transducer of ERBB2, 2	9.5
50	437444	H46008	Hs.31518	ESTs	9.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	9.5
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	9.5
	449226	AB002365	Hs.23311	KIAA0367 protein	9.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	9.4
55	420969	AI636310	Hs.28310	ESTs	9.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	9.4
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	9.4
	420805	L10333	Hs.99947	reticulon 1	9.4
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	9.4
60	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	9.4
	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	9.4
	425657	T89839	Hs.119471	ESTs	9.4
	428250	AW809208	Hs.183297	DKFZP566F2124 protein	9.4
	453293	AA382267	Hs.10653	ESTs	9.4
65	412446	AI768015	Hs.92127	ESTs	9.4
	441102	AA973905	Hs.331328	intermediate filament protein syncoilin	9.4
	421689	N87820	Hs.106826	KIAA1696 protein	9.4
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	9.4
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	9.4
70	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	9.4
	441499	AW298235	Hs.101689	ESTs	9.4
	420184	AA188408	Hs.95665	hypothetical protein	9.4
	420061	AW024937	Hs.29410	ESTs	9.4
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.4
75	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.3
	450580	N40087	Hs.15248	ESTs	9.3
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	9.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	9.3
	412639	AW961284	Hs.296235	ESTs	9.3
80	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	9.3
	446131	NM_000929	Hs.290	phospholipase A2, group V	9.3
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	9.3
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.3
	425139	AW630488	Hs.325820	protease, serine, 23	9.3

	448807	AI571940	Hs.7549	ESTs	9.3
	412505	AA974491	Hs.21734	ESTs	9.3
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	9.3
5	445704	AI493742	Hs.165210	ESTs, Moderately similar to I38022 hypot	9.3
	402855			NM_001839*:Homo sapiens calponin 3, acid	9.3
	428465	AW970976	Hs.293653	ESTs	9.3
	422564	AI148006	Hs.222120	ESTs	9.3
10	430027	AB023197	Hs.227743	KIAA0980 protein	9.2
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.2
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	9.2
	433862	D86960	Hs.3610	KIAA0205 gene product	9.2
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	9.2
	401558			ENSP00000220478*:SECRETORANIN III.	9.2
15	428634	AA811845	Hs.106290	Kelch motif containing protein	9.2
	437678	AA829860	Hs.122834	ESTs	9.2
	416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.2
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	9.2
20	431187	AW971146	Hs.293187	ESTs	9.2
	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	9.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	9.1
	430669	AW969657	Hs.291029	ESTs	9.1
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	9.1
25	448822	BE149845	Hs.289038	hypothetical protein MGC4126	9.1
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	9.1
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (	9.1
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	9.1
	434361	AF129755	Hs.117772	ESTs	9.1
30	443247	BE614387	Hs.333893	c-Myc target JPO1	9.1
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	9.1
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	9.1
	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	9.1
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	9.1
35	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	9.1
	418821	AA436002	Hs.183161	ESTs	9.1
	427213	AW007211	Hs.16131	hypothetical protein FLJ12876	9.1
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	9.1
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	9.1
40	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	9.1
	447033	AI357412	Hs.157601	ESTs	9.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	9.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	9.0
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	9.0
45	444984	H15474	Hs.132898	fatty acid desaturase 1	9.0
	445674	BE410347	Hs.13063	transcription factor CA150	9.0
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	9.0
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	9.0
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	9.0
50	432161	AK000400	Hs.292807	ESTs, Weakly similar to envelope [H.sapi	9.0
	405523			C8001409*:gil7441226 pir  S31212 collage	9.0
	416662	T25853	Hs.7538	ESTs	9.0
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	9.0
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	9.0
55	432897	AF155099	Hs.279780	NY-REN-18 antigen	9.0
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	8.9
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	8.9
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.9
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.9
60	414917	C04863	Hs.47191	ESTs	8.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	8.9
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	8.9
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	8.9
	424683	N87519	Hs.27196	ESTs	8.9
65	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	8.9
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	8.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	8.9
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	8.9
	441079	AW150697	Hs.107418	ESTs	8.9
70	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	8.9
	431316	AA502663	Hs.145037	ESTs	8.9
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	8.9
	433628	AI821784	Hs.188578	ESTs	8.9
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	8.9
75	453344	BE349075	Hs.44571	ESTs	8.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	8.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	8.9
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	8.9
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	8.9
80	433213	AW665130	Hs.137190	ESTs	8.9
	451573	AW130351	Hs.243549	ESTs	8.9
	408393	AW015318	Hs.23165	ESTs	8.8
	434725	AK000796	Hs.4104	hypothetical protein	8.8
	418876	AA740616		gb:ny97111.s1 NCL_CGAP_GCB1 Homo sapiens	8.8

	444558	AW181975	Hs.165892	ESTs	8.8
	417355	D13168	Hs.82002	endothelin receptor type B	8.8
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	8.8
5	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	8.8
	424956	AW198103	Hs.158154	ESTs, Weakly similar to granule cell mar	8.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	8.8
	444647	H14718	Hs.11506	Human clone 23589 mRNA sequence	8.8
	444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!!	8.8
10	409643	AW450866	Hs.257359	ESTs	8.8
	428647	AA830050	Hs.124344	ESTs	8.8
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	8.8
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	8.8
	425465	L18964	Hs.1904	protein kinase C, iota	8.8
15	424113	AI743880	Hs.12876	ESTs	8.8
	459324	AW080953		gb:xc28c12.x1 NCL_CGAP_Co18 Homo sapiens	8.8
	451684	AF216751	Hs.26813	CDA14	8.8
	451244	AW008798	Hs.267448	hypothetical protein FLJ20039	8.8
	439170	AA332365	Hs.165539	ESTs, Weakly similar to I38022 hypothe	8.8
20	424238	AA337401	Hs.137635	ESTs	8.8
	449686	AW072813	Hs.270868	ESTs, Moderately similar to ALUA_HUMAN A	8.8
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	8.8
	410870	U81599	Hs.66731	homeo box B13	8.8
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	8.8
25	429831	AA564489	Hs.137526	ESTs	8.8
	453468	W00712	Hs.32990	DKFZP566F084 protein	8.8
	428340	AF261088	Hs.154721	aconitase 1, soluble	8.8
	453345	AA302862	Hs.90063	neurocalcin delta	8.8
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	8.8
30	440486	BE243513	Hs.7212	hypothetical protein PP1044	8.7
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	8.7
	408949	AF189011	Hs.49163	putative ribonuclease III	8.7
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
35	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.7
	408242	AA251594	Hs.43913	PIBF1 gene product	8.7
	430848	AW021726		gb:df27e02.y1 Morton Fetal Cochlea Homo	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypothe	8.7
40	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	8.7
	425913	AA365799	Hs.50785	SEC22, vesicle trafficking protein (S. c	8.7
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	8.7
	427723	AI355260	Hs.279789	histone deacetylase 3	8.7
	441683	BE564214	Hs.102946	ESTs	8.7
45	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	8.7
	428259	AA424793	Hs.24144	ESTs	8.7
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	8.7
	420041	AB005142	Hs.94592	klotho	8.7
	432432	AA541323	Hs.115831	ESTs	8.7
50	452335	AW188944	Hs.61272	ESTs	8.7
	412673	AL042957	Hs.31845	ESTs	8.7
	430335	D80007	Hs.239499	KIAA0185 protein	8.7
	419904	AA974411	Hs.18672	ESTs	8.6
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	8.6
55	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	8.6
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.6
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	8.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	8.6
	419647	AA348947	Hs.91816	hypothetical protein	8.6
60	425907	AA365752	Hs.155965	ESTs	8.6
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	8.6
	424434	H87028	Hs.146861	hypothetical protein FLJ20580	8.6
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	8.6
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	8.6
65	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.6
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	8.6
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	8.6
	441790	AW294909	Hs.132208	ESTs	8.6
	441124	T97717	Hs.119563	ESTs	8.6
70	438160	AA779332	Hs.122671	ESTs	8.6
	433264	D85782	Hs.3229	cysteine dioxygenase, type I	8.6
	434851	AA806164	Hs.116502	ESTs	8.6
	420608	BE548277	Hs.103104	ESTs	8.6
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	8.6
75	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	8.5
	454058	AI273419	Hs.135146	hypothetical protein FLJ13984	8.5
	435614	R09718	Hs.20403	ESTs	8.5
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	8.5
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	8.5
80	447894	AW204253	Hs.21912	ESTs	8.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	8.5
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	8.5
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	8.5
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	8.5



	434747	AA837085	Hs.220585	ESTs	8.5
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	8.5
	450813	AI739625	Hs.203376	ESTs	8.5
5	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.5
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	8.5
	440840	AW629666	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	8.5
	407891	AA486620	Hs.41135	endomucin-2	8.5
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	8.5
10	432620	AA777749	Hs.5978	LIM domain only 7	8.5
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	8.5
	408170	AW204516	Hs.31835	ESTs	8.5
	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	8.5
	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	8.5
15	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	8.5
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	8.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	8.4
	418120	AA213437	Hs.192249	ESTs	8.4
	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	8.4
20	432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	8.4
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	8.4
	434384	AA631910	Hs.162849	ESTs	8.4
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	8.4
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	8.4
25	421622	AB037748	Hs.106204	KIAA1327 protein	8.4
	431160	AW971174	Hs.324330	ESTs	8.4
	449567	AI990790	Hs.188614	ESTs	8.4
	411088	BE247593	Hs.145053	ESTs	8.4
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	8.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.3
30	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	8.3
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	8.3
	438440	AA807228	Hs.225161	ESTs	8.3
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	8.3
35	422295	AF051151	Hs.114408	tol-like receptor 5	8.3
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	8.3
	425242	D13635	Hs.155287	KIAA0010 gene product	8.3
	432769	AA620814	Hs.144959	ESTs	8.3
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.3
40	427229	AI799751	Hs.5635	ESTs	8.3
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	8.3
	403149		NM_001450:Homo sapiens four and a half L	8.3	
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	8.3
	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
45	436476	AA326108	Hs.33829	bHLH protein DEC2	8.3
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	8.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	8.3
	453121	AI968264	Hs.232286	ESTs	8.3
	420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp434O0921 (f	8.3
50	426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	8.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	8.2
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	8.2
	440080	AW051597	Hs.143707	ESTs	8.2
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.2
55	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	8.2
	432695	D63480	Hs.278634	KIAA0146 protein	8.2
	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	8.2
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	8.2
	418051	AW192535	Hs.19479	ESTs	8.2
60	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	8.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	8.2
	417958	AA767382	Hs.193417	ESTs	8.2
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	8.2
	430468	NM_004673	Hs.241519	angiopoietin-like 1	8.2
65	407802	D84145	Hs.39913	novel RGD-containing protein	8.2
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.2
	414138	AA135884	Hs.3772	ESTs	8.2
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	8.2
	408267	AW380525	Hs.32675	tubulin-specific chaperone e	8.2
70	429692	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypotheti	8.2
	408108	AI580492	Hs.42743	hypothetical protein	8.2
	408418	AW963897	Hs.44743	KIAA1435 protein	8.2
	430334	AI824719	Hs.328700	ESTs	8.2
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	8.2

TABLE 59B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
409385	112523_1	AA071267 T65940 T64515 AA071334

409752 115301\_1 AW963990 AA078196 AW749482 AA077468 BE151571 AA376917  
 411479 1247077\_1 AW848047 AW848202 AW848631 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905  
 AW848214  
 5 411667 1253334\_1 BE160198 AW935898 T11520 AW935930 AW856073 AW861034  
 416913 163001\_1 AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499  
 418866 179788\_1 T65754 AA229857 AA229658  
 418876 179960\_1 AA740616 AA654854 AA229923  
 419536 185688\_1 AA603305 AA244095 AA244183  
 10 419544 185760\_2 AI909154 AA526337 AA244193 AI909153  
 423800 232161\_1 AA331156 AA331157 AA331155  
 426413 266650\_1 AA377823 AW954494 AI022688  
 429163 300543\_1 AA884766 AW974271 AA592975 AA447312  
 430848 324621\_1 AW021726 AA487752 AA488085  
 15 431121 328275\_1 AW971157 AA492575 AA492520  
 432189 342819\_1 AA527941 AI810608 AI620190 AA635266  
 432600 350959\_1 AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339  
 434415 385931\_1 BE177494 AW276909 AA632849  
 434579 38916\_1 T55958 T57205 AF147346  
 20 439518 47334\_1 W76326 AF086341 W72300  
 443161 561305\_1 AI038316 AI344631 AI261653  
 447974 745643\_1 R76886 AI453674 R77049

TABLE 59C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400860	9757499	Minus	151830-152104,152649-152744
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
402076	8117410	Plus	128316-128627
402812	6010110	Plus	25026-25091,25844-25920
402855	9662953	Minus	59763-59909
403047	3540153	Minus	59793-59968
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
403149	9799833	Plus	25034-25185
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404571	7249169	Minus	112450-112648
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

Table 60A lists about 1166 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 60A: ABOUT 1166 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	56.6
419526	AI821895	Hs.193481	ESTs	56.2
420154	AI093155	Hs.95420	JM27 protein	44.0
432441	AW292425	Hs.163484	ESTs	41.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	39.9
431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypopheti	37.9
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	36.0
446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	32.9
425075	AA506324	Hs.1852	acid phosphatase, prostate	31.1
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	30.0
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	29.8

	400302	N48056		folate hydrolase (prostate-specific memb	28.9
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	27.9
	432101	AI918950	Hs.123642	EphA3	26.3
5	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	26.2
	453096	AW294631	Hs.11325	ESTs	25.7
	400287	S39329	Hs.181350	kallikrein 2, prostatic	25.5
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	24.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	24.5
10	401424			NM_001172:Homo sapiens arginase, type II	24.5
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	22.4
	400292	AA250737	Hs.72472	BMP-R1B	22.3
	407202	N58172	Hs.109370	ESTs	22.3
	415989	AI267700		ESTs	20.2
15	407709	AA456135	Hs.23023	ESTs	20.0
	407168	R45175	Hs.117183	ESTs	19.6
	433444	AW975324	Hs.129816	ESTs	19.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	19.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	18.7
20	410929	H47233	Hs.30643	ESTs	18.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	17.9
	418961	AW967646	Hs.23023	ESTs	17.7
	452792	AB037765	Hs.30652	KIAA1344 protein	17.5
	403047			NM_005656*:Homo sapiens transmembrane pr	17.3
25	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3
	418396	AI765805	Hs.26691	ESTs	17.1
	433647	AA603367	Hs.222294	ESTs	16.9
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	16.7
	430487	D87742	Hs.241552	KIAA0268 protein	16.5
30	440260	AI972867	Hs.7130	copine IV	16.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	15.7
	429220	AW207206		ESTs	15.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	15.3
	418819	AA228776	Hs.191721	ESTs	14.8
35	421513	X00949	Hs.105314	relaxin 1 (H1)	14.8
	429918	AW873986	Hs.119383	ESTs	14.5
	420092	AA814043	Hs.88045	ESTs	14.5
	432473	AI202703	Hs.152414	ESTs	14.4
	450693	AW450461	Hs.203965	ESTs	14.4
40	431548	AI834273	Hs.9711	novel protein	14.4
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	14.3
	430187	AI799909	Hs.158989	ESTs	14.3
	441690	R81733	Hs.33106	ESTs	14.3
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	14.2
45	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	13.7
	450642	R39773	Hs.7130	copine IV	13.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	13.4
	432966	AA650114	Hs.325198	ESTs	13.4
	410330	AW023630	Hs.159425	ESTs	13.4
50	434666	AF151103	Hs.112259	T cell receptor gamma locus	13.1
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	13.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	12.8
	431474	AL133990	Hs.190642	ESTs	12.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	12.5
55	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	12.5
	434217	AW014795	Hs.23349	ESTs	12.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	12.3
	428398	AI249368	Hs.98558	ESTs	12.2
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	12.2
60	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	12.2
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	12.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	12.1
	436032	AA150797	Hs.109276	latexin protein	12.0
	432527	AW975028	Hs.102754	ESTs	12.0
65	434792	AA649253	Hs.132458	ESTs	12.0
	420424	AB033036	Hs.97594	KIAA1210 protein	11.9
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.9
	424846	AU077324	Hs.1832	neuropeptide Y	11.9
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	11.9
70	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	11.8
	432600	AI821085		gb:ns95a12.y5 NCL_CGAP_Pr3 Homo sapiens	11.8
	413597	AW302885	Hs.117183	ESTs	11.8
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	11.7
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	11.6
75	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	11.6
	432435	BE218886	Hs.282070	ESTs	11.5
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	11.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	11.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.5
80	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	11.0
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	10.8

	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.6
	400301	X03635	Hs.1657	estrogen receptor 1	10.5
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	10.5
5	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	10.5
	415539	AI733881	Hs.72472	BMP-R1B	10.4
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!!	10.4
	424432	AB037821	Hs.146858	protocadherin 10	10.3
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	10.3
10	434036	AI659131	Hs.197733	hypothetical protein MGC2849	10.3
	415263	AA948033	Hs.130853	ESTs	10.2
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	10.2
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	10.1
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
15	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	10.0
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	10.0
	432244	AI669973	Hs.200574	ESTs	10.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.9
	450164	AI239923	Hs.63931	ESTs	9.8
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	9.8
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	9.7
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	9.6
	433234	AB040928	Hs.65366	KIAA1495 protein	9.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	9.5
25	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.5
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	9.4
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	9.4
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	9.4
30	450325	AI935962	Hs.26289	ESTs	9.4
	427761	AA412205	Hs.140996	ESTs	9.4
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	9.4
	416795	AI497778	Hs.20509	HBV pX associated protein-8	9.3
	422805	AA436989	Hs.121017	H2A histone family, member A	9.3
35	418848	AI820961	Hs.193465	ESTs	9.2
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	9.2
	415788	AW628686	Hs.78851	KIAA0217 protein	9.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	9.1
	432437	W07088	Hs.293685	ESTs	9.1
40	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	9.1
	436962	AW377314	Hs.5364	DKFZP564I052 protein	9.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	9.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	9.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	9.0
45	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	8.8
	442082	R41823	Hs.7413	ESTs	8.8
	436671	AW137159	Hs.146151	ESTs	8.7
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	8.7
	440774	AI420611	Hs.153934	ESTs	8.7
50	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	8.7
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.6
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	8.6
	443646	AI085198	Hs.164226	ESTs	8.6
55	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	8.5
	428728	NM_016625	Hs.191381	hypothetical protein	8.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.5
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	8.5
	437866	AA156781		metallothionein 1E (functional)	8.5
60	453006	AI362575	Hs.303171	ESTs	8.4
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	8.3
	421040	AA715026	Hs.135280	ESTs	8.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	8.3
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	8.2
65	440749	W22335	Hs.7392	hypothetical protein MGC3199	8.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	8.2
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	8.2
	447156	AW274731	Hs.157920	ESTs	8.1
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.1
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	8.0
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.0
	435981	H74319	Hs.188620	ESTs	7.9
	442081	AA401863	Hs.22380	ESTs	7.9
	434988	AI418055	Hs.161160	ESTs	7.9
75	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	7.8
	420345	AW295230	Hs.25231	ESTs	7.8
	412324	AW978439	Hs.69504	ESTs	7.8
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	7.8
	408374	AW025430	Hs.155591	forkhead box F1	7.8
80	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	7.8
	453160	AI263307	Hs.239884	H2B histone family, member L	7.8
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp566J1922 (f	7.7
	416182	NM_004354	Hs.79069	cyclin G2	7.7
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	7.6

	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	7.6
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	7.5
	443180	R15875	Hs.258576	claudin 12	7.5
5	454119	BE549773	Hs.40510	uncoupling protein 4	7.5
	418693	AI750878	Hs.87409	thrombospondin 1	7.5
	426581	AB040956	Hs.135890	KIAA1523 protein	7.5
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	7.5
	439569	AW602166	Hs.222399	CEGP1 protein	7.4
10	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	7.4
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	7.4
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.3
15	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	7.3
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	7.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	7.3
	428218	AA424266	Hs.123642	EphA3	7.3
	434158	T86534	Hs.14372	ESTs	7.3
20	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	7.3
	430261	AA305127	Hs.237225	hypothetical protein HT023	7.3
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.3
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	7.2
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	7.2
25	420871	AA702972	Hs.65300	ESTs	7.2
	418278	AI088489	Hs.83937	hypothetical protein	7.1
	456516	BE172704	Hs.222746	KIAA1610 protein	7.1
	417511	AL049176	Hs.82223	chordin-like	7.1
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	7.1
30	414422	AA147224	Hs.249195	Homeo box A13	7.1
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	7.1
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.0
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.0
	437872	AK002015	Hs.5887	RNA binding motif protein 7	7.0
35	448148	NM_016578	Hs.20509	HBV pX associated protein-8	7.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.9
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	6.9
	457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo	6.9
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	6.9
40	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.9
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	6.9
	432887	AI926047	Hs.162859	ESTs	6.8
	444931	AV652066	Hs.75113	general transcription factor IIIA	6.8
	421823	N40850	Hs.28625	ESTs	6.8
45	426981	AL044675	Hs.173081	KIAA0530 protein	6.8
	425170	AU077315	Hs.154970	transcription factor CP2	6.8
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	6.8
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	6.8
	439492	AF086310	Hs.103159	ESTs	6.8
50	449919	AI674685	Hs.200141	ESTs	6.8
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	6.8
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	6.7
	441111	AI806867	Hs.126594	ESTs	6.7
	457498	AI732230	Hs.191737	ESTs	6.7
55	415293	R49462	Hs.106541	ESTs	6.7
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.7
	433908	AW298141	Hs.157975	ESTs	6.7
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.7
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.7
60	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6
	443745	AB039670	Hs.9728	ALEX1 protein	6.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	6.6
	447805	AW627932	Hs.302421	gemin4	6.6
	440995	T57773	Hs.10263	ESTs	6.6
65	422173	BE385828	Hs.250619	phorbol-in-like protein MDS019	6.6
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.6
	437052	AA861697	Hs.120591	ESTs	6.6
	444030	AW021254	Hs.135055	ESTs	6.6
	416836	D54745	Hs.80247	cholecystokinin	6.6
70	447033	AI357412	Hs.157601	ESTs	6.5
	428927	AA441837	Hs.90250	ESTs	6.5
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	6.5
	448779	BE042877	Hs.177135	ESTs	6.4
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	6.4
75	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.4
	432682	AI376400	Hs.159588	ESTs	6.4
	441499	AW298235	Hs.101689	ESTs	6.4
	441676	BE564206	Hs.49889	ESTs	6.4
	421077	AK000061	Hs.101590	hypothetical protein	6.4
80	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	6.4
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	6.4
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	6.3
	452277	AL049013	Hs.28783	KIAA1223 protein	6.3

	412953	Z45794	Hs.238809	ESTs	6.3
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	6.3
	453390	AA862496	Hs.28482	ESTs	6.3
5	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	6.3
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	6.3
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.3
	433610	AA806822	Hs.112547	ESTs	6.3
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	6.3
10	412977	AA125910	Hs.191461	ESTs	6.3
	441217	AI922183	Hs.213246	ESTs	6.3
	443912	R37257	Hs.184780	ESTs	6.3
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	6.2
	435021	AA922192	Hs.54709	ESTs	6.2
15	425465	L18964	Hs.1904	protein kinase C, iota	6.2
	418821	AA436002	Hs.183161	ESTs	6.2
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	6.2
	448106	AI800470	Hs.171941	ESTs	6.2
	408418	AW963897	Hs.44743	KIAA1435 protein	6.2
20	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.2
	427078	AI676062	Hs.111902	ESTs	6.2
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	6.2
	449907	AA004825	Hs.103281	ESTs	6.1
	458509	AA654650	Hs.282906	ESTs	6.1
25	437323	AA371145	Hs.194397	leptin receptor	6.1
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	6.1
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	6.1
	412673	AL042957	Hs.31845	ESTs	6.0
	410150	AW382942	Hs.260024	ESTs	6.0
30	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	6.0
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	6.0
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	6.0
	409047	AW961434	Hs.31539	ESTs	6.0
	418601	AA279490	Hs.86368	calmegin	6.0
35	425710	AF030880	Hs.159275	solute carrier family, member 4	6.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	6.0
	414905	H40873	Hs.175971	ESTs	6.0
	450295	AI766732	Hs.210628	ESTs	6.0
	412505	AA974491	Hs.21734	ESTs	6.0
40	428730	AA625947	Hs.25750	ESTs	6.0
	445413	AA151342	Hs.12677	CGI-147 protein	6.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	5.9
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	5.9
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	5.9
45	431359	AW993522	Hs.292934	ESTs	5.9
	404632			NM_022490:Homo sapiens hypothetical prot	5.9
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	5.9
	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	405523			C8001409*:gil7441226[pilr]S31212 collage	5.9
50	448807	AI571940	Hs.7549	ESTs	5.8
	404642			NM_021965*:Homo sapiens phosphoglucomuta	5.8
	452598	AI831594		ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.8
55	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.8
	419038	AW134924	Hs.190325	ESTs	5.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.7
	432432	AA541323	Hs.115831	ESTs	5.7
	435937	AA830893	Hs.119769	ESTs	5.7
60	414528	AA148950	Hs.188836	ESTs	5.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	5.7
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	5.7
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	5.7
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	5.7
65	420184	AA188408	Hs.95665	hypothetical protein	5.7
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	5.7
	443250	AI041530	Hs.132107	ESTs	5.7
	443324	R44013	Hs.164225	ESTs	5.7
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	5.7
70	448172	N75276	Hs.135904	ESTs	5.7
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.6
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	5.6
	452242	R50956	Hs.159993	glycosyltransferase	5.6
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	5.6
75	418019	R68911	Hs.176275	ESTs	5.6
	450813	AI739625	Hs.203376	ESTs	5.6
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	5.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.6
	451684	AF216751	Hs.26813	CDA14	5.6
80	427674	NM_003528	Hs.2178	H2B histone family, member Q	5.6
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	5.6
	417958	AA767382	Hs.193417	ESTs	5.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	5.6
	435176	AA744875	Hs.189413	ESTs	5.5

	428465	AW970976	Hs.293653	ESTs	5.5
	431316	AA502663	Hs.145037	ESTs	5.5
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCL_CGAP_Alv1 Homo sapiens	5.5
5	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	5.5
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.5
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.5
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	5.5
	416239	AL038450	Hs.48948	ESTs	5.4
10	421470	R27496	Hs.1378	annexin A3	5.4
	408177	AI241733	Hs.43871	ESTs	5.4
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	5.4
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	5.4
	448072	AI459306	Hs.24908	ESTs	5.4
15	420397	NM_007018	Hs.97437	centrosomal protein 1	5.4
	429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	5.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.4
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.4
20	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.4
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	5.4
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	5.4
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.3
25	412677	AW029608	Hs.17384	ESTs	5.3
	430412	AW341754	Hs.189305	ESTs	5.3
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	5.3
	421433	AI829192	Hs.22380	ESTs	5.3
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	5.3
30	458571	AV653731	Hs.282829	ESTs, Moderately similar to PC4259 ferri	5.3
	441054	AA913591	Hs.126480	ESTs	5.3
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	5.3
	433409	AI278802	Hs.25661	ESTs	5.3
	441102	AA973905		intermediate filament protein syncoilin	5.3
35	453387	AI990741	Hs.252809	ESTs	5.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.3
	433923	AI823453	Hs.146625	ESTs	5.3
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.2
	447574	AF162666	Hs.18895	tousled-like kinase 1	5.2
40	421896	N62293	Hs.45107	ESTs	5.2
	410870	U81599	Hs.66731	homeo box B13	5.2
	420729	AW964897	Hs.290825	ESTs	5.2
	425066	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	5.2
	429467	NM_004477	Hs.203772	F5HD region gene 1	5.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	5.2
	446553	AB021179	Hs.15299	HMBA-inducible	5.2
	453308	AW959731	Hs.323099	ESTs	5.2
	452576	AB023177	Hs.29900	KIAA0960 protein	5.2
	421437	AW821252	Hs.104336	hypothetical protein	5.2
50	422295	AF051151	Hs.114408	toll-like receptor 5	5.2
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.2
	400424	AJ276316	Hs.287374	zinc finger protein 304	5.2
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.2
	452588	AA889120	Hs.110637	homeo box A10	5.2
55	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.1
	413991	H44725	Hs.176090	ESTs	5.1
	444454	BE018316	Hs.11183	sorting nexin 2	5.1
	446795	AI797713	Hs.156471	ESTs	5.1
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.1
60	432340	AA534222		gb:nj21d02.s1 NCL_CGAP_AA1 Homo sapiens	5.1
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	5.1
	453293	AA382267	Hs.10653	ESTs	5.1
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	5.1
	409643	AW450866	Hs.257359	ESTs	5.1
65	427723	AI355260	Hs.279789	histone deacetylase 3	5.1
	438157	AW137011	Hs.49576	ESTs	5.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	5.1
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	5.1
	418051	AW192535	Hs.19479	ESTs	5.1
70	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.1
	425843	BE313280	Hs.159627	death associated protein 3	5.1
	440594	AW445167	Hs.126036	ESTs	5.1
	452449	AW068658	Hs.20943	ESTs	5.1
	429769	NM_004917	Hs.218366	kallikrein 4 (prostase, enamel matrix, p	5.1
75	428898	AB033070	Hs.194408	KIAA1244 protein	5.1
	415339	NM_015156	Hs.78398	KIAA0071 protein	5.1
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	5.1
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.0
	433023	AW864793	Hs.87409	thrombospondin 1	5.0
80	433862	D86960	Hs.3610	KIAA0205 gene product	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	418624	AI734080	Hs.104211	ESTs	5.0
	430291	AV660345	Hs.238126	CGI-49 protein	5.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.0

	429922	Z97630	Hs.226117	H1 histone family, member 0	5.0
	420218	AW958037	Hs.286	ribosomal protein L4	5.0
	425242	D13635	Hs.155287	KIAA0010 gene product	5.0
5	427176	AW381569	Hs.40334	ESTs	5.0
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.0
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.0
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	5.0
	450244	AA007534	Hs.125062	ESTs	5.0
10	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	5.0
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	5.0
	445866	H20899	Hs.13399	Homo sapiens clone 25032 mRNA sequence	4.9
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	4.9
15	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	4.9
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	4.9
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	4.9
	401451			NM_004496*:Homo sapiens hepatocyte nucle	4.9
20	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.9
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.9
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.9
	420608	BE548277	Hs.103104	ESTs	4.9
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.9
	424332	AA338919	Hs.101615	ESTs	4.9
25	430523	AW451385	Hs.161954	ESTs	4.9
	449300	AI656959	Hs.346514	ESTs	4.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	4.9
	438321	AA576635	Hs.6153	CGI-48 protein	4.9
30	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.9
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.8
	425174	D87450	Hs.154978	KIAA0261 protein	4.8
	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	4.8
	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	4.8
35	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	4.8
	449539	W80363	Hs.58446	ESTs	4.8
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.8
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	4.8
40	420210	AI557257	Hs.44811	ESTs	4.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.8
	428647	AA830050	Hs.124344	ESTs	4.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	4.8
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	4.8
45	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	4.8
	416030	H15261	Hs.21948	ESTs	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	4.8
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.7
50	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.7
	443684	AI681307	Hs.55098	ESTs	4.7
	415621	AI648602	Hs.55468	ESTs	4.7
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.7
	424433	H04607	Hs.9218	ESTs	4.7
55	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	4.7
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	4.7
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	4.7
	434973	AW449285	Hs.313636	EST	4.7
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.7
60	431587	NM_016179	Hs.262960	transient receptor potential channel 4	4.7
	452260	AA453208		RAB9, member RAS oncogene family	4.7
	412846	AW961245	Hs.55896	Homo sapiens PAC clone RP5-978E18 from 7	4.7
	418836	AI655499	Hs.161712	ESTs	4.7
	401558			ENSP00000220478*:SECRETOTRANIN III.	4.7
65	441647	AA534210	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H	4.7
	443881	R64512	Hs.237146	hypothetical protein FLJ12752	4.7
	417169	R13550	Hs.246773	ESTs	4.7
	423349	AF010258	Hs.127428	homeo box A9	4.7
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	4.7
70	444951	AI783767	Hs.148635	ESTs, Moderately similar to ALUB_HUMAN I	4.6
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.6
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.6
	423242	AL039402	Hs.125783	DEME-6 protein	4.6
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	4.6
75	419005	T86358	Hs.193931	ESTs, Weakly similar to I54374 gene NF2	4.6
	403046			NM_005656*:Homo sapiens transmembrane pr	4.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.6
	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	4.6
80	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	4.6
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	4.6
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	4.6
	452994	AW962587	Hs.31305	KIAA1547 protein	4.6
	446091	AW022192	Hs.200197	ESTs	4.6
	432908	AI861896	Hs.304505	ESTs	4.6



	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	4.6
	431673	AW971302	Hs.293233	ESTs	4.6
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	4.6
5	452355	N54926	Hs.29202	G protein-coupled receptor 34	4.6
	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	4.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	4.6
	409019	AW385412	Hs.9615	myosin regulatory light chain 2, smooth	4.6
	413812	AW188687	Hs.44748	ESTs	4.6
10	414343	AL036166	Hs.323378	coated vesicle membrane protein	4.6
	434423	NM_006769	Hs.3844	LIM domain only 4	4.5
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	421724	AB037832	Hs.107287	KIAA1411 protein	4.5
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.5
15	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	4.5
	446720	AI439136	Hs.140546	ESTs	4.5
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.5
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	4.5
	423412	AF109300		prostate cancer associated protein 5	4.5
20	433507	AI817336	Hs.191791	ESTs	4.5
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.5
	423782	AI472209	Hs.323117	ESTs	4.5
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.5
25	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	4.5
	428715	AW293716	Hs.53126	ESTs	4.5
	429857	AF089897	Hs.294030	topoisomerase-related function protein 4	4.5
	459561	AI547306		ESTs	4.5
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.5
30	414272	AI651603	Hs.46988	ESTs	4.5
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	4.5
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	4.5
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.5
	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	4.5
35	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	4.5
	401519			C15000476*:gij12737279[refXP_012163.1]	4.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.5
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.4
40	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	4.4
	433517	AW022133	Hs.189838	ESTs	4.4
	429559	AI985345	Hs.26425	ESTs	4.4
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.4
	409190	AU076536	Hs.50984	sarcoma amplified sequence	4.4
45	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.4
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.4
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	4.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	4.4
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	4.4
50	434384	AA631910	Hs.162849	ESTs	4.4
	444564	AI167877	Hs.143716	ESTs	4.4
	447500	AI381900	Hs.159212	ESTs	4.4
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.4
	408380	AF123050	Hs.44532	diubiquitin	4.4
55	448766	AI473827	Hs.31793	ESTs	4.4
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.4
	432810	AA863400		ESTs	4.4
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	4.4
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.4
60	434022	R18374	Hs.117956	ESTs	4.4
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	4.4
	417728	AW138437	Hs.24790	KIAA1573 protein	4.4
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
65	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	4.3
	448550	AL161983	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (f	4.3
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.3
	452335	AW188944	Hs.61272	ESTs	4.3
70	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	4.3
	450316	W84446	Hs.226434	hypothetical protein MGC4643	4.3
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	4.3
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	4.3
	424534	D87682	Hs.150275	KIAA0241 protein	4.3
75	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	4.3
	435023	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	4.3
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	4.3
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.3
	421163	AA375974	Hs.32450	ESTs, Weakly similar to T23762 hypotheti	4.3
80	420405	AA743396	Hs.189023	ESTs	4.3
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.3
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	4.3
	439764	T26535	Hs.22744	hypothetical protein MGC13105	4.3
	446351	AW444551	Hs.35380	x 001 protein	4.3

5	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.3
	414312	AA155694	Hs.191060	ESTs	4.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	4.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	4.3
	414680	AA743331		hemoglobin, alpha 2	4.3
10	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	4.3
	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.3
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	4.3
	434874	N62448	Hs.293970	methyilmalonate-semialdehyde dehydrogenas	4.2
	431429	AF072813		reticulon 3	4.2
15	413492	D87470	Hs.75400	KIAA0280 protein	4.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	4.2
	435846	AA700870	Hs.14304	ESTs	4.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	4.2
	450546	AA010200	Hs.175551	ESTs	4.2
20	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.2
	416445	AL043004	Hs.79337	KIAA0135 protein	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.2
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	4.2
25	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	4.2
	449685	AW296669	Hs.66095	ESTs	4.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
	450377	AB033091	Hs.74313	KIAA1265 protein	4.2
	419647	AA348947	Hs.91816	hypothetical protein	4.2
30	442049	AA310393	Hs.190044	ESTs	4.2
	430669	AW969657	Hs.291029	ESTs	4.2
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	4.1
	443634	H73972	Hs.134460	ESTs	4.1
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	4.1
35	422634	NM_016010	Hs.118821	CGI-62 protein	4.1
	445895	D29954	Hs.13421	KIAA0056 protein	4.1
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	4.1
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.1
	447752	M73700	Hs.105938	lactotransferrin	4.1
40	402855			NM_001839*:Homo sapiens calponin 3, acid	4.1
	443161	AI038316		gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_	4.1
	415827	H17462	Hs.23079	ESTs	4.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	4.1
	418365	AW014345	Hs.161690	ESTs	4.1
45	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	4.1
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	4.1
	446657	AI335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.1
	421141	AW117261	Hs.125914	ESTs	4.1
	430335	D80007	Hs.239499	KIAA0185 protein	4.1
50	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	4.1
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	4.1
	410592	R94088	Hs.43569	ESTs	4.1
55	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.1
	428634	AA811845	Hs.106290	Kelch motif containing protein	4.1
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	4.1
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.0
	443273	AI042063	Hs.132156	ESTs	4.0
60	428055	AA420564	Hs.101760	ESTs	4.0
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	4.0
	451294	AI457338	Hs.29894	ESTs	4.0
	430519	AF129534	Hs.49210	F-box only protein 4	4.0
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	4.0
65	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.0
	409706	BE158773	Hs.213207	ESTs	4.0
	447082	T85314		thioredoxin-like	4.0
70	418594	AI732083	Hs.187619	ESTs	4.0
	426501	AW043782	Hs.293616	ESTs	4.0
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	4.0
	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	4.0
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	4.0
75	425920	AL049977	Hs.162209	claudin 8	4.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	4.0
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.0
	433209	AB040907	Hs.278436	KIAA1474 protein	4.0
	428801	AW277121	Hs.254881	ESTs	4.0
80	419629	AB020695	Hs.91662	KIAA0888 protein	4.0
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.9
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	3.9
	400695			C11002514*:gil11280151 pir  E82756 beta-	3.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	3.9
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.sa	3.9
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	3.9
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.9

	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	3.9
	427615	BE410107	Hs.179817	CGI-82 protein	3.9
5	450649	NM_001429	Hs.25272	E1A binding protein p300	3.9
	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	3.9
	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.9
	431147	AI767751	Hs.20300	ESTs	3.9
	439192	AW970536	Hs.105413	ESTs	3.9
10	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.9
	451900	AB023199	Hs.27207	KIAA0982 protein	3.9
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	3.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.9
	442320	AI287817	Hs.129636	ESTs	3.9
15	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	3.9
	444636	T96667	Hs.17877	ESTs	3.9
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	3.9
	412576	AA447718	Hs.107057	ESTs	3.9
	423952	AW877787	Hs.136102	KIAA0853 protein	3.9
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
20	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	3.9
	447280	BE617907	Hs.97635	ESTs	3.9
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.8
	450580	N40087		ESTs	3.8
25	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.8
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.8
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.8
	412652	AI801777	Hs.260024	ESTs	3.8
30	426226	AA769045		gb:oa80h07.s1 NCI_CGAP_GCB1 Homo sapiens	3.8
	437816	AI823445	Hs.280699	ESTs	3.8
	444534	AW271626	Hs.42294	ESTs	3.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	3.8
	408242	AA251594	Hs.43913	PIBF1 gene product	3.8
35	443484	AI091458	Hs.134559	ESTs	3.8
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.8
	428043	T92248	Hs.2240	uteroglobin	3.8
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.8
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.8
40	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	3.8
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.8
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.8
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	3.8
	408547	AA574291	Hs.57837	ESTs	3.8
45	427635	BE397988	Hs.179982	tumor protein p53-binding protein	3.8
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.8
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.8
	453698	AA037615	Hs.42746	ESTs	3.8
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	3.8
50	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	3.8
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.8
	438138	R98299	Hs.177502	ESTs	3.8
	447906	AL050062	Hs.19999	DKFZP566K023 protein	3.8
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.7
55	435655	AW105663	Hs.6947	HSPC069 protein	3.7
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	3.7
	439398	AA284267	Hs.221504	ESTs	3.7
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	3.7
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
60	418576	AW968159	Hs.289104	Epithelial calcium channel 2, CaT-like A	3.7
	436024	AI800041	Hs.190555	ESTs	3.7
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.7
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.7
	442861	AA243837	Hs.57787	ESTs	3.7
65	448207	AI475490	Hs.170577	ESTs	3.7
	450628	AW382884	Hs.204715	ESTs	3.7
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.7
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	3.7
	443031	AW134696	Hs.49418	ESTs	3.7
70	447608	AW205042	Hs.18955	Homo sapiens cDNA FLJ20667 fis, clone KA	3.7
	408312	AF263613	Hs.44198	intracellular membrane-associated calciu	3.7
	412777	AI335773	Hs.270123	ESTs	3.7
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.7
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	3.7
75	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	3.7
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.7
	452129	AW291379	Hs.212827	ESTs	3.7
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	3.7
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.7
80	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	3.7
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
	423855	AA331761	Hs.254859	ESTs	3.7
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.7

	434470	AA634818	Hs.298138	ESTs	3.7
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	3.7
	420026	AI831190	Hs.166676	ESTs	3.7
5	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	3.7
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	3.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.7
	445941	AI267371	Hs.172636	ESTs	3.6
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.6
10	412533	AA679863	Hs.69606	ESTs	3.6
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	3.6
	442710	AI015631	Hs.23210	ESTs	3.6
	448212	AI475858		gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sapiens	3.6
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.6
15	453038	AW292415	Hs.20509	HBV pX associated protein-8	3.6
	427661	AA410292	Hs.104761	ESTs	3.6
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	3.6
	414844	AA296874	Hs.77494	deoxyguanosine kinase	3.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	3.6
20	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	3.6
	423482	BE280172	Hs.129228	galactokinase 2	3.6
	424677	U09414	Hs.151689	zinc finger protein 137 (clone pHZ-30)	3.6
	430160	AW968210	Hs.293957	ESTs, Weakly similar to ALUC_HUMAN !!!	3.6
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	3.6
	433887	AW204232	Hs.279522	ESTs	3.6
25	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	3.6
	411890	H92738	Hs.75811	N-acylsphingosine amidohydrolase (acid c	3.6
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6
	431724	AA514535	Hs.283704	ESTs	3.6
30	435703	AW630133	Hs.83313	GK003 protein	3.6
	445674	BE410347	Hs.13063	transcription factor CA150	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	3.6
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	3.6
35	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	3.6
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	3.6
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	3.6
	439379	AA835002	Hs.125611	ESTs	3.6
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.6
40	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	3.6
	451367	AA923729	Hs.26322	cell cycle related kinase	3.6
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	3.6
	431263	AW129203	Hs.322915	ESTs	3.6
	431952	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.6
45	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	3.6
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	3.5
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.5
	419440	AB020689	Hs.90419	KIAA0882 protein	3.5
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.5
50	419241	AA523939	Hs.165258	ESTs	3.5
	410762	AF226053	Hs.66170	HSKM-B protein	3.5
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.5
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.5
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.5
55	420390	AA330047	Hs.191187	ESTs	3.5
	416662	T25853	Hs.7538	ESTs	3.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	421991	NM_014918	Hs.110488	KIAA0990 protein	3.5
60	413950	AA249096	Hs.32793	ESTs	3.5
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	3.5
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.5
	411149	N68715	Hs.269128	ESTs	3.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.5
65	418334	AA319233	Hs.5521	ESTs	3.5
	422583	AA410506	Hs.27973	KIAA0874 protein	3.5
	425717	X07282	Hs.171495	retinoic acid receptor, beta	3.5
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.5
	434569	AI311295	Hs.344478	KIAA0196 gene product	3.5
70	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	3.5
	437296	AA350994	Hs.20281	KIAA1700	3.5
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	439605	AF086431	Hs.22380	ESTs	3.5
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3.5
	432589	AL135725	Hs.131708	ESTs	3.5
75	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.5
	421129	BE439899	Hs.89271	ESTs	3.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.5
80	434839	AI743069	Hs.134736	ESTs	3.5
	435166	AI391470	Hs.158618	ESTs	3.5
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.5
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.5
	453311	AW104911	Hs.126707	hypothetical protein FLJ11457	3.5

5	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
	449909	AA004681	Hs.59432	ESTs	3.5
10	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	3.5
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
15	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BE613337	Hs.234896	geminin	3.4
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
	423645	AI215632	Hs.147487	ESTs	3.4
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.4
20	434966	AA657494		gb:nt66f04.s1 NCL_CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902*:Homo sapiens progesteron induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
	436374	AA400709	Hs.96716	ESTs, Weakly similar to T17210 hypotheti	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
25	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056*:Plasma membrane calcium	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	449603	AI655662	Hs.197698	ESTs	3.4
30	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	437367	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.4
	430144	AI732722	Hs.187694	ERGL protein; ERGIC-53-like protein	3.4
35	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (	3.4
	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	3.4
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
40	408267	AW380525	Hs.343564	tubulin-specific chaperone e	3.4
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AI148006	Hs.222120	ESTs	3.4
	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	3.4
45	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AI056769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.4
	443242	BE243910	Hs.9082	nucleoporin p54	3.4
50	445469	AW298370	Hs.153714	complement-c1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.4
	433037	NM_014158	Hs.279938	HSPC067 protein	3.4
	423044	AA320829	Hs.97266	protocadherin 18	3.4
55	434128	W93170	Hs.284164	protein x 0004	3.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.4
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.4
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
	438825	BE327427	Hs.79953	ESTs	3.4
60	446874	AW968304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.4
	419131	AA406293	Hs.41167	ESTs	3.4
	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	433764	AW753676	Hs.39982	ESTs	3.4
65	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapi	3.3
	421234	AA907153	Hs.190060	ESTs	3.3
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.3
70	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
75	436664	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
	421476	AW953805	Hs.21887	ESTs	3.3
	422165	AL041199	Hs.1481	histidine decarboxylase	3.3
80	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263*:HSPC213.	3.3
	433404	T32982	Hs.102720	ESTs	3.3
	422546	AB007969	Hs.301478	KIAA0500 protein	3.3
	443884	N20617	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
5	444170	AW613879	Hs.102408	ESTs	3.3
	445474	AI240014	Hs.259558	ESTs	3.3
	450582	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
10	444324	AI301330	Hs.143838	ESTs	3.3
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	3.3
	400880			NM_000611*:Homo sapiens CD59 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
15	451968	H56196	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (fr	3.3
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
20	428523	AW974540		ESTs	3.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	3.3
	432363	AA534489		gb:mf76g11.s1 NCL_CGAP_Co3 Homo sapiens	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
25	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	3.3
	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hfrb1)	3.3
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.3
30	411373	BE326276	Hs.8861	ESTs	3.3
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
35	420969	AI636310	Hs.28310	ESTs	3.3
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	3.3
40	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.3
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.3
45	426775	AA384564		ESTs	3.3
	432378	AI493046	Hs.146133	ESTs	3.3
	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.3
50	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	3.2
	433002	AF048730	Hs.279906	cyclin T1	3.2
	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
55	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
	429377	AA813192	Hs.200596	KIAA0547 gene product	3.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.2
	420583	H77859	Hs.65450	reticulon 4	3.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.2
60	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	3.2
	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chai	3.2
	421029	AW057782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44656	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
65	408412	AW193033	Hs.124436	ESTs	3.2
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
	421887	AW161450	Hs.109201	CGI-86 protein	3.2
	432409	AA806538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
70	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	3.2
75	414342	AA742181	Hs.75912	KIAA0257 protein	3.2
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypothe	3.2
80	452295	BE379936	Hs.28866	programmed cell death 10	3.2
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.2

	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	415691	AW963979	Hs.24723	ESTs	3.2
5	433852	AI378329	Hs.126629	ESTs	3.2
	439735	AI635386	Hs.142846	hypothetical protein	3.2
	428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
10	415715	F30364	Hs.302204	ESTs	3.2
	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450963	Hs.119991	ESTs	3.2
	436401	AI087958	Hs.29088	ESTs	3.2
15	408784	AW971350	Hs.63386	ESTs	3.2
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.2
	405558			Target Exon	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
20	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AI128606	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	3.2
25	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	3.2
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
30	420131	F08286	Hs.95262	nuclear factor related to kappa B bindin	3.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE393767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220950	ESTs	3.1
	406627	T64904	Hs.163780	ESTs	3.1
35	438666	AW014493	Hs.126727	ESTs	3.1
	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.1
40	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
45	437083	AW082597	Hs.244862	ESTs	3.1
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	419965	H16382	Hs.70258	ESTs	3.1
50	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.1
	446146	AI287539	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.1
55	423947	AW451954	Hs.135941	KIAA1048 protein	3.1
	451893	AW192083	Hs.290855	ESTs	3.1
	447726	AL137638	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.1
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.1
60	443331	AI052026	Hs.149995	ESTs	3.1
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
65	430092	AI821399	Hs.16514	ESTs	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	H80696	Hs.233313	ESTs	3.1
	437756	AA767537	Hs.197096	ESTs	3.1
70	438979	AW976218	Hs.32565	ESTs	3.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
75	438308	AI343469	Hs.127685	KIAA1627 protein	3.1
	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
80	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AI249502	Hs.29669	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	412088	AI689496	Hs.108932	ESTs	3.1
	434361	AF129755	Hs.88474	ESTs	3.1
5	400664			NM_002425:Homo sapiens matrix metallopro	3.1
	436354	AI879252	Hs.5151	RAN binding protein 7	3.1
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
	410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	415245	N59650	Hs.27252	ESTs	3.1
10	418647	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	3.1
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
	453716	AA037675	Hs.152675	ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
	408705	AA312135	Hs.46967	HSPCO34 protein	3.0
15	430280	AA361258	Hs.237868	interleukin 7 receptor	3.0
	445919	T53519	Hs.334692	hypothetical protein MGC14141	3.0
	441790	AW294909	Hs.132208	ESTs	3.0
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
20	422788	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.0
	439703	AF086538	Hs.196245	ESTs	3.0
	444489	AI151010	Hs.157774	ESTs	3.0
	453878	AW964440	Hs.19025	DC32	3.0
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
25	433680	AI805366	Hs.199945	ESTs	3.0
	426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
	426044	AA502490	Hs.170290	ESTs	3.0
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
30	445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
	452737	AK001680	Hs.30488	DKFZP434F091 protein	3.0
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	3.0
	435712	AA694607	Hs.176956	ESTs	3.0
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
35	414993	AW819403	Hs.77724	KIAA0586 gene product	3.0
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
	421988	AW450481	Hs.161333	ESTs	3.0
	432833	N51075	Hs.110028	ESTs	3.0
	445210	H09323	Hs.27133	ESTs	3.0
40	447620	AW290951	Hs.224965	ESTs	3.0
	449375	R07114	Hs.271224	ESTs	3.0
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.0
	443967	AW294013	Hs.200942	ESTs	3.0
	441224	AU076964	Hs.7753	calumenin	3.0
45	448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
	435688	H72286	Hs.128387	ESTs	3.0
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.0
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
	415954	AA171850	Hs.42251	ESTs	3.0
50	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	3.0
	420077	AW512260	Hs.87767	ESTs	3.0
	443475	AI066470	Hs.132809	ESTs	3.0
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	3.0
	438436	AA807168	Hs.271552	ESTs	3.0
55	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
	443280	AA299688	Hs.24183	ESTs	3.0
	448264	AI478933	Hs.188260	ESTs	3.0
	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
	453843	D25215	Hs.35804	hect domain and RLD 3	3.0
60	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	3.0
	445943	AW898533	Hs.181574	ESTs	3.0
	432286	AW327432	Hs.255843	ESTs	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	3.0
	432675	AI791855	Hs.105884	ESTs	3.0
65	443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.0
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
	423583	AL122055	Hs.129836	KIAA1028 protein	3.0
70	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	3.0
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
	410011	AB020641	Hs.57856	PFTAIRES protein kinase 1	3.0
	411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
	438986	AF085888	Hs.269307	ESTs	3.0
75	445921	AW015211	Hs.146181	ESTs	3.0
	447124	AW976438	Hs.17428	RBP1-like protein	3.0
	452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

TABLE 60B

Pkey: Unique Eos probeset identifier number



CAT number: Gene cluster number  
Accession: Genbank accession numbers

	Pkey	CAT Number	Accessions
5	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
10	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	415989	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
	416288	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
15	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162496 BE161005 AA190449 AW513465 BE161006 BE162499
	417379	167238_1	AA196390 AA507837 AA196468
	418304	173658_2	AA215702 AA368006 AA215703 BE066555 BE006876
20	418647	177521_1	AA226198 AA226513 AA383773
	418866	179788_1	T65754 AA229857 AA229658
	419536	185688_1	AA603305 AA244095 AA244183
	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	423412	228001_1	AF109300 AI299378 AI202654
25	423800	232161_1	AA331156 AA331157 AA331155
	426226	262918_1	AA769045 AA372590 AW963633
	426413	266650_1	AA377823 AW954494 AI022688
	426503	268283_1	AA380153 AA380233 AW963529
	426775	271683_1	AA384564 AW966475 H02121 N41297 D63213 AA886888 AI922414 AW044240 AW196808 AI076736 AA599294 AI954433 AW117617 AI640323 H98134
30	426991	27415_1	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
	428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340
	429163	300543_1	AA884766 AW974271 AA592975 AA447312
35	429220	301384_1	AW207206 AW341473 AA448195 AI951341
	429258	301917_1	AA448765 C04967 C03045 AA658293
	430935	325772_1	AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
	430968	326269_1	AW972830 AA527647 AA489820 AA570362
	431429	33313_1	AF072813 AF119297 AA362885 AF059524 NM_006054 AA157365 AW163623 AA056148 AA227062 AA418057 AA227076 AA078753 AA233594 D58629 AA232373 AA233577 T35956 BE18035 AA354497 AA359082 T32010 AA134519 BE299901 BE268096 BE396826 AA324268 AL120308 AA187561 AA311680
40	432093	341283_1	H28383 AW972670 H28359 AA525808
	432125	341776_1	AW972667 AA526539 AI057032 AW167842
	432189	342819_1	AA527941 AI810608 AI620190 AA635266
45	432340	345248_1	AA534222 AA632632 T81234
	432363	345469_1	AA534489 AW970240 AW970323
	432600	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
	432810	354375_1	AA863400 AI991439 AW016017 AW014704 AI367512 H17550 AA744752 R46187 AW471324 AI126670 AA626033 AI276287 AI094253 AI286003 AI147163 AI911443 AW512612 AA972102 AA999975 AI684428 AI335035 D63102 AI524234 AI539156 AA565542
50	434579	38916_1	T55958 T57205 AF147346
	434966	396504_1	AA657494 AI582663 AI581639
	435023	398093_1	AI692552 AI393343 AI800510 AI377711 F24263 AA661876
	437866	44433_2	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188
55	438147	45074_1	AW250553 L07876 Z36843 R30693 AI190097 AW965317
	439092	468554_1	AA830149 AW978407 M85983 AW503637
	439518	47334_1	W76326 AF086341 W72300
	439904	479942_1	AW892676 AA853877 D44747
60	440840	50357_2	AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877
	441102	509604_1	AA973905 AI299888 AA917019 H63235 T90771
	442562	54500_2	BE379584 R34211 BE544768 AW973709 AI653056 AI653173 AI266043 AI656750 H74180 AI492830 AI376090 AI472184 D59940 AW170056 AI082443 AW021142 AI167921 AI348677 AI278577 AW130886 AA761517 AI698203 AA115535 AI264790 R34328 D59939 AW205074 AA554902 D62102 AI0007
65	443161	561305_1	AI038316 AI344631 AI261653
	445808	65133_1	AV655234 AW966332 AA340239
	447082	707248_1	T85314 AI360684 T85528 T91254
	448212	755099_1	AI475858 AW969013
70	449625	8113_1	NM_014253 AF100772 BE088769 AI022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
	450580	83929_1	AA164518 AA730973 W00417 W65303
75	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA855829 AW936878
	452260	9074_1	AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228 BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI659875 AW272338 AI423136 AI089270 AI160904 AA664354 BE1
	452598	92338_2	AI831594 AW970667 AW027959 AI129800 AI927949 AI650270 AI625105 AW514661 AI708393 AI138076 BE180510 AI926721 AI399955 AA749139 AI862160 AW874011 AI242763 AA262795 AA039864 H73499 AI093249 BE245661 AI816834 N25206 AA828301 AI084565 AI302816 AA026905 AA77255
80	452815	93255_1	AA418841 AI452657 AI768876 AA028973 BE179873 C00215 AA418930
	453802	981589_1	AL134757 AW079131
	455100	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034

457728 393853\_1 AW974811 AA651634 AA650072

TABLE 60C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402031	7656761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59968
403790	8084957	Minus	87826-87947,89835-90002
404571	7249169	Minus	112450-112648
404632	9796668	Plus	45096-45229
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6083

Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95<sup>th</sup> percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of prostate tumor to normal adult body tissue  
 R2: Ratio of prostate tumor to normal prostate tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2	42.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	3.2	26.5
420729	AW964897	Hs.290825	ESTs	3.7	15.8
401197			ENSP00000229263*:HSPC213.	3.0	12.6
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	12.4	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3	12.3
443271	BE568568	Hs.195704	ESTs	11.6	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.1	11.2
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4	9.4
417315	AI080042	Hs.180450	ribosomal protein S24	2.3	9.0
416182	NM_004354	Hs.79069	cyclin G2	8.4	8.4
421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	2.2	8.4
434217	AW014795	Hs.23349	ESTs	8.3	8.3
425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3	8.3
442501	AA315267	Hs.23128	ESTs	2.0	8.3
429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1	8.1
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.1	8.0
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	34.0	7.9
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5	7.5
419078	M93119	Hs.89584	insulinoma-associated 1	7.4	7.4
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	9.4	7.3
425018	BE245277	Hs.154196	E4F transcription factor 1	7.2	7.2
452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0	7.0
421552	AF026592	Hs.105700	secreted frizzled-related protein 4	4.0	6.6
409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3	6.3
411373	BE326276	Hs.8861	ESTs	3.2	6.3
423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7	6.2
422583	AA410506	Hs.27973	KIAA0874 protein	2.3	6.2
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1	6.1
437147	AL049964	Hs.8358	hypothetical protein FLJ20366	2.6	6.0

5	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.3	5.9
	431548	AI834273	Hs.9711	novel protein	15.7	5.8
10	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7	5.7
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.5	5.6
15	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.5	5.5
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
	451684	AF216751	Hs.26813	CDA14	3.9	5.4
20	421470	R27496	Hs.1378	annexin A3	5.3	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
	437571	AA760894	Hs.153023	ESTs	5.2	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
25	444917	R68651	Hs.144997	ESTs	5.1	5.1
	417318	AW953937	Hs.240845	ESTs	4.6	5.1
	434170	AA626509	Hs.122329	ESTs	5.1	5.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	3.3	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
30	421823	N40850	Hs.28625	ESTs	5.0	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
	425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
	439024	R96696	Hs.35598	ESTs	5.4	4.8
35	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
	451952	AL120173	Hs.301663	ESTs	4.7	4.7
	431676	AI685464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	9.1	4.7
40	452242	R50956	Hs.159993	glycosyltransferase	4.7	4.7
	401519			C15000476*:gi12737279 ref XP_012163.1	4.6	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	2.1	4.6
45	408380	AF123050	Hs.44532	diubiquitin	4.2	4.6
	425907	AA365752	Hs.155965	ESTs	2.2	4.6
	427078	AI676062	Hs.111902	ESTs	4.8	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
50	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
	443250	AI041530	Hs.132107	ESTs	8.1	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
55	428826	AL048842	Hs.194019	atractin	2.0	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2	4.2
	429900	AA460421	Hs.30875	ESTs	4.2	4.2
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.2	4.2
60	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
	443622	AI911527	Hs.11805	ESTs	2.2	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1	4.1
65	421129	BE439899	Hs.89271	ESTs	4.1	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
	433887	AW204232	Hs.279522	ESTs	4.1	4.1
70	436556	AI364997	Hs.7572	ESTs	4.1	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
	443646	AI085198	Hs.164226	ESTs	4.1	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0	4.0
75	433409	AI278802	Hs.25661	ESTs	4.0	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9	3.9
	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
80	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.9	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.4	3.8
	452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
	410330	AW023630	Hs.159425	ESTs	6.2	3.8

5	422975	AA347720	Hs.122669	KIAA0264 protein	2.2	3.8
	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.7	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	4.1	3.8
10	418821	AA436002	Hs.183161	ESTs	2.8	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.1	3.8
	453160	AI263307	Hs.239884	H2B histone family, member L	9.2	3.8
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7	3.7
15	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7	3.7
	448807	AI571940	Hs.7549	ESTs	3.6	3.7
	439209	AF087993	Hs.91954	ESTs	2.1	3.6
	420077	AW512260	Hs.87767	ESTs	4.4	3.6
	451009	AA013140	Hs.115707	ESTs	4.1	3.6
20	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.2	3.6
	447033	AI357412	Hs.157601	ESTs	7.7	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6	3.6
25	414680	AA743331		hemoglobin, alpha 2	3.5	3.5
	417380	T06809	Hs.332086	ESTs	3.5	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoeiti	3.5	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.2	3.5
30	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5	3.5
	432101	AI918950	Hs.123642	EphA3	16.5	3.5
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.3	3.5
	435513	AW404075	Hs.42785	DC11 protein	2.2	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	2.1	3.5
35	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	6.7	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	2.1	3.4
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.1	3.4
	440749	W22335	Hs.7392	hypothetical protein MGC3199	2.5	3.3
	408374	AW025430	Hs.155591	forkhead box F1	4.3	3.3
40	400277			Eos Control	2.4	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3	3.3
	443912	R37257	Hs.184780	ESTs	3.3	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	9.9	3.3
45	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.4	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.6	3.3
	451367	AA923729	Hs.26322	cell cycle related kinase	3.3	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	11.5	3.2
50	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	2.0	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2	3.2
	402802			NM_001397:Homo sapiens endothelin conver	4.3	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	2.7	3.2
55	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.8	3.2
	444489	AI151010	Hs.157774	ESTs	3.2	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2	3.2
60	453078	AF053551	Hs.31584	metaxin 2	2.1	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	10.6	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	2.8	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	2.1	3.1
	445840	AI277811	Hs.146291	ESTs	3.1	3.1
65	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	2.2	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1	3.1
	430519	AF129534	Hs.49210	F-box only protein 4	3.1	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	16.2	3.1
70	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	9.0	3.1
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	20.9	3.1
	420154	AI093155	Hs.95420	JM27 protein	27.4	3.1
	453293	AA382267	Hs.10653	ESTs	3.7	3.1
75	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypothe	2.4	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	2.9	3.0
	433285	AW975944	Hs.237396	ESTs	7.7	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0	3.0
80	445921	AW015211	Hs.146181	ESTs	4.3	3.0
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.5	3.0
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	2.5	3.0
	450580	N40087		ESTs	3.0	3.0
	447726	AL137638	Hs.19368	matrilin 2	3.9	2.9
	447816	NM_007233	Hs.274329	TP53 target gene 1	7.2	2.9
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	5.1	2.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	2.6	2.9

	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.9	2.9
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisoqu	2.9	2.9
	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	2.9	2.9
5	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
	442320	AI287817	Hs.129636	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
10	451796	AL133019	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (f	2.9	2.9
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.0	2.9
	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
	453628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
15	412324	AW978439	Hs.69504	ESTs	2.0	2.8
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.8	2.8
	433865	N29862	Hs.44104	ESTs	2.8	2.8
20	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
25	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
	444668	AA654650	Hs.282906	ESTs	2.2	2.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abl-interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
30	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
	450546	AA010200	Hs.175551	ESTs	2.2	2.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6	2.7
	458332	AI000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
35	412576	AA447718	Hs.107057	ESTs	2.7	2.7
	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
40	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
	447401	BE618582	Hs.97661	ESTs	2.7	2.7
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
45	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
	422805	AA436989	Hs.121017	H2A histone family, member A	13.6	2.7
	446238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	8.1	2.7
50	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
	410592	R94088	Hs.43569	ESTs	2.6	2.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.6	2.6
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.6	2.6
	433419	AI830342	Hs.211272	ESTs	2.9	2.6
55	447509	AF107454	Hs.107537	chromosome 7 open reading frame 2	2.0	2.6
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	2.4	2.6
	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
60	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
	414312	AA155694	Hs.191060	ESTs	2.6	2.6
	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
65	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.2	2.6
	406627	T64904	Hs.163780	ESTs	8.7	2.6
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.4	2.6
	425815	R94023	Hs.94560	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
70	431474	AL133990	Hs.190642	ESTs	9.3	2.5
	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
75	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.4	2.5
	403047			NM_005656*:Homo sapiens transmembrane pr	21.1	2.5
	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.5	2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
80	436401	AI087958	Hs.29088	ESTs	2.5	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

	446791	AI632278	Hs.195922	ESTs	2.5	2.5
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
	419791	AI579909	Hs.105104	ESTs	2.7	2.5
5	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.0	2.5
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	2.5	2.5
	447702	AI420256	Hs.161271	ESTs	2.1	2.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	2.4	2.4
10	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.4	2.4
	429128	AA446869	Hs.119316	ESTs	2.0	2.4
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	2.4	2.4
	435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
15	407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	4.3	2.4
	447713	AI420733	Hs.207083	ESTs	2.4	2.4
	456848	AL121087	Hs.296406	KIAA0685 gene product	2.2	2.4
20	437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
	432378	AI493046	Hs.146133	ESTs	5.2	2.4
	443180	R15875	Hs.258576	claudin 12	10.1	2.4
	445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
25	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.5	2.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
	421709	AA159394	Hs.107056	CED-6 protein	2.3	2.4
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
30	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
	433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
35	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.1	2.3
	450693	AW450461	Hs.203965	ESTs	2.3	2.3
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	2.3	2.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	4.1	2.3
40	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
	419438	AA406400	Hs.12482	glyceronephosphate O-acyltransferase	2.7	2.3
	443194	AI954968	Hs.279009	matrix Gla protein	2.1	2.3
	414869	AA157291	Hs.21479	ubiquitin 1	2.5	2.3
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.3	2.3
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
45	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	2.3	2.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hfr1)	4.1	2.3
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.2	2.3
	431147	AI767751	Hs.20300	ESTs	5.8	2.3
50	442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
	446091	AW022192	Hs.200197	ESTs	4.0	2.3
	431563	AI027643	Hs.120912	ESTs	2.2	2.3
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	3.5	2.3
55	405685			C2002829:gil4507689[ref]NP_003298.1] tra	2.3	2.3
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	2.3	2.3
	450378	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	2.3	2.3
	429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
	417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
60	429277	AW452016	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.6	2.2
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	4.5	2.2
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.9	2.2
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
	431542	H63010	Hs.5740	ESTs	7.0	2.2
65	401558			ENSP00000220478*:SECRETOTRANIN III.	2.2	2.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
	422295	AF051151	Hs.114408	toll-like receptor 5	2.2	2.2
	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.2	2.2
	447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
70	452994	AW962597	Hs.31305	KIAA1547 protein	4.0	2.2
	450325	AI935962	Hs.26289	ESTs	11.9	2.2
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6	2.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
75	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	4.2	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
	422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
80	433293	AF007835	Hs.32417	hypothetical protein MGC4309	11.0	2.2
	410733	D84284	Hs.66052	CD38 antigen (p45)	3.1	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
	408833	AW612232	Hs.254835	ESTs	3.0	2.2

5	422424	AI186431	Hs.296638	prostate differentiation factor	4.4	2.2
	433444	AW975324	Hs.129816	ESTs	11.7	2.2
	446354	AW449650	Hs.346335	ESTs	2.6	2.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	5.9	2.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
10	424036	AA770688		H2A histone family, member L	3.8	2.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.8	2.2
	404641			NM_021965*:Homo sapiens phosphoglucomuta	2.2	2.2
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
	406068			C2002008:gi 7303957 gb AAAF59000.1  (AE00	3.1	2.1
15	415162	AF035718	Hs.78061	transcription factor 21	2.1	2.1
	423349	AF010258	Hs.127428	homeo box A9	5.9	2.1
	424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
20	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	2.1	2.1
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	2.1	2.1
25	452959	AI933416	Hs.189674	ESTs	2.1	2.1
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
	408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
	418727	AA227609	Hs.94834	ESTs	2.1	2.1
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
30	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
	432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	2.5	2.1
	434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
35	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
	438520	AA706319	Hs.98416	ESTs	2.7	2.1
	414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
40	450861	AI523898	Hs.17617	ESTs	2.4	2.1
	419193	D29643	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.2	2.1
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
	407182	AA312551	Hs.230157	ESTs	2.1	2.1
45	421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
	432833	N51075	Hs.110028	ESTs	2.1	2.1
	425170	AU077315	Hs.154970	transcription factor CP2	2.6	2.0
	436278	BE396290	Hs.5097	synaptogyrin 2	2.8	2.0
	438719	AA357129	Hs.239625	integral membrane protein 2B	2.3	2.0
50	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.6	2.0
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.0	2.0
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
55	413627	BE182082	Hs.246973	ESTs	3.3	2.0
	414133	AW022188	Hs.41167	ESTs	2.3	2.0
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	14.7	2.0
	450244	AA007534	Hs.125062	ESTs	3.1	2.0
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
60	409219	AA393383	Hs.133331	ESTs	2.1	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
	421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
	434128	W93170	Hs.284164	protein x 0004	2.7	2.0
	434503	T96231	Hs.17762	ESTs	2.0	2.0
65	443292	AK000213	Hs.9196	hypothetical protein	2.0	2.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
	448172	N75276	Hs.135904	ESTs	6.0	2.0
	452039	AI922988	Hs.172510	ESTs	2.0	2.0
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
70	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	10.1	2.0
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
	451369	AA017321	Hs.269691	ESTs	2.1	2.0
	434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	5.4	2.0
75	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.7	2.0
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	5.5	2.0
	446783	AW138343	Hs.141867	ESTs	4.4	2.0
	437323	AA371145	Hs.194397	leptin receptor	2.5	2.0
	410076	T05387	Hs.7991	ESTs	2.9	2.0
80	421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	2.5	2.0

TABLE 61B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
10	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	419733	187589_1	AW362955 H59488 AI040666 W60959 W94209 H27231 T84625 H75715 W04957 W63676 AA659693 AA514302 W63789 BE046412 T91396 AI951970 AW044233 N20018 AW663548 T90114 AI139947 AA809643 AA846232 AA581966 AA789002
15	424036	23460_1	AA770688 H15373 AW161070 BE304523 BE378517 AA989300 AA904029 BE254211 AA449148 AI268420 AI300495 AI215637 AI300494 AI268551 AA928971 AA179427 AA947684 BE393792 H98018 AI885781 AI188567 AI290658 C15404
	426413	266650_1	AA377823 AW954494 AI022688
	429258	301917_1	AA448765 C04967 C03045 AA658293
	431676	336411_1	AI685464 AW971336 AA513587 AA525142
20	432689	35275_1	AB018320 H56457 AA247916 N83488 N87920 AA095653 T19858 AL134279 AA094167 AI673378 AI000340 R47500 W16595 AW152297 AI625937 AA002027 AI814851 AA902666 AI039729 AW975053 BE302243 AI240793 AA193203 N5581
	438869	46651_1	AF075009 R63109 R63068
	439518	47334_1	W76326 AF086341 W72300
	442677	548626_1	AI557914 W81031 AW473764 AI814081 W81068 AW182826 AW173296 AI376594 AI220500 BE257195 BE246486 R55637 C20788 AI014407 AI248353 AW028015
25	445808	65133_1	AV655234 AW966332 AA340239
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T613
	450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
30	453802	981589_1	AL134757 AW079131

TABLE 61C

35

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt\_position: Indicates nucleotide positions of predicted exons.

40

Pkey	Ref	Strand	Nt_position
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402802	3287156	Minus	53242-53432
403047	3540153	Minus	59793-59968
404641	9796810	Minus	32247-32362
405685	4508129	Minus	37956-38097
406068	9114084	Plus	382-543

45

50

Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95<sup>th</sup> percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

60	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
65	Unigene Title:	Unigene gene title			
	R1:	Ratio of prostate tumor to normal prostate tissue			
	Pkey	ExAccn	UnigenelD	Unigene Title	R1
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.5
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
	420729	AW964897	Hs.290825	ESTs	15.8
75	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	13.6
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	13.1
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	12.6
80	401197			ENSP00000229263*.HSPC213.	12.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	12.6
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4
	449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3
	443271	BE568568	Hs.195704	ESTs	11.6
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	11.2



	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419553	N34145	Hs.10177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
5	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
10	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AI080042	Hs.180450	ribosomal protein S24	9.0
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.0
15	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
	425174	D87450	Hs.154978	KIAA0261 protein	8.6
20	445701	AF055581	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	8.4
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	8.4
	434217	AW014795	Hs.23349	ESTs	8.3
25	417363	AW129357	Hs.329700	ESTs	8.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
30	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
	443837	AI984625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
35	436962	AW377314	Hs.5364	DKFZP564I052 protein	7.9
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	7.3
	451900	AB023199	Hs.27207	KIAA0982 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
45	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153684	frizzled-related protein	7.1
	433867	AK000596	Hs.3618	hippocalcin-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
50	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20196	adenylate cyclase 9	6.9
55	426759	AI590401	Hs.21213	ESTs	6.8
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.7
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
60	452859	AI300555	Hs.288158	hypothetical protein FLJ23591	6.7
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA622037	Hs.166468	programmed cell death 5	6.6
65	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	6.5
	443020	AI350058	Hs.106129	ESTs	6.5
	415752	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	6.4
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	6.3
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.3
75	411373	BE326276	Hs.8861	ESTs	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	6.2
	418196	AI745649	Hs.26549	KIAA1708 protein	6.1
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1
80	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	6.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447965	AW292577	Hs.94445	ESTs	5.9

	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	5.9
	431548	AI834273	Hs.97111	novel protein	5.8
5	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
10	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	5.8
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7
	431055	AL157645	Hs.48793	sialyltransferase 6 (N-acetylglucosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
15	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
	407938	AA905097	Hs.85050	phospholamban	5.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
20	406672	M26041	Hs.198253	major histocompatibility complex, class	5.5
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.5
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AF013168	Hs.79393	tuberous sclerosis 1	5.5
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
25	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.4
30	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
	451684	AF216751	Hs.26813	CDA14	5.4
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	5.4
	445757	AW449065	Hs.13264	KIAA0856 protein	5.4
	449907	AA004825	Hs.103281	ESTs	5.4
35	419159	AW974945	Hs.268049	hypothetical protein	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.3
	403851			C5002154*.gil7299015[gb]AAF54217.11 (AE0	5.3
40	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	5.3
	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
	424624	AB032947	Hs.151301	Ca2-dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
45	422746	NM_004484	Hs.119651	glypican 3	5.2
	437571	AA760894	Hs.153023	ESTs	5.2
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
50	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	5.2
	453204	R10799	Hs.191990	ESTs	5.2
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	5.1
	444917	R68651	Hs.144997	ESTs	5.1
55	414212	AA136569	Hs.10848	KIAA0187 gene product	5.1
	451593	AF151879	Hs.26706	CGI-121 protein	5.1
	417318	AW953937	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
	433600	R42833	Hs.22232	ESTs	5.0
60	434170	AA626509	Hs.122329	ESTs	5.0
	424090	X99699	Hs.139262	XIAP associated factor-1	5.0
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435706	W31254	Hs.7045	GL004 protein	5.0
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
65	432897	AF155099	Hs.279780	NY-REN-18 antigen	5.0
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	5.0
	410762	AF226053	Hs.66170	HSKM-B protein	5.0
	421823	N40850	Hs.28625	ESTs	5.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
70	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.9
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	4.9
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	4.9
75	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.9
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KIAA0010 gene product	4.8
80	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	4.8
	439024	R96696	Hs.35598	ESTs	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8
	430935	AW072916		zinc finger protein 131 (clone PHZ-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.7
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	4.7
5	451952	AL120173	Hs.301663	ESTs	4.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
	451831	NM_001674	Hs.460	activating transcription factor 3	4.7
	414522	AW518944	Hs.76325	step II splicing factor SLU7	4.7
	427176	AW381569	Hs.40334	ESTs	4.7
10	441390	AI692560	Hs.131175	ESTs	4.7
	447382	AW027790	Hs.182261	ESTs	4.7
	431676	AI685464		gb:tt88f04.x1 NCL_CGAP_Pr28 Homo sapiens	4.7
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7
15	401519			C15000476*:gij12737279[ref]XP_012163.1]	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.6
	414341	D80004	Hs.75909	KIAA0182 protein	4.6
20	408380	AF123050	Hs.44532	diubiquitin	4.6
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
	425907	AA365752	Hs.155965	ESTs	4.6
	419111	AA234172	Hs.137418	ESTs	4.6
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
	427078	AI676062	Hs.111902	ESTs	4.5
	419326	W94915	Hs.42419	ESTs	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.5
	408705	AA312135	Hs.46967	HSPCO34 protein	4.5
30	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
	449673	AA002064	Hs.18920	ESTs	4.5
	438440	AA807228	Hs.225161	ESTs	4.5
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	4.5
35	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	4.5
	456974	M12529	Hs.169401	apolipoprotein E	4.4
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.4
	436420	AA443966	Hs.31595	ESTs	4.4
40	443250	AI041530	Hs.132107	ESTs	4.4
	411962	AA099050		gb:zk85d12.r1 Soares_pregnant_uterus_NbH	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-li	4.4
45	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	4.4
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.4
	428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4
	436446	AW016809	Hs.119021	ESTs	4.3
50	450704	H85157	Hs.40696	ESTs	4.3
	438666	AW014493	Hs.126727	ESTs	4.3
	417308	H60720	Hs.81892	KIAA0101 gene product	4.3
	428826	AL048842	Hs.194019	atractin	4.3
	444212	AW503976	Hs.10649	basement membrane-induced gene	4.3
55	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
	447858	AW080339	Hs.80426	ESTs	4.3
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.3
	426827	AW067805	Hs.172665	methylentetrahydrofolate dehydrogenase	4.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	4.3
60	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.3
	417986	AA481003	Hs.97128	ESTs	4.3
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
	408088	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
	410853	H04588	Hs.30469	ESTs	4.3
65	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-lin	4.2
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	4.2
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	4.2
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2
70	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.2
	429900	AA460421	Hs.30875	ESTs	4.2
	437672	AW748265	Hs.5741	flavohemoprotein b5?	4.2
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	4.2
	450661	AW952160	Hs.146550	ESTs	4.2
75	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	456804	AI421645	Hs.139851	caveolin 2	4.2
	414291	AI289619	Hs.13040	G protein-coupled receptor 86	4.2
80	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	4.2
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	4.2
	429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
	443622	AI911527	Hs.11805	ESTs	4.1

	436576	AI458213	Hs.77542	ESTs	4.1
	443958	BE241880	Hs.10029	cathepsin C	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1
5	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.1
	421129	BE439899	Hs.89271	ESTs	4.1
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.1
	430383	AI861854	Hs.210778	hypothetical protein FLJ10989	4.1
10	431475	AI567669	Hs.40342	putative nuclear protein	4.1
	446468	AI765890	Hs.16341	MAWD binding protein	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
	404390			Target Exon	4.1
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	4.1
15	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
	433887	AW204232	Hs.279522	ESTs	4.1
20	436556	AI364997	Hs.7572	ESTs	4.1
	430157	BE348706	Hs.278543	ESTs	4.1
	451259	NM_006052	Hs.26146	Down syndrome critical region gene 3	4.1
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1
25	443646	AI085198	Hs.164226	ESTs	4.1
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
	413275	W94748	Hs.48821	ESTs	4.0
30	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	4.0
	433409	AI278802	Hs.25661	ESTs	4.0
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	4.0
	417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
35	421921	H83363	Hs.6820	translocase of inner mitochondrial membr	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
	415710	J04543	Hs.78637	annexin A7	4.0
	457794	AA689292	Hs.246850	ESTs	4.0
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
40	424401	H67220	Hs.169681	death effector domain-containing	4.0
	435905	AW997484	Hs.5003	KIAA0456 protein	4.0
	442731	AI868167	Hs.131044	ESTs	4.0
	418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9
45	439394	AA149250	Hs.56105	ESTs	3.9
	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
	436758	AW977167	Hs.155272	ESTs	3.9
	451030	H40697	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
	405934			Target Exon	3.9
50	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
55	412978	AI431708	Hs.820	homeo box C6	3.9
	414962	AF273304	Hs.235376	XPMC2 protein	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	3.9
	449590	AA694070	Hs.268835	ESTs	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.9
60	450899	T77447	Hs.177864	ESTs	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.8
	452588	AA889120	Hs.110637	homeo box A10	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
65	450506	NM_004460		fibroblast activation protein, alpha	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
	415156	X84908	Hs.78060	phosphorylase kinase, beta	3.8
70	422975	AA347720	Hs.122669	KIAA0264 protein	3.8
	403100			C2001027*:gij7296271[gb]AAF51562.1[AE0	3.8
	422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
	424806	AA382523	Hs.105689	MSTP031 protein	3.8
75	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
	443441	AW291196	Hs.92195	ESTs	3.8
	432529	AI989507	Hs.162245	ESTs	3.8
	432908	AI861896	Hs.304505	ESTs	3.8
80	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
	424855	AW204725	Hs.25560	ESTs	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	3.8

	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
5	453160	AI263307	Hs.239884	H2B histone family, member L	3.8
	416072	AL110370	Hs.79000	growth associated protein 43	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
10	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7
	417348	AI940507	Hs.318526	hypothetical protein FLJ12661	3.7
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
	448807	AI571940	Hs.7549	ESTs	3.7
15	413403	AA129105	Hs.198425	ESTs, Moderately similar to S65657 alpha	3.7
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
	408089	H59799	Hs.42644	thioredoxin-like	3.7
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.7
20	439209	AF087993	Hs.91954	ESTs	3.6
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	3.6
	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	3.6
	456619	AV647917	Hs.107153	inhibitor of growth family, member 1-lik	3.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
25	411213	AA676939	Hs.69285	neuropilin 1	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
30	452260	AA453208		RAB9, member RAS oncogene family	3.6
	439506	AI361238	Hs.41136	ESTs	3.6
	420077	AW512260	Hs.87767	ESTs	3.6
	451009	AA013140	Hs.115707	ESTs	3.6
	436473	AI193122	Hs.132275	ESTs	3.6
35	413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
	443067	AI077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.6
	433269	AI343543	Hs.126890	ESTs	3.6
40	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
	447033	AI357412	Hs.157601	ESTs	3.6
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6
45	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
	443399	AI452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
	401807			C7001350:gil6578126[gb]AAF17706.1[AF0496	3.5
	413979	BE218090	Hs.279453	ESTs	3.5
	414680	AA743331		hemoglobin, alpha 2	3.5
50	417380	T06809	Hs.332086	ESTs	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	3.5
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.5
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	446416	AV658299	Hs.163959	ESTs	3.5
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
	456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
60	432101	AI918950	Hs.123642	EphA3	3.5
	453565	BE298808	Hs.33363	DKFZP434N093 protein	3.5
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.5
	450066	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
65	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
	415528	R17236		gb:yg12c04.r1 Soares infant brain 1NIB H	3.5
	435513	AW404075	Hs.42785	DC11 protein	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	3.5
70	409068	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
	439132	H72803	Hs.38363	ESTs	3.5
	451173	AI765082	Hs.48317	ESTs	3.5
	422673	N59027		gb:yv59d11.r1 Soares fetal liver spleen	3.4
	401597	AA172106		Rag C protein	3.4
75	401744			Target Exon	3.4
	432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	3.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.4
80	435411	AW444619	Hs.138211	ESTs	3.4
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
	437158	AW090198		KIAA1150 protein	3.4
	416375	H95567	Hs.124700	ESTs	3.4
	419441	AW023731	Hs.274368	MSTP032 protein	3.4

	432741	AI732358	Hs.185118	ESTs, Moderately similar to A37413 calbi	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
5	428466	AF151063	Hs.184456	hypothetical protein	3.4
	447397	BE247676	Hs.18442	E-1 enzyme	3.4
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AL046851	Hs.153053	CD37 antigen	3.4
10	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	3.4
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
15	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.4
	444480	AI150730	Hs.265640	ESTs, Moderately similar to A47582 B-cel	3.4
	403389			C3001393*:gij3327090[dbj]BAA31613.1[AB	3.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	3.3
	408374	AW025430	Hs.155591	forkhead box F1	3.3
20	410494	M36564	Hs.64016	protein S (alpha)	3.3
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.3
	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
25	417295	AW993524	Hs.43148	ESTs	3.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
30	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
	425836	AW955696	Hs.90960	ESTs	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
35	436499	AJ276678	Hs.283102	HEF like Protein	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
	426848	H72531	Hs.36190	ESTs	3.3
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	3.3
40	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.3
	430280	AA361258	Hs.237868	interleukin 7 receptor	3.3
	408968	AI652236	Hs.49376	hypothetical protein FLJ20644	3.3
	453548	AL079983	Hs.116774	integrin, alpha 1	3.3
45	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
50	410366	AI267589	Hs.302689	hypothetical protein	3.2
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
55	439047	AW979177		gb:EST391287 MAGE resequences, MAGP Homo	3.2
	444451	AV650179	Hs.282431	ESTs	3.2
	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	406973	M34996	Hs.198253	major histocompatibility complex, class	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
60	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
	406247			Target Exon	3.2
	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
65	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984788		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
	441683	BE564214	Hs.102946	ESTs	3.2
70	417386	AL037228	Hs.82043	D123 gene product	3.2
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	422473	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
75	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.2
	435129	AI381659	Hs.267086	ESTs	3.2
	424894	H83520	Hs.153678	reproduction 8	3.2
80	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
	410185	BE294068	Hs.737	immediate early protein	3.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	3.2
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypotheti	3.2

	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
5	452413	AW082633	Hs.212715	ESTs	3.1
	409390	AI927212	Hs.3734	ESTs	3.1
	453078	AF053551	Hs.31584	metaxin 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	3.1
10	441124	T97717	Hs.119563	ESTs	3.1
	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	3.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	3.1
15	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
	427399	NM_014883	Hs.177664	KIAA0914 gene product	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
20	445840	AI277811	Hs.146291	ESTs	3.1
	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp434I1216 (f	3.1
	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
25	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
	400194			NM_003763:Homo sapiens syntaxin 16 (STX1	3.1
	400479			Target Exon	3.1
	402895			ENSP00000252117:Myelin transcription fac	3.1
30	403423			Target Exon	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
35	430519	AF129534	Hs.49210	F-box only protein 4	3.1
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	3.1
	422481	AL050163	Hs.117339	DNA-activation protein 10	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	3.1
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	3.1
40	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.1
45	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
50	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
	453293	AA382267	Hs.10653	ESTs	3.1
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	441527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
55	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.0
	411315	AW836547		gb:PM3-LT0032-030100-006-e08 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
60	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxin)	3.0
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
65	421786	AI188653	Hs.21351	ESTs	3.0
	433285	AW975944	Hs.237396	ESTs	3.0
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
70	445345	AW003850	Hs.12532	chromosome 1 open reading frame 21	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
75	428130	AW444985	Hs.77603	ESTs	3.0
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
	426448	R06054		gb:ye89g07.r1 Soares fetal liver spleen	3.0
80	445921	AW015211	Hs.146181	ESTs	3.0
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

451102	AA015683	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	3.0
416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

TABLE 62B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411962	126744_1	AA099050 AA099526 T47733
414279	143227_1	AW021691 AI537404 R45431 AI333439 AI741845 AI674468 R44190 R52535 R52617 AI220925 AI979148 AI744688 AW242437 AA618148
414680	147525_1	AI983837 AA399623 AI676204 AI420077 N24944 D51042 AA282786 AA137264 AW236107 AW769
415528	1539409_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288
416128	157163_1	AA708749 AA644620 AA652769 AA242975 AA151074 T19890
416882	162718_1	R17236 R52580 F11642
422673	219674_1	AA173632 AI174858 AA581361 AI700024 AA173988 BE165417 AI366964
426448	267323_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
430935	325772_1	AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
430968	326269_1	N59027 AA314694 N53937 R08100
431304	331286_1	R06054 AA378789 AW956453
431676	336411_1	AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
432125	341776_1	AW972830 AA527647 AA489820 AA570362
432363	345469_1	BE157283 BE157287 AA502438
437158	43392_5	AI685464 AW971336 AA513587 AA525142
437866	44433_2	AW972667 AA526539 AI057032 AW167842
439047	468139_1	AA534489 AW970240 AW970323
439518	47334_1	AW090198 AW173544 AW439860 AW007307 AI762577 W86516 AA160485 AA974203 AI589521 AW451857 AW450602 AI702529 AA630766
450506	836_1	AI801808 AW611634 AI393606 AW235356 AW000736 AW468599 AI582546 AA962057 AA523012 AW51
450580	83929_1	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
452260	9074_1	AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA04
453024	944876_28	AW979177 AA846994 AA829672
454573	1292917_1	W76326 AF086341 W72300
456719	222707_1	NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
		AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296
		N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
		AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228
		BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI
		AW846787 AW903370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352
		AW839043 AW839049 AW903372 AW846755 AW846767 AW903368 AW846766 BE146826 AW839056 AW846802 AW
		AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984795 AW984793
		AW984789 AW984823 AW984802 AW984800 AW984799 AW984825 AW984792 AW984821 AW984820 AW
		Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863
		AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW2

TABLE 62C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400479	8439786	Minus	115386-116348
400658	8118459	Minus	73525-73644
400750	8119067	Plus	198991-199168,199316-199548
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-66031
401744	2576349	Plus	14595-14751
401807	7331536	Plus	152325-152912
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402802	3287156	Minus	53242-53432
402895	9967547	Plus	85537-85671,86379-86469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	69340-69615
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39624-40072
405141	8980911	Plus	99861-100054
405934	6758795	Plus	159913-160605
406038	8389537	Plus	37764-37877
406247	7417725	Minus	46234-46461



Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75<sup>th</sup> percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigenelD:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of normal prostate tissue to prostate tumor tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M81650	Hs.1968	semenogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X83957	Hs.83870	nebulin	20.7
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.99949	prolactin-induced protein	11.8
415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	AI738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	AI791314		gb:ae46g12.y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	AI459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
405001	U58196		interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.266720	ESTs	6.2
435805	AW470260	Hs.48496	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	5.6
404606			Target Exon	5.6
432326	AI280308	Hs.274361	amiloride-sensitive cation channel 2, ne	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C11000936.gil3746443[gb]AAC63969.1[ AF0	4.8
416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	4.8
442082	R41823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440965	AI523646	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel, su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1NIB H	4.6
441040	AW449782	Hs.178803	ESTs	4.6
442764	AI762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
458895	AI535663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	AI801500	Hs.128457	ESTs	4.4
436781	AI914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004348*:Homo sapiens runt-related tra	4.3
442931	AI024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457136	AA428240	Hs.126083	ESTs	4.3
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
458840	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435866	AA704538	Hs.119740	ESTs	4.2
423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	4.2

	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
	400164			Eos Control	4.1
	435519	AI218950	Hs.125461	hypothetical protein FLJ11539	4.1
5	425094	AI955956	Hs.21417	ESTs	4.1
	415928	R46799	Hs.23966	ESTs	4.1
	415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
	426663	AI028767	Hs.262603	ESTs	4.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2)	4.1
10	404260			Target Exon	4.0
	453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
	401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	4.0
	415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
	402817	H24185		hypothetical protein	4.0
15	449233	BE048401	Hs.196511	ESTs	3.9
	435457	AA682421	Hs.59125	ESTs	3.9
	444105	AW189097	Hs.166597	ESTs	3.9
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
	411320	AW836646		gb:PM3-LT0032-090100-008-e05 LT0032 Homo	3.8
20	409679	BE250521		ras homolog gene family, member A	3.8
	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
	446175	AL036568	Hs.291	glutaryl aminopeptidase (aminopeptidase	3.8
	459707	AA631362	Hs.120866	gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens	3.8
	406917	X65964		gb:H.sapiens nestin gene.	3.8
25	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo	3.8
	443313	AI796730	Hs.55513	ESTs	3.8
	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W	3.8
	400499			C10001858:gil6679124[ref]NP_032759.1] ne	3.7
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
30	408229	AW176091		gb:QV0-BT0107-250899-007-b08 BT0107 Homo	3.7
	427318	AF186081	Hs.175783	zinc transporter	3.7
	417620	R02530	Hs.191198	ESTs	3.7
	404660			C9000841*:gil12654691[gb]AAH01185.1 AAH0	3.7
	409144	AW341187	Hs.279714	ESTs	3.7
35	436524	AA922236	Hs.221037	ESTs	3.7
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
	418833	AW974899	Hs.292776	ESTs	3.7
	424887	AA348112	Hs.259461	ESTs	3.7
	404984			Target Exon	3.7
40	454549	AW806910		gb:QV4-ST0023-160400-172-f04 ST0023 Homo	3.7
	426736	AA431615	Hs.130722	ESTs	3.7
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
	438040	AI222422	Hs.121846	ESTs	3.6
	443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
45	442097	AW015799	Hs.128474	ESTs	3.6
	435186	AL119470	Hs.145631	ESTs	3.6
	429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
	456521	AW373450	Hs.286212	hypothetical protein FLJ11729	3.6
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
50	400749			NM_003105*:Homo sapiens sortilin-related	3.6
	450295	AI766732	Hs.210628	ESTs	3.5
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
	434378	AA631739	Hs.335440	EST	3.5
	421342	AA504749		gb:aa63f08.r1 NCI_CGAP_GCB1 Homo sapiens	3.5
55	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
	429043	AI824977	Hs.145319	ESTs	3.5
	438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
	405258			Target Exon	3.4
	440207	AI371978	Hs.128326	ESTs	3.4
60	445045	AI652676	Hs.147256	ESTs	3.4
	406177			Target Exon	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	405735			ENSP00000252164*:KIAA1578 protein (Fragm	3.4
	445797	AI253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.4
65	444286	AI625304	Hs.190312	ESTs	3.4
	442027	AI652926	Hs.128395	ESTs	3.4
	447889	AW469180	Hs.346398	ESTs	3.4
	405152			Target Exon	3.4
	402460			C1001261*:gil2695979[emb]CAA70854.1] (Y0	3.4
70	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
	450588	AA010319	Hs.60389	ESTs	3.4
	447600	AI420990		ESTs	3.4
	406085			Target Exon	3.3
	417959	AW977642	Hs.291742	ESTs	3.3
75	418672	L44284	Hs.12915	ESTs	3.3
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.3
	446516	AW996692	Hs.257557	ESTs, Weakly similar to I38022 hypotheti	3.3
	415896	H08311	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.3
	410140	AL134435	Hs.247837	neurexin 3	3.3
80	458539	AI733837	Hs.145661	ESTs	3.3
	422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
	413381	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
	428561	AW973652	Hs.283105	ESTs	3.2

5	445608	AI830851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
	457733	AW974812	Hs.291971	ESTs	3.2
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	3.2
10	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AI423317	Hs.164680	ESTs	3.2
	418092	R45154	Hs.338439	ESTs	3.2
	411356	H45377		gb:yn99h03.r1 Soares adult brain N2b5HB5	3.1
15	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AJ010063	Hs.343603	titin-cap (telethonin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
	451686	AA059246	Hs.110293	ESTs	3.1
20	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
	401278			Target Exon	3.1
25	418087	AA961613	Hs.127838	ESTs	3.1
	421813	BE048255		gb:tz49b05.y1 NCI_CGAP_Brn52 Homo sapien	3.1
	402490			Target Exon	3.1
	448001	AW293237	Hs.202037	ESTs	3.1
	445316	AI219833	Hs.166767	ESTs	3.1
30	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
	433224	AB040919	Hs.210958	KIAA1486 protein	3.1
	421894	AI418464	Hs.190836	ESTs	3.1
35	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
	405422			ENSP00000216658*:HYPOTHETICAL 133.5 kDa	3.0
	420543	AA278221	Hs.173344	ESTs	3.0
40	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
	408025	AI692784	Hs.41767	PTD002 protein	3.0
	426349	AI308855	Hs.301497	arginyltransferase 1	3.0
45	444576	AI400974	Hs.182045	ESTs	3.0
	430661	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
	459647	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
	435713	AA699313	Hs.114071	ESTs	3.0
50	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_Ut4 Homo sapiens	3.0
	456103	Z39430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
	449245	AI636539	Hs.224296	ESTs	3.0
	428132	AA421765		gb:zu24g02.s1 Soares_NhHMPu_S1 Homo sapi	3.0
55	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.9
	432718	AA563943	Hs.244371	ESTs	2.9
	435534	AA830927	Hs.117306	ESTs	2.9
60	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypotheti	2.9
	410289	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr	2.9
	453126	AA032155	Hs.61622	ESTs	2.9
	459421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
	441543	AI733014	Hs.269715	ESTs	2.9
65	442252	AI733395	Hs.129124	ESTs	2.9
	419254	AI469453	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	2.9
	453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	2.9
70	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
	433942	AW272166	Hs.123465	ESTs	2.9
	400461			Target Exon	2.9
75	442640	AI205646	Hs.147220	ESTs	2.9
	438814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.9
	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCI_CGAP_Lym12 Homo sapien	2.8
	407142	AA412535		gb:zt99b10.s1 Soares_testis_NHT Homo sap	2.8
80	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypotheti	2.8
	442907	AI023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
	438690	AA815031	Hs.123598	ESTs	2.8
	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fis, clone A	2.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALU6_HUMAN A	2.8
	451632	BE005934	Hs.310625	EST	2.8

	426481	AW963941		gb:EST376014 MAGE resequences, MAGH Homo	2.8
	401656			Target Exon	2.8
	407269	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.8
5	435754	AA700752	Hs.117341	ESTs	2.8
	433565	AA599763	Hs.112520	ESTs	2.8
	451004	AA044967		gb:zf53d09.r1 Soares retina N2b4HR Homo	2.8
	425223	AA352825	Hs.146065	gb:EST60880 Activated T-cells XX Homo sa	2.8
	405770			NM_002362:Homo sapiens melanoma antigen,	2.8
10	456227	T84239	Hs.189788	ESTs	2.8
	454445	AW749432		gb:RC3-BT0386-301299-011-a09 BT0386 Homo	2.8
	419494	W01060	Hs.34382	ESTs	2.8
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	2.8
	428079	AA421020	Hs.208919	ESTs	2.7
15	406337			C14000021:gil7242973[dbj]BAA92547.1 (AB	2.7
	401884			Target Exon	2.7
	406881	D16154		gb:Human gene for cytochrome P-450c11, e	2.7
	428986	AA442884	Hs.201201	ESTs	2.7
	450044	R66444	Hs.51891	ESTs	2.7
20	403630			C3001708*:gil4758028[ref]NP_004360.1 co	2.7
	445514	AI241280	Hs.148906	ESTs	2.7
	446362	AW612481	Hs.104105	ESTs	2.7
	432492	AW275110	Hs.271106	ESTs	2.7
	430889	U22491	Hs.248117	G protein-coupled receptor 7	2.7
25	434316	AW411330	Hs.118796	annexin A6	2.7
	413155	BE067952		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	2.7
	433329	AF015041	Hs.199291	numb (Drosophila) homolog-like	2.7
	446523	NM_003063	Hs.334629	sarcophilin	2.7
	449923	BE258051		gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
30	453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hibr1)	2.7
	405678			CX001454:gil8393794[ref]NP_058681.1 myo	2.7
	432789	D26361	Hs.3104	KIAA0042 gene product	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	449109	AW270992	Hs.120949	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
35	436255	F01143	Hs.284284	zinc finger 1111	2.7
	415984	R19046	Hs.5010	gb:yq21f11.r1 Soares infant brain 1N1B H	2.7
	402844			C1000118*:gil9951913[ref]NP_062832.1 pr	2.7
	456666	AA452512	Hs.76719	U6 snRNA-associated Sm-like protein	2.7
	414620	AA150120	Hs.244621	ribosomal protein S14	2.7
40	404979			Target Exon	2.7
	412318	AW936911	Hs.326729	hypothetical protein MGC11082	2.7
	424361	AK001551	Hs.145944	Homo sapiens cDNA FLJ10689 fis, clone NT	2.7
	412542	AW961516	Hs.95097	ESTs	2.7
	441975	AW173248	Hs.344285	EST	2.7
45	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	457861	AW450205	Hs.305890	BCL2-like 1	2.7
	439204	AF087987	Hs.42696	EST	2.7
	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	2.7
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
50	443359	AI792583	Hs.135354	ESTs	2.7
	447336	AW139383	Hs.245437	ESTs	2.7
	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
	422185	AL117530	Hs.112822	DKFZP434B172 protein	2.7
	436030	R02287	Hs.121052	ESTs	2.7
55	449589	AW752437	Hs.135258	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
	436092	AI345995	Hs.127383	ESTs	2.6
	415054	AI733907		gb:zo86h09.y5 Stratagene ovarian cancer	2.6
	412908	AA121913	Hs.293896	pregnancy-associated plasma protein-E	2.6
	409583	AW440117	Hs.256879	ESTs	2.6
60	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
	435383	R61083		wee1 (S. pombe) homolog	2.6
	426629	AI203933	Hs.97142	ESTs	2.6
	415831	H15145	Hs.30509	ESTs	2.6
	412281	AI810054	Hs.14119	ESTs	2.6
65	434898	AW500458	Hs.29956	KIAA0460 protein	2.6
	422229	AF134414	Hs.113271	ABO blood group (transferase A, alpha 1-	2.6
	447518	T80061		gb:yd22f08.s1 Soares fetal liver spleen	2.6
	458546	AI215667	Hs.175044	ESTs	2.6
	438648	AA813125	Hs.146335	ESTs	2.6
70	450399	AW511049	Hs.202007	ESTs	2.6
	420833	R47948	Hs.188732	ESTs	2.6
	453903	AW299606	Hs.232777	ESTs	2.6
	443650	AI698330	Hs.151444	ESTs	2.6
	427419	NM_000200	Hs.177888	histatin 3	2.6
75	423741	AA330362		gb:EST34074 Embryo, 12 week II Homo sapi	2.6
	451577	N69101	Hs.40730	ESTs	2.6
	441358	AW173212	Hs.129041	ESTs	2.6
	402706			Target Exon	2.6
	436054	AI076262	Hs.119813	ESTs	2.6
80	402749			Target Exon	2.6
	442472	AW806859		gb:MR0-ST0020-081199-004-c03 ST0020 Homo	2.6
	445762	AI734002	Hs.264590	ESTs, Moderately similar to ALU5_HUMAN A	2.6
	441420	AA932872		gb:oo57d07.s1 NCL_CGAP_Lu5 Homo sapiens	2.6
	405564			Target Exon	2.6

	406003		Target Exon	2.6	
	459584	AI910884	Hs.346429	ESTs	2.6
	441597	AW135032	Hs.203625	ESTs	2.6
5	411280	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	2.6
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfami	2.6
	445060	AA830811	Hs.282908	ESTs	2.6
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
	428717	T78001	Hs.133546	hypothetical protein FLJ21120	2.6
10	401716			C16000902:gi 403440 gb AAA73168.1  (M817	2.6
	416628	W03955		gb:za62d04.r1 Soares fetal liver spleen	2.6
	443864	N37059	Hs.36250	ESTs, Weakly similar to I38022 hypotheti	2.6
	440702	AA904178	Hs.148233	ESTs	2.6
	456310	AA225522		gb:nc25c06.r1 NCI_CGAP_Pr1 Homo sapiens	2.6
15	451255	AA020857	Hs.90744	ESTs	2.6
	455737	BE072246		gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
	445326	AI220072	Hs.344672	ESTs	2.6
	408432	AW195262		gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.6
	445874	BE326671	Hs.170058	ESTs	2.6
20	441063	AA913819	Hs.188025	ESTs	2.6
	455505	AW970640	Hs.309071	ESTs	2.6
	453491	AL040177		gb:DKFZp434F0213_r1 434 (synonym: htes3)	2.6
	455048	AW852749		gb:PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	2.6
25	444130	AI125263	Hs.170410	ESTs	2.6
	422210	BE269319	Hs.171937	steroid dehydrogenase-like	2.5
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.5
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.5
	400427	AB044934	Hs.287388	histamine H4 receptor	2.5
30	410443	BE062906	Hs.28338	KIAA1546 protein	2.5
	455210	AW866599		gb:QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
	429909	AW977090	Hs.184860	CGI-203 protein	2.5
	441191	AI693930	Hs.148816	ESTs	2.5
	413489	BE144228		gb:MR0-HT0165-140200-009-d04 HT0165 Homo	2.5
35	448215	N34740	Hs.6658	ESTs	2.5
	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	2.5
	447610	AW296286	Hs.255534	ESTs	2.5
	450724	R55428		gb:yj79b05.r1 Soares breast 2NbHBst Homo	2.5
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	2.5
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	2.5
	447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755 protein,	2.5
	434152	AI792665	Hs.291190	ESTs	2.5
	412671	AW977734	Hs.37931	gb:EST389963 MAGE resequences, MAGO Homo	2.5
	456401	W28146		gb:43f11 Human retina cDNA randomly prim	2.5
45	404678			Target Exon	2.5
	408520	AA225063	Hs.161614	ESTs	2.5
	411332	AW837212		gb:QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.5
	429906	AL080137	Hs.193743	ESTs	2.5
50	433712	AF090887	Hs.306562	Homo sapiens clone HQ0085	2.5
	438353	BE539951	Hs.306996	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
	446224	AW450551	Hs.13308	ESTs	2.5

TABLE 63B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408229	1048462_1	AW176091 H24234
	408432	1058667_1	AW195262 R27868 AW811262
	409679	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
65	410483	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
	411320	1238624_1	AW836646 AW836580 AW836610 AW836636 AW836603 AW836632
	411332	1239102_1	AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
	411356	1240273_1	H45377 H21137 AW838640
	411426	1245515_1	BE141714 AW845993 AW845989
70	411829	1260309_1	AW865749 BE179419 BE179492
	411944	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	413155	1351148_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946
	413381	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
	413489	1373392_1	BE144228 BE144291
75	415054	151827_1	AI733907 AA159708 AI732614
	415098	1522174_1	D59687 D59694 D59656 D59589
	415131	1523680_1	D61119 D81508 D81734
	415386	1535560_1	Z43087 F07410 H15506 H54108 R95033 H98000
	415981	1564242_1	R35694 H12035 R53312
80	416628	1604848_1	W03955 H82332 H69247 H72486
	416935	163179_1	AA190712 AA190665 AA252564
	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	419896	1888662_1	Z99362 Z99363
	420778	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481

5	421342	201427_1	AA504749 AA287498
	421813	207654_1	BE048255 AA313083 AA298419
	422731	220507_1	AL138411 AL138412 AA315860
	423741	231582_1	AA330362 AW962525 H87796
	423772	23188_1	AA306637 NM_007241 AF156102 BE388339 BE614027 AW935016 AA315261 AW376418 AW304951 AI859820 AA367436 AW516957 BE614519
			AI453152 AI453149 AI453139 AW168378 AI139491 AI538368 AW468227 AI680027 AW090513 AA662830 F30995 AI351985 AI424349 AW009599
			C02215 AI6525
10	423871	232749_1	AA331906 AA332484
	426481	267878_1	AW963941 AW963944 AA379825 AA379564
	428132	287430_1	AA421765 AA456076 AI290275 AA455579
	431847	338402_1	AI791314 AI791434 AA516511
	434407	385744_1	AW815333 AW815409 AA632563
	435383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
15	436190	41555_1	AK001059 AA633055
	438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
	441420	516748_1	AA932872 W28068 W28643 T96110
	442472	543371_1	AW806859 AW806852 AF049582
	445797	650943_1	AI253414 AI366014 R34822
20	447518	724787_1	T80061 AI382804
	447600	728288_1	AI420990 AI399725 AI401757
	448516	766241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI525093
	449923	81926_1	BE258051 R45758 AA004732 BE255126
	450724	844585_1	R55428 AI820704 AI732283 R54983
25	451004	85453_1	AA044967 H86327 AA013079 AA058776 BE242713 AA019987
	452351	91233_1	AA025647 R45716 AW753786
	453412	966264_1	AJ003290 AJ003288 AW276947
	453491	969172_1	AL040177
	453752	979899_1	AL120800 BE378580
30	453826	982669_1	AL138129 AL138179 BE064231
	454445	1204468_1	AW749432 AW749434 R47332
	454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866611 AW866616
	455048	1250599_1	AW852749 AW852755 AW852620
	455210	1260650_1	AW866599 AW866294 AW866468 AW866467
35	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
	455737	1353892_1	BE072246 BE072229 BE072225 BE072210 BE072221 BE072256 BE072211 BE072242
	455791	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
	455887	1380836_1	BE154173 BE154098 BE154096
	456075	1476756_1	N73442 R98100 BE410380
40	456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
	456401	1844649_2	W28146 W28187

TABLE 63C

45	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
50	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	400461	9929654	Plus	32727-32846,32929-33051
	400499	9796071	Minus	148495-148806
55	400749	7331445	Minus	9162-9293
	400831	8576271	Minus	56502-57407
	401278	9799936	Plus	98428-98573
	401411	7799787	Minus	144144-144329
	401656	9100664	Minus	1-382
60	401716	6715703	Plus	174722-174911
	401884	8140731	Minus	89182-90053
	401896	8569194	Plus	115129-115294
	401917	9502466	Plus	25054-25229
	402422	9796344	Minus	32843-33008
65	402460	9796884	Minus	108901-109254,110246-110581,113613-113960
	402490	9797648	Plus	149982-150929
	402706	8894426	Minus	148640-148805
	402749	9212740	Minus	68787-68882,76602-76768
	402797	3421043	Minus	15758-15930
70	402817	6822166	Minus	48611-49012
	402844	9369286	Plus	54958-55313
	403451	9838240	Plus	77382-78300
	403612	8469060	Minus	94723-94859
	403630	8569999	Minus	13909-14466,15251-15760,16898-17431,41742-42440
75	403649	8705159	Minus	27141-27247
	404260	9366879	Plus	51396-51513
	404267	9581792	Minus	12209-12313,18241-18397
	404606	9212936	Minus	22310-23269
	404660	9797068	Plus	168215-168916
	404678	9797204	Plus	115196-115448
80	404979	4160139	Minus	87762-88217
	404984	6939882	Plus	87221-87505
	405001	6015406	Minus	104646-104819
	405150	9929758	Plus	126475-126773

405152	9965561	Minus	137662-137969
405258	7329310	Plus	129930-130076
405422	7243869	Minus	101938-102079, 102261-102443, 102896-103202
405564	2114222	Minus	16766-17344
405678	4079670	Plus	151821-152027
405735	9931101	Minus	29854-29976
405770	2735037	Plus	61057-62075
406003	8247800	Plus	42079-42516
406085	9123888	Plus	18665-18843
406177	7279760	Minus	18930-19148
406337	9213455	Plus	90117-90337
406398	9256276	Minus	118691-118959
406600	8248616	Minus	36296-36610

Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Cenbank accession number			
UnigenelD:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of BPH tissue to normal adult body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
420154	AI093155	Hs.95420	JM27 protein	49.6
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	47.2
419526	AI821895	Hs.193481	ESTs	43.6
432441	AW292425	Hs.163484	ESTs	42.7
431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypothe	30.2
407202	N58172	Hs.109370	ESTs	26.1
432101	AI918950	Hs.123642	EphA3	25.8
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	25.5
425075	AA506324	Hs.1852	acid phosphatase, prostate	24.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	24.4
410929	H47233	Hs.30643	ESTs	21.1
400287	S39329	Hs.181350	kallikrein 2, prostatic	20.3
446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	19.8
423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	18.6
415989	AI267700		ESTs	17.8
428336	AA503115	Hs.183752	microseminoprotein, beta-	17.3
450693	AW450461	Hs.203965	ESTs	16.7
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	16.7
407168	R45175	Hs.117183	ESTs	15.5
408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	15.5
454119	BE549773	Hs.40510	uncoupling protein 4	14.5
428819	AL135623	Hs.193914	KIAA0575 gene product	14.5
400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	14.4
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	14.3
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	14.2
433444	AW975324	Hs.129816	ESTs	13.8
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	13.5
428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	12.9
401424			NM_001172:Homo sapiens arginase, type II	12.7
432435	BE218886	Hs.282070	ESTs	12.5
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	12.3
446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	12.0
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.9
407275	AI364186		gb:qw34h07.x1 NCL_CGAP_U14 Homo sapiens	11.8
452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.7
432473	AI202703	Hs.152414	ESTs	11.3
410330	AW023630	Hs.159425	ESTs	11.2
431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	11.2
452792	AB037765	Hs.30652	KIAA1344 protein	11.2
418848	AI820961	Hs.193465	ESTs	10.9
400292	AA250737	Hs.72472	BMP-R1B	10.9
433647	AA603367	Hs.222294	ESTs	10.8
453160	AI263307	Hs.239884	H2B histone family, member L	10.8
409262	AK000631	Hs.52256	hypothetical protein FLJ20624	10.6
431474	AL133990	Hs.190642	CEGP1 protein	10.3
429220	AW207206		ESTs	10.3
428134	AA421773	Hs.161008	ESTs	10.2
408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	10.1
456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	9.8
434792	AA649253	Hs.132458	ESTs	9.7
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	9.5
428398	AI249368	Hs.98558	ESTs	9.4

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
5	429918	AW873986	Hs.119383	ESTs	9.1
	440260	AI972867	Hs.7130	copine IV	9.1
	453096	AW294631	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
10	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
15	450642	R39773	Hs.7130	copine IV	8.7
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
20	446336	AW815036	Hs.151251	ESTs	8.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417169	R13550	Hs.246773	ESTs	8.2
	453387	AI990741	Hs.252809	ESTs	8.2
25	434666	AF151103	Hs.112259	T cell receptor gamma locus	8.1
	417958	AA767382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
30	433923	AI823453	Hs.146625	ESTs	7.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441690	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoi	7.5
35	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	7.5
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
	409557	BE182896	Hs.211193	ESTs	7.3
40	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.3
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	7.1
	449300	AI656959	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	7.1
45	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AI799909	Hs.158989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	7.0
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	6.9
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	6.9
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	6.9
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
55	449821	AI671141	Hs.211122	ESTs	6.8
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.8
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	6.7
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
60	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	6.6
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
65	450164	AI239923	Hs.63931	ESTs	6.5
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
70	440911	AA909536	Hs.143562	ESTs	6.4
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	6.3
	435375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	6.3
75	431359	AW993522	Hs.292934	ESTs	6.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403667			Target Exon	6.1
	424846	AU077324	Hs.1832	neuropeptide Y	6.1
	439569	AW602166	Hs.222399	CEGP1 protein	6.1
80	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
	448004	AW451477	Hs.257456	ESTs	6.1
	431770	BE221800	Hs.268555	5'-3' exoribonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	6.0
	415621	AI648602	Hs.55468	ESTs	6.0



	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.0
	432527	AW975028	Hs.102754	ESTs	5.9
	447156	AW274731	Hs.157920	ESTs	5.9
5	404003			Target Exon	5.9
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
	438138	R98299	Hs.177502	ESTs	5.9
10	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.8
	434973	AW449285	Hs.313636	EST	5.8
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	5.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
	434485	AI623511	Hs.118567	ESTs	5.8
15	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	5.7
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
20	432966	AA650114	Hs.325198	ESTs	5.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	5.7
	425810	AI923627	Hs.31903	ESTs	5.6
	414312	AA155694	Hs.191060	ESTs	5.6
25	404571			NM_015902*:Homo sapiens progesteron induce	5.6
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
	427078	AI676062	Hs.111902	ESTs	5.6
	422805	AA436989	Hs.121017	H2A histone family, member A	5.6
30	417511	AL049176	Hs.82223	chordin-like	5.6
	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	5.6
	433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
	441676	BE564206	Hs.49889	ESTs	5.5
	421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
35	432682	AI376400	Hs.159588	ESTs	5.5
	435021	AA922192	Hs.54709	ESTs	5.5
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	5.5
	426581	AB040956	Hs.135890	KIAA1523 protein	5.5
	439079	AF085937	Hs.38348	ESTs	5.5
40	443635	AI080230	Hs.134214	ESTs	5.5
	400080			Eos Control	5.5
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
	436578	AI091435	Hs.134859	ESTs	5.5
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
45	450325	AI935962	Hs.26289	ESTs	5.4
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	5.4
	435072	AW592176	Hs.116932	ESTs	5.4
	428647	AA830050	Hs.124344	ESTs	5.4
50	441111	AI806867	Hs.126594	ESTs	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	450244	AA007534	Hs.125062	ESTs	5.3
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.3
	415539	AI733881	Hs.72472	BMP-R1B	5.3
55	437267	AW511443	Hs.258110	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
	446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
60	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cd	5.3
	423101	M83941	Hs.123642	EphA3	5.3
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
	450813	AI739625	Hs.203376	ESTs	5.3
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	5.2
65	415890	H08225	Hs.268712	ESTs	5.2
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	441054	AA913591	Hs.126480	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
70	448072	AI459306	Hs.24908	ESTs	5.2
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	5.2
	421040	AA715026	Hs.135280	ESTs	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
75	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	445238	AA883971	Hs.187506	ESTs	5.1
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
80	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	440995	T57773	Hs.10263	ESTs	5.0
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0

5	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	5.0
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	5.0
10	403696			C4001100*:gil5852342[gb]AAD54015.1] (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
15	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
	414422	AA147224	Hs.249195	Homeo box A13	4.9
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.9
20	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	435937	AA830893	Hs.119769	ESTs	4.8
	435136	R27299	Hs.10172	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
25	447058	AI939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29882		ESTs	4.8
	420871	AA702972	Hs.65300	ESTs	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
30	453843	D25215	Hs.35804	hect domain and RLD 3	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypothi	4.7
	452843	AI796769	Hs.208320	ESTs	4.7
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	4.7
35	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
	443361	AI792628	Hs.133273	ESTs	4.6
40	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AI831190	Hs.166676	ESTs	4.6
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.6
	415788	AW628686	Hs.78851	KIAA0217 protein	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
45	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	434408	AI031771	Hs.132586	ESTs	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
	447805	AW627932	Hs.302421	gemin4	4.6
	438875	AA827640	Hs.189059	ESTs	4.6
50	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
	418836	AI655499	Hs.161712	ESTs	4.5
55	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AI760833	Hs.293971	ESTs	4.5
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
60	420133	AA426117	Hs.155543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
	431060	AF039307	Hs.249171	homeo box A11	4.5
65	445372	N36417	Hs.144928	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
	418019	R68911	Hs.176275	ESTs	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
70	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412643	AW971239	Hs.136433	ESTs	4.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.4
	445210	H09323	Hs.27133	ESTs	4.4
75	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	4.4
	420608	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	444030	AW021254	Hs.135055	ESTs	4.4
80	435655	AW105663	Hs.6947	HSPC069 protein	4.4
	400533			ENSP00000209376*:PRED65 protein (Fragmen	4.4
	435285	AW272603	Hs.266134	ESTs	4.4
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
	432960	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	4.3
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	4.3

5	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW968065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.3
10	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	405348			C7001664:gi12698061 dbj BAB21849.1  (AB	4.3
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
15	449603	AI655662	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
	432887	AI926047	Hs.162859	ESTs	4.3
	420905	AA521307	Hs.186651	ESTs	4.2
20	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
	450597	AI701635	Hs.207077	ESTs	4.2
25	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	AB040907	Hs.278436	KIAA1474 protein	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
30	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	440594	AW445167	Hs.126036	ESTs	4.2
	458912	AI911066		ESTs	4.2
35	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
	436714	AA728964	Hs.293399	ESTs	4.1
40	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	430523	AW451385	Hs.161954	ESTs	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
45	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	449907	AA004825	Hs.103281	ESTs	4.1
	430487	D87742	Hs.241552	KIAA0268 protein	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
50	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL039402	Hs.125783	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
55	446416	AV658299	Hs.163959	ESTs	4.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.0
	442338	AI761976	Hs.156080	ESTs	4.0
60	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415861	Z43123	Hs.144513	ESTs	4.0
	418259	AA215404		ESTs	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
65	432229	AW290976	Hs.143587	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
70	448131	AI675054	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partia	4.0
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	4.0
75	452221	C21322	Hs.288057	hypothetical protein FLJ22242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
80	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	457498	AI732230	Hs.191737	ESTs	3.9
	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.9
	424940	AA985308	Hs.283902	ESTs	3.9

5	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	446862	AV660697	Hs.282700	ESTs	3.9
10	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.9
	401403			Target Exon	3.9
	448779	BE042877	Hs.177135	ESTs	3.9
	420533	AI809510	Hs.118971	ESTs	3.9
15	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
	423453	AW450737	Hs.128791	CGI-09 protein	3.9
	434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
20	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	419038	AW134924	Hs.190325	ESTs	3.9
	421129	BE439899	Hs.89271	ESTs	3.9
	424332	AA338919	Hs.101615	ESTs	3.9
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	3.9
25	447033	AI357412	Hs.157601	ESTs	3.9
	439306	BE220199		WD40 protein C1ao1	3.8
	410352	AW969725	Hs.150444	KIAA0373 gene product	3.8
	407961	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	3.8
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.8
30	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	3.8
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.8
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	3.8
35	447280	BE617907	Hs.97635	ESTs	3.8
	438379	N23018	Hs.171391	C-terminal binding protein 2	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	423044	AA320829	Hs.97266	protocadherin 18	3.8
40	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	3.8
	433507	AI817336	Hs.191791	ESTs	3.8
	437718	AI927288	Hs.196779	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
45	426981	AL044675	Hs.173081	KIAA0530 protein	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
50	433908	AW298141	Hs.157975	ESTs	3.8
	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypothe	3.7
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	3.7
55	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	423096	AA732684	Hs.278428	progesterone induced protein	3.7
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
	428055	AA420564	Hs.101760	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
60	451746	M86178	Hs.311258	ESTs	3.7
	453293	AA382267	Hs.10653	ESTs	3.7
	436671	AW137159	Hs.146151	ESTs	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	408418	AW963897	Hs.44743	KIAA1435 protein	3.7
65	420092	AA814043	Hs.88045	ESTs	3.7
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	3.7
	441865	AA384726	Hs.5722	hypothetical protein FLJ23316	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	431231	AA653552	Hs.116532	ESTs	3.7
70	418348	AI537167	Hs.96322	hypothetical protein FLJ23560	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
75	440947	AA910403		ESTs	3.7
	404561			trichorhinophalangeal syndrome I gene (T	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	3.6
	444794	AI419991	Hs.145225	ESTs	3.6
80	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.6
	431316	AA502663	Hs.145037	ESTs	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypothe	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	411067	AI681006	Hs.71721	ESTs	3.6
	436326	BE085236		aldo-keto reductase family 1, member B1	3.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

5	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	416239	AI038450	Hs.48948	ESTs	3.6
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
10	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	425465	L18964	Hs.1904	protein kinase C, iota	3.5
15	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C12000517*:gij4758712[ref]NP_004659.1  a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
20	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
	427304	AA761526	Hs.163853	ESTs	3.5
	434763	AA648618		gb:ns07a11.1 r1 NCI_CGAP_Ew1 Homo sapiens	3.5
25	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
	438680	AA906121	Hs.173421	ESTs	3.5
30	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5
35	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AI800041	Hs.190555	ESTs	3.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
40	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
	409047	AW961434	Hs.31539	ESTs	3.4
45	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfami	3.4
	436340	R42246	Hs.21606	ESTs	3.4
50	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
55	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
60	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.19928	hypothetical protein SP329	3.4
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.4
	408784	AW971350	Hs.63386	ESTs	3.4
65	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.4
70	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
75	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50128	Hs.173400	ESTs	3.3
	427615	BE410107	Hs.179817	CGI-82 protein	3.3
	429588	AI080271	Hs.134533	ESTs	3.3
80	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23606	ESTs	3.3

	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	436854	AA749167	Hs.173911	ESTs	3.3
	430865	AI073424	Hs.5232	HSPC125 protein	3.3
5	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	423645	AI215632	Hs.147487	ESTs	3.3
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	3.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
	418051	AW192535	Hs.19479	ESTs	3.3
10	418719	AW975590	Hs.161707	ESTs	3.3
	437714	AA766346	Hs.293242	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
15	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.3
	423412	AF109300		prostate cancer associated protein 5	3.3
	436962	AW377314	Hs.5364	DKFZP564I052 protein	3.3
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	3.3
20	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	433213	AW665130	Hs.137190	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.2
	428043	T92248	Hs.2240	uteroglobin	3.2
25	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	3.2
	423595	R82826	Hs.220702	ESTs	3.2
	407021	U52077		gb:Human mariner1 transposase gene, comp	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
30	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.2
	425657	T89839	Hs.119471	ESTs	3.2
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
35	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
	451025	AW028689	Hs.301985	ESTs	3.2
	401416			C14000338*:gij7459502 pir  S74665 outer	3.2
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
40	436995	AI160015	Hs.118112	ESTs	3.2
	428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	429037	X81895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	3.2
45	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	437866	AA156781		metallothionein 1E (functional)	3.2
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
50	410870	U81599	Hs.66731	homeo box B13	3.2
	438899	AF085833	Hs.135624	ESTs	3.2
	415862	R51034	Hs.144513	ESTs	3.2
	420969	AI636310	Hs.28310	ESTs	3.2
	415467	R60891	Hs.260274	ESTs	3.2
55	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	417380	T06809	Hs.332086	ESTs	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
60	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	452862	AW378065	Hs.8687	ESTs	3.2
	405548			Target Exon	3.1
	439584	AA838114	Hs.221612	ESTs	3.1
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
65	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
70	416836	D54745	Hs.80247	cholecystokinin	3.1
	432589	AL135725	Hs.131708	ESTs	3.1
	420512	AA262886	Hs.143817	ESTs	3.1
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
	423855	AA331761	Hs.254859	ESTs	3.1
75	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
80	421823	N40850	Hs.28625	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	445784	AI253155	Hs.146065	ESTs	3.1
	434384	AA631910	Hs.162849	ESTs	3.1
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1

5	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
	433610	AA806822	Hs.112547	ESTs	3.1
	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	444800	AW119071	Hs.153287	ESTs	3.1
10	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.1
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	3.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	3.1
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.1
	407349	AA825449	Hs.83332	Homo sapiens cDNA: FLJ22437 fis, clone H	3.1
15	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	425480	AB023198	Hs.158135	KIAA0981 protein	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
20	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	3.1
	433852	AI378329	Hs.126629	ESTs	3.0
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.0
	452242	R50956	Hs.159993	glycosyltransferase	3.0
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	3.0
25	405264			NM_030813*:Homo sapiens suppressor of po	3.0
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.0
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.0
	434497	AI821803	Hs.136580	ESTs	3.0
	420355	AW968263	Hs.123126	ESTs	3.0
30	403481			Target Exon	3.0
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.0
	416642	T96118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
35	426174	AA547959	Hs.115838	ESTs	3.0
	430459	BE178539	Hs.278634	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	446258	AI283476	Hs.263478	ESTs	3.0
	448686	AA158659	Hs.334712	hypothetical protein FLJ14744	3.0
40	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	3.0
	414441	AA234759	Hs.132950	ESTs	3.0
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	3.0
	437048	AA743240	Hs.91582	ESTs	3.0
	450963	AI864668	Hs.48832	ESTs	3.0
45	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.0
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.0
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
50	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	3.0
	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
55	437323	AA371145	Hs.194397	leptin receptor	3.0
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.0
	450580	N40087		ESTs	3.0
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.0
	418365	AW014345	Hs.161690	ESTs	3.0
60	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.0
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	418819	AA228776	Hs.191721	ESTs	3.0
	428634	AA811845	Hs.106290	Kelch motif containing protein	3.0
65	431869	AA521136	Hs.190176	ESTs	3.0
	435008	AF150262	Hs.162898	ESTs	3.0
	448880	AW205507	Hs.32360	ESTs, Highly similar to I38587 retroviri	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 64B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

80	Pkey	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1	AW846433 AW846159 AW846377 AW846528

5	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214 BE046680 BE046738 BE044958 BE064415 BE064430 BE064448 BE145899 BE145848 BE145849 BE145853 BE145927 BE145925 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086 Z43062 R13213 H14422 H51299 H44619 H46391 R86024 H51892 T72744 AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597 AA215404 AI990909 BE464132 AW271459 N74332 AI262061 T65754 AA229857 AA229658 AI217097 AW886090 W38035 W38792 AA232835 AW936043 AA603305 AA244095 AA244183 AA255652 AA280911 AW967920 AA262684 BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 AF109300 AI299378 AI202654 AA337221 AA336756 AW966196 AA377823 AW954494 AI022688 AA380153 AA380233 AW963529 AK001536 AA191092 AW510354 AI554256 AL353968 AA134266 AA418703 AA418711 BE071915 BE071920 BE071912 AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340 AA884766 AW974271 AA592975 AA447312 AW207206 AW341473 AA448195 AI951341 AW968485 AW968670 AA480922 BE350425 AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339 AJ003429 AJ003367 AA564825 H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320 AA648618 AW974389 H51771 N73895 AJ001872 BE085236 BE085317 X04236 AA577934 AA578392 AA502836 AA595852 AA578258 AW207091 AA507151 AA559152 T57040 BE503281 AW593405 AI825755 AI350499 AI655710 AI972281 AI654949 BE073961 BE073962 BE041399 AW750214 AA228488 BE074016 AI908706 AW270601 AW873282 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188 AA830149 AW978407 M85983 AW503637 BE220199 W01813 AF086118 N0760 BE221405 AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877 AA910403 AI815593 W58361 AW162520 AI816550 N99828 BE079873 AI110738 AF074645 AV653771 BE089370 AI458682 H24240 R14537 R18426 AW867082 AI151418 W60401 AW631238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053 AW889353 AA521308 AA001203 W92828 AI207798 AA746655 R78710 W24617 AA024605 C01747 AW173095 W61229 W92685 AA742467 H00789 R76925 AW1828 AA001793 AA001871 NM_014253 AF100772 BE088769 AI022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 AI692689 R14223 R18395 N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303 AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878 AA495800 AA495737 AA010736 AA654716 AA640726 BE173515 BE173560 AI902860 T79703 T96307 AL079725 AW998716 AW022148 N68020 AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892 AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 AW753456 AW753036 AW854868 AW854862 AW835767 AW835537 BE160187 AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033 BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362 BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464 AA493662 AW897396 BE154814 AI911066 AI933734 AI680888 AJ003599
---	--------	-----------	--

TABLE 64C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
------	-----	--------	-------------



5	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401403	7710966	Plus	146180-146294
	401416	7452889	Minus	121456-121626
	401424	8176894	Plus	24223-24428
	403242	7637817	Minus	11297-12511
10	403481	9965004	Plus	93496-93633
	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403696	3135242	Minus	143467-143634
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
15	404571	7249169	Minus	112450-112648
	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	405264	7329374	Plus	28556-28684
	405348	2914717	Minus	43310-43462
20	405510	7630909	Minus	101028-101174
	405548	1532158	Plus	11552-11686

Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85<sup>th</sup> percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of BPH tissue to prostate tumor tissue

	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	428134	AA421773	Hs.161008	ESTs	9.4
	446336	AW815036	Hs.151251	ESTs	9.3
40	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	8.9
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	400533			ENSP00000209376*:PRED65 protein (Fragmen	8.7
	418310	AA814100	Hs.86693	ESTs	8.7
45	404592			NM_022739*:Homo sapiens E3 ubiquitin lig	8.1
	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
	400080			Eos Control	7.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	7.4
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
50	438231	AW594539	Hs.155689	ESTs	7.3
	418387	R18085		gb:yg16b12.r1 Soares infant brain 1NIB H	7.2
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	6.9
55	404967			Target Exon	6.9
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	6.9
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	6.9
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	6.8
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	6.8
60	400440	X83957	Hs.83870	nebulin	6.6
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	6.6
	400086			Eos Control	6.4
	440911	AA909536	Hs.143562	ESTs	6.4
	425312	AA354940	Hs.145958	ESTs	6.4
65	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
	419015	T79262	Hs.14463	ESTs	6.3
	453789	AA628517	Hs.118502	ESTs	6.2
	424940	AA985308	Hs.283902	ESTs	6.1
	403667			Target Exon	6.1
70	429014	AI800518	Hs.118158	ESTs	6.0
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitte	6.0
	419999	AI760942	Hs.191754	ESTs	6.0
	405348			C7001664:gi 12698061 dbj BAB21849.1  (AB	6.0
	404003			Target Exon	5.9
75	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
	432319	AW510770	Hs.128386	ESTs	5.7
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
	443361	AI792628	Hs.133273	ESTs	5.6
80	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	5.6
	439079	AF085937	Hs.38348	ESTs	5.5
	422081	AW136820	Hs.196011	ESTs	5.5
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	5.5
	423529	T87318	Hs.120411	ESTs	5.5

	436578	AI091435	Hs.134859	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
5	414403	AW969551	Hs.76064	ribosomal protein L27a	5.4
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
10	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypothe	5.3
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
15	446495	D60923	Hs.153460	ESTs	5.2
	435375	AI733610	Hs.187832	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	5.2
	405321			Target Exon	5.1
20	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	438206	AA780385	Hs.187885	ESTs	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
25	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	440354	AA889386	Hs.125468	ESTs	5.0
	440388	AI693520	Hs.223000	ESTs	4.9
	421188	AA284658	Hs.261493	ESTs	4.9
	403481			Target Exon	4.8
30	438132	AA907076	Hs.122060	ESTs	4.8
	403333			NM_002518*:Homo sapiens neuronal PAS dom	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
35	452843	AI796769	Hs.208320	ESTs	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.205679	ESTs	4.7
40	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	442160	AI337127	Hs.156325	ESTs	4.6
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.6
	434589	AF147363		gb:Homo sapiens full length insert cDNA	4.6
	404995			ENSP00000251890*:Monocytic leukemia zinc	4.6
45	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
	405549			C7001976*:gij4758712[ref NP_004659.1  al	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sap	4.5
50	444800	AW119071	Hs.153287	ESTs	4.5
	403371			Target Exon	4.5
	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	4.5
	439752	T78968	Hs.14411	ESTs	4.5
55	414441	AA234759	Hs.132950	ESTs	4.5
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	4.5
	454585	BE069128		gb:QV3-BT0379-310100-071-g06 BT0379 Homo	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
60	418059	AA211586		gb:zn56d05.s1 Stralagene muscle 937209 H	4.4
	451469	NM_014809	Hs.26441	KIAA0319 gene product	4.4
	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	4.3
65	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	415467	R60891	Hs.260274	ESTs	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.3
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	4.3
70	441620	R59595	Hs.26675	ESTs	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	448108	AW300021	Hs.170685	ESTs	4.2
	436345	AA873008	Hs.121572	ESTs	4.2
	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	4.2
75	413525	BE145899		gb:MRO-HT0208-221299-204-b10 HT0208 Homo	4.2
	403305	NM_006825		transmembrane protein (63kD), endoplasmic	4.2
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	430124	AW204994	Hs.253450	ESTs	4.2
80	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	H54253	Hs.205241	ESTs, Weakly similar to S65657 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

	445206	AI350199	Hs.269990	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
5	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AI761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QV0-DT0020-090200-106-g05 DT0020 Homo	4.0
10	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
15	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.9
	453387	AI990741	Hs.252809	ESTs	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
20	454806	AW872430	Hs.273743	ESTs	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
25	407834	AW084991	Hs.26100	ESTs	3.9
	400398	AF137396	Hs.283879	ubiquilin 3	3.9
	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C14000482*:gil9790241[ref NP_062628.1] S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
30	444911	U06117	Hs.250	xanthene dehydrogenase	3.9
	436350	AA713661	Hs.121091	ESTs	3.9
	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321 Homo	3.8
	452320	AA042873	Hs.160412	ESTs	3.8
35	402145			Target Exon	3.8
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
40	434381	AA631834		gb:np77h05.s1 NCL_CGAP_Pr2 Homo sapiens	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	433523	H29882		ESTs	3.8
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
45	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
50	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
	449264	AI637649	Hs.196105	ESTs	3.8
	443635	AI080230	Hs.134214	ESTs	3.7
	428200	AI039624	Hs.98388	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
55	418759	AA227879	Hs.187621	ESTs	3.7
	450497	H64159	Hs.15328	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
60	448135	AI470874	Hs.343799	ESTs	3.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	3.7
65	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.7
70	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
75	440947	AA910403		ESTs	3.7
	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
80	429073	AA446167	Hs.47385	ESTs	3.6
	419002	T78625	Hs.268594	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	3.6

	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	AI671141	Hs.211122	ESTs	3.6
5	451193	N29850	Hs.44098	ESTs	3.6
	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	427235	AI126288	Hs.192232	ESTs	3.6
10	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.5
	401132			C12000517*:gij4758712[ref NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813*:Homo sapiens suppressor of po	3.5
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
15	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
20	403510			Target Exon	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	3.4
25	434497	AI821803	Hs.136580	ESTs	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769*:BG153O3.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
30	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.4
35	427033	AI457449	Hs.192817	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	410551	R36730	Hs.21816	ESTs	3.4
	423357	AI285124	Hs.157505	ESTs	3.4
	450582	AI339732		G-rich RNA sequence binding factor 1	3.4
40	437662	AA765387	Hs.145095	ESTs	3.4
	442388	AW663442	Hs.129485	ESTs	3.4
	445004	AI204616	Hs.148701	ESTs	3.4
	450597	AI701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
45	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
50	407344	AI038025	Hs.271418	gb:ox29f07.x1 Soares_total_fetus_Nb2HF8_	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
55	453328	AW292635	Hs.346145	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	449256	AA059050	Hs.59847	ESTs	3.3
	432550	AW297206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
60	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	3.3
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
65	452011	AW628911	Hs.211429	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	420355	AW968263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypothe	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
70	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501*:gij129092[sp P23270]OLF7_RAT O	3.2
	411552	AW851255		gb:IL3-CT0220-160200-066-H02 CT0220 Homo	3.2
75	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
	435786	H09175	Hs.26085	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
80	447183	AI554733	Hs.173182	ESTs	3.2
	426629	AI203933	Hs.97142	ESTs	3.2
	447892	AI435848	Hs.172978	ESTs	3.2
	457136	AA428240	Hs.126083	ESTs	3.2
	443585	AW466983	Hs.283949	enamelin	3.1

5	451399	AL042110	Hs.326728	ESTs	3.1
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	458251	AL040927	Hs.210422	ESTs	3.1
	439950	AW937417	Hs.293561	ESTs	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
10	403805			Target Exon	3.1
	422666	AA677981	Hs.119023	SMC2 (structural maintenance of chromoso	3.1
	408799	AA059412	Hs.47986	hypothetical protein MGC10940	3.1
	429350	AI754634	Hs.131987	ESTs	3.1
	430454	AW469011	Hs.105635	ESTs	3.1
15	441817	AW969706	Hs.293332	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	445758	R60715	Hs.25804	ESTs	3.1
	403291			Target Exon	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	455772	W28799		gb:52g11 Human retina cDNA randomly prim	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	438142	T90309	Hs.269651	ESTs	3.1
	416423	H54375	Hs.268921	ESTs	3.1
25	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	3.1
	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.1
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.1
	420721	AA927802	Hs.159471	ZAP3 protein	3.1
	436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L	3.1
30	441492	AI149998	Hs.146346	ESTs	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	435628	W88732	Hs.36107	ESTs	3.0
	444326	AI939357	Hs.270710	ESTs	3.0
35	413774	AA131782	Hs.182314	ESTs	3.0
	434352	AF129505	Hs.86492	small muscle protein, X-linked	3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	3.0
	416642	T96118	Hs.226313	ESTs	3.0
40	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	427813	D29833	Hs.2207	salivary proline-rich protein	3.0
	405733			NM_021140*:Homo sapiens ubiquitously tra	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	3.0
	410929	H47233	Hs.30643	ESTs	3.0
50	458187	D56919	Hs.265848	myomegalin	3.0
	429430	AI381837	Hs.155335	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0

## 55 TABLE 65B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408304	1050848_1	AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515 AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288 AW810263 AW810325 AW810443 AW8
65	409189	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
	410559	1208283_1	AW754192 W00554 AW857797 AW754203 AW754197 AW754193
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
70	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1	AW846433 AW846159 AW846377 AW846528
	411518	1248692_1	AW850246 AW850251 AW850302
	411552	1249255_1	AW851255 AW851432 AW850955
75	412701	1322288_1	AW984757 AW984797 AW984734 AW984745
	412988	1342150_1	BE046680 BE046738 BE044958
	413081	1348563_1	BE064415 BE064430 BE064448
	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	416009	1566379_1	Z43062 R13213 H14422
80	416422	1593811_1	H60457 H68709 H73528 H54335 R87154
	418059	171879_1	AA211586 F35799 AA211641 F29720 AW937387 AW937408
	418387	174731_1	R18085 AA219028 R17712 Z44345
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043

5	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	421926	209246_1	AA300591 AW963893 AA300493
	424200	236595_1	AA337221 AA336756 AW966196
	424686	242486_1	AA345504 AA345251 AW963243
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
10	432765	353907_1	AJ003429 AJ003367 AA564825
	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 AI792312 AI792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
15	436295	41733_1	N73895 AJ001872
	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE089370
	449570	81018_1	AA001793 AA001871
20	450317	831956_1	AI692689 R14223 R18395
	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
	453682	977454_1	T79703 T96307 AL079725
25	454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE069023 AW809375
	454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
30	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
35	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
	455490	1297826_1	AW953477 Z41970 F12435 T73989 T09387
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
40	455772	1363114_1	W28799 BE086078
	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
	457374	328758_1	AA493662 AW897396 BE154814

TABLE 65C

50	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
55	Pkey	Ref	Strand	Nt_position
	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401459	9212270	Minus	182001-183323
60	402145	8018280	Plus	113086-114800
	402454	7534025	Minus	14826-15803
	402703	8705069	Minus	15335-15500
	403242	7637817	Minus	11297-12511
	403291	7230870	Plus	95177-95435
	403305	8099945	Plus	114632-114805
65	403333	8568833	Minus	124794-124941
	403371	9087278	Plus	105655-106050
	403433	9719611	Minus	72225-72437
	403481	9965004	Plus	93496-93633
70	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403805	8140491	Minus	51483-51742,53429-53511
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
75	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	404967	7523744	Minus	89944-90729
	404995	6006247	Minus	154015-154123
	405264	7329374	Plus	28556-28684
80	405321	3419846	Minus	44654-45210
	405348	2914717	Minus	43310-43462
	405510	7630909	Minus	101028-101174
	405549	1552494	Plus	10878-11048
	405733	9884689	Plus	124832-125051

Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85<sup>th</sup> percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigenelD:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of BPH tissue to prostate tumor and normal body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
410929	H47233	Hs.30643	ESTs	21.1
450693	AW450461	Hs.203965	ESTs	16.7
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432473	AI202703	Hs.152414	ESTs	11.3
446336	AW815036	Hs.151251	ESTs	10.9
407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens	10.7
428134	AA421773	Hs.161008	ESTs	10.2
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
415293	R49462	Hs.106541	ESTs	9.1
458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
428927	AA441837	Hs.90250	ESTs	8.6
420345	AW295230	Hs.25231	ESTs	8.5
453387	AI990741	Hs.252809	ESTs	8.2
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	7.5
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4
400080			Eos Control	7.4
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
438231	AW594539	Hs.155689	ESTs	7.3
410330	AW023630	Hs.159425	ESTs	7.2
449300	AI656959	Hs.346514	ESTs	7.1
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	6.8
454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	6.6
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.6
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
424433	H04607	Hs.9218	ESTs	6.5
442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.4
425312	AA354940	Hs.145958	ESTs	6.4
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
440911	AA909536	Hs.143562	ESTs	6.4
400533			ENSP00000209376*:PRED65 protein (Fragmen	6.2
418310	AA814100	Hs.86693	ESTs	6.2
403667			Target Exon	6.1
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
404003			Target Exon	5.9
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.9
438138	R98299	Hs.177502	ESTs	5.9
424940	AA985308	Hs.283902	ESTs	5.8
434485	AI623511	Hs.118567	ESTs	5.8
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
443361	AI792628	Hs.133273	ESTs	5.6
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
439079	AF085937	Hs.38348	ESTs	5.5
430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5
436578	AI091435	Hs.134859	ESTs	5.5
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
435072	AW592176	Hs.116932	ESTs	5.4
435375	AI733610	Hs.187832	ESTs	5.4
444609	AW571659	Hs.278081	ESTs	5.4
416602	NM_006159	Hs.79389	nel (chicken)-like 2	5.4
433087	AI720686	Hs.152520	ESTs	5.3
439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.3
437267	AW511443	Hs.258110	ESTs	5.3
441916	AA993571	Hs.129075	ESTs	5.3
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypothesi	5.3

	423101	M83941	Hs.123642	EphA3	5.3
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
	415890	H08225	Hs.268712	ESTs	5.2
5	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
10	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.1
15	445238	AA883971	Hs.187506	ESTs	5.1
	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	440354	AA889386	Hs.125468	ESTs	5.0
20	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfo	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	4.9
25	450497	H64159	Hs.15328	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	414818	BE541217	Hs.23606	ESTs	4.8
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	433523	H29882		ESTs	4.8
30	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	443635	AI080230	Hs.134214	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	AI796769	Hs.208320	ESTs	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
35	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.7
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
40	405348			C7001664:gi12698061 dbj BAB21849.1  (AB	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	447058	AI939456	Hs.160870	ESTs	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
	430697	AA484207	Hs.211867	ESTs	4.5
45	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
	449821	AI671141	Hs.211122	ESTs	4.5
	420905	AA521307	Hs.186651	ESTs	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	420154	AI093155	Hs.95420	JM27 protein	4.4
55	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	4.4
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	433597	AA708205	Hs.100343	ESTs	4.3
60	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	4.2
65	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	420355	AW968263	Hs.123126	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
70	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
75	450597	AI701635	Hs.207077	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
80	438875	AA827640	Hs.189059	ESTs	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	404967			Target Exon	4.0
	427203	AW629517	Hs.244855	ESTs	4.0



5	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	4.0
	435136	R27299	Hs.10172	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
10	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurolypsin, moto	4.0
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
15	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.9
20	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
	456466	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	414441	AA234759	Hs.132950	ESTs	3.9
25	425810	AI923627	Hs.31903	ESTs	3.9
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	440450	AI333129	Hs.156147	ESTs	3.8
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
30	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
35	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
40	433908	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
	432101	AI918950	Hs.123642	EphA3	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
45	448568	AA149121	Hs.71947	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	436345	AA873008	Hs.121572	ESTs	3.7
	446862	AV660697	Hs.282700	ESTs	3.7
50	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
55	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
60	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	403481			Target Exon	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
	417565	AI203405	Hs.47831	ESTs	3.6
65	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021987	Hs.59970	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
70	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	420026	AI831190	Hs.166676	ESTs	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
75	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.5
	401132			C12000517*:gil4758712[ref]NP_004659.1] a	3.5
80	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5

5	430865	AI073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153287	ESTs	3.5
	428647	AA830050	Hs.124344	ESTs	3.5
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
10	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AI760833	Hs.293971	ESTs	3.4
	436714	AA728964	Hs.293399	ESTs	3.4
	404848			ENSP00000240769*:BG153O3.1 (similar to C	3.4
15	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
20	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
25	456995	T89832	Hs.170278	ESTs	3.4
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
30	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	433628	AI821784	Hs.188578	ESTs	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
35	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AI126288	Hs.192232	ESTs	3.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
40	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
	448108	AW300021	Hs.170685	ESTs	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
45	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	432229	AW290976	Hs.143587	ESTs	3.3
50	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
	416662	T25853	Hs.7538	ESTs	3.3
55	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
	428715	AW293716	Hs.53126	ESTs	3.3
	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	3.3
60	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AI821803	Hs.136580	ESTs	3.2
	439306	BE220199		WD40 protein C1a01	3.2
	420608	BE548277	Hs.103104	ESTs	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
65	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	3.2
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
70	402145			Target Exon	3.2
	448131	AI675054	Hs.200481	ESTs	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	447183	AI554733	Hs.173182	ESTs	3.2
75	447597	AI886036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
	434408	AI031771	Hs.132586	ESTs	3.2
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.2
80	453789	AA628517	Hs.118502	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AI458682		gb:tk13e01.x1 NCL_CGAP_Lu24 Homo sapiens	3.2
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

5	405321		Target Exon	3.1
	429569	AA454993	Hs.138343 ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941 ESTs	3.1
	452102	U04343	Hs.27954 CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	433444	AW975324	Hs.129816 ESTs	3.1
	410821	AI114811	Hs.92526 ESTs, Weakly similar to T00365 hypotheti	3.1
	415861	Z43123	Hs.144513 ESTs	3.1
	422299	AK000181	Hs.114556 hypothetical protein FLJ20174	3.1
10	432527	AW975028	Hs.102754 ESTs	3.1
	427773	AA412290	Hs.98124 ESTs	3.1
	441817	AW969706	Hs.293332 ESTs	3.1
	416812	H91010	Hs.44940 ESTs	3.1
	417958	AA767382	Hs.193417 ESTs	3.1
15	407426	AF129533	gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921 ESTs	3.1
	418037	AI990212	Hs.86447 ESTs	3.1
	419197	N48921	Hs.27441 KIAA1615 protein	3.1
	420179	N74530	Hs.21168 ESTs	3.1
20	436295	N73895	gb:za62d06.s1 Soares fetal liver spleen	3.1
	405548		Target Exon	3.1
	423595	R82826	Hs.220702 ESTs	3.1
	412533	AA679863	Hs.69606 ESTs	3.1
	434072	H70854	Hs.283059 Homo sapiens PRO1082 mRNA, complete cds	3.1
25	405264		NM_030813*:Homo sapiens suppressor of po	3.1
	410869	AW808361	gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	425354	U62027	Hs.155935 complement component 3a receptor 1	3.1
	441492	AI149998	Hs.146346 ESTs	3.1
	447078	AW885727	Hs.9914 ESTs	3.1
30	435021	AA922192	Hs.54709 ESTs	3.0
	408832	AW085690	Hs.63428 ESTs, Weakly similar to Z195_HUMAN ZINC	3.0
	450580	N40087	ESTs	3.0
	432319	AW510770	Hs.128386 ESTs	3.0
	453713	R20640	Hs.79133 cadherin 8, type 2	3.0
35	445784	AI253155	Hs.146065 ESTs	3.0
	416642	T96118	Hs.226313 ESTs	3.0
	418948	AI217097	gb:gd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997 ESTs	3.0
	439182	AF086030	Hs.21621 hypothetical protein DKFZp762O076	3.0
40	404995		ENSP00000251890*:Monocytic leukemia zinc	3.0
	444794	AI419991	Hs.145225 ESTs	3.0
	443634	H73972	Hs.134460 ESTs	3.0
	420133	AA426117	Hs.155543 ESTs	3.0
	407829	AA045084	Hs.29725 hypothetical protein FLJ13197	3.0
45	426743	AA383833	Hs.245022 ESTs	3.0
	442326	H92962	Hs.124813 hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016 ESTs	3.0
	454096	AW062757	gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	419622	AA452054	Hs.119338 ESTs	3.0
50	449745	AI668593	gb:yl38a05.x5 Soares breast 3NbHBst Homo	3.0
	428412	AA428240	Hs.126083 ESTs	3.0
	428200	AI039624	Hs.98388 ESTs	3.0
	414951	AW794931	Hs.100861 hypothetical protein FLJ14600	3.0
	431869	AA521136	Hs.190176 ESTs	3.0
55	451391	AA017410	Hs.40568 ESTs	3.0
	452959	AI933416	Hs.189674 ESTs	3.0

TABLE 66B

60	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
65	Pkey <sub>i</sub>	CAT Number	Accession	
	410790	1221131_1	AW803357 AW803423 AW812233 R06814	
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934	
			AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739	
			AW808704 AW808558 AW808714 AW808420 AW8	
70	411436	1245660_1	AW846433 AW846159 AW846377 AW846528	
	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069	
			AW848905 AW848214	
	412988	1342150_1	BE046680 BE046738 BE044958	
75	413081	1348563_1	BE064415 BE064430 BE064448	
	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925	
	416009	1566379_1	Z43062 R13213 H14422	
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043	
	420111	190755_1	AA255652 AA280911 AW967920 AA262684	
80	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280	
	424200	236595_1	AA337221 AA336756 AW966196	
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564	
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912	

428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438
		AI092404 AI085630 AA731340
430535	319643_1	AW968485 AW968670 AA480922 BE350425
432765	353907_1	AJ003429 AJ003367 AA564825
433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
434763	392847_1	AA648618 AW974389 H51771
436295	41733_1	N73895 AJ001872
439092	468554_1	AA830149 AW978407 M85983 AW503637
439306	47088_1	BE220199 W01813 AF086118 N70760 BE221405
440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
442481	543588_1	N99828 BE079873 AI110738 AF074645
445432	63943_1	AV653771 BE089370
448044	747196_1	AI458682 H24240 R14537 R18426 AW867082
449570	81018_1	AA001793 AA001871
449745	814534_1	AI668593 AI820774 R86205 H39971 H22177 H26241
450317	831956_1	AI692689 R14223 R18395
450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
		AA164518 AA730973 W00417 W65303
450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
452462	918580_1	BE173515 BE173560 AI902860
453682	977454_1	T79703 T96307 AL079725
454037	996287_1	AW998716 AW022148 N68020
454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
454457	1207274_1	AW753456 AW753036 AW854868 AW854862
454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
454860	1237732_1	AW835767 AW835537 BE160187
454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
455067	1252050_1	AW854538 AW854418 AW854412
455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
457374	328758_1	AA493662 AW897396 BE154814
458912	823104_1	AI911066 AI933734 AI680888 AJ003599

TABLE 66C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277595
400746	7329328	Minus	147703-147896
401132	8705350	Minus	85679-85795
402145	8018280	Plus	113086-114800
403242	7637817	Minus	11297-12511
403481	9965004	Plus	93496-93633
403510	7652047	Plus	61866-62027
403667	6850483	Minus	1344-1442,1545-1697
404003	8655948	Plus	198349-199096
404561	9795980	Minus	69039-70100
404592	9943965	Minus	39067-39225
404848	8248647	Minus	23955-24034,25143-25264
404967	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28556-28684
405321	3419846	Minus	44654-45210
405348	2914717	Minus	43310-43462
405510	7630909	Minus	101028-101174
405548	1532158	Plus	11552-11686

TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	65.0
	432441	AW292425	Hs.163484	ESTs	56.0
	446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
	400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	48.1
10	414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
	419526	AI821895	Hs.193481	ESTs	35.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
15	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
	400292	AA250737	Hs.72472	BMP-R1B	28.8
	400287	S39329	Hs.181350	kallikrein 2, prostatic	28.8
20	425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
	415539	AI733881	Hs.72472	BMP-R1B	27.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	25.5
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
	407168	R45175	Hs.117183	ESTs	24.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
	428336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
30	403047			NM_005656*:Homo sapiens transmembrane pr	23.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
	407709	AA456135	Hs.23023	ESTs	21.5
	401424			NM_001172:Homo sapiens arginase, type II	20.6
35	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
	434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
	415989	AI267700		ESTs	17.9
	437052	AA861697	Hs.120591	ESTs	17.8
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
40	431548	AI834273	Hs.9711	novel protein	16.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	16.5
	413597	AW302885	Hs.117183	ESTs	16.1
45	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	15.3
	407122	H20276	Hs.31742	ESTs	15.1
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
	426501	AW043782	Hs.293616	ESTs	13.9
	428898	AB033070	Hs.194408	KIAA1244 protein	13.7
	418961	AW967646	Hs.23023	ESTs	13.3
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	13.2
55	418848	AI820961	Hs.193465	ESTs	13.1
	428398	AI249368	Hs.98558	ESTs	13.0
	429220	AW207206		ESTs	12.7
	401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
60	419078	M93119	Hs.89584	insulinoma-associated 1	12.3
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.4
	429918	AW873986	Hs.119383	ESTs	11.3
65	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	412446	AI768015		ESTs	11.1
	433404	T32982		ESTs	10.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	10.4
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
	418278	AI088489	Hs.83937	hypothetical protein	10.3
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	10.2
75	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	10.1
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	10.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	10.0
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	9.8
	437718	AI927288	Hs.196779	ESTs	9.8
80	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
	453160	AI263307		H2B histone family, member L	9.7
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
	450325	AI935862	Hs.91973	ESTs	9.6
	434170	AA626509	Hs.122329	ESTs	9.6
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	9.6

	447033	AI357412	Hs.157601	ESTs	9.5
	401747			Homo sapiens keratin 17 (KRT17)	9.3
	434423	NM_006769	Hs.3844	LIM domain only 4	9.3
5	411887	AW182924	Hs.128790	ESTs	9.2
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	9.2
	415263	AA948033	Hs.130853	ESTs	9.2
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
	421896	N62293	Hs.45107	ESTs	9.1
10	432101	AI918950	Hs.123642	EphA3	9.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	8.9
	420218	AW958037		ribosomal protein L4	8.8
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
15	424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	8.5
	446100	AW957109	Hs.13804	hypothetical protein dJ462O23.2	8.5
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.5
20	416182	NM_004354	Hs.79069	cyclin G2	8.5
	431542	H63010	Hs.5740	ESTs	8.4
	447397	BE247676	Hs.18442	E-1 enzyme	8.3
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	8.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	8.1
25	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
	451684	AF216751	Hs.26813	CDA14	8.1
	437124	AA554458		KIAA0666 protein	8.0
	416239	AL038450	Hs.48948	ESTs	8.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
30	424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
	428728	NM_016625	Hs.191381	hypothetical protein	7.9
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.8
	442049	AA310393	Hs.190044	ESTs	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
35	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
	443180	R15875	Hs.258576	claudin 12	7.5
	433285	AW975944	Hs.237396	ESTs	7.5
	410870	U81599	Hs.66731	homeo box B13	7.4
	418836	AI655499	Hs.161712	ESTs	7.4
40	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
	431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	7.3
	432586	AA568548		ESTs	7.3
45	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
	435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.3
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
	426108	AA622037	Hs.166468	programmed cell death 5	7.1
	433323	AA805132	Hs.159142	ESTs	7.1
50	423349	AF010258	Hs.127428	homeo box A9	7.0
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
55	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
	418601	AA279490	Hs.86368	calmegin	6.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	6.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	6.8
	425465	L18964	Hs.1904	protein kinase C, iota	6.6
60	450377	AB033091		KIAA1265 protein	6.6
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	6.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	6.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	6.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
65	440774	AI420611	Hs.153934	ESTs	6.5
	413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
70	451027	AW519204	Hs.40808	ESTs	6.4
	436063	AK000028		ribosomal protein S24	6.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
75	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.2
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.1
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	6.1
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
80	448045	AJ297436	Hs.20166	prostate stem cell antigen	6.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.0
	433517	AW022133	Hs.189838	ESTs	6.0
	424036	AA770688		H2A histone family, member L	5.9

	420092	AA814043	Hs.88045	ESTs	5.9
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.8
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
5	418666	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	5.8
	450244	AA007534	Hs.125062	ESTs	5.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
	451952	AL120173	Hs.301663	ESTs	5.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
10	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	5.7
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	5.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
	415621	AI648602	Hs.55468	ESTs	5.7
15	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	5.5
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.4
20	425211	M18667	Hs.1867	progastricin (pepsinogen C)	5.4
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.4
	410762	AF226053	Hs.66170	HSKM-B protein	5.4
	440594	AW445167	Hs.126036	ESTs	5.4
25	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
	447805	AW627932	Hs.302421	gemin4	5.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
	453308	AW959731	Hs.323099	ESTs	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
30	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.2
	404632			NM_022490:Homo sapiens hypothetical prot	5.1
	450861	AI523898	Hs.17617	ESTs	5.1
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.1
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.1
35	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
	410037	AB020725	Hs.58009	KIAA0918 protein	5.1
	410240	AL157424	Hs.61289	synaptojanin 2	5.0
	403046			NM_005656*:Homo sapiens transmembrane pr	5.0
	419647	AA348947	Hs.91816	hypothetical protein	5.0
40	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	5.0
	450164	AI239923	Hs.63931	ESTs	5.0
	417318	AW953937	Hs.240845	ESTs	4.9
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
45	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
	433852	AI378329	Hs.126629	ESTs	4.9
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.8
50	441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
	453171	R76472	Hs.65646	ESTs	4.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	4.8
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	4.8
	419440	AB020689	Hs.90419	KIAA0882 protein	4.8
55	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.8
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
	421685	AF189723	Hs.105778	ATPase, Ca transporting, type 2C, member	4.7
60	431724	AA514535	Hs.283704	ESTs	4.7
	423242	AL039402	Hs.125783	DEME-6 protein	4.7
	434485	AI623511	Hs.118567	ESTs	4.7
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	4.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	4.6
65	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.6
	439735	AI635386	Hs.142846	hypothetical protein	4.6
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
70	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
	426006	R49031	Hs.22627	ESTs	4.5
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.5
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.5
75	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
	423583	AL122055	Hs.129836	KIAA1028 protein	4.4
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.4
80	429467	NM_004477	Hs.203772	FSHD region gene 1	4.4
	451752	AB032997		KIAA1171 protein	4.3
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.3
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.3
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
	427308	D26067	Hs.174905	KIAA0033 protein	4.3
	435706	W31254	Hs.7045	GL004 protein	4.3
5	416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	4.2
	410076	T05387	Hs.7991	ESTs	4.2
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.2
10	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
	442501	AA315267	Hs.23128	ESTs	4.2
	436761	AI817776	Hs.236557	ESTs	4.2
	420380	AA640891	Hs.102406	ESTs	4.2
	436556	AI364997	Hs.7572	ESTs	4.2
15	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
	446416	AV658299	Hs.163959	ESTs	4.2
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.2
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.1
20	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.1
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	4.1
	408418	AW963897	Hs.44743	KIAA1435 protein	4.1
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.1
25	432363	AA534489		gb:nf76g11.s1 NCL_CGAP_Co3 Homo sapiens	4.1
	447574	AF162666	Hs.18895	lousled-like kinase 1	4.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.0
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.0
	444108	R55784	Hs.140942	ESTs	4.0
30	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.0
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
35	438825	BE327427	Hs.79953	ESTs	4.0
	433233	AB040927	Hs.301804	KIAA1494 protein	4.0
	415276	U88666	Hs.78353	SFRS protein kinase 2	4.0
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
	407819	R42185		ESTs	4.0
40	450402	BE218027	Hs.89969	ESTs	4.0
	432527	AW975028	Hs.102754	ESTs	4.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.9
45	432435	BE218886	Hs.282070	ESTs	3.9
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	3.9
	411031	W37943	Hs.34892	KIAA1323 protein	3.9
50	429259	AA420450	Hs.292911	Plakophilin	3.9
	407813	AL120247	Hs.40109	KIAA0872 protein	3.9
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.9
	417958	AA767382	Hs.193417	ESTs	3.9
	427176	AW381569	Hs.40334	ESTs	3.9
55	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.8
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.8
	432675	AI791855		ESTs	3.8
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.8
	427479	BE410092	Hs.178471	KIAA0798 gene product	3.8
60	443162	T49951	Hs.9029	DKFZP434G032 protein	3.8
	413950	AA249096	Hs.32793	ESTs	3.8
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.8
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	3.8
65	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.8
	447620	AW290951		ESTs	3.8
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.8
70	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8
	459284	AF155660	Hs.300496	mitochondrial solute carrier	3.8
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	3.7
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	3.7
75	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.7
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.7
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.7
	453469	AB014533	Hs.33010	KIAA0633 protein	3.7
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	3.7
80	422072	AB018255	Hs.111138	KIAA0712 gene product	3.7
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420522	AW957137	Hs.98541	hypothetical protein	3.6
	408833	AW612232	Hs.254835	ESTs	3.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.6



	456177	NM_012391	Hs.79414	prostate epithelium-specific Els transcr	3.6
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate synth	3.6
	422424	AI186431	Hs.296638	prostate differentiation factor	3.6
5	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.6
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.6
	421887	AW161450	Hs.109201	CGI-86 protein	3.6
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
10	412520	AA442324	Hs.795	H2A histone family, member O	3.6
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.6
	441224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.5
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
15	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.5
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.5
20	428055	AA420564	Hs.101760	ESTs	3.5
	418827	BE327311	Hs.47166	HT021	3.5
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	3.5
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
25	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
	439671	AW162840	Hs.6641	kinesin family member 5C	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.4
30	443884	N20617	Hs.194397	leptin receptor	3.4
	403752			NM_002753*:Homo sapiens mitogen-activate	3.4
	427723	AI355260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
35	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.4
	433647	AA603367	Hs.222294	ESTs	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
40	437617	AI026701	Hs.5716	KIAA0310 gene product	3.3
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.3
	435655	AW105663	Hs.6947	HSPC069 protein	3.3
45	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
50	420568	F09247	Hs.247735	protocadherin alpha 10	3.3
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	3.3
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
55	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
	409960	BE261944		hexokinase 1	3.3
	433891	AA613792		gb:no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
60	419972	AL041465	Hs.182982	golgin-67	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.3
65	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.3
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
	414922	D00723		glycine cleavage system protein H (amino	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26691	ESTs	3.2
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.2
70	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
	401519			C15000476*:gil12737279[ret]XP_012163.1	3.2
75	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.2
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.2
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upt3, variant A	3.2
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
80	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
	439593	BE073597	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	AI249502	Hs.29669	ESTs	3.2
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2

5	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	425810	AI923627	Hs.31903	ESTs	3.2
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
10	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
	414222	AL135173		sorbitol dehydrogenase	3.1
	419749	X73608	Hs.93029	sparc/osteoneclin, cwcv and kazal-like d	3.1
15	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.1
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.1
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
20	436489	AJ272269	Hs.121429	zinc-binding protein Rbcc728	3.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.1
	445943	AW898533	Hs.181574	ESTs	3.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
25	432426	AW973152	Hs.31050	ESTs	3.1
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.1
	423453	AW450737	Hs.128791	CGI-09 protein	3.1
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.1
30	436278	BE396290	Hs.5097	synaptogyrin 2	3.1
	432908	AI861896		ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.1
35	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	409757	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
	434293	NM_004445	Hs.3796	EphB6	3.1
	410001	AB041036	Hs.57771	kallikrein 11	3.1
40	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278962	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
	448807	AI571940	Hs.7549	ESTs	3.1
45	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1
	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	3.0
50	429638	AI916662	Hs.211577	kineclin 1 (kinesin receptor)	3.0
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
55	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
	449459	BE546846	Hs.195048	ESTs	3.0
60	438523	H66220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.0
	429966	BE081342	Hs.283037	HSPC039 protein	3.0
65	412652	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	3.0
	436032	AA150797	Hs.109276	latexin protein	3.0
70	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
	415172	AF079529	Hs.78106	phosphodiesterase 8B	2.9
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
75	413142	M81740	Hs.75212	ornithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
	439609	AW971945	Hs.293236	ESTs	2.9
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
80	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420061	AW024937	Hs.29410	ESTs	2.9
	431663	NM_016569	Hs.267182	TBX3-iso protein	2.9
	417622	AW298163	Hs.82318	WAS protein family, member 3	2.9
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI632278	Hs.195922	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

5	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	2.9
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	2.9
10	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	2.9
	413125	BE244589	Hs.75207	glyoxalase I	2.9
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.9
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
15	437296	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.9
	445109	AF039916	Hs.12330	ecNucleoside triphosphate diphosphohyd	2.9
	423551	AA327598	Hs.89633	ESTs	2.9
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	2.9
20	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bromodomain-containing 1	2.8
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	2.8
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	2.8
25	444367	H54892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-melastatic cells 4, protein expresse	2.8
	418166	AI754416		Cdc42 effector protein 3	2.8
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
30	413550	W03011	Hs.306881	MSTP043 protein	2.8
	426170	BE161065	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
	425320	U29344	Hs.83190	fatty acid synthase	2.8
	431631	AA548906	Hs.122244	ESTs	2.8
35	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	2.8
40	439778	AL109729	Hs.99364	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
	450546	AA010200	Hs.175551	ESTs	2.7
	431674	AA098901	Hs.301642	G-protein coupled receptor	2.7
45	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	443181	AI039201	Hs.283316	ESTs	2.7
	448913	AA194422	Hs.22564	myosin VI	2.7
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	2.7
50	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	2.7
	434747	AA837085		ESTs	2.7
55	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	2.7
	447147	AA910363	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	2.7
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.7
60	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	2.7
	438157	AW137011	Hs.49576	ESTs	2.7
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	2.7
65	409648	AW451449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
	400301	X03635	Hs.1657	estrogen receptor 1	2.7
	453390	AA862496	Hs.28482	ESTs	2.7
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
70	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	2.7
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	2.7
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	2.7
75	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.7
	409650	T08490	Hs.288969	HSCARG protein	2.7
	452707	AI093823	Hs.45070	ESTs	2.7
80	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	2.7
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.7
	406627	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6

	440695	AW088363	Hs.246240	ESTs	2.6
	416941	BE000150	Hs.48778	niban protein	2.6
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.6
5	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	2.6
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
	401197			ENSP00000229263*:HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 f1s, clone H	2.6
	410297	AA148710		lumican	2.6
10	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.6
	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
15	408157	AA047685	Hs.62946	ESTs	2.6
	420805	L10333	Hs.99947	reticulon 1	2.6
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586L2022 (f	2.6
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	2.6
20	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
	425174	D87450	Hs.154978	KIAA0261 protein	2.6
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75360	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
25	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	2.6
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406670	W79632	Hs.256301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
30	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
	449518	BE395253	Hs.30861	ESTs	2.6
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.6
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.6
35	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.6
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.6
	434672	AW294020	Hs.117721	ESTs	2.6
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.6
	452576	AB023177	Hs.29900	KIAA0960 protein	2.6
40	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.6
	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
45	451040	AA324743	Hs.40808	ESTs	2.6
	445636	AW105401		ribosomal protein L29	2.6
	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.6
50	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.6
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	2.5
	406789	AI041403		ribosomal protein L29	2.5
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.5
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.5
55	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.5
	436165	AI373544	Hs.331328	intermediate filament protein syncollin	2.5
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.5
	452827	AI571835	Hs.55468	ESTs	2.5
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
60	431108	AA991508	Hs.105317	ESTs	2.5
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA826425	Hs.192375	ESTs	2.5
65	421091	W22821		ribosomal protein L26	2.5
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.5
	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.5
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.5
70	431615	AW295859	Hs.235860	ESTs	2.5
	433037	NM_014158	Hs.279938	HSPC067 protein	2.5
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
	450628	AW382884	Hs.204715	ESTs	2.5
75	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.5
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
80	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.5
	416737	AF154335	Hs.79691	LIM domain protein	2.5
	414869	AA157291	Hs.21479	ubiquitin 1	2.5
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.5
407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.5
414556	AW975063	Hs.343443	ribosomal protein L36	2.5
446911	N27605	Hs.16492	DKFZP564G2022 protein	2.5
435126	AI393666	Hs.42315	p10-binding protein	2.5
421866	M24470	Hs.1435	guanosine monophosphate reductase	2.5
426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.5
447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.5
443837	AI984625	Hs.9884	spindle pole body protein	2.5
421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
435021	AA922192	Hs.73962	ESTs	2.5
435750	AB029012	Hs.4990	KIAA1089 protein	2.5
435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.5
407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
425976	C75094	Hs.334514	NG22 protein	2.5
449458	AI805078	Hs.208261	ESTs	2.5
428013	AF151020	Hs.181444	hypothetical protein	2.5
424369	R87622	Hs.26714	KIAA1831 protein	2.5
431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
452779	AA418775	Hs.47234	ESTs	2.5
433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.5
438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.5
427515	T79526	Hs.179516	integral type I protein	2.5
418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.5

TABLE 67B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259
412446	63467_1	BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815 BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
433404	7392_1	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336
449625	249224_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AM93770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
453160	6028_5	AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422
432586	6633_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548
438869	52134_1	AF075009 R63109 R63068
450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164
436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
424036	6226_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465 AL531028 BG437151 BE868021 AA179427
450203	19009_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024796 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192
451752	10408_5	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295901 BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333 AW970240 AA534489 AW970323
432363	1234917_1	

5	422890	61426_1	AK057805 AW162343 AI190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 BI792383 BF056928 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI366013 AI867923 BG911906 D81142 C15616 AI538697 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 AI7038 H10064 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
10	417379 407819	1610005_1 7392_2	AA196390 AA507837 AA196468 AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185 AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706664 BE706539 BE153177 BF084925 AI133779 AW961788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826 AW973834 AI791932 AI791855 AI732640 AA558833 AA559897 AI821610 AI973051 AI400921 AI796154 AW241817 AW290951 NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AI602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA4456385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435520 AI356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677 BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296868 AI268977 AI168133 BM352065 AI262769 BF941976 AI056920 AA481861 BF763697 AI1565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111012 AA908246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AI154257 AW182329 AA613792 T05304 AW858385 BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI695677 AI562079 AI700926 AI470561 BF063058 AW196387 AU132984 BI064046 AI970157 R02122 H55924 AI521721 AA808206 AA725223 AI766003 AW339821 AA805951 AI287969 AW664827 BC021085 AL527872 AI526296 AL557087 BI255090 AU143499 AL560356 BG823170 BE736988 AU141388 AL580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726986 AL564735 BE155962 BE155979 BF741679 H67776 H55234 H89665 AW117774 AW274435 L29008 NM_003104 U07361 BF002824 BI222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW069877 AW015214 AI948718 BE219706 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI204449 AW275385 AI336950 BE501521 BF740566 AA311404 AA384639 BI772535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AL564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AL581093 AU158964 AU158917 AI282516 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 AI284986 AA857926 BF372568 AA570172 AI753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N55172 AW013929 AI826274 AI871237 C75260 AA934846 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AU106667 AU159238 AU1282517 AA406317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW438877 AI800550 AW328268 AI244886 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 N70983 H44325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AA706106 AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635 AF119847 AA437261 AA436987 AI132965 AF150424 AI861896 AA570057 AV738855 AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981 AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI376957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422 AK055915 BE867252 AI523348 AA765350 BF446858 Z43675 R19529 AI133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA376592 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI096810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA249732 AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974 AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102 AA602964 AA609200 AW976537 AI033582 AA837085 AA745261 AA648395 BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355 AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA661791 BM474307 BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893 AI989299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299 R70463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI624611 BG271780 AI497723 H88862 D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z39807 BF954386 NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099 AL538039 BG703131 BE255806 BF805256 F12128 AL1566773 BI828686 BF761480 AI204971 BG818818 BI199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AI534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833
70	407192 434747 410297	2200202_1 117643_1 2990_1	
75	424339	50559_1	
80			

445636 8561\_5 BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310  
AA090672

419175 35068\_1 AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331  
AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA365626  
Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618  
AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AI037576 AA534314 BE814964 BE973713 N49493 BE006634  
BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572  
AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403  
F02090 AI187299 AI609644 Z40516 AW952314

10 441128 20932\_1 BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071  
BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706  
N90525 AW973623 AI359627 BG674574 BE903322

15 406789 0\_0 AI041403 Z49148  
421091 24941\_2 AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161  
BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358396  
AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AL568301 AL567278 BI522445 BI754384  
BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116  
BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842  
H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896

20 400263 18977\_1 Z11692 X51466 NM\_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935  
BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095  
BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241  
BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685  
BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671  
BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206  
BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964  
BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 67C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA  
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401519	6649315	Plus	157315-157950
401785	7249190	Minus	165776-165996, 166189-166314, 166408-16656
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833, 5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 995 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 995 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UnigenelD: Unigene number  
Unigene Title: Unigene gene title  
R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	85.5
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	68.6
446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cali	65.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	AI821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fls, clone PL	44.9
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	40.9
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
5	400292	AA250737	Hs.72472	BMP-R1B	31.4
	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	31.4
	428819	AL135623	Hs.193914	KIAA0575 gene product	31.2
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	30.3
10	407168	R45175	Hs.117183	ESTs	29.6
	400287	S39329	Hs.181350	kallikrein 2, prostatic	29.6
	415539	AI733881	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.8
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	28.1
15	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.5
	403047			NM_005656*:Homo sapiens transmembrane pr	27.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	25.7
	428336	AA503115	Hs.183752	microseminoprotein, beta-	25.0
	401424			NM_001172:Homo sapiens arginase, type II	24.9
20	407709	AA456135	Hs.23023	ESTs	24.7
	407122	H20276	Hs.31742	ESTs	24.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	23.2
	415989	AI267700		ESTs	23.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.7
25	437052	AA861697	Hs.120591	ESTs	22.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	22.5
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	21.2
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	20.8
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	20.5
30	427958	AA418000	Hs.98280	potassium intermediate/small conductance	20.5
	431548	AI834273	Hs.9711	novel protein	19.8
	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.4
	426501	AW043782	Hs.293616	ESTs	19.3
	413597	AW302885	Hs.117183	ESTs	18.9
35	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	18.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	18.0
	429220	AW207206		ESTs	17.9
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.6
	418961	AW967646	Hs.23023	ESTs	17.3
40	428898	AB033070	Hs.194408	KIAA1244 protein	17.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.8
	428398	AI249368	Hs.98558	ESTs	16.3
	419078	M93119	Hs.89584	insulinoma-associated 1	15.8
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.4
45	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	15.2
	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
	447033	AI357412	Hs.157601	ESTs	14.9
	452594	ALU076405	Hs.29981	solute carrier family 26 (sulfate transp	14.7
50	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	14.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.4
	418848	AI820961	Hs.193465	ESTs	14.3
	429918	AW873986	Hs.119383	ESTs	14.2
55	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
	418278	AI088489	Hs.83937	hypothetical protein	14.1
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	13.9
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	13.3
	432101	AI918950	Hs.123642	EphA3	13.3
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	13.1
60	412446	AI768015		ESTs	12.7
	437718	AI927288	Hs.196779	ESTs	12.6
	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	12.6
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.5
65	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.5
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	12.4
	453160	AI263307		H2B histone family, member L	12.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	12.1
70	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	12.1
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	11.9
	424692	AA429834	Hs.151791	KIAA0092 gene product	11.7
	415263	AA948033	Hs.130853	ESTs	11.3
75	416182	NM_004354	Hs.79069	cyclin G2	11.3
	420218	AW958037		ribosomal protein L4	11.3
	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.2
80	450325	AI935962	Hs.91973	ESTs	11.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	11.1
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	11.0



5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_006769	Hs.3844	LIM domain only 4	10.6
	434170	AA626509	Hs.122329	ESTs	10.6
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.5
10	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
	401747			Homo sapiens keratin 17 (KRT17)	10.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
15	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247676	Hs.18442	E-1 enzyme	10.0
	433285	AW975944	Hs.237396	ESTs	10.0
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	9.8
20	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.190044	ESTs	9.6
	443180	R15875	Hs.258576	claudin 12	9.5
	406964	M21305		FGFES predicted novel secreted protein	9.5
25	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
	451684	AF216751	Hs.26813	CDA14	9.5
	440594	AW445167	Hs.126036	ESTs	9.4
30	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	calmegin	9.3
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
	437124	AA554458		KIAA0666 protein	9.2
	428728	NM_016625	Hs.191381	hypothetical protein	9.2
35	438869	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.9
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
	418836	AI655499	Hs.161712	ESTs	8.8
40	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofe	8.7
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	8.7
45	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	8.7
	425465	L18964	Hs.1904	protein kinase C, iota	8.5
	416239	AL038450	Hs.48948	ESTs	8.5
	436962	AW377314	Hs.5364	DKFZP564I052 protein	8.4
50	450164	AI239923	Hs.63931	ESTs	8.4
	452744	AI267652	Hs.245107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AI420611	Hs.153934	ESTs	8.3
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
	410870	U81599	Hs.66731	homeo box B13	8.3
55	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	8.2
	423349	AF010258	Hs.127428	homeo box A9	8.1
60	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.1
	432586	AA568548		ESTs	8.0
	426108	AA622037	Hs.166468	programmed cell death 5	8.0
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	8.0
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	7.9
65	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kallikrein 4 (prostase, enamel matrix, p	7.7
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
	433323	AA805132	Hs.159142	ESTs	7.7
70	451952	AL120173	Hs.301663	ESTs	7.7
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
	420092	AA814043	Hs.88045	ESTs	7.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	7.6
75	440749	W22335	Hs.7392	hypothetical protein MGC3199	7.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.4
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	7.4
80	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AI648602	Hs.55468	ESTs	7.4
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
	450244	AA007534	Hs.125062	ESTs	7.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AI623511	Hs.118567	ESTs	7.2

5	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	7.1
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
	436063	AK000028		ribosomal protein S24	7.0
10	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.9
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
	436476	AA326108	Hs.33829	bHLH protein DEC2	6.8
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
15	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	6.6
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
20	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0918 protein	6.5
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
	409648	AW451449	Hs.57749	ESTs	6.4
25	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.3
	404632			NM_022490:Homo sapiens hypothetical prot	6.3
30	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
	410762	AF226053	Hs.66170	HSKM-B protein	6.3
	436032	AA150797	Hs.109276	latexin protein	6.3
35	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	6.2
	424036	AA770688		H2A histone family, member L	6.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
40	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183161	ESTs	6.1
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	6.1
	432527	AW975028	Hs.102754	ESTs	6.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
45	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.0
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
	419647	AA348947	Hs.91816	hypothetical protein	6.0
50	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
	446416	AV658299	Hs.163959	ESTs	5.9
	407819	R42185		ESTs	5.9
55	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	5.9
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.9
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	5.8
	410240	AL157424	Hs.61289	synaptojanin 2	5.8
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	5.7
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.7
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	5.7
65	433852	AI378329	Hs.126629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	5.6
	419440	AB020689	Hs.90419	KIAA0882 protein	5.6
	435706	W31254	Hs.7045	GL004 protein	5.6
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
70	442409	BE208843	Hs.129544	hypothetical protein MGC15438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.6
	429638	AI916662	Hs.211577	kinectin 1 (kinesin receptor)	5.5
75	403046			NM_005656*:Homo sapiens transmembrane pr	5.5
	447805	AW627932	Hs.302421	gemin4	5.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	5.4
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
80	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	5.4
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	D26067	Hs.174905	KIAA0033 protein	5.4
	409151	AA306105		SEC22, vesicle trafficking protein (S. c	5.4
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.4
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88666	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
	417318	AW953937	Hs.240845	ESTs	5.3
5	429467	NM_004477	Hs.203772	FSHD region gene 1	5.3
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.2
10	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
	436420	AA443966	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
15	450832	AW970602	Hs.105421	ESTs	5.1
	448807	AI571940	Hs.7549	ESTs	5.1
	420568	F09247	Hs.247735	protocadherin alpha 10	5.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
20	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	452576	AB023177	Hs.29900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
25	407103	AA424881	Hs.256301	hypothetical protein MGC13170	5.0
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
30	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
	444108	R55784	Hs.140942	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.9
35	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.9
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.9
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.9
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.9
40	442501	AA315267	Hs.23128	ESTs	4.8
	439735	AI635386	Hs.142846	hypothetical protein	4.8
	451752	AB032997		KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
45	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	4.8
	433313	W20128	Hs.296039	ESTs	4.8
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.8
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	4.7
50	447574	AF162666	Hs.18895	tousled-like kinase 1	4.7
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.7
	411031	W37943	Hs.34892	KIAA1323 protein	4.7
55	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.7
	441224	AU076964	Hs.7753	calumenin	4.7
	407813	AL120247	Hs.40109	KIAA0872 protein	4.7
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.7
60	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.7
	414922	D00723		glycine cleavage system protein H (amino	4.7
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.79953	ESTs	4.7
	425174	D87450	Hs.154978	KIAA0261 protein	4.7
65	420380	AA640891	Hs.102406	ESTs	4.7
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.7
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.6
	436761	AI817776	Hs.236557	ESTs	4.6
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.6
70	404922			NM_003071:Homo sapiens SWI/SNF related,	4.6
	436556	AI364997	Hs.7572	ESTs	4.6
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	4.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.6
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.5
75	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.5
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.5
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.5
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.5
80	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.5
	453390	AA862496	Hs.28482	ESTs	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	4.5

	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.4
5	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.4
	417958	AA767382	Hs.193417	ESTs	4.4
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
15	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	4.3
	429259	AA420450	Hs.292911	Plakophilin	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	4.3
	459284	AF155660	Hs.300496	mitochondrial solute carrier	4.3
20	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.3
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
25	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	4.3
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
	450402	BE218027	Hs.89969	ESTs	4.3
	428055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.3
	432675	AI791855		ESTs	4.2
30	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
	445707	AI248720	Hs.114390	ESTs	4.2
	410297	AA148710		lumican	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
35	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
	447620	AW290951		ESTs	4.2
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.2
40	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	4.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	4.2
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	AI355260	Hs.279789	histone deacetylase 3	4.2
45	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	4.2
	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
50	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypothe	4.1
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	4.1
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.1
	427479	BE410092	Hs.178471	KIAA0798 gene product	4.1
55	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	4.1
	449459	BE546846	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
60	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	412520	AA442324	Hs.795	H2A histone family, member O	4.0
	448663	BE614599		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433647	AA603367	Hs.222294	ESTs	4.0
65	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	4.0
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014533	Hs.33010	KIAA0633 protein	4.0
70	418827	BE327311	Hs.47166	HT021	4.0
	446791	AI632278	Hs.195922	ESTs	4.0
	443884	N20617	Hs.194397	leptin receptor	4.0
	416857	AA188775	Hs.292453	ESTs	4.0
	401519			C15000476*.gil[12737279]ref[XP_012163.1]	4.0
75	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.0
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.9
	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AW105663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
80	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.9
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ubiquitin 1	3.9
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
	435021	AA922192	Hs.73962	ESTs	3.9
5	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
10	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421887	AW161450	Hs.109201	CGI-86 protein	3.8
	434614	AI249502	Hs.29669	ESTs	3.8
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.8
15	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.8
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.8
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
20	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	AI186431	Hs.296638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
25	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.8
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440695	AW088363	Hs.246240	ESTs	3.8
	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
30	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
	411190	AA306342	Hs.69171	protein Kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
35	432426	AW973152	Hs.31050	ESTs	3.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	3.7
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	AI861896		ESTs	3.7
40	432800	BE391046	Hs.278962	AIM-1 protein	3.7
	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	AL041465	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kallikrein 11	3.7
	432205	AI806583	Hs.125291	ESTs	3.7
45	401197			ENSP00000229263*:HSPC213.	3.7
	420061	AW024937	Hs.29410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284192	ESTs	3.7
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
50	420805	L10333	Hs.99947	reticulon 1	3.7
	401866			Target Exon	3.7
	457183	H91882	Hs.118569	Dvl-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	3.7
55	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451945	BE504055	Hs.211420	ESTs	3.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.6
60	454229	AW957744	Hs.278469	lacrimal proline rich protein	3.6
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.6
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
65	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	3.6
	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.6
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
70	450649	NM_001429	Hs.25272	E1a binding protein p300	3.6
	436489	AJ272269	Hs.121429	zinc-binding protein Rbccc728	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	3.6
75	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
	427715	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.6
	403752			NM_002753*:Homo sapiens mitogen-activate	3.6
80	418559	AA225048	Hs.104207	ESTs	3.6
	438523	H66220	Hs.278177	ESTs	3.6
	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	3.5
5	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
	433891	AA613792		gb.no97h03.s1 NCI_CGAP_Pr2 Homo sapiens	3.5
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434672	AW294020	Hs.117721	ESTs	3.5
10	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.5
	434970	AW272262	Hs.225767	ESTs	3.5
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.5
	445943	AW898533	Hs.181574	ESTs	3.5
15	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.5
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
20	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
	436087	BE300296	Hs.5054	CGI-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.5
25	439609	AW971945	Hs.293236	ESTs	3.5
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	3.5
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
30	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
	442323	AW016669	Hs.29190	ESTs	3.5
	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104336	hypothetical protein	3.5
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
35	450628	AW382884	Hs.204715	ESTs	3.4
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.4
40	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.4
	434293	NM_004445	Hs.3796	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
45	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	3.4
	411078	AI222020	Hs.182364	CocoaCrisp	3.4
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
50	431674	AA098901	Hs.301642	G-protein coupled receptor	3.4
	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.4
55	452295	BE379936	Hs.28866	programmed cell death 10	3.4
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
	439593	BE073597	Hs.124863	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.4
60	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412652	AI801777		ESTs	3.3
	415172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
65	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	3.3
	425010	T16837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
	442064	AI422867	Hs.88594	ESTs	3.3
70	431663	NM_016569	Hs.267182	TBX3-iso protein	3.3
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	3.3
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	3.3
75	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.3
	436278	BE396290	Hs.5097	synaptogyrin 2	3.3
	424560	AA158727	Hs.150555	protein predicted by clone 23733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418166	AI754416		Cdc42 effector protein 3	3.3
80	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.2
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase I	3.2

	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.2
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	3.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	3.2
5	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	3.2
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	3.2
	422173	BE385828	Hs.250619	phorbolin-like protein MDS019	3.2
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	3.2
10	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.2
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.2
	406214			NM_016371:Homo sapiens hydroxysteroid (1	3.2
15	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.2
	438714	AA814859	Hs.160074	ESTs	3.2
	433213	AW665130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	3.2
20	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	3.2
	437179	AA393508		serologically defined colon cancer antig	3.2
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.2
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.2
25	450546	AA010200	Hs.175551	ESTs	3.2
	409995	AW960597	Hs.129206	ESTs	3.2
	408739	W01556	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638:Homo sapiens hypothetical prot	3.2
30	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	3.1
	414341	D80004	Hs.75909	KIAA0182 protein	3.1
	423044	AA320829	Hs.97266	protocadherin 18	3.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
35	423551	AA327598	Hs.89633	ESTs	3.1
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
	413550	W03011	Hs.306881	MSTP043 protein	3.1
	431933	AI187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99364	putative transmembrane protein	3.1
40	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.1
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
	421254	AK001724	Hs.102950	coat protein gamma-cop	3.1
	424339	BE257148		endoglycan	3.1
45	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	3.1
	425320	U29344	Hs.83190	fatty acid synthase	3.1
	426170	BE161085	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.1
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	3.1
	417622	AW298163	Hs.82318	WAS protein family, member 3	3.1
50	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	433036	AA574091	Hs.105964	ESTs	3.1
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.1
	408380	AF123050	Hs.44532	diubiquitin	3.1
55	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	3.1
	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.1
	437296	AA350994	Hs.20281	KIAA1700	3.1
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	3.1
60	448913	AA194422	Hs.22564	myosin VI	3.1
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.0
	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
65	437546	AW074836	Hs.173984	T-box 1	3.0
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
70	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	3.0
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406627	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
75	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	3.0
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	3.0
	431416	AA532718		ESTs	3.0
	431631	AA548906	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
80	434974	AA778711		eukaryotic translation initiation factor	3.0
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	3.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279938	HSPC067 protein	3.0

	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
5	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	3.0
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	3.0
	432810	AA863400	Hs.23054	ESTs	3.0
10	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.0
	445596	R89543	Hs.12942	vesicle trafficking protein	3.0
	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.0
15	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.0
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.9
	425920	AL049977	Hs.162209	claudin 8	2.9
	409927	T69981		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
20	447881	BE620886		GCN1 (general control of amino-acid synt	2.9
	439584	AA838114	Hs.221612	ESTs	2.9
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CGI-83 protein	2.9
25	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.9
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.9
30	429351	AK001490	Hs.200016	hypothetical protein FLJ10628	2.9
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
35	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.9
	428801	AW277121	Hs.254881	ESTs	2.9
	430462	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98806	hypothetical protein	2.9
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
40	418222	AI675881	Hs.86538	ESTs	2.9
	433009	AA761668		gb:nz24c08.s1 NCL_CGAP_GCB1 Homo sapiens	2.9
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.9
45	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371048	Hs.93758	H4 histone family, member H	2.9
	409650	T08490	Hs.288969	HSCARG protein	2.9
50	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas	2.9
	412719	AW016610		ESTs	2.9
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	439621	AI200281	Hs.123910	ESTs, Highly similar to B34087 hypothe	2.9
	437050	AA766420		ESTs	2.9
55	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
	416941	BE000150	Hs.48778	niban protein	2.9
	421694	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
60	436823	AW749865		ESTs, Weakly similar to I38022 hypothe	2.8
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	2.8
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
65	400860			Target Exon	2.8
	436165	AI373544	Hs.331328	intermediate filament protein syncoilin	2.8
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	2.8
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.8
70	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
	435703	AW630133	Hs.83313	GK003 protein	2.8
	431108	AA991508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40808	ESTs	2.8
	443837	AI984625	Hs.9884	spindle pole body protein	2.8
75	418196	AI745649	Hs.26549	KIAA1708 protein	2.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.8
80	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.8
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	2.8



	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467064	Hs.5740	ESTs	2.8
5	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
	452827	AI571835	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	2.8
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	2.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor , S. cerev	2.8
10	419286	AA236005	Hs.128764	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266619	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
15	440080	AW051597		ESTs	2.8
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	2.8
	431525	AA506656	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.8
20	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.8
	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41690	desmocollin 3	2.8
	442013	AA506476	Hs.10600	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
	453038	AW292415	Hs.20509	HBV pX associated protein-8	2.8
25	419175	AW270037		KIAA0779 protein	2.8
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75360	carboxypeptidase E	2.8
30	432651	AW973744	Hs.293100	ESTs	2.8
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
35	414556	AW975063	Hs.343443	ribosomal protein L36	2.8
	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.7
	440340	AW895503	Hs.125276	ESTs	2.7
40	410339	AI916499	Hs.298258	ESTs	2.7
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
45	410099	AA081630		KIAA0036 gene product	2.7
	422000	M30599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
	432745	AI821926		gb:n78f05.x5 NCL_CGAP_Pr3 Homo sapiens	2.7
50	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.7
	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rii-related antigen, integr	2.7
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	2.7
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.7
55	400263			Eos Control	2.7
	435750	AB029012	Hs.4990	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.7
	421709	AA159394	Hs.107056	CED-6 protein	2.7
	421077	AK000061	Hs.101590	hypothetical protein	2.7
60	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
65	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	2.7
	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW206942	Hs.253594	intron of: trichorhinophalangeal syndro	2.7
	420223	N27807		ribosomal protein L4	2.7
70	427515	T79526	Hs.179516	integral type I protein	2.7
	447673	AI823987	Hs.182285	ESTs	2.7
	411960	R77776	Hs.18103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613416	Hs.336425	Homo sapiens, clone MGC:17296, mRNA, com	2.7
75	441551	AA318224	Hs.296141	ESTs	2.7
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA806164	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.7
80	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
	432450	AI990739	Hs.158184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.7
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.7

	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.7
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.7
	431615	AW295859	Hs.235860	ESTs	2.7
5	418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.7
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.7
	438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
15	441094	U33819	Hs.7647	MYC-associated zinc finger protein (puri	2.7
	451356	AA748418	Hs.164577	ESTs	2.7
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2.7
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	2.7
20	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	2.7
	404913			NM_024408*:Homo sapiens Notch (Drosophil	2.7
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.7
	441054	AA913591		ESTs	2.6
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.6
25	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein Lsm8	2.6
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443666	AI458179	Hs.41528	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	2.6
30	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.6
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	2.6
35	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.6
	430341	NM_006348	Hs.239631	golgi transport complex 1 (90 kDa subuni	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
40	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	420164	AW339037	Hs.24908	ESTs	2.6
	443444	AW952619	Hs.17235	Homo sapiens clone TCCCIA00176 mRNA sequ	2.6
45	412774	AA120865	Hs.23136	ESTs	2.6
	445922	AI337316	Hs.147998	ESTs	2.6
	429925	NM_000786		cytochrome P450, 51 (lanosterol 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
50	417327	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famil	2.6
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
	408743	AL110246	Hs.47367	KIAA1785 protein	2.6
	434011	AW953437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.6
55	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	2.6
60	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.6
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	446258	AI283476	Hs.263478	ESTs	2.6
65	440191	AI990417		tubulin, beta 5	2.6
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
70	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	2.6
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.6
	416751	T48130	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	2.6
75	458946	AA009716	Hs.42311	ESTs	2.6
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.6
	449458	AI805078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	2.6
80	442336	AW340958	Hs.7572	ESTs	2.6
	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

5	436972	AA284679	Hs.25640	claudin 3	2.6
	426809	BE313114	Hs.29706	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
	457638	AI792670	Hs.144405	ESTs	2.6
	442821	BE391929	Hs.8752	transmembrane protein 4	2.5
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L36	2.5
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
10	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	2.5
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	2.5
15	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.5
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	456050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
20	414528	AA148950	Hs.188836	ESTs	2.5
	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-like	2.5
25	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	2.5
	408796	AA688292	Hs.170345	ESTs	2.5
	407627	AI419020	Hs.62620	chromosome 6 open reading frame 1	2.5
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthase	2.5
	415862	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.5
35	449500	AW956345	Hs.12926	ESTs	2.5
	457090	AL080243	Hs.180920	ribosomal protein S9	2.5
	445389	NM_016831	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
40	450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.5
	419430	AI878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA260722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	2.5
45	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40696	ESTs	2.5
	400262			Eos Control	2.5
50	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
	418039	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypotheti	2.5
	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.5
55	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
	431188	W05656	Hs.169755	ESTs	2.5
60	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437762	T78028	Hs.154679	synaptotagmin I	2.5
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.5
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.5
65	451585	AK001171	Hs.326422	hypothetical protein MGC4549	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.5
	446054	AB014537	Hs.13604	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
70	421026	AL047332	Hs.101067	GCN5 (general control of amino-acid synt	2.5
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 68B

75	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
80	Pkey	CAT Number	Accession	
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236	
	429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259	

449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
412446	63467_1	BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
433404	7392_1	BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433
453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336
420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
437124	59408_1	AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 NA9381 R49886 D61278 BI756612 AA508234 R49885 BF850422
438869	52134_1	AF075009 R63109 R63068
428342	6712_1	AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967
450203	19009_1	AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
432586	6633_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024796 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192
450377	12109_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548
436063	5483_1	AB033091 AI520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AI050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866
424036	6226_1	AI699181 N73808 H08164
407819	7392_2	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
409151	4123_1	NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465 AL531028 BG437151 BE868021 AA179427
422890	61426_1	AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185
451752	10408_5	NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA4456385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA34066 BG435520 AI356111 H00525 AV749060 BG944497 BG292031
432363	1234917_1	AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677
417379	1610005_1	AK057805 AW162343 AI190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 BI792383 BF056928 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735
414922	1563_2	AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW955110 AI366013 AI867923 BG911906 D081142 C15616 AL538697 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW540771 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
419733	7612_3	AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295901 BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333 AW970240 AA534489 AW970323
432675	1237917_1	AA196390 AA507837 AA196468
410297	2990_1	BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI695677 AL562079 AI700926 AI470561 BF063058 AW196387 AU132984 BI064046 AI970157 R02122 H55924 AI521721 AA808206 AA725223 AI766003
429163	1238297_1	AW339821 AA805951 AI287969 AW664827
447620	687223_1	AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706684 BE706539 BE153177 BF084925 AL133779 AW961788 AA659693 AA347970
407192	2200202_1	AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698
434194	62680_1	BE841554 BI045099 T84625 AW129678 BG770826
448663	16112_4	AW973834 AI791932 AI791855 AI732640 AA558833 AA559897 AI821610
429163	1238297_1	BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355
447620	687223_1	AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA661791 BM474307
407192	2200202_1	BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893
434194	62680_1	AI899299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303
448663	16112_4	R1349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299
429163	1238297_1	W0463 AI383586 AA827189 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI624611 BG271780 AI497723 H88862
447620	687223_1	D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59373 AI12223 AI935759 AI362553 D60006
407192	2200202_1	N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441
434194	62680_1	W19723 R32966 BE883841 R61003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z39807 BF954306
448663	16112_4	AI973051 AI400921 AI796154 AW241817 AW290951
429163	1238297_1	AA602964 AA609200
447620	687223_1	AF119847 AA437261 AA436987 AI132965
407192	2200202_1	BE966763 AA659765 AI961656 AI520918 AA761743 AA281477 N66431 BE463652 AA281329 AW272944 AA058687 BM145087 AA045516
434194	62680_1	AW341820 AA112515 AA258766 AI886639 AA741133 AA768245 AA035533 AI630459 T20165 AW971268 BE966269 AA522722
448663	16112_4	AW974271 AA592975 AA447312 AA884766



			AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314
5	421091	24941_2	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AI568301 AL567278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896
10	441128	20932_1	BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322
15	406789	0_0	AI041403 Z49148
	410099	16732_1	AK055674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 BI917678 BG819395 BG911971 BG820167 AI174254 AA348720 AA364503 BG714279 AW893230 AA081774 Z42222 AV727176 BF875715 AA081630 BE000834 AA334880 AI563737 BG029709 W52882 AI439658 BE551237 AA283724 BF109530 AI457096 AI805992 BE467736 AA693467 AI697593 AI887863 AI167419 AW901980 AW901768 BE702179 AA484549 T23811 BE327043 AA716027 AA917004 AA167714 BF339675 AA084618 AI418634 T31586 AA436630 AI366472 AA706191 AI422304 AI204899 AI041169 AA211402 AW827081 AA788593 T32736 AI767935 AA747914 T03534 AW959843 AL119527 BE327037 AW901982 AW993370 AW901977 AW902071 W60090 N79906 D26885 T07735 BE702069 BE702172 T08671 BE767117 BE767113
20	432745	112643_1	AA658826 AI821926 AI791191 AA635129 AA564492
	400263	18977_1	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI99487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084
30	411605	10026_3	BG256892 H10532 NA46614 R52610 AW977696 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09686 BI838226 BF034269 AA429173 BE741829 AW867495 AI123683 AW006831 BE831162 AW452753 AV742717 W86152 BF115102 AI633815 BF921562 AA094230 BE092587 W86151 AA526153 AI672156 BF914496 R12579 BF852352 AA699780 T57386 BF903022 R09933 AA678298 BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672
35	420223	191648_1	N27807 AA256634 BE276324
	423476	32437_1	AF263306 BF951698 T66089 F11783 F11794 H29379 R19493 H18042 AL133995 AW134660 AI299437 AA057405 AA917450 AI002692 T09262 R43839 H29290 T65008 N78357
40	441054	2641490_1	AI221207 AI659856 AA913591 AI220302
	429925	33135_1	NM_000786 U23942 BI601050 BG771947 BG773455 BI561558 BI460206 BG714348 BM126447 AU129411 AU129401 AL119303 AV724389 AU099323 AU127089 BG701614 BM150364 D55653 AV702235 BE090408 AU151526 AW149661 BG054754 W42624 W52098 AV709923 W79867 W74235 AV709052 AI217668 AA399409 BE182318 BM128040 AI693998 AW615411 AW070426 AI124550 AW778736 AA477781 AW263013
45	434976	121716_1	AI459619 AA860513 BF809548 AA643635 AA864975 H42020 AW901189 AA904786 BF432722 BI916393 BM470755 BI333211 AA095636 BI256415 U47727 BG773392 N58531 AA226450 BG679564 AA292178 W56883 BE813131 C03646 BG287974 AA386261 H47580 R48858 T91611 H42019 BI869421 BG502073 BG425943 W37290 W31363 BE004451 BF208311 BI048717 N78122 AA226597 AI525334
	440191	MH790_2	AI963821 AA657925 AA935436 AW975068
50			BC000222 AL136871 NM_032261 BC009497 BM461705 BG470749 BG826905 BG285127 BI253235 BE397026 BG704967 AW961225 BM352817 BI227161 BG820180 AA454463 AA255685 N31549 AA326504 BC019924 BG257230 BI092368 BI869896 BG251883 BF034444 BG286577 BE280391 AA599912 BF686779 AI755222 AA452272 AW241170 AU155656 F28259 T16319 AA362505 N64515 BM016416 BM458963 BG739972 AV729565 BE268285 BE867433 BM011110 BG285856 AI922439 BE270975 AL119339 BF956085 AI565178 AL554305 AL573240 AL572917 AI129627 AL546640 BE392285 AI092843 AI371057 BE302410 AI608753 AW674261 AI750057 AI052649 N47822 AL156249 AI589903 BG258439 AI123662 AI126014 AA778101 AA243218 AW498837 AA748311 AI754395 T15728 AA775369 AA858195 W73625 AA216784 AW513778 AW243958 AI061112 AI783806 AL569622 AA070466 BF229936 N58159 H80288 N32598 H80293 H80279 AL581253 AW571884 AI361698 AW073321
55			AA876464 H95640 T34421 AA331419 N99897 H80274 BI262120 AA205826 AA070716 AA653206 AA653483 BG389811 W20432 AA670295 AA653197 D51888 AA362527 BG056668 AW118162 AW073071 BE293868 BF792321 BF792258 BG107176 T56604 BM193566 H03238 AA618045 AA906004 BI085686 AA564566 AI221630 D52045 C14510 AA029390 W60153 H98743 AI682641 H28485 AA723093 AI081730 AA641309 AA687083 BI224818 AW204722 AI309186 AI215122 AI200785 BE467373 BM352502 AI304400 AI193071 AI742483 AW003408 AI400201 AI656740 AW665173 AI215120 AI147599 AI803429 AI076110 AI754349 AW205103 AI262491 AI808243 AI281007 AI051273 AI004801 AW768918 AW103289 AI474637 AI264446 AI699509 BE704420 AA989278 AA918256 AA830956 AA989425 AA911929 AA262598 BE740563 BE727592 BE781003 BG030940 BE256750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H94863 N69544 AA181762 D20132 T55734 T60692 R76858 AA022948 AW770291 R50934 AA205918 R97811 H40328 R86252 AA936029 AI813809 AA933607 AA129695
60			AA548261 AA714393 AA775006 AA653439 AA983808 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007 AA489663 D52138 D51696 D55942 D52740 AI000118 AL516304 AL534259 N54940 AL579194 AI669399 AI342925 BE939201 AA633000 BI222963 AI619676 AW190306 BF035010 AW087897 AI864969 T57243 R48211 AA113880 R26594 C14467 C14444 BI195459 BE896346 BE270780 AL568073 BG389833 BE891549 BI223147 AW381001 AA448464 AW799744 AA412194 AA948107 AA927157 AA983841 BF752571 BE731304 AI380443 AI240179 AA977516 AA884643 AW079380 AW294316 AI913755 AI864320 AI685770 H25135 AI972654 AI538592
65	440409	588375_1	AI174783 R12271 R83569
	444610	2145292_1	AI274757 AI559500 AW022192
	446091	515091_1	AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818
	431843	445334_1	C15161 D60184 D60656
70	400262	18977_1	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI99487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084
75			
80			TABLE 68C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859,56369-56511
404922	7341893	Plus	13248-13428
401519	6649315	Plus	157315-157950
401197	9719705	Plus	176341-176452
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833,5708-5895
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401785	7249190	Minus	165776-165996,166189-166314,166408-16656
406214	7342036	Plus	86320-86523
403532	8076842	Minus	81750-81901
400860	9757499	Minus	151830-152104,152649-152744
404913	7341740	Plus	97717-97976

Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

TABLE 69A:

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

Pkey	ExAccn	UnigenelD	Unigene Title	R1
424806	AA382523	Hs.105689	MSTP031 protein	1.51
418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.94
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1.60
442802	AL133035	Hs.8728	hypothetical protein DKFZp343G171	1.73
417944	AU077196	Hs.82985	collagen, type V, alpha 2	1.48
410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	1.91
452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.59
425139	AW630488	Hs.25338	protease, serine, 23	1.63
402463			NM_014624:Homo sapiens S100 calcium-bind	1.50
423798	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon	1.31
412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (	2.06
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
441457	AW996651	Hs.43838	ESTs	1.30
408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	1.87
413795	AL040178	Hs.142003	ESTs	1.64
441689	AI123705	Hs.289068	ESTs	1.44
412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
424432	AB037821	Hs.146858	protocadherin 10	1.65
432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	1.31
418683	U90908	Hs.87241	hypothetical protein from clones 23549 a	1.42
453085	AW954243		KIAA0251 protein	1.47
438887	R68857	Hs.265499	ESTs	1.49
436729	BE621807		transmembrane 4 superfamily member 1	1.91
400494			ENSP00000238970*:CIG30 (Fragment).	1.34
442506	BE566411		ESTs	1.54
425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	1.55
414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	2.65
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
422389	AF240635	Hs.115897	protocadherin 12	1.38
417124	BE122762	Hs.25338	ESTs	2.13
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	1.54
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
450534	AI570189	Hs.25132	KIAA0470 gene product	1.43
449618	AI076459	Hs.15978	KIAA1272 protein	1.42
446098	AW072215	Hs.208470	ESTs	1.53
413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
448674	W31178	Hs.154140	ovary-specific acidic protein	1.47
407061	X97748		gb:H.sapiens PTX3 gene promotor region.	1.33

	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
5	453789	AA628517	Hs.118502	ESTs	1.41
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.62
	401234			mitogen-activated protein kinase 8 inter	1.48
	420174	AI824144	Hs.199749	ESTs	1.75
10	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
	418693	AI750878	Hs.87409	thrombospondin 1	1.89
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	1.64
15	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.49
	422099	AA156022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	445119	AF035121	Hs.12337	kinase insert domain receptor (a type II	1.40
20	438142	T90309	Hs.269651	ESTs	1.45
	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.51
	442711	AF151073	Hs.8645	hypothetical protein	1.42
25	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	1.32
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA659037	Hs.163780	(AB075832) KIAA1952 protein [Homo sapien	1.76
	418825	AA228881	Hs.22394	hypothetical protein FLJ10893	1.40
30	417805	U38545	Hs.82587	phospholipase D1, phosphatidylcholine-spe	1.35
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
35	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	1.75
	452298	AI039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T59538		gb:yb65g12.s1 Stratagene ovary (937217)	1.52
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
	433374	AI821409	Hs.304471	EST	1.45
40	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.14
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.52
	453983	H94997	Hs.16450	ESTs	1.94
	406506			Target Exon	1.97
45	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW580939	Hs.97199	complement component C1q receptor	2.36
	426696	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.61
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	1.41
50	450152	AI138635	Hs.22968	intron of VEGFR	1.70
	437269	AA334384	Hs.149420	ESTs	1.60
	445279	R41900	Hs.22245	ESTs	1.59
	409509	AL036923	Hs.322710	ESTs	1.52
	410240	AL157424	Hs.61289	synaptotagmin 2	1.61
55	424711	NM_005795	Hs.152175	calcitonin receptor-like	1.96
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	1.81
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	1.91
	410057	R66634	Hs.268107	multimerin	1.85
	446727	AB011095	Hs.16032	KIAA0523 protein	1.67
60	412564	X83703		cardiac ankyrin repeat protein	1.51
	414786	AI246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.71
	410276	AI554545	Hs.71832	angiopoietin-2	1.91
	406627	T64904	Hs.163780	ESTs	1.76
	405025			Bone morphogenetic protein 6	1.69
65	422648	D86983	Hs.118893	Melanoma associated gene	2.33
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.78
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	1.79
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.02
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.93
70	429276	AF056085	Hs.198612	G protein-coupled receptor 51	1.65
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.48
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	2.01
	434398	AA121098	Hs.3838	serum-inducible kinase	1.83
	416851	AW963951	Hs.85618	ESTs	1.65
75	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.69
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.71
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.86
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	1.65
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	1.83
80	428206	AB020643	Hs.183006	KIAA0836 protein	1.77
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	2.00
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	1.94



	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	1.74
	444409	AI792140	Hs.49265	ESTs	1.88
	421340	F07783	Hs.1369	decay accelerating factor for complement	1.74
5	445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
	444009	AI380792	Hs.135104	ESTs	1.90
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.16
	416940	N75620	Hs.43157	ESTs	2.03
	418922	AW956580	Hs.42699	ESTs	2.09
10	431548	AI834273	Hs.9711	novel protein	1.81
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
	434558	AW264102	Hs.39168	ESTs	1.93
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
	428438	NM_001955	Hs.2271	endothelin 1	2.46
15	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
	439410	AA632012	Hs.188746	ESTs	1.93
	453467	AI535997	Hs.30089	ESTs	2.39
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
20	417933	X02308	Hs.82962	thymidylate synthetase	1.70
	436420	AA443966	Hs.31595	ESTs	1.97
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	1.80
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
	413745	AW247252	Hs.75514	nucleoside phosphorylase	1.99
	405121			mitogen-activated protein kinase 8 inter	2.99
30	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
	421937	AI878857	Hs.109706	hematological and neurological expressed	1.65
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
35	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
	408243	Y00787	Hs.624	interleukin 8	2.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
	407891	AA486620	Hs.41135	endomucin-2	2.34
	407891	AA486620	Hs.41135	endomucin-2	2.34
40	436032	AA150797	Hs.109276	latexin protein	2.24
	439382	BE247684	Hs.103070	ESTs	2.07
	419172	AW338625	Hs.22120	ESTs;similar to TRANSMEMBRANE 4 SUPERF	2.00
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.33
	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
45	432128	AA127221	Hs.296502	ESTs	2.27
	417426	NM_002291	Hs.82124	laminin, beta 1	2.11
	434217	AW014795	Hs.23349	ESTs	2.03
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	2.08
	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
50	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.37
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	2.55
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.09
	449722	BE280074	Hs.23960	cyclin B1	1.76
55	413794	AF234532	Hs.61638	myosin X	2.01
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	2.15
	406964	M21305		gb:Human alpha satellite and satellite 3	3.08
	448231	AI701916	Hs.202509	ESTs	2.27
	408989	AW361666	Hs.49500	KIAA0746 protein	1.43
60	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	2.18
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
	417308	H60720	Hs.81892	KIAA0101 gene product	1.86
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	2.92
65	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
	400666			NM_002425:Homo sapiens matrix metallopro	2.59
	431728	NM_007351	Hs.268107	multimerin	2.72
	440086	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom	2.25
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.76
70	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	3.37
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	3.11
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
	444330	AI597655	Hs.49265	ESTs	3.08
	422424	AI186431	Hs.296638	prostate differentiation factor	2.96
75	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	11.91

TABLE 69B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey CAT Number Accession

453085	10017_1	BC017336 BG716430 BG501286 BI458528 AI582223 N98532 AI338138 AI273442 AW102617 AA831177 AA745642 AA412583 AA355375 BG547492 AW954243 BI766546 BG057641 AI192435 AI338935 AI312651 AI708679 AI191125 AI206832 AA676899 AI078010 AI888718 AA452830 BF445542 N69930 AA715017 BF446713 BE046852 AW771909 AA907729 AI143749 AI761290 AA890233 BF925759 AI783713 AI767267 AA814538 W56778 AA918481 BG743526 BE454242 AI025328 AI298436 AI290445 H27710 AI475034 BG740023 AI090348 AI340003 BI602481 W38495 AI183314 AI927418 BG397181 AA878310 W19369 W56507 C05751 AW380760 AW380770 AW380790 BF930729 H28425 AA037326 AA375805 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AI574095 AI576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL555866 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 NM_002640 L40377 BG227962 AI925897 W60100 BG980023 AA853496 AA360401 AW956168 W61361 AI074846 AA373798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068728 AW976385 AI121194 AI767324 BM054718 AW366882 AA156151 Z25109 C05177 AW975688 AA731063 N67084 AF147374 T59538 T59589 T59598 T59542 X83703 NM_014391 BC018667 AU139209 BE924924 BE924899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA969184 BE924898 BF229066 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943776 AA488072 AA486364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 C04160 C04483 BF229048 AW975183 AA973583 AI365103 AI699495 AI301787
--------	---------	--

TABLE 69C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402463	9796896	Minus	8818-8952
400494	9714719	Plus	169845-170272
401234	9929642	Plus	120173-120337
406506	7711374	Minus	6843-8077
405025	7107727	Plus	105267-105343, 106184-106294, 106387-10653
405121	8102330	Minus	35816-36004, 36587-36684
400666	8118496	Plus	17982-18115, 20297-20456

TABLE 70A:

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigenelD:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of the mean of the vessel AI's to the mean of the HUVEC AI's

Pkey	ExAccn	UnigenelD	Unigene Title	R1
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	0.99
439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.06
412636	NM_004415		desmoplakin (DPI, DPII)	1.25
426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.36
414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.50
417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.55
414572	AU077174	Hs.288181	cathepsin H	1.64
415314	N88802	Hs.5422	glycoprotein M6B	1.70
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	1.75
406973	M34996	Hs.198253	major histocompatibility complex, class	1.88
456974	M12529	Hs.169401	apolipoprotein E	1.90
430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.91
406828	AA419202	Hs.84298	CD74 antigen (invariant polypeptide of m	1.97
422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	1.99

5	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	2.12
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	2.15
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.17
	437536	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.26
	446945	AI193115	Hs.16611	tumor protein D52-like 1	2.27
10	422639	AI929377	Hs.173724	creatine kinase, brain	2.29
	427451	AI690916	Hs.178137	transducer of ERBB2, 1	2.31
	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pseudosarcosin)	2.38
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	2.39
15	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
	427393	AB029018	Hs.177635	KIAA1095 protein	2.47
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.49
	414063	H26904	Hs.75736	apolipoprotein D	2.50
20	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	2.51
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	2.51
	410532	T53088	Hs.155376	hemoglobin, beta	2.56
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	2.58
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.58
25	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427980	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8603	p8 protein (candidate of metastasis 1)	2.62
30	425751	T19239	Hs.1940	crystallin, alpha B	2.63
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	2.63
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.66
	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	2.67
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.67
35	452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
	425869	AA524547	Hs.160318	FXYD domain-containing ion transport reg	2.73
	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
40	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.86
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		plakophilin 4	2.94
45	429123	AB011099	Hs.196647	KIAA0527 protein	2.97
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.01
	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.01
	425622	AW360847	Hs.16578	ESTs	3.01
	420195	N44348	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.04
50	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
	407869	AI827976	Hs.24391	hypothetical protein FLJ13612	3.06
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
55	414840	R27319	Hs.23823	hairy/enhancer-of-split related with YRP	3.14
	424651	AI493206		ESTs	3.17
	443932	AW888222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	3.20
60	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.20
	423961	D13666	Hs.136348	periostin(OSF-2os)	3.24
	447384	AI377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.25
	447023	AA356764	Hs.17109	integral membrane protein 2A	3.25
65	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	3.25
	406972	M32053		gb:Human H19 RNA gene, complete cds.	3.26
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	3.29
70	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
	410614	AI091195	Hs.65029	growth arrest-specific 1	3.35
	451529	AI917901	Hs.208641	ESTs	3.35
	430310	U60115	Hs.239069	four and a half LIM domains 1	3.37
	424897	D63216	Hs.153684	frizzled-related protein	3.37
75	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	3.41
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
	407938	AA905097	Hs.85050	phospholamban	3.48
80	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	3.51
	452877	AI250789	Hs.32478	ESTs	3.52
	419577	L36531	Hs.91296	integrin, alpha 8	3.52
	404277			NM_019111*:Homo sapiens major histocompa	3.54

5	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	3.64
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	3.71
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	3.75
10	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	3.77
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.80
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	3.86
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	3.89
15	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.90
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	4.01
20	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	4.09
	421823	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	4.25
25	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	4.26
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	4.29
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.34
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78065	complement component 7	4.37
30	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	4.41
	452114	N22687	Hs.8236	ESTs	4.43
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
35	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxin)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108623	thrombospondin 2	4.73
40	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
	414290	AI568801	Hs.71721	ESTs	4.98
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416784	AA334592	Hs.79914	lumican	5.20
45	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
	408221	AA912183	Hs.47447	ESTs	5.65
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	5.87
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
50	426406	AI742501	Hs.169756	complement component 1, s subcomponent	7.94
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev9)	9.91
55	TABLE 70B Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers				
	Pkey	CAT Number	Accession		
60	412636	1438_1	M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827		
			AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592		
			BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316		
			BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737		
65			AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046		
			BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674		
			BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510		
			AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276		
70			BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421		
			BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845		
			AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723		
			AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211		
			AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599		
75			BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583		
			AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516		
			AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612		
			AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435		
80			AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207		
			AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181		
			H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654		
			AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320		
			AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474		
			BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE114064 BE713903 BE713868 BE713763		
			BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406		

5	454042	30254_1	BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284000 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487
			AJ420458 AI018523 AA708686 BF949633 AL119553 BF945960 AI081305 AA041432 AI921013 AI684910 AI654847 AW874199 AI206120 AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366468 N64350 AA779107 AW025969 R49056 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202561 AA788851 AI494436 BF856114 H22570 AW964381 BG007409 BM314056 AA465642 T30661 T33111 Z42834 C04542 BF948152 BF944325 BF858895 AA935284 AI267360 N64249 W67500 F07962 AA322394 BI489987 BE644965 BM313782 AA910364 AI809246 AA836750 BF115228 AA829730 N27413 BM141766 AI742325 AA455261 AA938708 AI420241 AI130039 BF222341 BF941301 AA771807 Z41034 BF447457 BF447426 AW515347 T03874 F02360 F02302 N34898 AI678586 AA807824 AA948556 AW204638 BM142045 BF446775 AV648364 AI801368 AA971739 AI017351 AA760722 AI460007 AI458383 AI694152 AA226536 BE467282 N47808 BE348825 BE830581 BE830583 N53009 N59351 N41056 W67501 AA016246 H43293 F21282 R59121 R56280
10	440820	3091_1	BG435302 BM083687 AA904035 AA488889 W76175 AA761874 H28767 AA910081 AA837086 AI521825 BG986378 AI478562 AA743152 AA746092 H88863 BG986375 AA635644 AI493206 AA669979 BE245127 BG986430 BG986529 BF665873 BG030157 BG622575 AA766495
15	424651	46029_5	

20	TABLE 70C		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.	
25	Strand:	Indicates DNA strand from which exons were predicted.	
	NL_position:	Indicates nucleotide positions of predicted exons.	

Pkey	Ref	Strand	NL_position
404277	1834458	Minus	91665-91946

30	TABLE 71A: 774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES		
----	---	--	--

35	Table 1A lists 774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.		
----	---	--	--

40	Pkey:	Unique Eos probeset identifier number	
	ExAccn:	Exemplar Accession number, Genbank accession number	
	UnigeneID:	Unigene number	
	Unigene Title:	Unigene gene title	
	R1:	75th percentile of ewing sarcoma to 85th percentile of body map	

45	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	104659	AW969769	Hs.105201	ESTs	70.3
	101447	M21305		gb:Human alpha satellite and satellite 3	64.7
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	50.5
	115881	NM_005756	Hs.184942	G protein-coupled receptor 64	48.8
50	121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	46.7
	101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	46.6
	110278	AF061573	Hs.19492	protocadherin 8	46.1
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	41.4
	116752	AL008583	Hs.91622	neuronal pentraxin receptor	40.9
55	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	39.6
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	36.9
	110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	35.5
	121362	AF050147	Hs.97932	chondromodulin I precursor	34.7
	131291	NM_004350	Hs.170019	runt-related transcription factor 3	33.0
60	101063	D54745	Hs.80247	cholecystokinin	31.7
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	28.7
	122651	AW975398	Hs.293836	ESTs	28.0
	100299	D49493	Hs.2171	growth differentiation factor 10	26.5
	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.2
65	123619	AA602964		gb:nc097c02.s1 NCL_CGAP_Pr2 Homo sapiens	26.1
	124006	AI147155	Hs.279727	ESTs; homologue of PEM-3 [Clona savignyi	23.1
	116301	AW969706	Hs.293332	ESTs	22.6
	121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	22.3
	106533	AL134708	Hs.145998	ESTs	22.3
70	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	21.3
	131313	R96290	Hs.75874	ribosomal protein L44	20.8
	116790	AW161357		microtubule-associated protein tau	18.7
	105316	AI671245	Hs.24835	hypothetical protein FLJ14594	18.2
	102123	NM_001809	Hs.1594	centromere protein A (17kD)	17.8
75	126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	17.8
	119791	AA554907	Hs.58291	ESTs	16.7
	113003	AW292315	Hs.7215	ESTs	16.3
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	16.3
	126799	AW753865	Hs.74376	olfactomedin related ER localized protei	16.3
80	105298	BE387790	Hs.26369	hypothetical protein FLJ20287	15.5
	107160	AA314490	Hs.27669	KIAA1563 protein	14.8
	115313	AA808001	Hs.184411	albumin	14.6
	123308	C14187	Hs.103538	ESTs	14.2

	126077	M78772	Hs.210836	ESTs	14.0
	100698	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	106821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
	110288	H40665	Hs.31564	ESTs	13.8
5	106498	AI221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;calsyntenin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	128639	AW582962	Hs.102897	CGI-47 protein	13.2
10	125698	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119456	AA248897	Hs.48784	ESTs	12.2
	135155	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	106614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
15	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
	132968	AF234532	Hs.61638	myosin X	11.7
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6616	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
	104968	AI249502	Hs.29669	ESTs	11.1
20	123532	AA608733		gb:ae56f06.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125556	AB033064	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, t	10.6
25	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	10.6
	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
30	110730	N67655	Hs.26411	ESTs	10.3
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (importin) beta 3	10.1
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
40	105091	AA148859	Hs.179909	hypothetical protein FLJ22995	9.6
	106146	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.5
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
45	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
	121910	AI204600	Hs.96978	hypothetical protein MGC10764	9.2
	130625	AF176012	Hs.260720	J domain containing protein 1	9.2
	129755	R42216	Hs.7759	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	9.0
50	111109	AI940675	Hs.20914	hypothetical protein FLJ23056	9.0
	120217	AA862257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-lin	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	AI085153	Hs.143764	ESTs, Weakly similar to unknown [H.sapie	8.8
55	113903	AI368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
	105253	AW997484	Hs.5003	KIAA0456 protein	8.6
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
60	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.5
	102725	AB026187	Hs.159156	protocadherin 11	8.5
	130298	AI347487	Hs.132781	class I cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
65	106575	AW970602	Hs.105421	ESTs	8.2
	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	8.1
	119499	AI918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244930	Hs.166895	ESTs	8.0
70	107098	AI823593	Hs.27688	ESTs	8.0
	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894638	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	7.9
75	133063	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.8
	105730	AW377314	Hs.5364	DKFZP564I052 protein	7.8
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	7.8
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	7.8
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	7.7
80	125400	AL110151	Hs.128797	DKFZP586D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AI608657	Hs.95097	ESTs	7.7
	129075	BE250162	Hs.83765	dihydrofolate reductase	7.6

5	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	7.6
	132438	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A (	7.6
	118036	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	7.6
	131170	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	7.5
	104548	R39398	Hs.91559	ESTs	7.5
10	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.4
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
	132559	AF119848	Hs.270863	hypothetical protein PRO1580	7.3
15	101050	AU077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW893940	Hs.59698	ESTs	7.1
	105127	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	7.1
	128478	AA708205	Hs.100343	ESTs	7.1
20	110456	H52348	Hs.36636	ESTs	7.1
	118846	AW299598	Hs.50895	homeo box C4	7.1
	120934	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	7.1
	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	7.0
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	7.0
25	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	106213	N45018	Hs.8769	hypothetical protein DKFZp761J17121	6.9
	118013	AI674126	Hs.94031	ESTs	6.9
	120147	AI917116		hemoglobin, beta	6.8
30	118267	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	6.8
	120325	AA195651		AP-2 beta transcription factor	6.8
	133276	AW978439	Hs.69504	ESTs	6.8
	127742	AW293496	Hs.180138	ESTs	6.7
35	127664	AA806164	Hs.116502	ESTs	6.7
	108778	AF133123	Hs.90847	general transcription factor IIIC, polyp	6.6
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	6.6
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.6
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
40	115197	R18656		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
	126967	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937	6.4
	118499	N67274	Hs.50141	EST	6.4
45	105301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AI869372	Hs.17207	Homo sapiens cDNA FLJ11922 fis, clone HE	6.3
	127968	AA830201	Hs.124347	ESTs	6.3
	134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
50	115844	AI373062	Hs.332938	hypothetical protein MGC5370	6.3
	121885	AA934883	Hs.98467	ESTs, Highly similar to AF257737 1 cilia	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
	132256	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	6.2
55	106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	6.2
	135186	U73328	Hs.172648	distal-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
	109261	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	6.1
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	6.1
60	128501	AL133572	Hs.199009	protein containing CXXC domain 2	6.1
	109747	AI223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-5301/15	6.0
	104689	AA420450	Hs.292911	Plakophilin	6.0
65	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121830	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypotheti	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
	109841	H01052		gb:yj32h01.s1 Soares placenta Nb2HP Homo	5.9
	115622	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.8
70	122969	AW821252	Hs.104336	hypothetical protein	5.8
	109872	R65841	Hs.28653	ESTs	5.8
	114208	AL049466	Hs.7859	ESTs	5.8
	113494	T91451	Hs.86538	ESTs	5.8
	127684	AA668631	Hs.159971	KIAA0379 protein	5.8
75	129300	W94197	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
	105909	AA195191		hypothetical protein FLJ20729	5.8
	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
80	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	5.7
	130723	BE247676	Hs.18442	E-1 enzyme	5.7
	107230	AI034467	Hs.34650	ESTs	5.7
80	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

	117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
5	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
10	106668	R49390	Hs.254129	KIAA1678	5.4
	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109606	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13675 fis, clone PL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
15	131185	BE280074	Hs.23960	cyclin B1	5.4
	111227	T06701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
20	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
	115121	AI634549	Hs.325422	ESTs	5.3
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.3
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	5.3
25	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (	5.3
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040884	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypotheti	5.2
30	120830	AI568170	Hs.96886	ESTs	5.2
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	5.2
	103316	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49163	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
35	116680	AW902848	Hs.273829	ESTs	5.2
	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161885	Hs.269745	ESTs	5.1
	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
40	110799	AI089660	Hs.323401	dpy-30-like protein	5.1
	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
45	125321	T86652	Hs.178294	ESTs	5.1
	102627	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
	116814	H50834	Hs.77899	gb:yp86a10.s1 Soares fetal liver spleen	5.0
50	130622	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	5.0
	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127765	AA971146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RU2S	4.9
	120484	AA253170	Hs.96473	EST	4.9
55	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
	129012	R81936		ribosomal protein L44	4.9
	124973	AI476066	Hs.102243	ESTs, Weakly similar to I78885 serine/th	4.9
	124648	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
60	131526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.9
	130637	AA356764	Hs.17109	integral membrane protein 2A	4.8
	126769	AA083456		gb:zn09g08.r1 Stratagene hNT neuron (937	4.8
	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	4.8
	100169	AL037228	Hs.82043	D123 gene product	4.8
65	130262	D63216	Hs.153684	frizzled-related protein	4.8
	109260	AW978515	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
70	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	4.8
	105848	AW954064	Hs.24951	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129706	AA443241		ribosomal protein L44	4.7
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126629	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	4.7
	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW352149	Hs.102314	ESTs	4.7
	126521	AI475110	Hs.203933	ESTs	4.7
	110343	AW136703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6



5	113974	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindi	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
	103487	AA743603	Hs.172108	nucleoporin 88kD	4.6
	125353	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	4.6
10	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	4.6
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
15	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.5
	104912	AA813192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AI571940	Hs.7549	ESTs	4.5
	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.5
20	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
	106489	AA452054	Hs.119338	ESTs	4.5
	122792	AW188551	Hs.99519	hypothetical protein FLJ14007	4.5
25	112651	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123596	AA421130	Hs.112640	EST	4.5
	125447	AI582222	Hs.128686	ESTs	4.5
	106178	AL049935	Hs.301763	KIAA0554 protein	4.4
30	102250	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334842	tubulin alpha 1	4.4
	127496	AI031650		ESTs	4.4
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	4.4
	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
35	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61939	Hs.103822	ESTs	4.4
	120922	AA481003	Hs.97128	ESTs	4.3
	115167	AA749209	Hs.43728	hypothetical protein	4.3
40	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PRO0659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
	103616	NM_002647	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
45	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	135098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	4.3
	106246	AL036917	Hs.288821	KIAA1638 protein	4.3
50	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
	129650	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
55	106073	AL157441	Hs.17834	downstream neighbor of SON	4.2
	105403	AI473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	4.2
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	4.2
60	106012	AI240665		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.2
	130832	AW838006	Hs.20082	zinc finger protein 3 (A8-51)	4.2
	125960	AI754693	Hs.145968	ESTs	4.2
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
65	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	4.2
	101266	L36645	Hs.73964	EphA4	4.2
70	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.1
	116133	AW449597	Hs.313652	EST, Weakly similar to I38022 hypothetic	4.1
	129001	AA443323	Hs.107812	BPOZ protein	4.1
75	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	4.1
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	4.1
	126107	H75477	Hs.93361	ESTs	4.1
	115333	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	4.1
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	4.1
80	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153746	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	CDC28 protein Kinase 2	4.1
	129948	AI537162	Hs.263988	ESTs	4.1
	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW088276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15069	ESTs	4.1
	118872	AI039201	Hs.283316	ESTs	4.1

5	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retroviru	4.0
	127153	AI732303	Hs.186518	hypothetical protein MGC2599 similar to	4.0
	124105	H11484	Hs.79133	ESTs	4.0
10	100031			AFFX control - DapX-M	4.0
	106897	AF039023	Hs.167496	RAN binding protein 6	4.0
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.0
	126965	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.0
15	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	4.0
	118751	N74210	Hs.50454	ESTs	4.0
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	4.0
	111387	AI244489	Hs.285724	ESTs	4.0
20	118676	N45312	Hs.46506	ESTs	4.0
	107348	AW973753	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	4.0
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
25	115399	AF151534	Hs.92023	core histone macroH2A2.2	4.0
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gb:yy54c08.s1 Soares_multiple_sclerosis_	4.0
	126522	W31912	Hs.21168	gb:zc76d03.s1 Pancreatic Islet Homo sapi	4.0
	131965	W79283	Hs.35962	ESTs	3.9
30	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
	105808	AI133161	Hs.286131	CGI-101 protein	3.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
35	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112996	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
	118967	AI668670	Hs.216756	ESTs	3.9
	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
40	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	3.9
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos	3.9
45	131971	BE567100	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.106985	ESTs	3.9
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
	112921	R91095	Hs.4276	KIAA1701 protein	3.9
50	120820	AA347417	Hs.96869	EST	3.8
	106459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
	105476	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.8
	122682	AA984531	Hs.159293	ESTs	3.8
55	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
	129785	H19006	Hs.184780	ESTs	3.8
	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	3.8
60	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H60720	Hs.81892	KIAA0101 gene product	3.8
	106140	AB006624	Hs.14912	KIAA0286 protein	3.8
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
65	103319	X83492	Hs.82359	tumor necrosis factor receptor superfami	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA296874	Hs.77494	deoxyguanosine kinase	3.8
	127262	AA828125		gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens	3.7
	126872	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	3.7
70	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.7
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	3.7
	126962	R12014	Hs.20976	ESTs	3.7
	116203	AW137166	Hs.87306	ESTs	3.7
	123377	AW969183	Hs.271297	ESTs	3.7
75	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123654	PCF11p homolog	3.7
	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
	131163	AA099524	Hs.23754	ESTs	3.7
80	126708	AW962593	Hs.135260	ESTs	3.7
	117417	AI241733	Hs.43871	ESTs	3.7
	106272	AW959731	Hs.323099	ESTs	3.7
	110834	AW273860	Hs.5759	ESTs	3.7
	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109260A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W96141	Hs.220687	ESTs	3.7

5	130850	AB040922	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
	105150	AA631977	Hs.155995	KIAA0643 protein	3.6
	103163	AU077018	Hs.3235	keratin 4	3.6
10	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW664072	Hs.60136	ESTs	3.6
	113577	AI300699	Hs.111334	PRO0470 protein	3.6
	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.6
15	127563	AB035898	Hs.150587	kinesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.6
	114118	F01598	Hs.175930	ESTs	3.6
	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.6
	125174	W51835	Hs.231082	EST	3.6
20	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	3.6
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	3.6
	135191	X16866	Hs.333497	cytochrome P450, subfamily IID (debrisoq	3.6
	124367	AI683183	Hs.99348	distal-less homeo box 5	3.6
	113560	T91015		ESTs	3.6
25	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	3.6
	113988	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88252	ESTs	3.6
	126600	AA699949	Hs.191385	ESTs	3.6
	127256	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
30	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	115691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
35	134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	3.6
	128468	T23625	Hs.150580	putative translation initiation factor	3.6
	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	3.5
40	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	3.5
	125562	AI494372	Hs.98968	hypothetical protein FLJ23058	3.5
	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.5
45	125558	R59305		gb:yh16c10.r1 Soares infant brain 1N1B H	3.5
	117265	AA451966		RAB9-like protein	3.5
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
	109482	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	3.5
50	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117613	AW029507	Hs.161102	ESTs	3.5
	100944	L07518		mucin 6, gastric	3.5
	105226	R58958	Hs.26608	hypothetical protein MGC15880	3.5
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	3.5
55	123720	AA609734	Hs.112755	EST	3.5
	128846	AA730767	Hs.285753	SCG10-like-protein	3.5
	116443	AW962196	Hs.339808	LBP protein 32	3.5
	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
	106918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.5
60	131244	AI638429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	insulin receptor substrate 2	3.5
	111223	AA852773	Hs.334838	KIAA1866 protein	3.5
	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	3.5
	105395	AI580880	Hs.268149	putative methyltransferase	3.5
65	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	106367	AA504747	Hs.136102	KIAA0853 protein	3.5
	103392	X94563		gb:H.sapiens dbi/acbp gene exon 1 & 2.	3.5
	101086	AA382524	Hs.250959	histatin 1	3.5
70	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	3.5
	114096	AF060219	Hs.27007	chromosome condensation 1-like	3.4
	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
75	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
	109734	AI927212	Hs.3734	ESTs	3.4
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	3.4
80	106685	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
	108687	BE544475	Hs.54347	ESTs	3.4
	113115	AI141426	Hs.8705	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.4
	123110	AA486256	Hs.193510	EST	3.4
	131019	W28614		chorionic somatomammotropin hormone 1 (p	3.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N63753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C186 protein	3.4
5	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	3.4
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	3.4
10	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	3.4
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115506	AB037756	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	3.4
15	106691	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
	105169	BE245294	Hs.180789	S164 protein	3.4
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126638	AA649257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
20	106650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	3.3
	108859	AL121500		ESTs	3.3
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypotheti	3.3
	125693	H23989	Hs.169743	Homo sapiens clone 25121 neuronal olfact	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
25	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.3
	124691	R05835	Hs.110153	ESTs	3.3
	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	gb:ym37a05.r1 Soares infant brain 1NIB H	3.3
30	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	3.3
	107908	AF087999		ESTs	3.3
	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	3.3
35	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
	105463	AA825974	Hs.32646	hypothetical protein FLJ21901	3.3
	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	3.3
40	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
	113283	T66813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133160	N54968	Hs.66309	hypothetical protein MGC11061	3.3
45	134076	AF086215	Hs.78980	gb:Homo sapiens full length insert cDNA	3.3
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
	127728	AW404061		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
	127506	T61039	Hs.76067	ribosomal protein L10a	3.3
50	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
	126666	AA648886	Hs.151999	ESTs	3.3
	130453	U80735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3
55	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
	121292	AA401807		gb:zv65f11.s1 Soares_total_fetus_Nb2HF8_	3.3
	123284	AA488988	Hs.293796	ESTs	3.3
	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
60	114988	AA251089		gb:zs04f05.s1 NCL_CGAP_GCB1 Homo sapiens	3.3
	132867	AF226667	Hs.58553	CTP synthase II	3.3
	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AI521936	Hs.107149	novel protein similar to archaean, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
65	111520	AI985369	Hs.301134	ESTs	3.3
	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA768242	Hs.80618	hypothetical protein	3.3
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	3.3
70	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	3.3
	116734	AW900992	Hs.93796	DKFZP586D2223 protein	3.3
	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326683	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
75	129284	AA318224	Hs.296141	ESTs	3.3
	119127	AA708035	Hs.12248	ESTs	3.3
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	118397	BE139479	Hs.161492	ESTs	3.3
80	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
	126735	M69113	Hs.226795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	3.2
	106103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
5	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	3.2
	133761	AF041430	Hs.75922	brain protein l3	3.2
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
10	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
	129673	D38552	Hs.1191	KIAA0073 protein	3.2
	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	126722	N66148	Hs.11125	HSPC033 protein	3.2
	109966	H09103	Hs.30897	EST	3.2
15	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
	109517	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
	105252	AB039670	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
20	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
	134869	AL157518	Hs.90421	PRO2463 protein	3.2
	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
25	129056	AI769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN !!!!	3.2
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
	103038	AA926960		CDC28 protein kinase 1	3.2
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1	3.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	3.2
	132305	AI806090	Hs.44344	hypothetical protein FLJ20534	3.2
30	131136	AB033099	Hs.23413	KIAA1273 protein	3.2
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117639	AA377165	Hs.44833	ESTs	3.2
	127076	AI422951	Hs.146162	ESTs	3.2
35	126153	H85692	Hs.40730	ESTs	3.2
	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypotheti	3.2
	104946	AW242407	Hs.73848	carcinoembryonic antigen-related cell ad	3.2
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
40	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	3.2
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	3.2
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.2
	119651	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108812	hypothetical protein FLJ22004	3.2
45	134964	AI803516	Hs.272891	hippocalcin-like protein 4	3.1
	105551	AW005822	Hs.25292	ribonuclease HI, large subunit	3.1
	119750	AI538880	Hs.94812	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
	104590	AW373062		nuclear receptor subfamily 1, group I, m	3.1
50	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
	116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.1
	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14967 fis, clone TH	3.1
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
	128538	R44214	Hs.101189	ESTs	3.1
55	129179	AW969025	Hs.109154	ESTs	3.1
	108793	AA129395	Hs.71139	ESTs	3.1
	108807	AI652236	Hs.49376	hypothetical protein FLJ20644	3.1
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.1
	132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	3.1
60	134937	AI251449	Hs.171939	ESTs	3.1
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	3.1
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	3.1
	128179	AW293689	Hs.127116	ESTs	3.1
65	117121	H95044	Hs.321386	EST	3.1
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
	128403	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA809672	Hs.123304	ESTs	3.1
	114250	AI914699	Hs.13297	ESTs	3.1
70	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	3.1
	117997	N52090	Hs.47420	EST	3.1
	104558	R56678	Hs.88959	hypothetical protein MGC4816	3.1
	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
75	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
	127521	AW297206	Hs.164018	ESTs	3.1
	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nucleolar protein NOP5/NOP58	3.1
	105024	AA126311	Hs.9879	ESTs	3.1
80	123485	AI308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	LIM domain binding 2	3.1
	115348	AA281562	Hs.766	ESTs	3.1
	117297	AW779829		gb:hn88a05.x1 NCL_CGAP_Kid11 Homo sapien	3.1

5	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
	115188	AK000219	Hs.88367	hypothetical protein FLJ20212	3.1
	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.1
	106472	AI207162	Hs.3815	stathmin-like-protein RB3	3.0
10	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
15	112435	NM_013255	Hs.288791	muskelin 1, intracellular mediator conta	3.0
	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	3.0
	106651	AA460421	Hs.30875	ESTs	3.0
	109597	AA989362	Hs.293780	ESTs	3.0
	132342	AW162758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
20	106057	BE614474	Hs.289074	F-box only protein 22	3.0
	106378	AA824298	Hs.21331	hypothetical protein FLJ10036	3.0
	128660	AA011597	Hs.177398	ESTs	3.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	3.0
25	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	3.0
	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	3.0
	133966	BE280478	Hs.182695	hypothetical protein MGC3243	3.0
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131586	AA460352	Hs.26966	KIAA1171 protein	3.0
30	100237	D30715		Human PAP (pancreatitis-associated prote	3.0
	105515	T24968	Hs.23038	HSPC071 protein	3.0
	123073	AA485061	Hs.105652	ESTs	3.0
	111375	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.0
	130724	AK001507	Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
35	129928	AI338993	Hs.134535	ESTs	3.0
	118922	AW206193		hypothetical protein DKFZp761B2423	3.0
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	3.0
40	122219	AA436002	Hs.183161	ESTs	3.0
	132195	BE018717	Hs.42124	ESTs	3.0
	102298	AA382169	Hs.54483	N-myc (and STAT) interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.0
	126997	AI377150	Hs.150914	ESTs	3.0
45	128902	AA036637	Hs.107052	ESTs	3.0
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	3.0
	106711	BE390125	Hs.143187	hypothetical protein	3.0
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	3.0
50	135029	H58818		hydroxysteroid (17-beta) dehydrogenase 7	3.0
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	3.0
	106735	R77698	Hs.337778	ESTs	3.0
	126628	N49776	Hs.170994	hypothetical protein MGC10946	3.0
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
55	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	3.0
	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	3.0
	129601	AB032964	Hs.115726	KIAA1138 protein	3.0
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	3.0
	128695	NM_003478	Hs.101299	cullin 5	3.0
60	123470	AW303285		Human DNA sequence from clone RP11-110H4	3.0
	109252	BE440157	Hs.85944	ESTs	3.0
	101445	M21259		gb:Human Alu repeats in the region 5' to	3.0
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	3.0
	116475	AA733050	Hs.334612	small nuclear ribonucleoprotein polypept	3.0
65	106573	AA223447	Hs.12835	A kinase (PRKA) anchor protein 7	3.0
	103106	W27172	Hs.1857	phosphodiesterase 6G, cGMP-specific, rod	3.0
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	3.0
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	3.0
	126887	H20832		gb:ym48d03.s1 Soares infant brain 1NIB H	3.0
70	117960	AA310417	Hs.47044	ESTs	3.0
	133626	AW836130	Hs.75277	hypothetical protein FLJ13910	3.0
	113179	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind	3.0
	109968	H09232	Hs.26484	HIRA-interacting protein 3	3.0
75	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

TABLE 71B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
------	------------	-----------

792

5	106012	96214_1	AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 AI360919 H03502 BE208298 R68588 AI350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933 AJ003322 AJ003324 AW404061 R09654 T67160 N50566 N53259 R81936 D78695 D78806 D78780 C17009 AA004406 AA122102 R70625 AA148932 H59583 H81146 H80378 H49863 H21182 H46534 H51478 H20702 H46515 H40200 H50046 H23647 H50439 H18383 H21846 H23849 H40182 R12924 H01290 H01283 H42464 W31947 W39660 AA046219 H03539 H01741 R22008 AA043911 AA156838 D78832 R36616 R66039 AI492481 AA088608 R69918 R36334 H80281 N58483 AI075154 AI086754 AA595787 H81051 H01187 AI057251 T96992 H59584 T47016 R31800 H13647 H01193 N74660 AA156601 H03455 R66040 R81937 R92416 H89486 R36617 R65795 AI088338 AI373324 H66992 R96235 AI494132 R16678 AA088178 AA705356 AA962143 AA148933 R09231 AI160937 R70525 T46980 AI200046 H02301 AA367587 R35968 T97106 D78703 N78072 D78668 D63268 R28197 AA085579 R63766 R92415 W00998 R80766 R67875 R27583 R09343 H13646 R27682 T89007 AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227 AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655 AI193667 AI341984 N92658 T32870 R52664 N50428 AW089291 AI934175 AI423737 D60665 AA226198 AA226513 AA383773 R18656 AW968014 AA262288 AW968002 X93079 AJ002788 R51324 AI381600 D80031 AW500520 AW593740 F09382 AA810597 AA262174 AA810595 AA810596 AA443241 R23784 R67255 R00047 AI457612 R63254 R28645 R27616 H01310 R78329 R76046 R76055 AA369734 N57914 H94864 AI953638 R31669 AW769278 R82398 AA131925 R21776 R79031 AI129553 N70340 AI276116 AA709381 N63734 AI342605 AA327133 AI805980 AA005377 AW611716 T86946 AA369083 R67250 H00240 R32578 W86279 R80248 R23734 H00977 R21732 R78932 AA368675 R16780 R26523 H40161 W93671 R99823 R77956 H61601 R98785 R09738 H78317 H53537 H81056 T53780 H12600 R82345 AA653499 AW953717 R63207 R33888 H54071 H66993 T48748 AI702300 R30775 H68996 AI014957 AA369082 AF075351 AI110886 AI742050 AW954245 AI768458 C19062 AI393674 C18911 C18029 AA708613 AI168432 R67389 AI168453 H00188 R21233 H03055 R53822 AA367558 R75872 W04151 AI220869 AI090290 AA368730 R94434 H81153 H70950 AA367783 H81514 H53536 C16968 C17797 C17677 C17064 AA082581 C17044 D63217 C18791 D78839 D63290 D78838 N91085 H54070 R80360 H78318 H40199 R33887 R02529 H94918 R00900 T87029 AA131924 R99891 AA004267 D78764 D78757 H61600 C18615 H60972 R98784 W86323 R09737 C17492 D78811 R67494 D78775 AA368244 H12650 D79043 AW957062 R82759 C19002 H01715 W28614 W27435 AI983043 AA364395 AW572472 AW190386 AI129278 AI913081 AW473549 AA830713 AI982871 AI638647 AI828466 AW572486 N52583 N89687 AW075567 AI571047 AI887479 AI559469 AI685802 AA805256 AI458777 AA974369 AI866929 AI886032 AI823925 AI823566 AW198135 AI287510 AI565910 AA765775 AI866019 AI263697 AI355825 R42668 AA894603 AW105585 AI824555 AW339175 D20479 NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 AW303285 AW117396 AA888929 BE174517 Z70704 AL042292 H54958 AA310063 AW499643 AW501380 AW501202 AW501293 AW501596 AW630166 AL041326 AA780690 L40517 U21556 AI093182 AW062487 AA883387 AA931302 BE252601 BE258381 AA827330 AL043930 AA356337 AW962830 AW393814 Z70703 AW389484 T62231 AW780049 AL043931 BE149744 AW963292 BE439669 BE091737 BE091657 AA484004 AI673095 AA599106 AW601545 AI538739 AI538730 AI521786 AW366369 AW021010 AA362576 AI289927 AA382592 AA608733 T74884 AA620552 U42359 N57493 H01052 AW206193 AW137594 AI953685 AI919143 AI424371 AW007698 AW025681 AI954289 R40438 AW070364 AI679653 AI679081 AI623213 AI652310 AI631411 AI565384 AI566734 AA149597 AI538172 AI040831 AI770021 AI914287 AA279311 W73001 AI493117 AI693374 AI802007 AI990645 N29752 R94559 AA806475 AA806828 R90998 R94558 AW300112 W24097 AW003016 N91920 T47910 AA029703 T91015 AF093097 AI869509 T27070 AA326718 AA024743 W23922 AA479593 AI765668 W23908 U92986 AA081632 N50578 AA065245 AW365046 AW365014 AA961091 AA150231 H53426 AA234651 N50522 T79343 T87399 N91858 H41179 AW009453 AA024744 T27069 AI346379 H88431 AA152289 R45373 AA477432 AI745607 AI807602 H41152 AA065244 AI242569 AI091032 AI251849 F03857 H88369 AI174488 AI002696 H53427 T87293 N91869 W35270 AA453723 AA453705 AW071829 AI393866 AW071807 W23592 AI342074 D31158 AA833756 AI991896 AA447791 AI864125 AW377239 AA295365 AI687970 R34076 F07607 AA521310 AW499865 R94584 R21283 AA350256 H68126 M21305 N24829 X94563 H58818 AA211777 AA401807 AA195191 AA190578 AI632307 AA195227 AA743633 AI823408 AI832203 AI653114 AA205307 AW021913 AI687980 AI674198 AI675663 AI417935 AA707350 AA135157 AI434721 AI151036 AI038305 R52643 AA780141 AW207645 D19691 AI474370 AA401739 N22905 N70378 D30715 AA251089 AA598484
---	--------	---------	--

Table 72A shows the Seq ID No, Pkey, ExAccn, UnigeneID, and Unigene Title for all of the sequences in Table 73.

80	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title



Seq ID No: Seq ID number correlation for those sequences in Table 73

	Pkey	ExAccn	UnigeneID	Unigene Title	Seq ID No
5	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	Seq ID No B1 & B2
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	Seq ID No B3 & B4
	101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	Seq ID No B5 & B6
	447761	AF061573	Hs.19492	protocadherin 8	Seq ID No B7 & B8
	428183	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	Seq ID No B9 & B10
10	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	Seq ID No B11 & B12
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	Seq ID No B13, B14, & B15
	104659	AW969769	Hs.105201	ESTs	Seq ID No B16
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	Seq ID No B17 & B18
	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	Seq ID No B19 & B20
15	100299	D49493	Hs.2171	growth differentiation factor 10	Seq ID No B21 & B22
	116301	AW969706	Hs.293332	ESTs	Seq ID No B23 & B24
	106533	AL134708	Hs.145998	ESTs	Seq ID No B25-B27
	131313	R96290	Hs.75874	ribosomal protein L44	Seq ID No B28 & B29
	105316	AI671245	Hs.24835	hypothetical protein FLJ14594	Seq ID No B30 & B31
20	113003	AW292315	Hs.7215	ESTs	Seq ID No B32
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	Seq ID No B33 & B34
	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	Seq ID No B35-B40
	123308	C14187	Hs.157208	ESTs	Seq ID No B41 & B42
	120147	AI917116		hemoglobin, beta	Seq ID No B43
25	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	Seq ID No B44 & B45
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	Seq ID No B46 & B47
	105301	AW352357	Hs.7457	MAGE1 protein	Seq ID No B48 & B49
	128478	AA708205	Hs.100343	ESTs	Seq ID No B50-B53
	106111	AW875398	Hs.6451	PRO0659 protein	Seq ID No B54 & B55
30	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	Seq ID No B56 & B57
	120830	AI568170	Hs.96886	ESTs	Seq ID No B58 & B59
	127664	AA806164	Hs.116502	ESTs	Seq ID No B60
	102725	AB026187	Hs.159156	protocadherin 11	Seq ID No B61 & B62
35	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	Seq ID No B63 & B64
	130637	AA356764	Hs.17109	integral membrane protein 2A	Seq ID No B65 & B66
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	Seq ID No B67 & B68
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	Seq ID No B69 & B70
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	Seq ID No B71 & B72
	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	Seq ID No B73 & B74
40	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	Seq ID No B75 & B76
	420462	AF050147	Hs.97932	chondromodulin I precursor	Seq ID No B77 & B78
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No B79 & B80
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	Seq ID No B81 & B82
45	416836	D54745	Hs.80247	cholecystokinin	Seq ID No B83 & B84

Table 72B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

50	Pkey	CAT Number	Accession
	131307	3138_1	NM_000025 X72861 X70811 M29932 X70812 S53291 AW015148 AW581776 AI276134
	131313	93372_1	R96290 H02411 C18327 AA367588 AA367557 H89632 C17954 AA568860 AI752983 AA699451 H04260 AI128118 AW193364 N94503
55			AA029995 T40536 AA368746 AI189909 BE047384 AA747591 R22855 AI032539 AI151343 AA148534 H63941 T49595 AA694405 H74226
			AI200363 R79731 AA702947 AI400076 AI088494 C17938 AA599478 H02962 R77665 C17370 R56618 H73711 R58545 D79189 AW265710
			R77664 T52101 AW953745 AW953739 D79107 AA029105 AW953738 AA456487 R67000 AA156623 AA368336 H63662
	116301	52669_2	AW969706 AA456258 AA491881 BE501639 D62113 AW969710 AI591236 AI379869 AW968997 AA040053 AI807206 AW663917 AA454645
60	103080	17092_1	AA489238 BE241958 AA743491
			AU077231 AA852219 M74092 X59798 M64349 NM_001758 AA226806 M73554 BE409154 AA160096 BE384352 AA160820 BE382880
			BE261734 AA113821 BE407745 AA156380 BE390287 BE390020 AA100854 AA127152 AW794066 AW367101 AW367093 U47703 AI347077
			W05266 AI824103 AI499061 AA642944 AI042556 AA906539 W60380 AI571777 AL135581 AA112340 N75459 AA592929 AI085348 AI278890
			AA126942 AI023701 AI873252 AA156319 AI190622 W60289 AI274886 R81309 AA100801 AA227161 AI568929 AA160603 AI074344 AI344561
65			AI150778 AA852218 AA158286 N20142 AA622148 AA864225 AA576367 AW182124 T89175 AI758455 AA780573 N71757 R81200 AI659596
			AI674613 AA642544 AW503909 AA128851 W39350 N40420 AA113072 BE168116 AI620604 AI298125 BE075272 N40078 BE075109 BE080779
			AI918938 BE168117 BE087369 AW995539 BE080949 BE080727 BE075271 BE075108 BE080955 BE089655 BE081115 AW750304 H66084
			AI146884 BE075154 AW992247 AI186525 AI752230 AW263140 W03329 N26056 AA948080 AA113073 H99284 AA227101 AA631077
70			AA148042 AI740837 BE082728 AA149570 W44495 BE089351 AA375044 N26775 H27771 AA064705 BE091204 R89337 N32676 N27141
			BE164704 H98049 W67603 AA425549 W31090 AA807411 BE173280 BE000178 T09020 W23852 AA062709 BE167894 AA076515 R97329
			BE541980 N42086 AA102307 AA113772 BE276181 H20622 W44436 W67604 W46412 AW771113 AI700678 AA502628 AA133137 BE274186
			BE396090 BE613371 BE612645 W46650 W95203 W92651 AI087288 R76299 AW604781 N55320 AI912334 AA403248 AW169156 H24970
			AW298822 AW080962 AI073747 W24123 AA577596 H21715 H27925 H26436 AI288304 AA148043 AA204678 BE047090 W48631 AA908347
			AA599485 AI276505 AI953979 AA563710 H25674 H51747 AA425389 AA516104 AI095335 T77237 AA151696 T92084 AI689037 AI624162
75			W49709 AW514883 AA100676 AI366087 AA069474 AA525859 AW771076 AA029402 AA994114 AI351505 AW770816 AI333594 AI289794
			AI346589 AA487700 AI081104 AA613344 AI377520 AI284911 AI311390 AA622062 AI055890 AI660881 AI366117 AA403090 AI272818
			AI073353 W46300 AA062689 AI755078 AI753397 AI633564 AI273471 AI339890 AA699584 AA983722 AI079968 AI752231 AA076431 AA113245
			AI168564 AA918965 AI066484 AI123599 AI921518 W94586 AA535600 AA064665 AA705388 AA064623 AA962503 AI924926 AW131206
80			AW275281 AI280632 T29597 W48728 AW954336 W38317 W94768 AI084717 W46567 AI245645 AW302501 N72201 AW510563 AW079132
			AA207064 AI143740 AW440672 AA632154 AI290286 AI350704 AI271377 AA025369 AI864756 T77451 H97348 AA852165 AI932951 N98526
			AA487486 R92970 AA934071 AI080448 AA063257 C05786 N99099 R42969 AA887065 AA662686 AA533833 AA662304 H51748 BE539444
			AI382164 AI814595 BE537043 AI168307 BE408935 AA453606 R89428 AA936527 AA936890 AW369618 AW264602 R18074 AI474189
			AW372354 AI094358 R37210 AA948510 AA226909 BE172527 AI086652 BE408324 AW292848 AI768962 BE540703 BE409478 AA931692

5	132520	45737_1	AA257992 AA317029 AA362097 D17042 H48100 AW838107 AW838106 AW838110 AW838231 AW610241 AW838442 AA045061 AW384991 BE000988 AA131806 BE180577 AW838269 AL039831 AI754380 C06051 AA131737 AW838239 AI767465 AI480134 AA610312 AW838190 AA379252 AW838282 AA484027 AI423413 AI685064 BE328307 AI241857 AW838281 AW838284 AI671267 AI814928 AA828367 AI476306 AI270180 AA622362 AI076497 AI635919 AI444994 AI194028 AI669159 AI928131 AA448853 AI350143 AW079289 AW467807 AA480442 AA522935 BE180570 AW380087 AW380109 AI081015 AI690818 AI589485 AI698510 AA642019 AA714366 AI580433 AA985527 AI740475 C21398 AA257993 AI302393 AI689018 AW770194 AW753750 AI079164 BE550338 AA559851 T16108 AI864822 AI932827 AA045095 AA045062 AI954225 AA768569 AA709308 AW958363 N35020
10	117602	10565_4	AB026187 NM_014522 U79247 F13304 AA224524 F10902 R39431
	102725	11582_1	AW753865 F07644 F11280 F06355 F08136 U79299 F07459 F08750 F12419 F12842 F06488 F08585 F13403 F05921 F05512 F11683 F05416
	102745	13186_1	F12841 F12810 F05418 F12850 R24551 F06276 H11803 H10237 H11542 H22894 R59563 H19351 H18722 F11237 F08507 H23123 R61595 F07796 F06201 F12289 F07107 T78113 F08734 F13344 F05760 F11784 F08780 F05835 R20588 F07739 F11497 R17410 H17414 R20440 T66090 R25292 T66236 T78766 T79908 R25286 R60071 C14761 AW905192 AA331914 AW965291 H09000 F05212 F08313 F05825 H06399 H15135 H11378 R66424 R61541 AA235405 AI205041 R59564 H23124 H18638 R37359 AI571275 R41780 T66174 T66159 R54102 W07657 H10794 R52337 R42890 H14354 R40952 T17391 H12068 R56797 R51000 R60011 R37617 R39434 H29286 T16403 H09129 R49114 H15161 H11729 R39160 H10468 H24454 H11432 R54433 H08768 H24042 H09511 H17281 H15292 R37849 AI991965 R52815 R42850 T17390 T16438 T17388 T16285 R48963 R50782 R44247 R46729 R59558 R40696 R43575 R44420 T17403 R37754 R46637 R51039 R40513 T23785 F10433 T16350 H10191 R43688 T23543 H08591 R44351 R37575 R49508 F04379 F04056 F05067 F02010 F09158 F10036 F08900 F02559 F09914 F09434 F05034 H17415 F02644 H10650 F10451 H14589 F10444 T16440 R44517 R46643 F03993 F10443 F02170 F09343 F10414 F04794 F11122 F04997 F03894 AW005932 F02767 F10941 F01777 R45260 F03386 R45261 T65009 F10990 F08942 F01673 H23253 F04533 F02082 F01669 F03689 H09568 R40763 H06400 R50958 N80570 AI082296 AI198226 T23763 AA814486 AW015823 AI886272 H06514 H0515969 F10049 AI984267 AI886279 AA558516 F02071 AI783843 AI804884 F01468 AA730438 AF035301 R38389 R41440 R59468 R14437 T89036 R43560 H10821 R52850 R56722 R14559 T09299 H10467 R25829 F13546 R56796 R51151 D82657 T32952 T68257 H06569 F12430 T74326 H08489 R34430 R13083 H23364 R21134 T77098 AW957157 H24150 H11403 R52336 F12830 T77173 T74281 T77663 T74736 H10649 H12067 R20092 T74735 R54530 R17552 R59557 R54529 H17280 T75171 H14694 T74975 H15291 R18574 R54157 R13446 H15221 R35120 R35031 R21277 R19632 R35820 R50899 R13923 R36771 R26485 R33061 R20100 H24426 H09184 H15958 R19253 H15196 H09510 R36032 R19691 H14402 H14885 T17068
25	119082	34131_1	AF252297 N27888 F13415 R34552 R14377 AA323962 AW611514 AW614097 AW195487 AI026040 AI097663 AA012834 AW969885 AA988198 R49069 AW873673 R37774 F08840 AA484668 AW873664 AA170805 AA170825 AA585275 AA585280 AA012833 U94320 NM_006174 U66275
30	102836	25380_1	AA143045 AW271802 AI017093 AA450183 W93694 AI885044 AI890068 AW264522 AW073559 AI355325 AI051302 AI567686 AI143554
	125770	16581_2	AA527891 AW468784 AI567693 AW884460 AI424892 AA401298 AW244098 AI122936 N24824 AA552932 AA873164 AI308810 N26098 H81852 N20798 AW263947 AI696267 AA494222 AW877967
35	120147	386607_2	AI917116 AA633698 AI580389 Z39483
	113003	420161_1	AW292315 AI090408 AW517041 AI928695 AI092060 AA716741 N98235 T23629
	104659	82594_1	AW969769 AA484137 AI291362 N64753 AL133784 AA007153 BE046923 D59990 C15166 D59991 D60194 AA648108 N76160 D61027 D06030 U29690 AF272890 AA708166 AA010748 R23839 H59572 R23383 AI625747 AA011176 AW665324 H02674 H59573 AA757931 H12502 R66851 AA702310 AA748431 AA749352 C01127 AI003679 T96352
40	105301	27795_5	AW352357 AA852419 T80568 AA332510 AW149659 AA341609 AA809550 AI183690 AA730875 T31719 AW965361 AA779709 T05461 AA564806 AI142536 AI553857 D53384 D53747 D54101 D55112 AW071935 AI082447 AI290911 AW168872 AI4199743 AI091646 AI246702 AI271662 AW117296 AI032138 AI741489 AI538705 AA233541 AI682685 AW136268 AI689641 AA599916 AI174443 AI432175 AI131328 AW136277 AA852418 AA240335 T03902 C15551 D52660 H08108 AA844525 AI420648 AI282445 AW068986 AW497637 AA779042 AA298564 BE262936
45	105316	181763_1	AI671245 D81062 AI085879 AI193252 AI870535 N23132 H97661 H18098 AA552173 AA233924 AA503379 H19618 D60732 F04762 H11343 AW590283
	127664	394361_1	AA806164 AA678564 AW978234 AW023951 AA651859 AI699785 AA913686 AW974569 AI681287
	106111	4671_1	AW875398 AI064861 NM_014138 AF090943 BE071887 BE547232 BE622599 AI345700 AA284315 AA147700 AW376340 BE220170 BE348475 AA025037 AA057284 AA025038 T16193 AW130196 AW594516 AI989991 AI139091 AW675747 AA830435 AI924977 AI670778 AI051887 AA912574 AW130213 AI828335 AI570587 AI332760 AI313115 AA804653 AA477920 AA147645 AI916912 AW768839 AA715098 AA292723 AA732421 T33122 AI631560 AI698686 AI185386 R43829 AA421638 AA961400 C00503 AA604025 AA554026 AA553885 BE172244 R24040 AA708205 H15963 R20851 L13829 AI934608 AI950163 H92893 AI267243 N66614 H28983 R42031 H06198 AI468628 H92779 L13828 T34896 H09748 R61554 AA350215 R40551
50	128478	370722_2	AI568170 AA731212 AW294848 AW466878 AA568908 AI281804 AI923633 AA347885 AI718854 AA714940
	105782	246361_1	NM_002975 AF020044 AB009244 BE620464 AA541683 AW000991 AW089850 AW664612 AI636676 AI627854 AI885823 AI864548 AI554122
	120830	244476_1	AI499682 AI570905 AI376008 AI871364 AI074230 AI383719 AA905016 AA977446 AA844732 T78922 AW244007 AI924747 AI968230 AI824575
	128797	20410_1	AI699224 AI569490 AW379856 AW292314 AI016874 AW292037
55	106533	305354_1	AL134708 AW206610 AW665919 AW594227 AI917093 AI498361 AA635141 AA453786 D54178 D53224 AI804341 D53111 M78885 AL134707 AA453903 AI278054 AI343349 AI380496 AW235939 D60373 D60993 D81246
60	121619	284072_1	AA528339 AI017218 AA416911
	123049	30801_1	BE047680 AF177395 NM_014421 AB033208 AB035181 W55979 AI093106 AI863392 AA715452 AA300480 AW022313 AA648103 AA720544 D61856 AA481794 AA737112 AW316551 AA714937 AW974378 AI370632 AI184289 AI333962 AA714945
65	129703	64196_1	BE388665 AA740614 AI394542 AA484451 AW070575 AA877654 AI360981 AI475799 BE349560 AI037351 N29437 AI246453 AW083444 AA844441 AI150871 AI440477 AI889061 AA682422 AA680053 AA740212 AI858728 AA490589 AW243692 AI249450 AI304448 AA534421 AI500317 AI273337 AW027729 AI979132 C06120 AI860916 AW591923 AI803174 AI559264 BE250500 AW675522 AA883284 T71033 AI346838 AI066754 AI197913 AA931979 AA427599 AI304730 AI285159 AI273325 AI038450 AI033760 N74972 AA136517 AI304446 AI262652 AA401348 AW514617 AI361795 AW514389 N30307 N93439 AI190775 BE349902 AI342114 AI186831 AA039628 H74242 AI914825 AI955761 AI343851
70			AA693856 T71096 AI498539 AA778995 AA084278 AI274678 AI022673 AW339621 AA704929 AW089735 AA041252 AA161337 AI185333 AW189397 AI160990 AI082392 AI935848 AI144404 AI141633 AA447987 AA464241 AI342103 AW026118 AA834025 AW664459 AA603777
			AA630752 AA115450 N49944 AW166071 AW769795 AA991877 AA873609 AW083441 H99130 AA910538 AA486199 AW083358 AA151767 AI161193 N54945 AA180193 AI423477 AI188387 AI608747 N58900 AI038449 AA136852 AA565913 AA180502 H61741 AA701125 AI127678
			AI278541 R76523 AA666187 H85083 F24755 R77729 AA135137 BE250395 R76239 AW794625 AW794044 H61957 AA308197 AW996031
			AA345524 N52726 AA354360 AA179785 N57375 R16447 AA160645 W21481
75	100299	2801_1	D49493 NM_004962 D49492 AA948479 AA993843 AA017558 AA992567 AA912897 AI185363 AA018254 N93253 AA297544 T19187 R53287
			AA069337 AA297489 N62906 AW023929 AA018253 AA017615 W25110 R52085 R52633 W16549 H88916 H89134 AA069338
	129977	2039_1	NM_000399 AA018140 AF139463 J04076 AW390694 AW361756 AI079830 AI190587 AA731059 AA742743 AI635915 AA878209 AI262612
			AI264201 AA446300 AA715016 AA446027 AI274101 AA593330 AA593338 AW015388 AI681724 AI347984 AL045275 AA970069 AA018188
			AW014396 AW769445 AI588869 AW338296 AI801548 AI367702 AI888410
80	123308	322009_1	C14187 AA496211 D80456 AA484051 D80455 AA528446
	101104	26442_2	AW862258 L07615
	130637	7040_1	AA356764 NM_004867 AF038953 W16828 R50284 AI929589 R01594 AA010474 W37917 N64212 N78175 R57511 AA329322 W77834
			AA169869 AA285240 AA356670 T93146 AA325779 AA357064 AA328151 AA306939 AA306801 N31260 AA306202 AA312530 BE242703
			AA354371 N42259 AL021786 H50965 H38038 AI655965 AI566732 AI953952 AW972835 AI077300 AI948482 AI760966 AA648335 W72197
			N32815 AA768073 AW338181 AW001742 AI819896 AI015666 N58011 AA677584 AI183750 AW105514 W37875 AW301679 AA775257

			AA730357 AI128690 AA630149 AW241515 AI147003 AI183499 N90923 AI968582 AA354145 AI147297 BE550502 AI085777 AI709087 AA773947 AA469192 AI199289 AI127085 H89232 N30719 AI028165 AW029469 AI709314 AA780834 AA778057 H89125 AI654762 T93061 N59622 AI360625 AA719982 AI248242 AA233925 AW262512 AW438666 AA010378 AA484010 AW438790 N22875 AA483718 AI185407 AA736720 AA664587 AA648672 AA503406 AA508123 AA503140 H46638 N75812 AA730938 D60546 AA483039 AA507705 AA480448 AI768654 AA658955 AA730803 AA330312 AW021127 BE172031 AW961052 AA339070 AA648172 BE172892 AA174175 AA492012 AA491590 AW118733 AA484130 AA730783 AA730510 D62577 D62828 AI469294 AI801343 N53447 AA740226 AI831983 AA516146 D79799 AI758212 AA484040 H38039 AI038772 AI039410 AA528387 AA730576 AA527231 AA748111 D62946 U38439 AA721708 H22130 AA559229 H51620 AA283355 AA730970 R01595 N72450 AA469123 AA579389 AA480477 AA283306 AA347822 AA328013 AW248508 AI278454 AI369343 AW291235 AI343946 AI347189 AA970152 AI279668 AI971894 AA664359 AI191039 AA084598 AA081641 AA316181 BE439545 AC005053 AF186249 AW386101 AC004969 AA730199 AA032221 AI686139 AI167942 AA809228 AI184070 AI394674 AW969977 AA032279 AW079284 AA513174 AA888312 AI453179 AA483363 AA528432 AA579511 AU077228 U61145 AL044256 AA206185 AL044975 NM_004456 X95653 AW890905 AA332806 AW965453 BE299226 U52965 BE275009 AA428252 AA769212 AA312778 AA810901 AA461315 AI969286 AI953668 AW296248 AI291422 AA704747 Z44716 BE541235 AW608806 AA588583 AW403788 AW408386 AA053521 T87571 AA581163 BE183241 T97906 R89149 AI808196 BE618521 AI970278 AI652680 AW130143 AI970272 AW197254 BE550449 AI628403 AA010143 AW005107 AA251815 AA805836 N53459 AA055309 AA643678 AI345616 AI345618 AI635728 AI871286 AI018437 AI262514 H75287 AI033155 AI203388 AA205802 AI475265 AW594186 AI696059 AI333312 AW264710 AA876764 AA864892 AA173156 AI292066 T79837 W93995 AA506427 AA815135 AI376342 AA010144 AI310421 AI223350 AA970576 N33926 T89364 AI090913 N55098 AA101673 AA626665 AA251840 N68857 AI890053 H05930 AI474199 AI436166 AA628810 N64452 AI205538 AA055310 BE244495 AI365179 T99536 AI203088 Z40549 AW139858 AA599627 R91847 AA483681 AW068982 H51746 AA091201 H13030 AA459732 T99430 AI051764 R45991 D54745 AU077189 NM_000729 R71188 H87563 R80701 AW956319 AA376289 R82442 H46452 R22481 R64323 AW043690 L00354 AW005571 H19813 AI745597 AI769202 AI205982 AW205841 R64324 AI201975 H46993 C18067 R71189 N29729 AI799838 AI091209 H87455 R82443 AW970995 AW072136 N40841 H13148 AI219052 N30191 T28007 AI817428 AA503602 AF050147 NM_007015 AB006000 AB005999 BE218114 AI703147 AI985891 BE222034 BE549774 BE327618 AI651459 BE549987 AI657194 BE222414 BE046984 AW470357 AW339338 C02526 AW590220 AI298082 AW296998 AI333135 AI867816 AA730514 BE348513 AA405500 AW136179 AA327834 BE327350 BE327366 AW969726 AA424028 AI266636 AI271571 AA423988 AI266634 AA702780 AA452037 AI424866 AA742931 AA483361 AA737106 N35765 N35779 AF086045 N30152 AW374028 AI478237 AA923562 AI382236 AA846668 AI627389 AI371709 H98083 H95983 H26576 H95984 AA745021 AA639180 H26575 AF061573 NM_002590 AA780138 AW135620 AI197884 AA483348 R05468 AW969724 H29216
5			
10	410102	117657_1	
	410268	11897_1	
	414761	14860_1	
15			
20	416836	16233_1	
25	420462	19379_1	
	428183	287965_1	
	439221	46993_1	
30	447761	7355_1	

Table 73: Sequences

Seq ID NO: B1 DNA sequence  
Nucleic Acid Accession #: NM\_053056.1  
Coding sequence: 210..1097

5	1	11	21	31	41	51	
	CACACGGACT	ACAGGGGAGT	TTTGTGAAG	TGCAAAAGTC	CTGGAGCCTC	CAGAGGGCTG	60
10	TCGGCGCAGT	AGCAGCGAGC	AGCAGAGTCC	GCACGCTCCG	GCGAGGGGCA	GAAGAGCGCG	120
	AGGGAGCGCG	GGGCGAGCAG	AGCGAGAGCC	GAGCGCGGAC	CCAGCCAGGA	CCCACAGCCC	180
	TCCCCAGCTG	CCCAGGAAGA	GCCCCAGCCA	TGGAACACCA	GCTCCTGTGC	TGCGAAGTGG	240
	AAACCATCCG	CCGCGCGTAC	CCCGATGCCA	ACCTCCTCAA	CGACCGGGTG	CTGCGGGCCA	300
	TGCTGAAGGC	GGAGGAGACC	TGCGCGCCCT	CGGTGTCTTA	CTTCAAATGT	GTGCAGAAGG	360
15	AGGTCTCTGC	GTCCATGCCG	AAGATCGTCG	CCACCTGGAT	GCTGGAGGTC	TGCGAGGAAC	420
	AGAAAGTGCA	GGAGGAGGTC	TTCGCCCTGG	CCATGAACCTA	CCTGGACCGC	TTCCTGTGCG	480
	TGGAGCCCTG	GAAAAAGAGC	CGCCTGCAGC	TGCTGGGGGC	CACCTGCAATG	TTCGTGGCCT	540
	CTAAGATGAA	GGAGACCATC	CCCCTGACGG	CCGAGAAGCT	GTGCATCTAC	ACCGACAACCT	600
	CCATCCGGCC	CGAGGAGCTG	CTGCAAAATG	AGCTGCTCCT	GGTGAACAAG	CTCAAGTGGA	660
20	ACCTGGCCCG	AATGACCCCG	CACGATTTCA	TTGAACACTT	CCTCTCCAAA	ATGCCAGAGG	720
	CGGAGGAGAA	CAAAAGATC	ATCCGCAAAAC	ACGCGCAGAC	CTTCGTGTC	CTCTGTGCCA	780
	CAGATGTGAA	GTTCAATTTCC	AATCCGCCCT	CCATGGTGGC	AGCGGGGAGC	GTGGTGGCCG	840
	CAGTGCAAAG	CCTGAACCTG	AGGAGCCCCA	ACAACTTCCT	GTCCCTACTAC	CGCCTCACAC	900
	GCTTCTCTCT	CAGAGTGATC	AAGTGTGACC	CAGACTGCCT	CCGGGCGCTG	CAGGAGCAGA	960
25	TCGAAGCCCT	GCTGAGTCA	AGCCTGCGCC	AGGCCACGCA	GAACATGGAC	CCCAAGGCCG	1020
	CCGAGGAGGA	GGAAGAGGAG	GAGGAGGAGG	TGGACCTGGC	TTGCACACCC	ACCGACGTGC	1080
	GGGACGTGGA	CATCTGAGGG	GCCAGGCGAG	GCGGGCGCCA	CCGCCACCCG	CAGCGAGGGC	1140
	GGAGCGCGCC	CCAGGTGCTC	CCCTGACAGT	CCCTCCTCTC	CGGAGCATTT	TGATACCAGA	1200
	AGGGAAAGCT	TCATTCTCCT	TGTTGTGTTG	TGTTTTTTCC	TTTGTCTCTT	CCCCCTTCCA	1260
30	TCTCTGACTT	AAGCAAAAGA	AAAAGATTAC	CCAAAAACTG	TCTTTAAAG	AGAGAGAGAG	1320
	AAAAAAGAAA	TAGTATTTGC	ATAACCTTGA	GCGGTGGGGG	AGGAGGGTTG	TGCTACAGAT	1380
	GATAGAGGAT	TTTATACCCC	AATAATCAAC	TCGTTTTTAT	ATTAATGTAC	TTGTTTCTCT	1440
	GTTGTAAGAA	TAGGCATTAA	CACAAAGGAG	GCGTCTCGGG	AGAGGATTAG	GTTCATCCTT	1500
	TTACGTGTTT	AAAAAAAGC	ATAAAAACAT	TTTAAAAACA	TAGAAAAATT	CAGCAAAACCA	1560
35	TTTTTAAAGT	AGAAGAGGGT	TTTAGGTAGA	AAAACATATT	CTTGTGCTTT	TCTTGATAAA	1620
	GCACAGCTGT	AGTGGGCTTC	TAGGCATCTC	TGTACTTTGC	TTGCTCATAT	GCATGTAGTC	1680
	ACTTTATAAG	TCATTGTATG	TTATTATATT	CCGTAGGTAG	ATGTGTAACC	TCTTCACTCT	1740
	ATTTCATGGT	GAAGTCACCT	CTTGGTTACA	GTAGCGTAGC	GTGGCCGTGT	GCATGTCCCT	1800
	TGCGCCTGTG	ACCACCACCC	CAACAAACCA	TCCAGTGACA	AACCATCCAG	TGGAGGTTTG	1860
40	TCGGGCACCA	GCCAGCGTAG	CAGGGTCGGG	AAAGGCCACC	TGTCCCACTC	CTACGATACG	1920
	CTACTATAAA	GAGAAGACAG	AATAGTGACA	TAATATATTC	TATTTTTATA	CTCTTCTAT	1980
	TTTTGTAGTG	ACCTGTTTAT	GAGATGCTGG	TTTTCTACCC	AACGGCCCTG	CAGCCAGCTC	2040
	ACGTCCAGGT	TCAACCCACA	GCTACTTGGT	TTGTGTTCTT	CTTCATATT	TAAACCATTT	2100
	CCATTTCCAA	GCACCTTTCA	TCCAATAGGT	GTAGGAAATA	GCGCTGTTTT	TGTTGTGTGT	2160
45	GCAGGGAGGG	CAGTTTCTTA	ATGGAATGGT	TTGGGAATAT	CCATGTACTT	GTTTGCACAGC	2220
	AGGACTTTGA	GCAAGTGTG	GGCCACTGTG	GTGGCAGTGG	AGGTGGGGTG	TTTGGGAGGC	2280
	TGCGTGCCAG	TCAAGAAGAA	AAAGGTTTGC	ATTCTCACAT	TGCCAGGATG	ATAAGTTCCT	2340
	TTCTTTTCT	TTAAAGAAAT	TGAAGTTTAG	GAATCCTTTG	GTGCCAACTG	GTGTTTGAAA	2400
	GTAGGGAACCT	CAGAGGTTTA	CCTAGAGAAC	AGGTGGTTTT	TAAGGGTTAT	CTTAGATGTT	2460
50	TCACACCCGA	AGGTTTTTAA	ACACTAAAT	ATATAATTTA	TAGTTAAGGC	TAAAAAGTAT	2520
	ATTTATTGCA	GAGGATGTTT	ATAAGGCCAG	TATGATTTAT	AAATGCAATC	TCCCTTGAT	2580
	TTAAACACAC	AGATACACAC	ACACACACAC	ACACACACAC	AAACGCTCTG	CCTTTGATGT	2640
	TACAGATTTA	ATACAGTTTA	TTTTTAAAGA	TAGATCCTTT	TATAGGTGAG	AAAAAACA	2700
	TCTGGAAGAA	AAAAACCA	CAAGACATT	GATTACGCCT	GTTTGGCGTT	TCCAGAGTC	2760
55	ATCTGATTGG	ACAGGCATGG	GTGCAAGGAA	AATTAGGGTA	CTCAACCTAA	GTTGCGTTCC	2820
	GATGAATTTT	TATCCCCTGC	CCCTTCTCTT	AAAAAATTTA	GTGACAAAAT	AGACAATTTG	2880
	CACATCTTGG	CTATGTAAAT	CTTGTAAATT	TTATTAGGA	AGTGTGAAG	GGAGGTGGCA	2940
	AGAGTGTGGA	GGCTGACGTG	TGAGGGAGGA	CAGGCGGGAG	GAGGTGTGAG	GAGGAGGCTC	3000
	CCGAGGGGAA	GGGCGGCTGC	CCACACCGGG	GACAGGCCGC	AGCTCCATTT	TCTTATTGCG	3060
60	CTGCTACCGT	TGACTTCCAG	GCACGGTTTG	GAAATATTCA	CATCGCTTCT	GTGTATCTCT	3120
	TTCACATTGT	TTGCTGCTAT	TGGAGGATCA	GTTTTTTGTT	TTACAATGTC	ATATACTGCC	3180
	ATGTACTAGT	TTTAGTTTTT	TCTTAGAACA	TTGTATTACA	GATGCCTTTT	TTGTAGTTTT	3240
	TTTTTTTTTT	ATGTGATCAA	TTTTGACTTA	ATGTGATTAC	TGCTCTATTC	CAAAAAGGTT	3300
	GCTGTTTCAC	AATACCTCAT	GCTTCACTTA	GCCATGGTGG	ACCCAGCGGG	CAGGTTCTGC	3360
65	CTGCTTTGGC	GGGCAGACAC	GCGGGCGCGA	TCCCACACAG	GCTGGCGGGG	GCCGGCCCCG	3420
	AGGCGCGCTG	CGTGAGAAC	GCGCGGCTGT	CCCCAGAGAC	CAGGCGTGTG	CCCTCTTCTC	3480
	TTCCCTGCGC	CTGTGATGCT	GGGCACTTCA	TCTGATCGGG	GGCGTAGCAT	CATAGTAGTT	3540
	TTTACAGCTG	TGTTATTCTT	TGCGTGTAGC	TATGGAAGTT	GCATAATTAT	TATTATTATT	3600
	ATTATAACAA	GTGTGCTCTA	CGTGCCACCA	CGGCGTTGTA	CCTGTAGGAC	TCTCATTCCG	3660
70	GATGATTGGA	ATAGCTTCTG	GAATTTGTTC	AAGTTTGGGG	TATGTTTAAT	CTGTATGTA	3720
	CTAGTGTCTT	GTTTGTATT	GTTTGTGTTA	TTACACCATA	ATGCTAATTT	AAAGAGACTC	3780
	CAAATCTCAA	TGAAGCCAGC	TCACAGTGCT	GTGTGCCCGG	GTCACCTAGC	AAGCTGCCGA	3840
	ACCAAAGAA	TTTGACCCCC	GCTGCGGGCC	CACGTGGTTG	GGGCCCCGCC	CTGGCAGGGT	3900
	CATCCTGTGC	TCGGAGGCCA	TCTCGGGCAC	AGGCCACACC	CGCCCCACCC	CTCCAGAACCT	3960
75	CGGCTCACGC	TACCTCTCAAC	CATCCTGGCT	GCGGCGTCTG	TCTGAACCAC	GCGGGGGCCT	4020
	TGAGGGACGC	TTTGTCTGTC	GTGATGGGGC	AAGGGCACAA	GTCCTGGATG	TTGTGTGTAT	4080
	CGAGAGGCCA	AAGGCTGGTG	GCAAGTGCAC	GGGGCACAGC	GGAGTCTGTG	CTGTGACCGG	4140
	CAAGTCTGAG	GGTCTGGGGC	GCGGGCGGCT	GGGTCTGTGC	ATTTCTGGTT	GCACCGCGGC	4200
80	GCTTCCACGC	ACCAACATGT	AACCGCATG	TTTCCAGCAG	AAGACAAAAA	GACAAACATG	4260
	AAAGTCTAGA	AATAAAACTG	GTAAACCC	AAAAA	AAAAA		

Seq ID NO: B2 Protein sequence  
Protein Accession #: NP\_444284.1

1 11 21 31 41 51  
797

MEHOLLCEVE ETIRRAYPDA NLLNDRVLRA MLKAEETCAP SVSYFKCVQK EVLPSMRKIV 60  
 ATWMLEVCEE QKCEEEVFPL AMNYLDRFLS LEPVKKSRLO LLGATCMFVA SKMKETIPLT 120  
 AEKLCTYTDN SIRPEELLQM ELLLVNKLKW NLAAAMTPHDF IEHFLSKMPE AEENKQIIRK 180  
 HAQTFVALCA TDVKFISNPP SMVAAGSVVA AVQGLNLRSP NNFLSYRLT RFLSRVIKCD 240  
 PDCLRACQEQ IEALLESSLR QAQQNMDFKA AEEEEEEEEEE VDLACTPTDV RDVDI

Seq ID NO: B3 DNA sequence  
 Nucleic Acid Accession #: XM\_044166  
 Coding sequence: 1..1576

1 11 21 31 41 51  
 CTTTGTTC GCCATGCCTA GTCTAGTGGT ATCTGGAATA ATGGAAAGAA ATGGGGGCTT 60  
 TGGAGAAGCTA GGATGTTTCG GGGGAAGCGC TAAGGACCGA GGGCTGCTGG AAGACGAGCG 120  
 CGCCCTTCAG CTGGCTCTCG ATCAACTCTG CCTCCTGGGT TTGGGGGAGC CCCCCGCCCC 180  
 CAGGGCGGGC GAGGACGGGG GAGGTGGGGG GGGCGGCGCC CCGCGCGAGC CGACAGCCCC 240  
 CCGCGAGCGC GCGCGCGCGC GCGCGCCCGC GCGCGCCCGC GCGCGCCCGA CGACGGCCCC 300  
 CGCAGCGCAG ACGCCCCAGC CCCCCACCGC CCCCCAAGGG GCGAGCGAGC CCAAGCTCTG 360  
 CGCTCTCTAC AAAGAGGGCG AGCTGCGCCT GAAGGGCAGC AGCAACACCA CGGAGTGTGT 420  
 TCCGTGCCCC ACCTCCGAGC ACGTGGCCGA GATCGTGGGC AGGCAAGGCT GCAAGATTAA 480  
 GGCCTTAGAG GCCAAGACCA ACACCTACAT CAAGACACCG GTGAGGGGCG AGGAACCAAGT 540  
 GTTCATGGTG ACAGGGCGAC GGGAGGACGT GGCCACAGCC GCGCGGGAAT TCATCTCAGC 600  
 AGCGGAGCAC TTCTCCATGA TCCGTGCTCT CCGCAACAAG TCAGGCGCCG CCTTTGGTGT 660  
 GGCTCCTGCT CTGCGCGGCC AGGTGACCAT CCGTGTGCGG GTGCGCTACC GCGTGGTGGG 720  
 GCTGGTGGTG GCGCCCAAGG GGGCAACCAT CAAGCGCATC CAGCAGCAAA CCAACACATA 780  
 CATTATCACA CCAAGCCGTG ACCGCGACCC CGTGTTCGAG ATCAGCGGTG CCCCAGGCAA 840  
 CGTGAGCGGT GCGCGGAGAG AGATCGAGAC GCACATCGCG GTGCGCACTG GCAAGATCCT 900  
 CGAGTACAA AATGAAACAG ACTTCCTGGC GGGGAGCCCC GACGACGCAA TCGATAGCCG 960  
 CTACTCCGAC GCGTGGCGGG TGCACACAGC CCGCTGCAAG CCGCTCTCCA CCTTCCGGCA 1020  
 GAACAGCCAG GCGTGCATCG GCGAGTGGCG AGTGGACTCT GGCTTTGAGG CCCCACGCCCT 1080  
 GGGTGAAGCAG GCGGGGGACT TTGGCTACGG CCGGTACCTC TTTCCGGGCT ATGGCGTGGG 1140  
 CAAGCAGGAT GTGTACTACG GCGTGGCCGA GACTAGCCCC CCGCTGTGGG CGGGCCAGGA 1200  
 GAACGCCAGC CTGCTGGGGG TGCTCTTCTC CTCTGCTCTC TCCTCCTCCT CTTCTTCCGC 1260  
 CAAGGCCCGC GCTGGGCCCC CCGCGCCACA CCGTCCCCCT GCCACTTCCG CGGGACCCGA 1320  
 GCTGGCCGGA CTCCCAGGCG GCGCCCCGGG AGAGCCGCTC CAGGGCTTCT CTAAACTTGG 1380  
 TGGGGGCGCG CTGCGGAGCC CCGGCGGCGG GCGGGATTGC ATGGTCTGCT TTGAGAGCGA 1440  
 AGTGACTGCC GCCTTTGTGC CCGTGGGACA CAACCTGTTC TGCATGGAGT GTGCAGTACG 1500  
 CATCTGCGAG AGGACGGAGC CAGAGTGTCC CGTCTGCCAC ATCAGAGCCA CGCAAGCCAT 1560  
 CCGAATATTC TCCTAAGCCC CGTGCCCATC GCCTCCGGGG CCGACTCCAC TGGGCCCAAC 1620  
 CTGGAGCTGT TTTCCACTAA AGCCTTTTGG AAAGCGGTGA TTTGAGGGGC AAGGTGCTTA 1680  
 GAGTACTCG CTGCTGGGGG AAGGGGGGAG GGAGGCAAGT GTGGCTGGAG GGTGCGCCAC 1740  
 TTTCAAGACC TCTGGTCACC CTGTCTTGA AAGATTGGA GGGGGCCAGA CTGAAATTT 1800  
 TACTAGAGTT ACAACTCTGA TACCTCAACA CACCTTAAA TCTGGAAGCA GCTAAGAGAA 1860  
 ACTTTTGTGT TGCCAGAGGT GCGCACTAAG GCATCTGAC GCGCTCTGCC CACCTCCCCC 1920  
 GCTGTGTGTC ACTCCACCCC TTCTTCCGAG GAGGGGGTGG GTAAAAGGGA GAGGGAGAA 1980  
 TACCACCTGT ATCTAGAGT GCTCTTGA ATCCCTAAGC CCTCTGGTCC TGACCTCCGA 2040  
 CCTCCAGCT CTGTCTTGT CTGTGTCTTT GTCTTTCTTC CCTTCCCCCT GCCCTGCCC 2100  
 CTACCAGCC AGCTTTGGGG ACACCATCCT TCTGGGGAGA AGTAGGGGGA GGAATATTG 2160  
 GATGGTCCCT CCATCTCCT CTAGGCATCT GGAGGCCCTC TCCCCACTC CTCAAAGAA 2220  
 ACATCTCAA TTATTGATGG AATGTATCCC CATCTCAGT GAAATGTGA GGAGGGGACT 2280  
 AATACTGGG TAAAGGGTCA AACCCACACC TTCATCTA TGGGCATTAT ATTAGGGAG 2340  
 TAGTTCTTGG GCTGGATTCT CTGGTTGTGG AAGTGGGGGC GCCAGAGTAG TGTGTCTGCT 2400  
 ATTTAAAGGA GCAGGAAGGG GCGTGAGGCA GGAGGAGAGA CTGGTGGAGG GAAGAGCTGC 2460  
 TCCTCCCATG CAGTGCCCGA CTCCTGAC CCGCTCAAC CTGACCTGAA CCTTTATTGA 2520  
 ATCCTTATTA GCTTGAATCC TTATTAGCTT GAATCCTCCA TGCAATCAT GGAGTCTGTG 2580  
 TCCCACTTGA TGTGGTTGAG GAGAAGCCAG GTCTTCAAAG AGGGGTGAGC TGTGGGCAAA 2640  
 GCAGGACTGG GGGGAGGGGG GCAGCAGGGC CTATTCTGAG AATCACATAT TGTTACAGGC 2700  
 CTTGCACCCC GTTGTCTGCT TCCCTCTGCG TCATTGTTGGG CTGCCACAG CTCTCCACCC 2760  
 TCCTGGTTCC CTGGCCGGG CCAAGAGAGG ATGGAGGAT GGGAGTCCCA GGAGATCCTT 2820  
 GTAAATAGTG GGGTGGGACT GTTCTGAGTG ATCAGCCGAG CACTTAAAGC TCCAGAGTCC 2880  
 CATTTCTCCT GGATGGAGCA GGTGGAGGTG CAGAGGGGAT TTCTCTCTCT CCTTCTCTCT 2940  
 GTCGAGAAT AACACCTCT CACAGCCTTC CCGTCCAGAA CACAGCCAG GGAGGGGTGG 3000  
 GGAAGGAGGT CACAGCCAAG AAACTGCCCT TGTGACGACT TCCCTCTCTC CCGCTATGT 3060  
 GAGCCATCCT GAGATGTCTG TACAATAGAA ACCAAACCAA ATGGGCACCC TCGTTGCCG 3120  
 GGGGGCAGGT GGGGAGGGGG GTGGGAAGAA GGGATGTCTG TCTGTCGTCC CCTTCCCCCT 3180  
 CTCACCTCT TACCCACAAA GGCAGAAGAC TGTACACTA GGGGGCTCAG CAAATTCAT 3240  
 CCCACCTTA CCAATTGAGC CAAACCTAGA AACAAACACA AACACGAAT AGTGAGAGAC 3300  
 AAAATAGAG AGAGAAAGAG AGCATGAGAG GGAGCGAGAC AGGCGACCAA CACAGAGGAG 3360  
 AGAAACAAA AATAGCAAAA AAAAAAATAA AAAGCAGTTC TTTATAATTT AATATTCTAT 3420  
 TTTAATAAAG GCGTTTATTA CCATATAAAT GTAGCAAGA ACCTGGGCTA ATATGAA

Seq ID NO: B4 Protein sequence  
 Protein Accession #: XP\_044166.2

1 11 21 31 41 51  
 FCFAMPSLVV SGIMERNGGF GELGCFGGSA KDRGLEDER ALQLALDQLC LLGLGEPPAP 60  
 RAGEDGGGGG GGAPAQPTAP PQPAPPPPPA APPAAPTAP AAQTPQPPTA PKGASDAKLC 120  
 ALYKEAELRL KGSSNTTECV PVPTSEHVAE IVGRQCKIK ALRAKTNTYI KTFVRGEEPV 180  
 FMVTGRREDV ATAREIISA AEHFSMIRAS RNKSGAAGV APALPGQVTI RVRVPRVVG 240  
 LVVGPKGATI KRIQQQTNTY IITPSRDRDP VFEITGAPGN VERAREEIEI HIAVRTGKIL 300  
 EYNNENDFLA GSPDAIDSR YSDAWRVHQP GCKPLSTFRQ NSLGCIGECG VDSGFAPRL 360  
 GEQGGDFGYG GYLFPYGVG KQDVYYGVAE TSPPLWAGQE NATPSTVLFS SASSSSSSSA 420

KARAGPPGAH RSPATSAGPE LAGLPRRPPG EPLQGFSLKG GGGLRSPGGG RDCMVCFESE 480  
 VTAALVPCGH NLFCECAVR ICERTDPECP VCHITATQAI RIFS

Seq ID NO: B5 DNA sequence  
 Nucleic Acid Accession #: NM\_000909.1  
 Coding sequence: 209..1363

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55

1	11	21	31	41	51	
CATTCCCACC	CTTCTTCTT	TAATAAGCAG	GAGCGAAAAA	GACAAATTCC	AAAGAGGATT	60
GTTTCAGTTC	AGGGAATGAA	GAATTCAGAA	TAATTTTGGT	AAATGGATTC	CAATATCGGG	120
AATAAGAATA	AGCTGAACAG	TTGACCTGCT	TTGAAGAAAC	ATACTGTCCA	TTTGTCTAAA	180
ATAATCTATA	ACAACCAAAC	CAATCAAAAT	GAATTCACAA	TTATTTTCCC	AGGTTGAAAA	240
TCATTTCAGT	CACCTCTAAT	TCTCAGAGAA	GAATGCCCCAG	CTTCTGGCTT	TTGAAAATGA	300
TGATTGTCTC	CTGCCCTTGG	CCATGATATT	TACCTTAGCT	CTTGCTTATG	GAGCTGTGAT	360
CATTCTTGGT	GTCTCTGGAA	ACCTGGCCTT	GATCATATTC	ATCTTGAAAC	AAAAGGAGAT	420
GAGAAATGTT	ACCAACATCC	TGATTGTGAA	CCTTCTCTTC	TCAGACTTGC	TTGTTGCCAT	480
CATGTGTCTC	CCCTTTACAT	TTGTCTACAC	ATTAATGGAC	CACCTGGGCT	TTGGTGAGGC	540
GATGTGTAAG	TTGAATCCTT	TTGTGCAATG	TGTTTCAATC	ACTGTGTCCA	TTTCTCTCT	600
GGTTCCTCATT	GCTGTGGAAC	GACATCAGCT	GATAATCAAC	CCTCGAGGCT	GGAGACCAAA	660
TAATAGACAT	GCTTATGTAG	GTATTGCTGT	GATTGGGGTC	CTTGCTGTGG	CTTCTTCTTT	720
GCCTTTCTCT	ATCTACCAAG	TAATGACTGA	TGAGCCGCTC	CAAAATGTAA	CACCTGTATGC	780
GTACAAAAGC	AAATACGTC	GCTTTGATCA	ATTTCCATCG	GACTCTCATA	GGTGTCTTAA	840
TACCACTCTC	CTCTTGGTGC	TGCAGTATTT	TGGTCCACTT	TGTTTATAT	TTATTTGCTA	900
CTTCAAGATA	TATATACGCC	TAAAAAGGAG	AAACAACATG	ATGGACAAGA	TGAGAGACAA	960
TAAAGTACAG	TCCAGTGAAA	CCAAAAGAAT	CAATATCATG	CTGCTCTCCA	TTGTGGTAGC	1020
ATTTGCAGTC	TGCTGGCTCC	CTCTTACCAT	CTTTAACTAT	GTGTTTGATT	GGAATCATCA	1080
GATCATTTGCT	ACCTTGAAC	ACAATCTGTT	ATTCCTGCTC	TGCCACCTCA	CAGCAATGAT	1140
ATCCACTTGT	GTCAACCCCA	TATTTTATGG	GTTCTGAAC	AAAAACTTCC	AGAGAGACTT	1200
GCAGTTCTTC	TTCAACTTTT	GTGATTTCCG	GTCTCGGGAT	GATGATTATG	AAACAATAGC	1260
CATGTCCACG	ATGCACACAG	ATGTTTCCAA	AACTTCTTTG	AAGCAAGCAA	GCCAGTCGCG	1320
ATTTAAAAAA	ATCAACAACA	ATGATGATAA	TGAAAAATC	TGAAACTACT	TATAGCCTAT	1380
GGTCCCGGAT	GACATCTGTT	TAAAAACAAG	CACAACCTGC	AACATACTTT	GATTACCTGT	1440
TCTCCCAAGG	AATGGGGTTG	AAATCATTTG	AAAATGACTA	AGATTTTCTT	GTCTTGCTTT	1500
TTACTGCTTT	TGTTGTAGTT	GTCAATAAT	CATTGGAAC	AAAAGGTGTG	GGCTTTGGGG	1560
TCTTCTGGAA	ATAGTTTTGA	CCAGACATCT	TTGAAGTGCT	TTTTGTGAAT	TTATGCATAT	1620
AATATAAAGA	CTTTTATACT	GTACTTATTG	GAATGAAATT	TCTTTAAAGT	ATTACGATGC	1680
GCTGACTTCA	GAAGTACCTG	CCATCCAATA	CGGTCAATAG	ATTGGGTCTC	TGTGATTAGA	1740
TTAGATTAGA	TTAGATTCTG	AACGAGTTGG	GCCATCCTTA	CTTTATGATA	GGCATCATTT	1800
TAGTGTGTTA	CAATAGTAAC	AGTATGCAAA	AGCAGCATTC	AGGAGCCGAA	AGATAGTCTT	1860
GAAGTCATT	AGAAGTGGTT	TGAGGTTTCT	GTTTTTGGT	GGTTTTTGT	TGTTTTTTTT	1920
TTTTTTCACC	TAAAGGGAGT	CTTTCAATTC	CTCCGACTG	ATTGTCACCT	AAATCAAAAT	1980
TTAAAAATGA	ATAAAAGAG	ATACTTCTCA	GCTGCAAAAT	TTATGGAGAA	TTGGGCACCC	2040
ACAGGAATGA	AGAGAGAAAG	CAGCTCCCCA	ACTTCAAAAC	CATTTTGATA	CCTGACAACA	2100
AGAGCATTTT	AGAGTAAAT	ATTTAATAAA	GTAAATTAGT	ATTGCTGCAA	ATAGCTAAAT	2160
TATATTTATT	TGAATTGATG	GTCAAGAGAT	TTTCCATTTT	TTTACAGAC	TGTTTCAGTG	2220
TTGTCAAGCT	TCTGCTCTAA	TATGTACTCG	AAAGACTTTC	CGCTTACAAT	TTGTAGAAAC	2280
ACAAATATCG	TTTTCCATAC	AGCAGTGCTT	ATATAGTGAC	TGATTTTAA	TTTCAATGTC	2340
CATCTTTCAA	AGGAAGTAAC	ACCAAGGTAC	AATGTTAAAG	GAATATTCAC	TTTACCTAGC	2400
AGGGAAAAAT	ACACAAAAAC	TGCAGATACT	TCATATAGCC	CATTTTAACT	TGTATAAACT	2460
GTGTGACTTG	TGGCGTCTTA	TAAATAATGC	ACTGTAAAGA	TTACTGAATA	GTTGTGTCT	2520
GTTAATGTGC	CTTCAAGTGC	GTATCTTGTA	ATCATGATTG	AGCCTCAGAA	TCATTGGAG	2580
AAACTATATT	TAAAGAGACA	AGACATACCT	CAATGTATTA	TACAGATAAA	GTATTACATG	2640
TGTTTGATTT	TAAAGGGCG	GACATTTTAT	TAAATCAAT	ATTGTTTTTG	CTTTTCTGTA	2700
GGAGTCTCTT	CAGTTTCTAT	TTTTTCTCAT	CCCATGACTT	CCCTCCGATG	GT	

Seq ID NO: B6 Protein sequence  
 Protein Accession #: NP\_000900.1

60  
 65  
 70

1	11	21	31	41	51	
MNSTLFSQVE	NHSVHSNFSE	KNAQLLAFEN	DDCHLPLAMI	FTLALAYGAV	IILGVSGNLA	60
LIIIIILKQKE	MRNVTNILIV	NLSFSDLLVA	IMCLPFTFVY	TLMDSHVVFE	AMCKLNPFVQ	120
CVSITVSIFS	LVLIAVERHQ	LIINPRGWRP	NNRHAYVGIA	VIWVLAVASS	LPFLIYQVMT	180
DEPFQNVITLD	AYKDKYVCFD	QFPDSHRLS	YTTLLVLQY	FGPLCFIFIC	YFKIYIRLKR	240
RNNMMDKMRD	NKYRSSETR	INIMLLSIVV	AFAVCWLPIT	IFNTVFDWNH	QIIATCNHNL	300
LFLLLCHLTAM	ISTCVNPIFY	GFLNKNFQRD	LQFFNFCD	RSRDDDYETI	AMSTMHTDVS	360
KTSLKQASPV	AFKKNNNDD	NEKI				

Seq ID NO: B7 DNA sequence  
 Nucleic Acid Accession #: NM\_002590.2  
 Coding sequence: 204..3416

75  
 80

1	11	21	31	41	51	
GCTTCTGTAA	GAGACGGAGA	GGCGCAGAGT	GAGGGCGGGT	CCGCGCGTCC	TCAGAGCCCG	60
CTGGAGGCTC	GGAGCTGCTA	CCCGCAGACT	TCTCCCGCAC	AGGGCTCGCA	AAGAGCGTGA	120
TTCCGAGAGC	CTGAGACTGA	CGCCCGACCT	GGAAACCAGA	GAAGACTTCC	TTAGCCTTTC	180
GGATCGCACT	TGAGGCTGGA	GGCATGAGTC	CTGTGAGGCG	TTGGGGCAGC	CCCTGCCCTT	240
TCCCCTTGCA	GCTCTTCAGC	CTCTGCTGGG	TGCTCTCAGT	GGCCCGAGAG	AAAACAGTCC	300
GATACAGCAG	CTTCGAGGAG	GATGCCCCCG	GCACGGTCA	CGGGACCCCTG	GCCGAGGACC	360
TGCATATGAA	AGTATCGGGT	GACACAAGCT	TCCGCCTGAT	GAAGCAATTC	AACAGCTCTC	420
TGCTCCGGGT	GCGGAAGGCG	GACGGGCAGC	TGACCGTCCG	GGACGCCGGC	CTGACCGCGG	480
AGCGGCTGTG	TGGCCAGGCC	CCGAGTGCG	TGCTGGCCTT	CGATGTGGTC	AGCTTCTCGC	540

5 AGGAGCAGTT CCGGCTGGTG CACGTGGAGG TAGAGGTGAG GGACGTCAAC GACCACGCGC 600  
 CGCGCTTCCC CAGGGCCAG ATCCCGTAG AGGTGTCCGA GGGTGCAGCA GTGGGCACGC 660  
 GCATCCCTTT GGAGGTGCCG GTGGACGAGG ACGTGGGCGC CAACGGGCTG CAGACCGTGC 720  
 GCCTGGCCGA GCCGACAGC CCCTTTCCGC TGGAGCTGCA GACGCGAGCG GACGGCGCTC 780  
 AGTGCAGAGA CCTGGTGGTG CTGCAGGAGC TGGACCGCGA GAGCCAGGCC GCCTACAGCC 840  
 TGGAGCTGGT GGCCAGGAC GGGGCGGCC CGCGCGCTC CGCCACGGCT GCCCTCAGCG 900  
 TGGCGTCTCT GGATGCGAAT GACCACAGCC CGGCCTTCCC GCAGGGCGCC GTGGCCGAAG 960  
 TGGAGCTGGC GGAAGACGCG CCCGTGGGCT CCCTGCTTCT CGACCTGGAC GCAGCCGACC 1020  
 CGCAGCAGGG ACCTAACGGC GACGTGGTGT TCGCATTTGG CGCCCGCACC CCGCCGAGG 1080  
 CGCGCCGCTT CTTCGGCTT GACCCGCGAT CAGGCCGCT CACCCTGGCC GGGCCCGTGG 1140  
 ACTACGAGCG TCAGGACACC TACGAGCTGG ACGTGCGGGC GCAGGACCGC GGACCCGGGC 1200  
 CCCGCGCTGC CACCTGCAAG GTCATCGTGC GCATCCGAGA CGTCAATGAC AACGCACCCG 1260  
 ACATCGCCAT CACCCCGCTG GCCGCCCCAG GCGCGCCGGC AACCTCACCC TTCGCCGCTG 1320  
 CCGCCGCGCC CGCTGCACCT GGGGGAGCGG ACGTAGCTC GCGGCGGGA GCCGGGACGC 1380  
 15 CGGAGGCTGG TGCCACTTCG CTGGTGCCGG AGGGGGCGGC GCGGAGAGC CTGGTGGCCC 1440  
 TGGTCAGCAC CTCGACAGG GACTCGGGCG CCAACGGGCA AGTGCCTGTC GCCCTCTATG 1500  
 GGCACGAGCA CTTCCGCGTG CAGCCGGCCT ACGCGGGCAG CTACCTGGTG GTGACCGCGG 1560  
 CGTGCCTGGA CCGCGAAGC ATCGCCGAGT ACAACTTGAC GCTGGTGGCC GAGGATCGCG 1620  
 20 GCGCGCCCCC GCTGCGCACA GTGCGGCCCT ACACGGTGCG TGTGGGCGAG GAGAACGACA 1680  
 ACGCGCCGCT CTTACGCGGG CCGGTCTATG AGGTGTCCGT GCGCGAGAAC AACCCGCCAG 1740  
 GCGCCTACCT GGCCACGGTG GCCGCCCGCG ACCGGGACCT GGGCCGCAAC GGCCAGGTCA 1800  
 CCTACCGGCT GCTGGAGGCC GAGGTGGGCC GCGCGGGGGG CGCCGTGTCC ACTTATGTCT 1860  
 CGGTGGACCC AGCTACCGGA GCCATCTACG CGCTGCGCAG CTTGCACTAT GAGACGCTGC 1920  
 25 GCCAACTCGA CGTTCGCATC CAAGCTAGCG ACGGCGGCTC CCCTCAGCTT TCCAGCAGCG 1980  
 CCCTAGTGCA AGTGCGCGTG CTGGACACGA ACGACCATGC GCCAGTCTCT GTGCACCCGG 2040  
 CGCCAGCCAA TGGCTCCCTA GAAGTGGGCG TGCTTGGGCG CACCGCAAAG GACACGGTTG 2100  
 TGGCCCGTGT GCAGGCCCGG GATGCAGACG AGGGAGCCAA CGGGAGAGCTG GCGTTCGAGC 2160  
 TGCAGCAGCA GGAGCCGCGC GAAGCCTTCG CCATCGGCGG CCGCACGGGG GAGATACTGC 2220  
 TCACCGGCGA CCTCTCGCAG GAGCCACCCG GTCGCGTGT CAGGGCGCTC CTGGTTCATAT 2280  
 30 CCGACGGCGG CCGTCCCCCG CTCACACCA CCGCAACTGT CAGCTTCTGT GTAACAGCAG 2340  
 GGGGCGGGCG TGGGCGGCTG GCGCTGCCA GTGCAGGAAG CCCGAGCGT TCCGCCCCG 2400  
 CTGGCTCTCG GCTCGGGGTG TCCGGGTGCG TGCTGCAATG GGACACGCCG CTGATCGTCA 2460  
 TCATCGTGTG GGCCGGGAGC TGCACGCTGC TGCTGGCCGC CATCATCGCC ATCGCCACCA 2520  
 35 CCGTCAACCG CCGCAAGAAG GAGGTGCGCA AAGGGGGGCG CCTCGGGGAA GAGCGGCCG 2580  
 GGGCGGCGGG CGCGGAGGCC TCGGCTCCCG GCTCCCCGGA GGAGGCCGCC CGGGGAGCCG 2640  
 GGCCCAAGGC CAACATGTTT GACGTGCTCA CCTTCCCTGG CACCGGCAAA GCGCCCTTTG 2700  
 GCAGCCCGCG GCGGACGCGG CCTCGCCTG CGGTGCGCGC GGGCGAAGTG CCGGGCTCAG 2760  
 AGGGCGGCGG CGCCACTGGG GAAAGCGCCT GTCACTTCGA GGGGCGAGC CGGCTCCGCG 2820  
 40 GCGCGCACGC CGAGCCCTAC GGTGCTTCCC CGGGTTTGG AAAGGAGCCG GCGCCCCCTG 2880  
 TGGCGGTGTG GAAAGGACAC TCCTTCAACA CCATTTCTGG CAGAGAAGCA GAGAAGTTCA 2940  
 GCGGCAAGA CAGCGTAAAG GGGGACAGTG ATTTCAACGA CAGCGATTCC GACATCAGCG 3000  
 GGAAGCTCT GAAAGAGGAT CTCATCAACC ACATGCAGAG TGGACTGTGG GCGTGCACCG 3060  
 CTGAGTGTA GATCCTGGGC CACTCTGACC GCTGTGGAG CCATCCTCTG AGCGGGCCCA 3120  
 45 ACGCACATCC ATCGCCTCAC CCACAGCCCC AGATGTCAAC CTTCTGTAAG AGCACGTCAC 3180  
 TGCTCGGGA TCCTCTGCGC AGGGACAATT ACTACAGGCG CCAGCTGCCC AAGACAGTGG 3240  
 GGTGTCAGAG CGTCTATGAG AAGTACTGCG ACAGAGACTA TGACAGGACA GTCACCTCTG 3300  
 TCTCCCCCTC CCGTCCAGGG AGGCTCCCG ACCTGCAGGA GATTGGAGTA CCCCTCTACC 3360  
 AGTCCCTTCC TGGCAGGTAC CTGTCCCCGA AGAAGGGAGC CAATGAAAAT GTGTAATCCC 3420  
 50 ATGCTGCATG TCTTCAACA TATACAGGTC ACTCCGAGAA GCCCTAAGT TATTGACCCG 3480  
 TTTCACTGTT GTATATATAA ATATGCAAGA TGTGCTTAC AATGAAGTTG TTGGAAGCTA 3540  
 TTTCAATCA CATTGGTACT GTTGGTATT TGCAAAACAA AATGTAGTTA ATGTAATTTT 3600  
 TATGAAATGT GTGCAGTATT TAATTTTCT TATGCTATTG ACTTTGATT CAATTGCGGC 3660  
 TTGCCATTTT CTTAGTGTGT TTAACCTGTA CATTGTGTAA TGTAATGTTT GTATATAATG 3720  
 55 AAAATTTGTT ATATTTTTAT ATAATAAAG CTAAAGTGGG AGTTATTGCC AAAGGAACTG 3780  
 TCTGTAAGAC AAAAAACAAA ACATGTTGGA ATTACTTAAT TGAATTTAT CTTTCACTG 3840  
 AAACAACCTA GTGTTTGAGA AATTTTGCTT TGCCAAGTAT AACTTGTATA TCTTGACTCT 3900  
 GTGGTAGATT TCAAGTTCAA TGTATTATTA TTACATTTGG TTTTCCGTAA ACCGTGTCAC 3960  
 60 TTATAAGCAC AGTAATAAAA GATTGTGCAT GTGTTTGAAG AAAAAAATAA AAAAAAATAA 4020  
 AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA

Seq ID NO: B8 Protein sequence  
 Protein Accession #: NP\_002581.2

65 1 11 21 31 41 51  
 MSPVRRWGSP CLFPLQLFSL CWVLSVAQSK TVRYSTFEED APGTVIGTLA EDLHMKVSGD 60  
 TSFRLMKQFN SSLLRVREGD QQLTVGDAGL DRERLCGQAP QCVLAFDVVS FSQEQFRLVH 120  
 VEVEVRDVND HAPRFRAQI PVEVSEGA AV GTRIPLEVPV DEDVGANGLQ TVRLAEPHSP 180  
 70 FRVELQTRAD GAQCADLVLL QELDRESQAA YSLELVAQDG GRPPRSATAA LSVRVLDAND 240  
 HSPAPFPQGA AEVELAEDAP VGSLLLDLDA ADPDEGPNGD VVFAFGARTP PEARRLFRLD 300  
 PRSGRLTLAG PVDYERQDTY ELDVRAQDRG PGPRAACTKV IVRIRDVNDN APDIAITPLA 360  
 APGAPATSPF AAAAAAALG GADASSPAGA GTPEAGATSL VPEGAARESL VALVSTSDRD 420  
 SGANGQVRCA LYGHEHFRLO PAYAGSYLVV TAASLDRERI AEYNLTVAE DRGAPFLRTV 480  
 RPYTVRVGD NDNAPLFTFP VYEVSVRENN PPGAYLATVA ARDRDLGRNG QVTVRLLAE 540  
 75 VGRAGGAVST YVSVDPATGA IYALRSFDYE TLRQLDVRIQ ASDGSGPQLS SSALVQVRVL 600  
 DQNDHAPVLV HAPAPVLSLE VAVPGRTAKD TVVARVQARD ADEGANGELA FELOQOEPRE 660  
 APAIGRRITGE ILLTGDLSE PPGRVFRALL VISDGRPPL TTTATVSVFV TAGGGRGPAA 720  
 PASAGSPERS RPPGSRGLVS GSVLQWDTPL IVIIVLAGSC TLLLAIIAI ATTCNRRKKE 780  
 80 VRKGALREE RPGAAGGGAS APGSPPEEAR GAGPRPNMFD VLTFFGTGKA PFGSPAADAP 840  
 PPAVAAAEVP GSEGGSATGE SACHFEGQOR LRGAHAEPYG ASPFGKEFA PPVAVWKHGS 900  
 FNTISGREAE KFSKDGSKG DSDFNDSDD ISGDALKKDL INHMQSGLWA CTAECKILGH 960  
 SDRCWSPSCS GPNAPSPHP PAQMSTFCKS TSLPRDPLRR DNYQAQLPK TVGLQSVYEK 1020  
 VLHRDYDRTV TLLSPRPFRG LPDLQIEGVP LYQSPFGRYL SPKKGANENV

Seq ID NO: B9 DNA sequence  
Nucleic Acid Accession #: AL121939.12  
Coding sequence: 185..1426

```

5      1      11      21      31      41      51
|      |      |      |      |      |
AGCGGAGTST CAGTGGCGAG CTCCGGGTGC TGTGGCCCCG CCTTGGCGGG GCGGCCTCCG 60
GCTCAGGCTG GCTGAGAGGC TCCCAGCTGC AGCGTCCCCG CCCGCCTCCT CGGGAGCTCT 120
GATCTCAGCT GACAGTGCCC TCGGGGACCA AACAAAGCCTG GCAGGACAAA ATTAGAAGAT 180
10     CAAAATGGAA AATATGCTGT TTTGGTTGAT ATTTTTCACC CTGGGGTGA CCCTCATTTA 240
TGGATCTGAA ATGGAATGGG ATTTTATGTG GCACTTGAGA AAGGTACCCC GGATTGTCAG 300
TGAAAGGACT TTCCATCTCA CCAGCCCCCG ATTTGAGGCA GATGCTAAGA TGATGGTAAA 360
TACAGTGTGT GGCATCGAAT GCCAGAAAGA ACTCCCAACT CCCAGCCTTT CTGAATTGGA 420
GGATTATCTT TCCTATGAGA CTGTCTTTGA GAATGGCACC CGAACCTTAA CCAGGGTGAA 480
15     AGTTCAAGAT TTGGTTCTTG AGCCGACTCA AAATATCACC ACAAAGGGAG TATCTGTTAG 540
GAGAAAGAGA CAGGTGTATG GCACCGACAG CAGGTTGAGC ATCTTGAGCA AAAGGTTCTT 600
AACCAATTTT CCTTTCAGCA CAGCTGTGAA GCTTTCACG GGCTGTAGTG GCATTCTCAT 660
TTCCCTTCAG CATGTTCTAA CTGCTGCCCA CTGTGTTTCA GATGGAAGG ACTATGTCAA 720
AGGGAGTAAA AAGCTAAGGG TAGGGTTGTT GAAGATGAGG AATAAAAGTG GAGGCAAGAA 780
20     ACCTCGAGGT TCTAAGAGGA GCAGGAGAGA AGCTAGTGGT GGTGACCAAA GAGAGGGTAC 840
CAGAGAGCAT CTGCAGGAGA GAGCGAAGGG TGGGAGAAGA AGAAAAAAAT CTGCCCGGGG 900
TCAGAGGATT GCCGAAGGGA GGCTTCTCTT TCAGTGGACC CGGGTCAAGA ATACCCACAT 960
TCCGAAGGGC TGGGCACGAG GAGGCATGGG GGACGCTACC TTGGACTATG ACTATGCTCT 1020
CTCGGAGCTG AAGCGTGTCT ACAAAAAGAA ATACATGGAA CTTGGAATCA GCCCAACGAT 1080
25     CAAGAAAATG CCTGGTGGAA TGATCCACTT CTCAGGATTT GATAACGATA GGGCTGATCA 1140
GTTGGTCTAT CGGTTTTCGA GTGTGTCYGA CGAATCCAAT GATCTCCTTT ACCAATAYTG 1200
CGATGCTGAG TCGGGCTCCA CCGGTTCCGG GGTCTATCTG CGTCTGAAAG ATCCAGACAA 1260
AAAGAATTGG AAGCGCAAAA TCATTGCGGT CTAATCAGGG CACCAGTGGG TGGATGTCCA 1320
CGGGGTTTCA AAGGACTACA ACAGTGTGCT TCGCATCACT CCCCTAAAAT ACGCCAGAT 1380
30     TTGCCTCTGG ATTCACGGGA ACGATGCCAA TTGTGCTTAC GGCTAACAGA GACCTGAAAC 1440
AGGGCGGTGT ATCATCTAAA TCACAGAGAA AACCAGCTCT GCTTACCCTA GTGAGATCAC 1500
TTCATAGGTT ATGCTCTGAC TTGAACCTCT TCAATAGCAT TTCWACATTT TTCAAAATCA 1560
GGAGATTTTC GTCCATTTAA AAAATGTATA GGTGCAGATA TTGAAACTAG GTGGGCACTT 1620
CAATGCCAAG TATATACTCT TCTTTACATG GTGATGAGTT TCATTGTAGT AAAAATTTTG 1680
35     TTGCCTTCTT AAAAATTAGA CACACTTTAA ACCTTCAAAC AGGTATTATA AATAACATGT 1740
GACTCCTTAA TGGACTTATT CTCAGGGTCC TACTCTAAGA AGAATCTAAT AGGATGCTGG 1800
TTGTGTATTA AATGTGAAAT YGCATAGATA AAGGTAGATG GTAAAGCAAT TAGTATCAGA 1860
ATAGAGACAG AAAGTTACAA CACAGTTTGT ACTACTCTGA GATGGAYCCA TTCAGCTCAT 1920
GCCCTCAATG TTTATATTGT GTTATCTGTT GGGTCTGGGA CATTAGTTT AGTTTTTTTG 1980
40     AAGAATTACA AATCAGAAGA AAAAGCAAGC ATTATAACA AAACATAATA CTGTTTACT 2040
GCTTTAAGAA ATAACAATTA CAATGTGTAT TATTTAAAAA TGGGAGAAAT AGTTTGTCT 2100
ATGAAATAAA CCTAGTTTAG AAATAGGGGA GCTGAGACAT TTTAAGATCT CAAGTTTTTA 2160
TTTAACATAT ACTCAAATA TGGACTTTTC ATGTATGATC AGGGAAGACA CTTCAAAAT 2220
TATGAATGAT CATGTGTTGA AAGCCACATT ATTTTATGCT ATACATTCTA TGTATGAGGT 2280
45     GCTACATTTT TAGGACAAAG AATTCTGTAA TCTTTTTCAA GAAAGAGTCT TTTTCTCCTT 2340
GACAAATCC AGCTTTTGTG TGAGGACTAT AGGGTGAATT CTCTGATTAG TAATTTTAGA 2400
TATGTCCTTT CCTAAAATG AATAAAATT ATGAATATGA CTTAAAAAAA AARWCGACG 2460
CGGCCCGCAA TTTAGTAGTA GTAGTCGACC CGGGAATTCC GGACCGGTAC CTGCAGGCGT 2520
ACCAGC

```

Seq ID NO: B10 Protein sequence  
Protein Accession #: CAC35071.1

```

55     1      11      21      31      41      51
|      |      |      |      |      |
MENMLLWLIF FTPGWTIDG SEMEWDFMWH LRKVPRIVSE RTFHLTSPAF EADAKMMVNT 60
VCGIECQKEL PTPSLSELED YLSYETVFEN GTRTLTRVKV QDLVLEPTQN IITKGVSVRR 120
KRQVYGTDSR FSILDKRFLT NFFPSTAVKL STGCSGILIS PQHVLTAHCH VHDGKDYVK 180
60     SKLRLVGLLK MRNKGSGKKR RGSKRSRREA SGGDQREGTR EHLRERAKGG RRRKKSRRGQ 240
RIAEGRPSPQ WTRVKNTHIP KGWARGMGMD ATLDYDYALL ELKRAHKKKY MELGISPTIK 300
KMPGGMIHFS GFDNDRADQL VYRFCVSDE SNDLLYQYCD AESGSGTSGV YLRKLDPKK 360
NWKRIIAVY SGHQWVDVHG VQKDYNAVVR ITPLKYAQIC LWHGNDANC AY

```

Seq ID NO: 11 DNA sequence  
Nucleic Acid Accession #: NM\_002035.1  
Coding sequence: 108..1106

```

70     1      11      21      31      41      51
|      |      |      |      |      |
AGGCGCCCGC CCGCCGCGCG TGATTCTCGC CTCGCCGCGC CCCAGCCCTG CGCGCCTTGC 60
CCGGCGGCCC CCGCCGCGCC GCTCCGGGCC CCTGGCCCCG CGGAGCGATG CTGCTGCTGC 120
CTGCCGCTTT CCTCGTGGCC TTCGTGCTGC TGCTGTACAT GGTGCTCTCC CTCTACAGCC 180
75     CCAAGCCCTT CGCCCTGCCC GGGGCGCATG TGGTGGTTAC AGGAGGTTCC AGTGGCATCG 240
GGAAAGTGAT TGCATCGAG TGCTATAAAC AAGGAGCTTT TATAACTCTG GTTGACAGAA 300
ATGAGGATAA GCTGCTGACG GCAAGAAAG AAATTGAAAT GCACTCTATT AATGACAAAC 360
AGTGGTGCTT TTGCATATCA GTTGTGTAT CTCAAGACTA TAACCAAGTA GAGAATGTCA 420
TAAAAACAAG ACAGGAGAAA CTGGGTCCAG TGGACATGCT GGTAAATTGT GCAGGAATGG 480
CAGTGTGACG AAAATTGAA GATCTTGAAG TTAGTACCTT TGAAAGTTTA ATGAGCATCA 540
80     ATTACTGGG CAGCGTGTAC CCCAGCCGGG CCGTGATCAC CACCATGAAG GAGCGCCGGG 600
TGGGCAGGAT CGTGTGTTG TCCCTCCAGG CAGGACAGTT GGGATTATTC GGTTCACAG 660
CCTACTCTGC ATCCAAGTTT GCCATAAGGG GATTGGCAGA AGCTTTGAG ATGGAGGTGA 720
AGCCATATAA TGTCTACATC ACAGTTGCTT ACCCACCAGA CACAGACACA CCTGGCTTTG 780
CCGAAGAAAA CAGACAAAG CCTTTGGAGA CTCGACTTAT TTCAGAGACC ACATCTGTGT 840
GCAAAACCAGA ACAGGTGGCC AAACAAATTG TTAAGATGTC CATAAGAGGA AATTTCACAA 900

```



GTTCCCTTGG CTCAGATGGG TACATGCTCT CGGCCCTGAC CTGTGGGATG GCTCCAGTAA 960  
 CTTCATTAC TGAGGGGCTC CAGCAGGTGG TCACCATGGG CCTTTTCCGC ACTATTGCTT 1020  
 TGTTTTACCT TGAAGTMTT GACAGCATAG TTCGTCGCTG CATGATGCAG AGAGAAAAAT 1080  
 CTGAAAATGC AGACAAAAC CTCTAATCTT CTACCCCTT GGAAGAAGAC TGTTCCTCAA 1140  
 TAAATTGAAC AGCTTGCTGC TAAATGGGAC CCAATTTTGG GCCTATAGAC ACTTATGTAT 1200  
 TGTTCCTGAA TACGTACAGT TGGACCAGTG CTCTTCAGGA ATGTGGCTGC AAGCAAGGGG 1260  
 CTAGAAGTTC ACCTCCTGAC AGTATTATTA ATACTATGCA AATATGGAAT AGGAGACCAT 1320  
 TTGATTTTCT AGGCTTTGTG GTAGAGAGGT GAAGGTATGA GAATTAATAG CGTGTGAACA 1380  
 AAGTAAAGAA CAGGATTCCA GAATGATCAT TAAATTTGTT TCTATTATT CTTTTTGGCC 1440  
 CCCCTAGAGA TTAAGTCCAG AAATGTACTT TCTGGCACAT AAAGAAATCT TGAGGACTTT 1500  
 GTTTAAACCT TCCATAAAAA AACAAATTTT GGTTCCTCGG GTTCCTCTCT TCTGCTCTCT 1560  
 TGTCTCTCTG TCTCTCTGTC TCTCTGCTCT TCTCTCTCTC TCTCTTTCTT TCTTTGTGTA 1620  
 TTTTATTCAA GATGAGTTGG ACCCATTGCC AGTGAGTCTG AATGTCTACT ACAGCCCTGT 1680  
 GTTGTGCTCA GGAATCCTCT TGCTGCTGGT GGAACCTCAT GGCTTCTCTC TCTCTTTGAT 1740  
 CCCATAAAGC TACGAGGGGG ACCGGAGAGG GCAGTGCAAT GGAAGTAA GAGATATTTT 1800  
 CCAGTAGGAA AAGCAATGCT TTCTGTCTTT TAGACTCAAA TGCTTAGGGA ACCTTTTCATT 1860  
 TCTCATTATG GGGGAAAGGC AGCCTCCTTA AATGTTTCTT GAAGAGCGGT AAAATCTAGA 1920  
 AGCTTAAGAA TTTACAGTTC CTTCATAAAC CATGATGACC TGAAGTTTAC CTATCCCAT 1980  
 TTAGCATCTA CTGTGTTTTT CCATCTCTTC CTTTCCAATT TTGCTTATAC TGCTGTAATA 2040  
 TTTTGTGAAA AAAAAAATAA AAGGAAAAAA AAGACCAGCT AAAATTTTCC ACTTGACTTT 2100  
 TTAACCTAAC TCATGAAATTA ATTAAGCAA ATGAAAAAAT TAAAAAGTGT GACTTTTCT 2160  
 CGGAGCATAT ATGTAGCTTT TAGGAAAGGC TGATGATGGT ATAAAGTTTG CTCATTAAGA 2220  
 AAAAAAGACA AGGCTGATTT TGAAGAGAGT TGCTTTTGAA ATAAATGAT CA

Seq ID NO: B12 Protein sequence  
 Protein Accession #: NP\_002026.1

1 11 21 31 41 51  
 MLLLAAPFLV AFVLLLYMVS PLISPKPLAL PGAHVVTGG SSGIGKCIAT ECVKQGAFFIT 60  
 LVARNEKLL QAKKEIEMHS INDKQVLCI SVDVSQDYNQ VENVIKQAE KLGPVMDLVN 120  
 CAGMAVSGKF EDLEVSTFER LMSINVLGSV YPSRAVITM KERRVGRIVF VSSQAGQLGL 180  
 FGFTAYSASK FAIRGLAEAL QMEVKPNVY ITVAYPPDT TPGFAENRT KPLETRLISE 240  
 TTSVCKPEQV AKQIVKDAIQ GNFNSSLGSD GYMLSALTGC MAPVTSITEG LQQVVTMGLF 300  
 RTIALFYLGS FDSIVRRMM QREKSENADK TA

Seq ID NO: B13 DNA sequence  
 Nucleic Acid Accession #: CAT Cluster

1 11 21 31 41 51  
 CTTGGGATGC ATTATATATT GCATTATATT TGCCGGTAAA ACTCGGTAA TTTTAAAAAT 60  
 CGGCAAAATA TTGGTGCTTT TCCCGAAATT TGCTCCGGGG CTCCCTTATA GGATAATTGG 120  
 TTTGGATTGG TTAAGTCCAA TTATTAATG CTGCGGTTTC AAATTCCAG CTGGAAGGAC 180  
 CACCCATTTA AAAACTTCAG AAGGCAGGAT CCTGCTCAAT TTATAAGGCT TTGGAATAAT 240  
 CCAGGCATTG GTTTGACATA TTTCCAGAGC TCAAACTGTC AGTGTTCCAC ATGCACATAC 300  
 AAGATCCAGA GTCTCATGTT AAATCACTT ACATACCCAG AAAGACCACC ACTTTGCAGG 360  
 TATAATATTG TACTTAAAGA CAGAGAGGAA GTGTTTCTTA ATCCAAACAC ATGTACACCA 420  
 AAGAACACAT AAGATGCCTT CTTCATCAA ATGCACTTGC TTGTGAATTA ATGGACTTGT 480  
 AATGAAACA ATGCAATCAG TCTTTTATAA TGCACCTGTC AATTGAGAT TCAAGTATTT 540  
 CTATTTCTTG GAAAAAATTT TAAGAATCAA AATAAAGAA AATAAAAGT GCATACAGTT 600  
 AAACATTTCA AAAAAAAAAA AA

Seq ID NO: B14 DNA sequence  
 Nucleic Acid Accession #: XM\_086767.1  
 Coding sequence: 276..611

1 11 21 31 41 51  
 CTTGTTTCATG GCATCTTTAG AAACAACTG CAATTTTATT TCATTTCCTT GTCGTTTATA 60  
 CAAAGATTAC AAGACTAGCT TATGTGTGGA CTGTGACTGT TTTAAGGAAA AATCATGTCC 120  
 TCGGCTGGGT TATCAAGCCA AGCTATTTAA AGGTGTTTAA AAAGAAAGGA TGGAAAGGAG 180  
 ACCTCTTAGG ACCACTGTGT TTTTGGATAC AAGTGGTACA TATCCATTCT GTAGCCTATT 240  
 ATTTTGTCTT CAGTATAATT GTTCCAGATA AAATATGAT GGATGGCTCG TTTTCATTTA 300  
 AATTATTAAT TCAGCTTGAAG ATGATTGAAG AGCCAAGGCT TTATGAAAAG AACAAACCAT 360  
 TTTATAAAGT TCAAGAAGTC AAGATTCTTG CTCAATTTTA TAATGACTTT GTAATATTT 420  
 CAGCATTTGG TTTGACATAT TTCCAGAGCT CAAATCTGCA GTGTTCCACA TGCACATACA 480  
 AGATCCAGAG ACTCATGTTA AAATCACTTA CATACCCAGA AAGACCACCA CTTTGCAGGT 540  
 ATAATATTGT ACTTAAAGAC AGAGAGGAAG TGTTCCTTAA TCCAAACACA TGTACACCAA 600  
 AGAACACATA AGATGCCTTC TTCCATCAA TGCACCTGCT TGTGAATTAA TGGACTTGTA 660  
 AATGAAACA TGCAATCAGT CTTTATAAT GCACGTGTTA ATTTGAGATT CAAGTATTTT 720  
 TATTTCTTGG AAAAAATTTT AAGAAATCAA AATAAAGAAA ATAAAAATG CATACAGTTA 780  
 AACATTCC

Seq ID NO: B15 Protein sequence  
 Protein Accession #: XP\_086767.1

1 11 21 31 41 51  
 MMDGSFSLK LNQLGMIEEP RLYEKNKPFY KLQEVKILAQ FYNDFVNISS IGLTYFQSSN 60  
 LQSTCTYKI QRIMLKSLTY PERPPLCRYN IVLKDRREEVF LNPNTCTPKN T

Seq ID NO: B16 DNA sequence

Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
5	TTTTTTTTTT	TTTTTTTTTT	TTAAATGCAA	AGGAGCAACA	AAATTTATTG	ACTGAATTAA	60
	ACACAACAGT	AAAATGGCAG	TGTTGTRAAT	TCATTTTCAG	ATGTTTGAAT	GGAACAAGAA	120
	AAGTGCTATT	AGCCCAAGCT	TCTTACATTC	ATTAAAAGAG	TGACTATCAA	AAACAGCAAC	180
	ATGCACAATG	GTACATATGC	ACAAAATGGA	ATTATATCAA	CAAATATACA	AAATACCCAA	240
	AATAAAATAT	TTACAGGTTT	AAAAATATAA	ACATTGATTC	CTCTATCCCA	TTAAACCATT	300
10	GGAGTGGAGA	AAGGAGGAAA	GACCCATTG	CTATTTAGAA	TCCTTTTAA	AACAAGTTTT	360
	TAAAACATAG	AAATTAGTCT	AGGAGACAAT	TTTTGATGTT	TTTCAGGGGT	TTAACATTCT	420
	ATTATAAAAA	TAACATCTAT	AAACCTACTA	ACAATTTTCC	TCCTGTGCAC	AAAAATAATA	480
	CTGCCAAAAC	CTGTCCCTCA	AGACATGCCT	GACTTTTCAGG	AAAGCTAATT	ATGGAAATGG	540
	AGTTTCTCGT	TTGGGTTATC	TTTGTACTA	TTTTCAAATA	ACCAGCAACT	CCCTATATTA	600
15	CACGTAGATA	CTTTATATAA	ATAACGTGGG	CGAAACCTGA	AGTTCACAA	GAGCCTGCTA	660
	GGTAGCTGGT	GTCAAGTACA	AATGATAGGA	ATTGACTTTG	CTCAACACAT	CAAAAGCATT	720
	TTCCCTGATA	TTCTGTATAG	ACCTACCACT	ATCAGATCCT	CCATATTCAA	TAAGATTAT	780
	CCTGGAAGCA	ATGAAATGT	TAAATATTAC	TTTGTAGAG	TTTCTCCTCC	TTTATTTAGA	840
20	AATAAATGTG	TAGTGGGGAC	CAGTGGTTGT	AATGTAGATA	CTTGAGAAGT	TTCATTGATT	900
	CCTTCAGACC	CATGCCG					

Seq ID NO: B17 DNA sequence

Nucleic Acid Accession #: NM\_022898.1

Coding sequence: 268..2739

	1	11	21	31	41	51	
25	TTTTCTTGCT	TTTCTTCCCT	TTTTTTTCTT	TTTGCAACA	AAACAAAAAA	CAGCATAGAA	60
	GAAAGAGCAA	AATAAAGAA	AAGAAGAGGA	GGAAGAGAGG	GAAAGAGAGG	AAGGGAAAAA	120
30	AAACACCAAC	CCGGGCAGAG	GAGGAGGTGC	GGCGGCGGCG	CGCGGCGGCG	CAGCGGCGGC	180
	AGCGGCGGCG	CGGCGGCTCG	GACCCCTCC	CCCGGCTCCC	CCCATCAGTG	CAGCTCTCCG	240
	GGCGATGCCA	GAATAGATGC	CGGGGCAATG	TCCCGCCGCA	AACAGGGCAA	CCCGCAGCAC	300
	TTGTCCCAGA	GGGAGCTCAT	CACCCAGAG	GCTGACCATG	TGGAGGGCCG	CATCCTCGAA	360
	GAAGACGAGG	GTCTGGAGAT	AGAGGAGCCA	AGTGGCCTGG	GGCTGATGGT	GGGTGGCCCC	420
35	GACCCTGACC	TGCTCACCTG	TGGCCAGTGT	CAAAATGAAC	TCCCTTGGG	GGACATCCTG	480
	GTTTTTATAG	AGCACAAGAG	GAAGCAGTGT	GGCGGCAGCT	TGGGTGCTCG	CTATGACAAG	540
	GGCCTGGACA	AGGACAGCCC	GCCACCCCTC	TCACGCTCCG	AGCTCAGGAA	AGTGTCCGAG	600
	CCGGTGGAGA	TGGGATCCCA	AGTCACCCCC	GACGAAGATG	ACCACCTGCT	CTCACCCACG	660
	AAAGGCATCT	GTCCCAAGCA	GGAGAACATT	GCAGGTAAAG	ATGAGCCTTC	CAGCTACATT	720
40	TGCACAACAT	GCAAGCAGCC	CTTCAACAGC	GCGTGGTTCC	TGCTGCAGCA	CGCGCAGAAC	780
	ACGCACGGCT	TCCGCATCTA	CCTGGAGCCC	GGGCGCGCCA	GCAGCTCGCT	CACGCCGCGG	840
	CTCACCATCT	CGCCGCGGCT	CGGCGCGGAG	GCCGTGGGCG	AGTCCCGGCT	CATGAATTTC	900
	CTGGGCGACA	GCAACCCCTT	CAACCTGCTG	CGCATGACGG	GCCCATCCT	GCGGGACCA	960
	CCGGGCTTGG	GCGAGGGCCG	CCTGCCGGGC	ACGCCGCCCTC	TCTTCAGTCC	CCCGCGCGGC	1020
45	CACCACTTGG	ACCCGCACCG	CCTCAGTGCC	GAGGAGATGG	GGCTCGTCGC	CCAGCACCCC	1080
	AGTGCCTTGG	ACCGAGTCTA	GCGCCTGAAC	CCCATGGCCA	TCGACTCGCC	CGCCATGGAC	1140
	TTCTCGCGCG	GGCTCCGCGA	GCTGGCGGGC	AACAGCTCCA	CGCCGCGGCC	CGTGTCCCGG	1200
	GGCCGCGGCA	ACCCTATGCA	CCGGCTCCTG	AACCCCTTCC	AGCCAGCCCC	CAAGTCCCGG	1260
	TTCTTGAGCA	CGCCGCGGCT	CGCGCCCATG	CCCCCTGGCG	GCACGCGGCC	CCCGCAGCCG	1320
50	CCAGCCAAGA	GCAAGTCGTG	CGAGTTCTGC	GGCAAGACCT	TCAAGTTCCA	GAGCAATCTC	1380
	ATCGTGCAAC	GGCGCAGTCA	CACGGGCGAG	AAGCCCTACA	AGTGCCAGCT	GTGCGACCA	1440
	GCGTGCTCGC	AGGCCAGCAA	GCTCAAGCGC	CACATGAAGA	CGCACATGCA	CAAGCCCGGC	1500
	TCGCTGGCCG	GCCGCTCCGA	CGACGGGCTC	TCGGCCGCCA	GCTCCCCCGA	GCCCGGCACC	1560
	AGCGAGCTGG	CGGGGAGGGG	CCTCAAGGCG	GCCGACGGTG	ACTTCCGCCA	CCACGAGAGC	1620
55	GACCCGTCCG	TGGGCCACGA	GCCGGAGGAG	GAGGACGAGG	AGGAGGAGGA	GGAGGAGGAG	1680
	GAGCTGTCTA	TGGAGAACGA	GAGCCGGCCC	GAGTCGAGCT	TCAGCATGGA	CTCGGAGCTG	1740
	AGCCGCAACC	GCGAGAACGG	CGGTGGTGGG	GTGCCCCGGG	TCCCGGGCGC	GGGGGGCGGC	1800
	GCGGCCAAGG	CGCTGGCTGA	CGAGAAGGCG	CTGGTGTCTG	GCAAGGTCAT	GGAGAACGTG	1860
	GGCCTAGGCG	CATGCGCGCA	GTACGGCGAG	CTCCTGGCCG	ACAAGCAGAA	GCGCGGCGCC	1920
60	TTCTTGAAGC	GTGCGGCGGG	GCGCGGGGAC	GCGGCGGACG	ACGACGACGC	GGGCGGCTGC	1980
	GGGGACGCGG	GCGCGGGCGG	GCGGCTCAAC	GGGCGCGGGG	GCGGCTTCGC	GCCAGGCACC	2040
	GAGCCCTTCC	CCGGGCTCTT	CCCGCGCAAG	CCCGCGCGCG	TGCCAGCCCC	CGGGCTCAAC	2100
	AGCGCCGCCA	AGCGCATCAA	GGTGGAGAA	GACCTGGAGC	TGCCGCCCCG	CGCGCTCATC	2160
	CCGTCCGAGA	ACGTGTACTC	GCAGTGGCTG	GTGGGCTACG	CGGCGTCGCG	GCACTTCATG	2220
65	AAGGACCCCT	TCCTGGGCTT	CACGGACGCA	CGACAGTCGC	CCITCGCCAC	GTGCTCCGAG	2280
	CACTCGTCCG	AGAACGCGAG	CCTGCGCTTC	TCCACGCGCG	CCGGGGACCT	GCTGGACGGC	2340
	GGCCTCTCGG	GCCGCGAGCG	CACGGCCAGC	GGAGGCGAGC	CCCCGACCT	GGGCGGCCCG	2400
	GGCCCCGGGC	GCCCGAGCTC	CAAGGAGGGC	CGCCGCGAGC	ACACGTGCGA	GTACTGCGGC	2460
	AAGGTGTTCA	AGAAGTGCAG	CAACTTGACG	GTGCACCGGC	GGAGCCACAC	CGGCGAGCGG	2520
70	CCTTACAAGT	GCGAGCTGTG	CAACTACGCG	TGCGCGCAGA	GCAGCAAGCT	CACGCGCCAC	2580
	ATGAAGAGCG	ACGGGACGAT	CGGCAAGGAG	GTGTACCGCT	GCGACATCTG	CCAGATGCC	2640
	TTCAGCGTCT	ACAGCACCTT	GGAGAAACAC	ATGAAAAAGT	GGCACGGCGA	GCACTTGCTG	2700
	ACTAACGACG	TCAAAATCGA	GCAGGCCGAG	AGGAGCTAAG	CGCGCGGGCC	CCGCGGCCCC	2760
	GCACCTGTAC	AGTGGAAACG	TTGCCAACCG	AGAGAATGCT	GACCTGACTT	GCCTCCGTGT	2820
75	CACCGCCACC	CCGCAACCCG	CGTGTCCCGG	GGGCCCCAGG	GAGGCGGCAC	TCCAACCTAA	2880
	CCTGTGTCTG	CGAAGTCCTA	TGGAAACCCG	AGGGTTGATT	AAGGCAGTAC	AAATTGTGGA	2940
	GCCTTTTAAC	TGTGCAATAA	TTTCTGTATT	TATTGGGTTT	TGTAATTTT	TTGGCATGTG	3000
	CAGGTACTTT	TATTATTAT	TTTTCTGTT	TGAATTCCTT	TAAGAGATTT	TGTTGGGTAT	3060
	CCATCCCTTC	TTTGTTTTTT	TTTTAACCCG	GTAGTAGCCT	GAGCAATGAC	TCGCAAGCAA	3120
80	TGTTAGAGGG	GAAGCATATC	TTTTAAATTA	TAATTGGGGG	GGAGGGGTGG	TGCTGCTTTT	3180
	TTGAAATTTA	AGCTAAGCAT	GTGTAATTTT	TTGTGAAGAA	GCCAACTCTC	AAATGACTTT	3240
	TAAAGTTGTT	TACTTTTCTA	TTCTTCTCTT	TTTTTGTGCC	TGAAATAAAA	AGTGGCATGC	3300
	AGTTTTTTTT	TAAATATTAT	TTAATTTTTT	TTTTTGGTTT	TGTTTTTTGG	GGTGGGGGGT	3360
	GTGGATGTAC	AGCGGATAAC	AATCTTTCAA	GTCGTAGCAC	TTTGTTCAG	AACTGGAATG	3420

5 GAGATGTAGC ACTCATGTCG TCCCGAGTCA AGCGGCCTTT TCTGTGTTGA TTTCGGCTTT 3480  
 CATATTACAT AAGGGAAACC TTGAGTGGTG GTGCTGGGGG AGGCACCCCA CAGACTCAGC 3540  
 GCCGCCAGAG ATAGGGTTTT TGGAGGGCTC CTCTGGGAAA TGGCCCGACA GCATTCTGAG 3600  
 GTTGTGCAATG ACCAGCAGAT ACTATCCTGT TGGTGTGCCC TGGGGTGCCA TGGCTGCTAT 3660  
 TCGCTGTAGA TTAGGCTACA TAAATGGGC TGAGGGTACC TTTTGGGGA GATGGGGTGG 3720  
 10 CCTGCAGTGA CACAGAAAGG AAGAACTAG CGGTGTCTCT TTAGGCGTTT TCTGGCTTGA 3780  
 CGGCTTCTCT CTTTTTTTAA ATCACCCCA CCACATAAAT CTCAAATCCT ATGTTGCTAC 3840  
 AAGGGGTGAT CCATCATTTT CCAAGCAGAC GAATGCCCTA ATTAATTGAA GTTAGTGTTC 3900  
 TCTCATTTAA TGCACACTGA TGATATTGTA GGGATGGGTG GGGTGGGGAT CTGCAAAAT 3960  
 TCTATTCTCT TTTACTGAAA AAGCAGGGGA TGAGTTCCAT CAGAAGGTGC CCAGCGCTAC 4020  
 TTCCAGGTT TTTATTTTTT TTTTCTATC TCATTAGGTT GGAAGGTACT AAATATTGAA 4080  
 CTGTTAAGAT TAGACATTTG AATCTGTGTG ACCCGCACTT TAAAGCTTTT GTTTGCATT 4140  
 AAATTAATG GCCTTCTAAC AAGAAATTGC AGCATATTCT TCTCTTTGGC CCAGAGGTGG 4200  
 15 GTTAACTGT AAGGGACAGC TGAGATTGAG TGTCAGTATT GCTAAGCGTG GCATTACAA 4260  
 TACTGGCACT ATAAAGAACA AAATAAATA ATAATTATA GGACAGTTTT TCTACTGCCA 4320  
 TTCAATTGA TGTGAGTGC TTGAAAAC TGAACTCTAT TTGAGTCTCT TGAGACAAAT 4380  
 GCAAACTTT TTTTGTGAAA TGAAAGACT TTTTAAAAA GTAAACAAG AAAAGTACAT 4440  
 TCTTTAGAAA CTAAACAAGC CACATTTACT TTAAGTAAAA AAAAAAATA TTCTGTTGA 4500  
 20 AGATAGAGGA TATGAAATGC CATAAGACCC AATCAAAATGA AGAAATAAAC CCAGCACAA 4560  
 CTTGGACATC CATTAGCTGA ATTATCTCTA GCCCTTTTG TTTTGGGAC AACGCTGCTT 4620  
 AGATATGGAG TGGAGGTGAT TTACTGCTGA ATTAAACTC AAGTGACACA AGTTACAAGT 4680  
 TGATATCGTT GAATGAAAAG CAAAACAAA ACAATTGAGG AACAACGGCT AATTTTTTCT 4740  
 AAAGTTAAAT TTAGTGCACT CTGTCTTAAA AATACGTTTA CAGTATTGGG TACATACAAG 4800  
 25 GGTAATAAATA AAATTTGTGT TATGTGTGTT GGAGCGATCT TTTTCTTCA AAGTTTGCTT 4860  
 AATAGGTTAT ACAAAATG CACAGTGGCC GCGTGTATAT TGTTTTCTTT TGGTGACGGG 4920  
 GTTTTAGTAT ATATTATATA TATTAATAAT TCTTGATTAC TGTAAAGTG GACCAGTATT 4980  
 TGTAATAATC GAGAATGCCT GGGCATTTTA CAAAACAAGA AAAAAATAC CCTTTTCTTT 5040  
 TCCTTGAATA TGTGTGAGTA AAATTTAAAT GGTGGGTCTA TAAATTTGTT CTGTGTACAG 5100  
 30 TAACGTGAAA GTCGGAGTTT TAGTAAATTT TTTTCTGCTT TGGGTGTTGA ATTTTATTT 5160  
 CAAAAAATA GTATAGAAAC TTGTATTG GGTATCAAAG GGGATTGCTA CACCATGTAG 5220  
 AAAAAGTATG TAGAAAAAAA GTGCTTAATA TTGTATTGCT TTTGCAGAAA AAAAAAAT 5280  
 CACATTTCTG ACCTGTACTT ATTTTCTCT TCCCGCTCC CTCTGGAATG GATATATTGG 5340  
 TTGTTTCATA TGATGTAGGC ACTTGCTGTA TTTTACTG AGCTCGTAAAT TTTTAACTG 5400  
 35 TAAGCTTGTC CTTTAAAGG GATTAAATGT ACCTTTTGT TAGTGAATTT GGAATAAAA 5460  
 AGAAAAAATA AACAAAAACA AACAGGCTGC CATAATATAT TTTTTAATT TGGCAGGATA 5520  
 AAATATTGCA AAAAAACAC ATTTGTATGT TAAGTCCTAT TGTACAGGAG AAAAAGGGTT 5580  
 GTTTCAGAAC CTTTGAGAAA AAGAAACAAA AGGAAGTAGT TAAATGCTTT GGTTCACAAA 5640  
 TCATTAGTT GTATATATT TTTGTCGGA TGGCCTACA CAGAGAACCG TTCGTGTTGG 5700  
 40 GCTTCTCTCT GAACGCCCCG AACCTTGCA CAAGGCTCCT TGGTGTGGCC ACAGCAGACC 5760  
 AGATGGGAAA TTATTGTGT TGAGTGGAAA AAAATCAGTT TTTGTAAAGA TGTCAAGTAA 5820  
 ATTCACATCT GTCCCTCCCT TCTCTAAGAG GCCATCTCTA AGATGTCAGA TGTAGAGGAG 5880  
 AGAGAGCGAG AGAACATCTT CCTTCTCTAC CATCACTCCT GTGGCGGTCA CCACCACCAC 5940  
 CTCTCCCGCC CTTACCAGCA GAAAGCAATG CAACTGAGC TGCTTTAGTC CTTGAGAAAT 6000  
 45 TGTGAACAAA ACACAAATAT CATAAAGGA GCTGGTGATT CAGCTGGGTC CAGGTGAAGT 6060  
 GACCTGCTGT TGAGACCGGT ACAAATTGGA TTTCAGGAAG GAGACTCCAT CACAGCCAGG 6120  
 ACCTTTCGTG CCATGGAGAG TGTGGCCTC TTGTCTTCT TCCCTGCTTT GCTGCTTTGC 6180  
 TCTCTGAAAC CTACATTCCG TCAGTTTCCG AATGCCAGGG CCTGGGATGA ATTTGGTGCC 6240  
 TTTCCATATC TCGTTCTCTC TCCTTCCCTC GCGTTTCCCT TCCATCCTTC ATCCTCCATT 6300  
 50 GTTCCTTTT TTTTCTTCA TTTTATTTT AATTTCTTT CTCTCTGCT GTTCTCTCCC 6360  
 TAATCTCTA TTTTATTTT ATTTTGTGA AAGCCAAAGT GCTTTAAGAT AAAGTGGTGG 6420  
 TCTTTTGGAT GAGGGAATAA TGCATTTTAA AATAAATAC CAATATCAGG AAGCCATTTT 6480  
 TTTATTTT CAGG AAATGTAAAG AACCATTATT TCAGGTTATG AAAGTATAAC CAAGCATCCT 6540  
 TTTGGGCAAT TCCTTACCAA ATGCAGAAGC TTTTCTGTT GATGCACTCT TTCTCCTTG 6600  
 55 CCACTTACCT TTGCAAGTT AAAAAAAGG GGGGAGGGAA TGGGAGAGAA AGCTGAGATT 6660  
 TCAGTTTCTT ACTGCAGTTT CCTACCTGCA GATCCAGGGG CTGCTGTTGC CTTTGGATGC 6720  
 CCCACTGAGG TCCTAGAGTG CCTCCAGGGT GGTCTTCTCT TAGTCATAAC AGCTAGCCAG 6780  
 TGCTCACCAG CTCACCAAGT TGCCAGGACT AAGCCATCCC AAAGCACAAG CATTGTGTGT 6840  
 CTCTGTGACT GCAGAGAAGA GAGAATTTTG CTTCTGTTT GTGTTTAAAA AACCAACACG 6900  
 60 GAAGCAGATG ATCCCGAGAG AGAGGCTCTC AGCATGGGTG ACCCAGCCGA CCTCAGGCCG 6960  
 GTTTCCGCAC TGGCACAACT TTGTTCAAAG TTGCCCCCAA TTGGAACCTG CCCTTGGA 7020  
 TTAGAGGGTC TTTTCATGGG AGAGAAGGAG ACTGAATTAC TCTAAGCAAA ATGTGAAAAG 7080  
 TAAGGAAATC AGCCTTTTAT CCGGCTCCTA AGTAACCGTC AGCCGAAGGT CTCGTGGAAC 7140  
 ACAGGCAAA CCGTGATTTT GGTGCTCCTT GTAACCTAGC CTTGCAAGC AAAGTCCCAT 7200  
 65 TGATTTAAGT TGTGTCATT TGTACTGGCA AGGCAAAATA TTTTATTAC CTTTCTATT 7260  
 ACTTATTGTA TGAGCTTTTG TTGTTTACTT GGAGGTTTGT TCTTTTACTA CAAGTTTGGG 7320  
 ACTATTTATT ATTGCTTGGT ATTTGTGCTC TGTTTAAAGAA ACAGGCACCT TTTTATTA 7380  
 TGGATAAAT GTTGAGATGA CAGGAGGTCA TTTCAATATG GCTTAGTAAA ATATTTATTG 7440  
 TTTCTTTATT CTCTGTACAA GATTTTGGGC CTCCTTTTCT CTTAATGTC ACAATGTTGA 7500  
 70 GTTCAGCATG TGTCTGCCAT TTCATTTGTA CGCTTGTTCA AAACCAAGTT TGTCTGTT 7560  
 TCAAGTTATA AAAATAAAT GGACATTTAA CTTGATCTCC AAA

Seq ID NO: B18 Protein sequence  
 Protein Accession #: NP\_075049.1

75 1 11 21 31 41 51  
 MSRRKQGNPQ HLSQRELITP EADHVEAAIL EEDEGLEIEE PSGLGLMVGG PDPDLLTCGQ 60  
 CQMFPLGLDI LVFLIEHKRQ CCGSLGACXD KALDKDSPPP SSRSELKVS EPVEIGIQVT 120  
 80 PDEDDHLLSP TKGICPKQEN IAGKDEPSSY ICTCKQPFN SAWFLQHAQ NTHGFRIYLE 180  
 PGPASSSLTP RLTIPLPLPG EAVAQSLPMN FLGDSNPFNL LRMTGPILRD HPGFGEGRLP 240  
 GTPPLFSPPP RHLLDPHRLS AEEMGLVAQH PSAFDRVMRL NPMAIDSPAM DFSRRLRELA 300  
 GNSSTPPFVS PGRGNPMHRL LNPFQSPKPS PFLSTPPLPP MPPGPTPPPQ PPAKSKSCEF 360  
 CGKTFKFQSN LIVHRSHTG EKPYKCQLCD HACSQASKLK RHMKTHMHKA GSLAGRSDDG 420  
 LSAASSPEPG TSELAGEGLK AADGDFRHE SDPSLGHEPE EDEDEDEDEE ELLLENESR 480

PESSFSMDSE LSRNRENGGG GVPVPGAGG GAAKALADEK ALVLGKVMEN VGLGALPQYG 540  
 ELLADKQKRG AFLKRAAGGG DAGDDDDAGG CGDAGAGGAV NGRGGGFAPG TEPFPGLFPR 600  
 KPAPLPSPGL NSAAKRIKVE KDLELPPAAL IPSENVYSQW LVGYAASRHF MKDPFLGFTD 660  
 ARQSPFATSS EHSSENGSLR FSTPPGDLDD GGLSGRSGTA SGGSTPHLGG PGPGRPSSKE 720  
 GRRSDTCEYC GKVFKNCSNL TVHRRSHTGE RPYKCELCNY ACAQSSKLTR HMKTHGQIGK 780  
 EVYRCDICQM PFSVYSTLEK HMKKWHGEHL LTNDVKIEQA ERS

Seq ID NO: B19 DNA sequence  
 Nucleic Acid Accession #: NM\_000399.2  
 Coding sequence: 339..1769

1 11 21 31 41 51  
 | | | | |  
 15 TAACTGAGCG AGGAGCAATT GATTAATAGC TCGGCGAGGG GACTCACTGA CTGTTATAAT 60  
 AACACTACAC CAGCAACTCC TGGCTTCCCA GCAGCCGGAA CACAGACAGG AGAGAGTCAG 120  
 TGGCAAAATAG ACATTTTCTT TATTTCCTAA AAAACAGCAA CTTGTTTGCT ACTTTTATTT 180  
 CTGTTGATTT TTTTTCCTTG GTGTGTGTGG TGGTTGTTT TAAGTGTGGA GGGCAAAAGG 240  
 AGATACCATC CCAGGCTCAG TCCAACCCCT CTCCAAAACG GCTTTTCTGA CACTCCAGGT 300  
 20 AGCGAGGGAG TTGGGTCTCC AGGTTGTGCG AGGAGCAAAT GATGACCGCC AAGGCCGTAG 360  
 ACAAATCCC AGTAACTCTC AGTGGTTTGT TGCACCACTG GTCTGACAAC ATCTACCCGG 420  
 TGGAGGACCT CGCCGCCACG TCGGTGACCA TCTTTCCTAA TGCCGAACCT GGAGGCCCTT 480  
 TTGACCAGAT GAACGGAGTG GCCGGAGATG GCATGATCAA CATTGACATG ACTGGAGAGA 540  
 AGAGGTCGTT GGATCTCCCA TATCCAGCA GCTTTGCTCC CGTCTCTGCA CCTAGAAACC 600  
 25 AGACCTTAC TACATGGGC AAGTTCTCCA TTGACCTCTA GTACCTTGGT GCCAGCTGCT 660  
 ACCCAGAAGG CATAATCAAT ATTGTGAGTG CAGGCATCTT GCAAGGGGTC ACTTCCCCAG 720  
 CTTCAACCAC AGCCTCATCC AGCGTCACCT CTGCCTCCCC CAACCCACTG GCCACAGGAC 780  
 CCCTGGGTGT GTGCACCATG TCCACAGACC AGCCTGACCT GGACCACTCT TACTCTCCGC 840  
 CACCGCCTCC TCCTCCTTAT TCTGGCTGTG CAGGAGACCT CTACCAAGGAC CCTTCTGCGT 900  
 30 TCCTGTAGC AGCCACACCT TCCACCTCTT CTTCTCTGGC CTACCCACCA CCTCCTTCTT 960  
 ATCCATCCCC CAAGCCAGCC ACGGACCCAG GTCTCTTCCC AATGATCCCA GACTATCTCT 1020  
 GATTCTTTCC ATCTCAGTGC CAGAGAGACC TACATGGTAC AGCTGGCCCA GACCGTAAGC 1080  
 CCTTTCCCTG CCCACTGGAC ACCCTGCGGG TGCCCCCTCC ACTCACTCCA CTCTCTACAA 1140  
 TCCGTAACCT TACCTGGGG GGGCCCAAGT CTGGGTGAC CGGACCAAGG GCCAGTGGAG 1200  
 35 GCAGCGAGGG ACCCGGCTG CCTGGTAGCA GCTCAGCAGC AGCAGCAGCC CCGCGCCGCG 1260  
 CCGCCTATAA CCCACACCAC CTGCCACTGC GGCCTATTCT GAGGCTCGC AAGTACCCCA 1320  
 ACAGACCCAG CAAGACGCCG GTGCACGAGA GGCCCTACCC GTGCCACGA GAAGGCTGCG 1380  
 ACCGGCGGTT TCCTCGCTCT GACGAGCTGA CACGGCACAT CCGAATCCAC ACTGGGCATA 1440  
 AGCCCTTCCA GTGTGCGATC TGCATGCGCA ACTTCAGCCG CAGTGACCAC CTCACCACCC 1500  
 40 ATATCCGCAC CCACACCCGT GAGAAGCCCT TCGCCTGTGA CTACTGTGGC CGAAAGTTTG 1560  
 CCCGGAGTGA TGAGAGGAAG CGCCACACCA AGATCCACCT GAGACAGAAA GAGCGGAAAA 1620  
 GCAGTGCCCC CTCTGCATCG GTGCCAGCCC CCTCTACAGC TCCTGCTCT GGGGGCGTGC 1680  
 AGCCTGGGGG TACCTGTGTC AGCAGTAACA GCAGCAGTCT TGGCGGAGGG CCGCTCGCCC 1740  
 CTTGCTCCTC TCGGACCCCG ACACCTTGAG ATGAGACTCA GGCTGATACA CCAGCTCCCA 1800  
 45 AAGGTCCCGG AGGCCCTTTG TCCACTGGAG CTGCACAACA AACACTACCA CCCTTTCCCT 1860  
 TCCTCTCTC CTTTGTGTTG GCAAAGGGCT TTGTTGGAGC TAGCACTGCC CCCTTTCCAC 1920  
 CTAGAAGCAG GTTCTTCTTA AAACCTAGCC CATTCTAGTC TCTCTTAGGT GAGTTGACTA 1980  
 TCAACCAAG GCAAAGGGGA GGCTCAGAAG GAGGTGGTGT GGGGATCCCC TGGCCAAGAG 2040  
 GGCTGAGGTC TGACCTGCTT TTAAGGGT GTTTGACTAG GTTTTGCTAC CCCACTTCCC 2100  
 50 CTATTTTTGA CCCATCACAG GTTTTGTGACC CTGGATGTCA GAGTTGATCT AAGACGTTTT 2160  
 CTACAATAGG TTGGGAGATG CTGATCCCTT CAAGTGGGGA CAGCAAAAAG ACAAGCAAAA 2220  
 CTGATGTGCA CTTTATGGCT TGGGACTGAT TTGGGGGACA TTGTACAGTG AGTGAAGTAT 2280  
 AGCCTTTATG CCACACTCTG TGGCCCTAAA ATGGTGAATC AGAGCATATC TAGTTGTCTC 2340  
 55 AACCTTGAA GCAATATGTA TTATATACTC AGAGAACAGA AGTGCAATGT GATGGGAGGA 2400  
 ACGTAGCAAT ATCTGCTCTT TTTGAGTTG TTTGAGAAAT GTAGGCTATT TTTTCAGTGT 2460  
 ATATCCACTC AGATTTTGTG TATTTTGTAT GTACCCACAC TGTCTCTTAA ATTCTGAATC 2520  
 TTTGGGAAAA AATGTAAAGC ATTTATGATC TCAGAGGTTA ACTTATTTAA GGGGGATGTA 2580  
 CATATTCTCT GAAACTAGGA TGCATGCAAT TGTGTTGGAA GTGTCTTGG TCGCCTTGTG 2640  
 TGATGTAGAC AAATGTTACA AGGCTGCATG TAAATGGGTT GCCTTATTAT GGAGAAAAAA 2700  
 60 ATCACTCCCT GAGTTTATGA TGGCTGTATA TTTATGCCTA TTAATATTTG GAATTTTTTT 2760  
 TAGAAAGTAT ATTTTGTAT GCTTTGTTT GTGACTTAAA AGTGTACCT TTGTAGTCAA 2820  
 ATTTAGATA AGAATGTACA TAAATGTACC GGAGCTGATT TGTTTGGTCA TTAGCTCTTA 2880  
 ATAGTTGTGA AAAAATAAAT CTATTTCTAAC GCAAAACCAC TAACTGAAGT TCAGATATAA 2940  
 TGGATGGTTT GTGACTATAG TGTAAATAAA TACTTTTCAA CAAT

Seq ID NO: B20 Protein sequence  
 Protein Accession #: NP\_000390.2

1 11 21 31 41 51  
 | | | | |  
 70 MMTAKAVDKI PVTLSGFVHQ LSDNIYPVED LAATSVTIFP NAEELGGPFDQ MNGVAGDGM 60  
 NIDMTGEKRS LDLPYPSSFA PVSAPRNQTF TYMGKFSIDP QYPGASCYPE GIINIVSAGI 120  
 LQGVTSPTAS TASSSVTSAS ENPLATGPLG VCTMSQTQPD LDHLYSPPPP PPPYSGCAGD 180  
 LYQDPSAFLS AATTSTSSSL AYPPPPSYPS PKPATDPGLF PMIPDPGFF PSQQRDLHG 240  
 75 TAGPDRKFPF CPLDTRLVPP PLTPLSTIRN FTLGGPSAGV TGPAGSGGSE GPRLPSSSSA 300  
 AAAAATAAAY NPHHLPLRPI LRPRKYPNRP SKTPVHERPY PCPAEGCDRR FSRSEDLTRH 360  
 IRIHTGHPKF QCRICMRNFS RSDHLTTHIR THTGKPFAC DYCGRKFARS DERKRTKIH 420  
 LRQKERKSSA PSASVPAPST ASCSGGVQPG GTLCSSNSSS LGGGFLAPCS SRTRTP

Seq ID NO: B21 DNA sequence  
 Nucleic Acid Accession #: NM\_004962.2  
 Coding sequence: 457..1893

1 11 21 31 41 51  
 | | | | |

5  
10  
15  
20  
25  
30  
35  
40  
45

CACACACGGG CGCACGCACA CGGCAGCCGG GCCAGGGACG ACCCTGTCAG CTGCAGCCCC 60  
 AGAGGTCCGG GGCAGCGCAGC CGGGTCCCTT CGAGGGCCGA GCCGGCCGCC CCGCCCGGCC 120  
 CCTCGAAGCA GCCGGGCCGG GCGCGCAGTG GGCTACAAAC TTTGCGCAGC CGAGTCCGCC 180  
 AAGGCAGCGC GCCGACTCGG GCTCGGCTCG GCTCTGCGCT GCTCCGACG GCTGTGACCG 240  
 CTGGCCGGGG GCTCGGGCCG CCGGTACCCA CGGACCGCGC GCCCGGGTGC CTGCTCCGCT 300  
 AAGCCCCCTG CCCCAGCGCG ACCTCGGTAT CCAGCGCCCT GCTGCCCGGG CTCTCCCCGC 360  
 GCGCCCTACT GCCGCGAGGT CAGTCCGCG CCTCCGGTGC GCCAGCGCTC GCCTTCCTCC 420  
 TCCTGGACTT CGGCCCTTTG CCGCCCTCAC CACGCCATGG CTCATGTCCC CGCTCGGACC 480  
 AGCCCGGGAC CCGGCCCCCA GCTGCTGCTG CTGCTGCTGC CGTTGTTTCT GCTGTTGCTC 540  
 CGGGATGTGG CCGGCAGCCA CAGGGCCCCC GCCTGGTCCG CACTGCCCGC GGCCGCCGAC 600  
 GGCCCTGCAGG GGGACAGGGA TCTCCAGCGG CACCCTGGGG ACAGCGCCGC CACGTTGGGC 660  
 CCCAGCGCCC AGGACATGGT CGCTGTCCAC ATGCACAGGC TCTATGAGAA GTACAGCCGG 720  
 CAGGGCGCGC GGCCGGGAGG GGGCAACACG GTCCGCAGCT TCAGGGCCAG GCTGGAAGTG 780  
 GTCGACCAGA AGGCCGTGTA TTTCTTCAAC CTGACTTCCA TGCAAGACTC GGAATGATC 840  
 CTTACGGCCA CTTTCCACTT CTACTCAGAG CCGCCTCGGT GGCTTCGAGC GCTCGAGGTG 900  
 CTATGAAGC CGCGGCCCAA GAACGCTTCA GGCCGCCCGC TGCCCTGGGG CCGGCCCA 960  
 CGCCAGCACC TGCTCTTCCG CAGCCTCTCG CAGAACACGG CCACACAGGG GCTACTCCGC 1020  
 GGGGCCATGG CCCTGGCGCC CCCACGCGC GGCTGTGGC AGGCCAAGGA CATCTCCCC 1080  
 ATCGTCAAGG CGGCCCGCCG GGATGGCGAG CTGCTCCTCT CCGCCAGCT GGATTCTGAG 1140  
 GAGAGGGACC CGGGGGTGCC CCGGCCAGC CCCTATGCGC CCTACATCT AGTCTATGCC 1200  
 AACGATCTGG CCATCTCGGA GCCCAACAGC GTGGCAGTGA CGCTGCAGAG ATACGACCCC 1260  
 TTCCCTGCCG GAGACCCCGA GCCCGCGCA GCCCCCAACA ACTCAGCGGA CCCCGCGTG 1320  
 CGCCGAGCCG CGCAGGCCAC TGGGCCCTTC CAGGACAACG AGCTGCCGGG GCTGGATGAG 1380  
 AGCCCGCCCG CGCCCCACGC ACAGCACTTC CACAAGCACC AGCTGTGGCC CAGCCCCCTC 1440  
 CGGGCGCTGA AACCCTGGCC AGGGCGCAAA GACCCGAGGA AGAAGGGCCA GGAGGTGTTT 1500  
 ATGGCCGCCT CGCAGGTGCT GGACTTTGAC GAGAAGACGA TGCAAGAACG CCGGAGGAAG 1560  
 CAGTGGGATG AGCCGAGGGT GTGCTCCCGG AGGTACCTGA AGGTGGACTT CGCAGACATC 1620  
 GGCTGGAATG AATGGATAAT CTCACCGAAA TCTTTTGATG CCTACTACTG CGCGGGAGCA 1680  
 TGTGAGTTCC CACTGCCTAA GATCGTTCGT CCATCCAACC ATGCCACCAT CCAGAGCATT 1740  
 GTGAGGGCTG TGGGCATCAT CCCTGGCATC CCAGAGCCCT GCTGTGTTCC CGATAAGATG 1800  
 AACTCCCTTG GGGTCTCTTT CTTGGATGAG AATCGGAATG TGGTCTGTA GGTGTACCCC 1860  
 AACATGTCCG TGGACACCTG TGCCTGCCGG TGAGACCACT CCAGGGTGGA AAGAAGCCAC 1920  
 GCCCAGCAGA GCTGCCTTCT CGGAGCCTTC TGCAACACAG ACTTGTGGTG CAGCTGCAGA 1980  
 CACAGAGCAC AGCTCATGGT CAACATCACT GGGGCCCAGA GAGAGCTGTC CGCCAGTGCA 2040  
 TCATTAGGGG GTCTTTTATT GCTAGTGACT AGCCCCCTAA ATGCCAGCCT GAGTACCTGA 2100  
 AGGAATCTGG GAATTAGCCC TGGCCTGAAA GTGGCCCATC ATTCATACCC ACTGTTCTGA 2160  
 AGGCTTGAAA ACAAAACATA TCCACAACAT TGGCTTGATG TGATCATCAT CTCATAACTG 2220  
 AGCAAGAAGA CTATGCAAAAT CTTAGGGCGC TCGCTCCCTG CACACGGAAG GAACTCTGTT 2280  
 TAAATGCTCA GTTCAGAAC CAATTGGGCCA CATAGTGATT TTGGAACACA GGATAATCGT 2340  
 GGTGTAATAG AGTGTTCCTT TTCAAAGTCC ACTGCAGAGC TTTTATCCAT ATGGTATGCA 2400  
 CATGTAGCCA ATATTGTTTT CTTTTTCTTA ATATATATAT TTTATTTTAA AACAAACAAA 2460  
 AGGGAGGGCG TTGACACCAT TCCCCACAGA GATAGTCATG CTGAGTGTGG GTTGTTTAAA 2520  
 CATGCATATT GAAATAACAC ATATAGTAAC GTGGGAATAC TAAAAAATAA CCAAGATTTT 2580  
 ATATTTTGTG AAATTATACT TTCTATACTG TAGATTGTGT ATGTTATGTG TTTTATGGA 2640  
 AAGCTAATAA ATTAAAGGTA CAGTGGTATC TTGA

Seq ID NO: B22 Protein sequence  
 Protein Accession #: NP\_004953.1

50  
55  
60

1 11 21 31 41 51  
 | | | | |  
 MAHVPARTSP GPGPQLLLLL LPLFLLLLRD VAGSHRAPAW SALPAAADGL QGDRDLQRHP 60  
 GDAAATLGPS AQDMVAVMHM RLYEKYSRQG ARPGGGNTVR SFRARLEVVD QKAVYFFNLT 120  
 SMQDSEMLLT ATFHIFYSEPL RWPRALEVLC KPRAKNASGR PLPLGPPTRO HLLFRSLSQN 180  
 TATQGLLRGA MALAPFPFRL WQAKDISPIV KAARRDGELL LSAQLDSEER DPGVPRPSPY 240  
 APYILVYAND LAISEPNSVA VTLQRYDPFP AGDPEPRAAP NNSADPRVRR AAQATGPLQD 300  
 NELPGLDERP PRAHAQHFKH QLNWPSFPRA LKPRFGRKDR RKKQGEVFMA ASQVLDLDEK 360  
 TMQKARRRQW DEPRVRSRRY LKVDFAIDGW NEWIISPKSF DAYYCAGACE FPMPIKIVRS 420  
 NHATIQSIVR AVGIIPGIPE PCCVPDKMNS LGVLFLENR NVVLKVYFNM SVDTCACR

Seq ID NO: B23 DNA sequence  
 Nucleic Acid Accession #: AK026322.1

65  
70  
75  
80

1 11 21 31 41 51  
 | | | | |  
 ATTCTTTAAA TACTTAAACA TGGTTATAAC AGCTGTGTTT TAAGCTCCTT GTCTGTTAAT 60  
 TCCATCATCT GTCACTTTTG CATCTGTTT TATTGACTAA CTTTCTTCTT CATCATGGTC 120  
 ACATATCCTT GCTTCTTCCC ATATTAGTA AAGTTTAGTT GGATGCTGGA TTGTTTAAAT 180  
 TTAGCATTTT GGAGTGACTG CTTTTCGACT TGCCTTTAAA AGTATTGGAC TTCGTTTGA 240  
 TAGTTGAATT ACTTGCAAA CAGCTTGATC ATTCTGAGAC TTGTTTAA CTTTGTGCGA 300  
 AAAGGCTATG CTACTTCAAG TATAATAAAA CCTAGTTTGA GTTTTATCCT ATAATAAGG 360  
 CATGTGTTCA ATTTGAATGT CTCCAACCT GTGTGAAC TCAGTCTCCA 420  
 ATTTGCGAGT AATTTTCTT GTTCAGCCTT GCAGTCTCAT CCTACTCAAG TGTGGCTCTG 480  
 TATCCAACAA CAGTCTTGGA GATCTCATGA AGATTCTGA AACTTTTGCT CTGCAGGATA 540  
 CCTTCTCTTG TGGTATGTC CCTGAAAC TCCAGCCTCC GTGTCTTCAA TTCAGTGAAA 600  
 CTACTACTCT GCTTGGATT CCCTCTTATA CAATGGTCTA CCAAGTGACT GCAACACAGAA 660  
 ATCTAAGGGA ATTTAGAGG TCACCTCATT TATTTTCTT TTTTTCAGGG ATTATAGTAG 720  
 TACTATACCA CTGTGAGCC AATGTGTGAG AATGGTGGT TCATACATT TCTCCAATTC 780  
 TTTCTTGTGA CAGGAGCCTC CATTACTTTT CAAACAGTAA TGCAGTTGCA GTTGCCTCTC 840  
 CTTTCTTCTA TTATGTGTTT ATCTCTGGCA GTTTGAGCCA AGAGAGGGCA CGGAGAAGTA 900  
 CAATGACTAG AGAGCACTTC TGTGAGGCT CATTCTATGA CCCCTACCCC AGTGCCTTAT 960  
 GAATGTGTGC TGCAGATGTC ATACAGCATC ACAGCTTCTT CTCTAATTTA TGAGGCATAA 1020  
 TTTTCTTTT TGTATTTTGA TTGTATTACC TGCTTGGTTC CAAGAGGATG ATGAGGAGGA 1080  
 CTACTATAGG ATAAATTGT TTTTATAGAG CAATTCTCA TGGGTACGA GGGATAGTAC 1140

TCCATTTTCC TCACTGATAT CGGCTTGATC ATCTGAGTCA GTGGGCTCAT TGTGGAAACA 1200  
 TATGGAATCC TTTATGCTTT TTCTCAGGCT GCTTCTGTGA CATGAAATAA AGCCAGAGTT 1260  
 GATTGTGAAA AAAAAAAAAA AAAA

5 Seq ID NO: B24 DNA sequence  
 Nucleic Acid Accession #: cat cluster

	1	11	21	31	41	51	
10	TGTATACATT	CCTTTCAAAT	AAAGACCTTG	AGAAAACAGC	AGAGCCAAGT	GAAGATCACC	60
	TAAAGAACTT	TGTGGCTAAT	TTTACTTCA	TGTAGTAGCA	GTGGGTACTG	GGCAGGGTCT	120
	CTTTCCTCACT	CTGATGATTT	GTGCTCTTAT	TTTTCTCTAGA	TTTACCTCAT	CTAGGGCATA	180
	TTCTTTTCCC	TCTTCTCTT	TACCTTTCCT	GGTCTGTATC	CCTCTGTACT	CAGTTCCCCT	240
15	AAATTATTGG	ACTACAAACT	AATATACTAG	AAAAGCATAC	ACTTATTTTA	TTTGAATGCA	300
	GAAATGCTAT	CTATCAGTAT	ATATACATAA	GAATGTATAT	TACAGTATAT	CTATATATAC	360
	TTAACACTGT	AACCTTTCAGT	ATTCCCCAGT	TAGCGTACCT	AACCTCTCTG	TGGGTATATG	420
	TAATTCTTAT	TAGACTACTA	GAGAAAAACC	AACCTGGCAGT	TTGCTAAGCA	TATCTACTGG	480
	TGTTGTTTCT	GCGCCCTCTT	TTGGCTAATT	GATGTAATTA	TACTGGCTCT	AAAGATTAC	540
20	TGCCCATATA	GTAATAGTA	TAGCCACATT	CTGAACATAT	CAAAAGTACA	AACCTAGGAG	600
	GAGTGTATGT	ACAAATATGT	AAAATTTTAT	GAAAATGAAC	ATGTTTTTAT	GATGTTATTT	660
	CTAGTCTATA	AGAATGTGAT	GACTGCTTTG	CTTCATTAT	GTACGTTCCC	ATTATATTCT	720
	TGCTGTCAAT	CAATCACAAA	TTTATATCAG	ATTAGGATAA	ACTAAGCCAT	TTTATGTATT	780
	TTATTTTAAA	CCTTATTTTG	GCAGAGTAAT	TCCTTAGAAT	TGGAAAAGCT	GTTACTTTGA	840
25	AATTACCAAT	TTATTACAAA	ACATAGAAAT	GTATTGTAGC	TACAAAGACA	ACCAAGCATT	900
	TTCTGTGTTT	TAATGAATAT	CTAAAAAAT	ACATTAGTAT	TATTTTACTC	AGTTTGTAAA	960
	TGATTTTTTT	ACTGGCTCTA	TTGCCCTTAA	ATACTAAGA	GATTAATGAT	TCTTTGTATA	1020
	ATTTTCCTTT	TCTTTGTTCT	TTTTTTTACA	TTTCGCAGAG	TTATATCTAT	AGTTTTAGTA	1080
	ACAAATTTCT	ATGATTTCTG	GATAACTGAA	AACAACATAA	GGTGTGGGCG	ATTAGAAAAAT	1140
	AATTGTGAGC	AGTAGAATTA	CTGATGTAAT	ATGTATGTTG	GACTGAAGTA	TTTCTTTATA	1200
30	AACATTCTAT	TTGATTTTAA	GCAAAATGTA	TGTTAAAGCA	TGTTTTTACA	TCAGTAAAGT	1260
	CATTGTGCGA	CCTTCTGGAA	ATGAAAGGTT	TTTACCTAGA	TACTGTAAAGT	TACACCTCCT	1320
	TAACAATCAT	ATTTGTCAAT	GTTGTTTTCT	GCAACAAAAA	ATGTTTATGG	GCTTCATGTA	1380
	GGCTTAAGAT	TGTAGGCAAA	AATGGACTGA	GTTCAGGACC	CTTCAAGCAG	TAGGCATTCA	1440
	GTTACAGAGC	AGTTGGTACT	TTGTAACCCA	GACTTACAGT	TTAAAAATAT	CAAGTTAGCT	1500
35	GATGTTTCAT	TATAATAAAA	ATACTATTTT	GCTTAAGAGT	TGTATTACAA	ATATTGTGTC	1560
	TTAACATTAG	AAATAGCTGT	TTTAAATTGT	AGTTTAACATA	TTAAGTTTAT	CAGAAAAAAA	1620
	GCATGGTTTA	TTTTTAATAA	TGAAATAGAG	AACATAATAC	GTAATGTTCA	GTATAACAGC	1680
	TGAGTTAAAA	CATCTGCCAG	GATTAACATC	AGTGCCTTTT	TGCCAATGCA	TAGAGGCATT	1740
40	TTTCTCTAAG	TATGATGGCT	AATGATAACT	ATTCCTTTGT	ACACATTCAA	GTCACTCCCA	1800
	TACAAGTAAC	TAGTGGGTGA	TATGTTTCAC	TCCAAGGGGT	GTATTAATTC	TGAATGCTAA	1860
	TCATGAAGAC	TTAAGTTAGG	ACAACACTTC	AAACCAGGAA	GTGTGAACCTG	ATTTA	

Seq ID NO: B25 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..1144

	1	11	21	31	41	51	
50	ATGGAGCGCG	GGATGCACCT	CGGTGCAGCG	GCCGCGGCGG	AGGACGACCT	CTTCCTGCAC	60
	AAGAGCCTGA	GCGCCTCCAC	CTCCAAGCGC	TTGGAAGCGG	CTTCCGCTC	CACGCCCCCG	120
	GGCATGGACC	TGTCCCTGGC	GCCGCCGCGT	CGGGAACGCC	CGGCGTCCCT	CTCCTCGTCG	180
	CCCTCGGGCT	GCTTCGAGCC	GGCTGACCCC	GAGGGGGCAG	GGCTGCTGTT	GCCGCCGCGT	240
	GGAGGAGGCG	GCGGCGGAGC	GCGGGGAAGT	GCGGCGGCGG	GCGGCGGCGG	GGTGGGTGTC	300
55	CCCGGGCTGC	TAGTAGGTTT	AGCCGGCGTT	GGGGGGCAGC	CTAGCCTAAG	CAGCCTGCCG	360
	GCCGGGGCGG	CCCTTTGCCT	CAAGTACGGC	GAAAGCGCGA	GCCGGGGCTC	GGTGGCGGAG	420
	AGCAGCGGCG	GCGAGCAGAG	CCCGGAGGAC	GACAGCGACG	GTGCTGCGCA	GCTCGTCTG	480
	CGGGCCGGAG	TAGCCGACCC	GCGGGCCTCC	CCGGGAGCGG	GAGGTGGTGG	GCGGAAGGCA	540
	GCCGAGGGCT	GCTCGAATGC	CCACCTCCAC	GCGGCGGCCA	GCGTCCCCCC	GGGGGGCCTG	600
60	GGCGGCGGCG	GCGGCGGGGG	TAGCAGCAGC	GGTAGCAGTG	GCGGCGGTGG	CGGTAGCGGT	660
	AGCGGCAGCG	GCGGCAGCAG	CAGCAGCAGC	AGCAGCAGCA	GCAAGAAATC	CAAAGAGCAA	720
	AAGGCGCTGC	GCGTTAATAT	CAATGCCCGA	GAGCGCCGGC	GGATGCACGA	CCTGAACGAC	780
	GCGCTGGACG	AGCTGCGCGC	GGTGATCCCC	TACGCGCACA	GCCCCCTCGT	GCGAAAGCTC	840
	TCCAAGATCG	CACGCTGCT	GCTCGCCAAG	AACTACATCC	TCAATGCAGG	GCAGGCCCTG	900
65	GAGGAGATGC	GCGCCTAGT	CGCCTACCTC	AACCAGGGCC	AGGCCATCTC	GGCTGCTCTC	960
	CTGCCAGCT	GCGGCGTGC	AGCGGCAGCA	GCTGCTGCCC	TGCACCCGGC	GCTCGGCGCC	1020
	TACGAGCAGG	CAGCCGGCTA	CCCGTTTACG	GCCGGAAGTG	CCCCGGCTGC	CTCCTGCCCG	1080
	GAGAAGTGC	CCCTGTTTAA	CAGCGTCTCC	TCCAGCCTCT	GCAACAGTGC	CACGGAGAAG	1140
	CCTT						

70 Seq ID NO: B26 Protein sequence  
 Protein Accession #: FGENESH predicted

	1	11	21	31	41	51	
75	MERGMHLGAA	AAGEDDLFLH	KSLSASTSKR	LEAAFRSTPP	GMDLSLAPPP	RERPASSSSS	60
	PLGCFEPADP	EGAGLLPLPP	GGGGGGSAGS	GCGGGGGVGV	PGLLVGSAGV	GDPSSLSSLP	120
	AGAAALCLKY	ESASRGSVAE	SSGGEQSPDD	DSGRCLELV	RAGVADPRAS	PGAGGGGAKA	180
	ABGRNSNAHL	GGASVPPGGL	GGGGGGGSSS	GSSGGGGGSG	SGSGGSSSSS	SSSSKKSKSQ	240
	KALRLNINAR	ERRRMHDLND	ALDELRAVIP	YAHSPSVRKL	SKIATLLLLAK	NYILMQAQL	300
80	EEMRRLVAYL	NQGQAISAAS	LPSSAAAAAA	AAALHPALGA	YEQAAGYPFS	AGLPAAASCP	360
	EKCALFNSVS	SSLCKQCTEK	P				

Seq ID NO: B27 DNA sequence  
 Nucleic Acid Accession #: cat cluster

	1	11	21	31	41	51	
5	TTTTTTTTTT	TTTTTTTAA	ATGTTTGATC	AAAATATTTT	AATAAAGATT	CTTCTGACA	60
	TAGATACACA	TACAAATGGT	CGTACATAGC	TGTCATAGTC	TGATTGACCT	ATTTAATATA	120
	TATATCATTC	TTTACACATC	CAAAACCCGC	CAACAGATCC	ATCACAGCTC	CCAACCTACC	180
	ATCCAACTG	ACAAACTGAA	TTTGTATTAT	CTGCAAGGAG	TGGAAAATAG	CAGGACTCCA	240
	TTTTTAAAAA	AGATTTTCTT	GATTTTCATA	GGGCGGAAAG	GCAGTCAAA	AGCCATGCAG	300
10	AACTAAAACT	GAAAGCTCAC	TTTGGGTAAA	TAGCTTCTTG	TTCTTCCTTA	GTTTTCTTTC	360
	TTTTTAAATT	TTATTTTTTT	AGAAAAATAA	CAAAGGATTT	CACACCATAG	GCAAAATCAA	420
	CCAGTCTTTT	AACTTAAATA	ATTCTCCACA	GTAAATAATA	CATATATGTA	CATATATATT	480
	AAAAGCAATT	AAATTAGACC	TTTTAAAAAT	GCACAGCACA	GCCTGGAAAA	ATATTGTGCT	540
	AGCATGTTCT	TACGTATAGC	AACTATTGCT	GTGATGTTTT	TCCCTTTTGG	AATGTAAAGG	600
15	AGTCCCTCTT	CAAAAAAGAG	ATCAATTTCAT	TCATCAATTA	AGAATACACC	TTTCTGTAA	660
	TTTTTGGACT	GAAGCAATTT	ATTAAAGCTC	AAATTAATA	CAGGGATGAT	GCAACTGAAA	720
	ATATCCAGGT	GACCTTTCAT	AAACCTAAGC	AGCTCAGATA	CATCAATATT	TCTCTTCATA	780
	CTTGTTGGCA	AAATAAACCTT	TAAACACTTG	GCACACAGCA	TAAAGTAATCT	ATAAAACAA	840
	TTTAGAGGCA	TTAAAAAAT	CTGCACATAA	GACCCATGAC	TTTAACACAT	GATAAATACT	900
20	GTGATGTGG	AAGGGTCATT	GAAGAATAAC	AAATAAATAC	CATGAATTGT	TAATACATCA	960
	TTGCAGAGTA	GAAAGTAACA	AGGTGCACAT	AAATATTTTT	AAATGCAATT	CTTTCAGCCA	1020
	CAGTCAGTTT	TTTTATATCA	CTCTCGCCAA	AACTTTGAGC	ATTTTCACAG	GATTAAAGTT	1080
	CAGAGACAAT	AAAAAATACA	AGTCTTTCAT	AGTAACATGT	TCTCTCTCTC	TGCTCTGGG	1140
	TTTTATTTC	CCCTCACCTA	AGTCAACATT	TCAAGTTTTT	CTCCTGGCTC	AGAATCAAAA	1200
25	TTTATTTTCA	AGTGCCCTTT	CTGATTTGTC	TGAATGAATA	TTCCATCTCT	CATGCTACCG	1260
	ATCCGCT						

Seq ID NO: B28 DNA sequence  
Nucleic Acid Accession #: NM\_002581.2  
Coding sequence: 368..5251

30	1	11	21	31	41	51	
	GGGGGAGGGA	ATTCAGCGGA	TCAGTCTTAA	GAGGAGCTTT	TTTTTGGAGC	GAGAAATCAT	60
35	ATAAAAATAA	ATGAAATAAA	ACAAGGAGGA	AGGCAACCAG	CTGTTAGGGG	GAAAAATAAG	120
	CAGATAAAGG	AGCGGGGAGA	GAAATTAATT	GCCAAACCAG	AGGAGTTGGG	CTGTATTTTT	180
	CAAGAGTGGG	GAGAGTGGAG	CACACACCTT	GAGGAGGAAA	GCGAGAAAGA	AAAGAAAAAA	240
	GCAAGTGAAG	GGGGGCTCGC	CCAAGAAAGG	TGAAGAACGC	AAGAAAGTCG	AGGCGCCGAG	300
	GCTCCCAAAG	CTGGCAGCTC	CGGGTGGCGG	TGCAGGGGCG	AAGGGGGGGG	CGGGGGGAAC	360
40	GTGCGCATG	CGGCTCTGGA	GTGGGTGCTG	GCACCTGGGG	CTGCTGAGCG	CCGCGCTGGG	420
	CTGCGGGCTG	GCCGAGCGTC	CCGCGCGGGC	CCGAGAGAGC	CCGCGGGCCG	GCCGACCCCC	480
	GCGCCGCCGC	GCCGCGCCCG	CCACCTGCGC	CACCCGCGGC	CCGCGGCCGC	CGCGCTCGC	540
	CGCGCGCGCC	GCCGCGCCCG	GGCGTGCCTG	GGAAGCCGTG	CGCGTCCCCC	GGCGGCGGCA	600
	GCAGCGGGAG	GCGAGGGGCG	CCACCGAGGA	GCCGAGCCCG	CCGAGCCGGG	CGCTCTATTT	660
45	CAGCGGGCGA	GGCGAGCAGC	TGCGAGTCCT	CCGGGCCGAC	CTCGAGCTGC	CCCGGGACGC	720
	GTTCACGCTG	CAAGTGTGCG	TGCGAGCGGA	GGGGGGCCAG	AGGTCTCCGG	CAGTGATCAC	780
	AGGGGTGTAT	GACAAATGTT	CTTATATCTC	ACGTGACCGA	GGATGGGTCT	TGGGCATTCA	840
	CACCATCAGT	GACCAAGACA	ACAAAGACCC	ACGCTACTTT	TTCTCTTTGA	AGACAGACCG	900
	AGCCCCGCAA	GTGACCACCA	TCAATGCCCA	CCGCGAGCTAC	CTCCCAGGCC	AGTGGGTATA	960
50	CCTAGCTGCC	ACCTATGATG	GGCAGTTCAT	GAAGCTCTAT	GTGAATGGTG	CCCAGGTGGC	1020
	CACCTCTGGG	GAACAAGTGG	GTGGCATATT	CAGCCCACTG	ACCCAGAAAT	GCAAAAGTGT	1080
	CATGTTAGGG	GGCAGTGCCT	TGAATCACAA	CTACCGGGGC	TACATCGAGC	ACTTCAGTCT	1140
	GTGGAAGGTG	GCCAGGACTC	AGCGGGAGAT	ACTGTCTGAC	ATGGAACCC	ATGGCGCCCA	1200
55	CACCTGCTCA	CCTCAGCTCC	TCCCTCAGGA	GAACCTGGGAC	AATGTGAAGC	ATGCCCTGGT	1260
	CCCCATGAAG	GATGGCAGCA	GCCCCAAAGT	GGAATTCAGC	AATGCCCAAG	GCTTTCTGCT	1320
	GGACACGAGT	CTGGAGCCTC	CTCTGTGCGG	ACAGACATTG	TGTGACAAAC	CAGAGGTCAT	1380
	TGCCAGCTAC	AATCAGCTCT	CAAGTTTCCG	CCAGCCCAAG	GTGGTGCCTG	ACCGCTGGT	1440
	CAACCTCTAT	GAAGATGATC	ATAAGAACCC	GACGGTGACG	CGCGAGCAGG	TGGACTTCCA	1500
60	GCACCATCAG	CTGGCTGAGG	CCTTCAAGCA	ATACAACATC	TCCTGGGAGC	TGGACGTGCT	1560
	GGAGGTGAGC	AACTCTCTCC	TTGCGCGCCG	CCTCATCTCT	GCCAACTGTG	ACATCAGCAA	1620
	GATTGGGGAT	GAGAACTGTG	ACCCCGAGTG	CAACCACACG	CTGACGGGCC	ACGACGGCGG	1680
	GGATTGCGCG	CACCTGCGCC	ACCCTGCTTT	CGTGAAGAAG	CAGCACACAC	GGGTGTGTGA	1740
	CATGGAGTGC	AACTATGAAC	GGTTCACATT	TGATGGTGGA	GAGTGTCTGT	ACCCTGAAAT	1800
	CACCAATGTC	ACTCAGACTT	GCTTTGACCC	CGACTCTCCA	CACAGAGCCT	ACTTGGATGT	1860
65	TAATGAGCTG	AAGAACATTC	TTAAATTGGA	TGGATCAACA	CATCTCAATA	TTTTCTTTGC	1920
	AAAATCCTCA	GAGGAGGAGT	TGGCAGGAGT	AGCAACTTGG	CCATGGGACA	AGGAGGCCCT	1980
	GATGCACTTA	GGTGGCATTG	TCTTGAACCC	ATCTTTCTAT	GGCATGCTTG	GGCACACCCA	2040
	CACCATGATC	CATGAGATTG	GTCAACAGCT	GGGCTCTCT	CACGTCTTCC	GAGGCATCTC	2100
	AGAAATCCAG	TCCTGACAGT	ACCCCTGCAT	GGAGACAGAG	CCCTCTCTCG	AGACTGGAGA	2160
70	CCTCTGCAAT	GATACCAACC	CAGCCCCATA	ACACAAGTCC	TGTGGTGACC	CAGGGCCAGG	2220
	AAATGACACC	TGTGGCTTTC	ATAGCTTCTT	CAACACTCCT	TACAACAAC	TCATGAGCTA	2280
	TGCAGATGAC	GACTGTACGG	ACTCCTTCAC	GCCCAATCAA	GTGCGCCAGAA	TGCATGTTA	2340
	CCTGGACCTG	GTCTACACAG	GCTGGCAGCC	CTCCAGGAAA	CCAGCGCTTG	TTGCCCTCGC	2400
	CCCCCAAGTT	CTGGGCCACA	CAACGGACTC	TGTGACACTG	GAGTGGTTCC	CACCTATAGA	2460
75	TGGCCATTTC	TTTGAAAGAG	AATTGGGATC	AGCATGTGAT	CTTTGCTTGG	AAGGGAGAA	2520
	CCTGGTGACG	TATGCTTCCA	ACGCTTCTCT	CCCAATGCCC	TGCAGCCCAT	CAGGACACTG	2580
	GAGCCCTCGT	GAGCAGAGAG	GTCATCTTGA	TGTTGAACAG	CCCTGTAAAT	CCAGTGTCCG	2640
	CACCTGGAGC	CCAAATTTCAG	CTGTCAACCC	ACACACGGTT	CCTCCAGCCT	GCCCTGAGCC	2700
	TCAAGGCTGC	TACCTCGAGC	TGGAGTTCCT	CTACCCCTTG	GTCCCTGAGT	CTCTGACCAT	2760
80	TTGGGTGACC	TTTTGTCTCA	CTGACTGGGA	CTCTAGTGGG	GCTGTCAATG	ACATCAAACT	2820
	GTTGGCTGTC	AGTGGGAAGA	ACATCTCCCT	GGGTCTCTCAG	AATGTCTTCT	GTGATGTCCC	2880
	ACTGACCATC	AGACTCTGGG	ACGTGGGCGA	GGAGGTGTAT	GGCATCCAAA	TCTACACGCT	2940
	GGATGAGCAC	CTGGAGATCG	ATGCTGCCAT	GTTGACCTCC	ACTGCAGACA	CCCCACTCTG	3000
	TCTACAGTGT	AAGCCCCCTGA	AGTATAAGGT	GGTCCGGGAC	CCTCTCTTCC	AGATGGATGT	3060
	GGCCTCCATC	CTACATCTCA	ATAGGAAATT	CGTAGACATG	GATCTAAATC	TTGGCAGTGT	3120

5  
10  
15  
20  
25  
30  
35  
40

```

GTACCAGTAT TGGGTCATAA CTATTTTCAGG AACTGAAGAG AGTGAGCCAT CACCTGCTGT 3180
CACATACATC CATGGACGCTG GGTACTGTGG CGATGGCATT ATACAAAAG ACCAAGTGA 3240
ACAAATGCGAC GACATGAATA AGATCAATGG TGATGGCTGC TCCCTTTTCT GCCGACAAGA 3300
AGTCTCCTTC AATTGTATTG ATGAACCCAG CCGGTGCTAT TTCCATGATG GTGATGGGGT 3360
ATGTGAGGAG TTTGAAACAA AAACCCAGCAT TAAGGACTGT GGTGTCTACA CGCCCCAGGG 3420
ATTCTTGGAT CAGTGGGCGT CCAATGCTTC AGTATCTCAT CAAGACCAGC AATGCCCAGG 3480
CTGGGTATC ATCGGACAGC CAGCAGCATC CCAGGTGTGT CGAACCAAGG TGATAGATCT 3540
CAGTGAAGGC ATTTCCAGC ATGCCTGGTA CCCTTGCAAC ATCAGCTACC CATATTCCCA 3600
GCTGGCTCAG ACCACTTTTT GGTCCCGGGC GTATTTTCT CAACCAATGG TTGCCGAGC 3660
TGTCATTGTC CACCTGGTGA CGGATGGGAC ATATTATGGG GACCAAAAGC AGGAGACCAT 3720
CAGCGTGCAG CTGCTTGATA CCAAAGATCA GAGCCACGAT CTAGGCCTCC ATGTCCTGAG 3780
CTGCAGGAAC AATCCCCTGA TTATCCCTGT GGTCCATGAC CTGAGCCAGC CCTTCTACCA 3840
CAGCCAGGCG GTACGTGTGA GCTTCAGTTC GCCCTTGGTC GCCATCTCGG GGGTGGCCCT 3900
CCGTTCCTTC GACAACCTTG ACCCCGTCAC CCTGAGCAGC TGCCAGAGAG GGGAGACCTA 3960
CAGCCCTGCC GAGCAGAGCT GCGTGCACCT CGCATGTGAG AAAACTGACT GTCCAGAGCT 4020
GGCTGTGGAG AATGCTTCTC TCAATTGCTC CAGCAGCGAC CGCTACCACG GTGCCAGTG 4080
TACTGTGAGC TGCCGAGACG GCTACGTGCT CCAGATACGG CGGGATGATG AGCTGATCAA 4140
GAGCCAGACG GGACCCAGCG TCACAGTGAC CTGTACAGAG GGCAAGTGA ATAAGCAGGT 4200
GGCCTGTGAG CCAGTCGACT GCAGCATCCC AGATCACCAT CAAGTCTATG CTGCTCTCTT 4260
CTCTGCCCCC GAGGGCACCA CCTTTGGCAG TCAATGTTC TTCCAGTGCC GTCAACCTGC 4320
ACAATTGAAA GGCAACAACA GCCTCCTGAC CTGCATGGAG GATGGGCTGT GGTCTCTCCC 4380
AGAGGCCCTG TGTGAGCTCA TGTGCTCTCG TCCACCCCT GTGCCCAATG CAGACCTCCA 4440
GACCGCCCGG TGCCGAGAGA ATAAGCAAA GGTGGGCTCC TTCTGCAAA ACAAATGCAA 4500
GCCTGGATAC CATGTGCCCTG ATCCTCTCG GAAGTCAAAG AAACGGGCCT TCAAGACTCA 4560
GTGTACCCAG GATGGCAGCT GGCAGGAGGG AGCTTGTGTT CCTGTGACCT GTGACCCACC 4620
TCCACAAAA TTCCATGGGC TCTACCATG TACTAATGGC TTCCAGTTCA ACAGTGAGTG 4680
TAGGATCAAG TGTGAAGACA GTGATGCCCTC CCAGGGACTT GGGAGCAATG TCATTCAATTG 4740
CCGGAAGATG GGCACCTGGA ACGGCTCCTT CCATGTCTGC CAGGAGATGC AAGGCCAGTG 4800
CTCGGTTCGA AACGAGCTCA ACAGCAACCT CAAACTGCAG TGCCCTGATG GCTATGCCAT 4860
AGGGTCGGAG TGTGCCACCT CGTGCTTGA CAACAACAGC GAGTCCATCA TCCTGCCAAT 4920
GAACGTGACC GTGCGTGACA TCCCCACTG GCTGAACCCC ACACGGGTAG AGAGAGTTGT 4980
CTGCACTGCT GGTCTCAAGT GGTATCCCTCA CCCTGCTCTG ATTCACCTGT TCAAGGCTG 5040
TGAGCCCTTC ATGGAGAGACA ATTATTGTGA TGCCATCAAC AACCGAGCTC TTTGCAACTA 5100
TGACGGTGGG GATTCTGCA CCTCCACAGT GAAGACCAAA AAGGTCAACC CATTCCCTAT 5160
GTCCTGTGAC CTACAAGGTG ACTGTGCTTG TCGGACCCC CAGGCCAAG AACACAGCCG 5220
GAAAGACCTC CGGGGATACA GCCATGGCTA AGGAAGGACA AGAAGTTGTC AAAGAATTCC 5280
CAACGCCAGG ACCACATCC CTTTGGTATT GATTTACAG TCAGCTGCTC AACGGAATGG 5340
CCTCTCCACA CAGGGATCC TTAGACCCA ACCGGTCTGC CTTTAATTTT ACCCAGGAAG 5400
GACTCACATT GGGGCGAATG AACCAAGTTT CGCCATGCTG GATGATGAAA TGGATTCCCA 5460
TCCAAAGTC TGAGATGGAT TGCATATACA GTGTGCAGTC CCAGAGCCTC CTAATAATTCT 5520
AGCCATTTGT CACACAACCA CAGCAAAAA AAA

```

Seq ID NO: B29 Protein sequence  
Protein Accession #: NP\_002572.1

45  
50  
55  
60  
65  
70  
75

```

1 11 21 31 41 51
MRLWSVWLHL GLLSAAALGCG LAERPRRARR DPRAGRPPRP AAGPATCATR GPRPPRLAAA 60
AAAAGRAWEA VRVPRRRQR EARGATEEPS PPSRALYFSG RGEQLRVLRA DLELPDRAFT 120
LQVWLRAGEG QRSAPVITGL YDKCSYISRD RGWVVGIIHTI SDQDNKDPYR FFSLKTDRLR 180
QVTINAHRS YLPQGWVYLA ATYDGFQMKL YVNGAQVATS GEQVGIFSP LTQKCKVLML 240
GGGALNHNRY GYIEHFSWLK VARTQREILS DMETHGAHTA LPQLLLQENW DNVKHAWSM 300
KDGSSPKVEF SNAHGFLDDT SLEPPLCGQT LCDNTEVIAS YNQLSSFRQP KVVRYRVVNL 360
YEDDHKNPTV TREQVDFQHH QLAFAFKQYN ISWELDVLEV SNSSLRRRLI LANCDISKIG 420
DENDPECNH LLTGHDDGDC RHLRHPAFVK QHNGVCDMD CNYERFNFDG GECCDPEITN 480
VTQTCFDPDS PHRAYLDVNE LKNILKLDGS THLNIFFAKS SEELAGVAT WPWDKEALMH 540
LGGLVILNPSF YGMPGHTHTM IHEIGHSLGL YHVFGRGISEI QSCSDPCMET EPSFETGDL 600
NDTNPAKPKF SCGDPGPGND TCGFHSFNT PYNNFMSYAD DDCTDSFTPN QVARMHCYLD 660
LVYQGWQPSR KPAPVALAPQ VLGHITDSVT LEWFPPIDGH FFERELGSAC HLCLEGRILV 720
QYASNASSPM PCSPSGHWSP REAEGHPDVE QPKSSVRTW SPNSAVNPHT VPPACPEPQG 780
CYLELEFLYP LVPESLTIWV TFSVDWDSS GAVNDIKLLA VSGKNISLGP QNVFCDVPLT 840
IRLWDVGEV YGIQIYTLDE HLEIDAAMLT STADTPLCLQ CKPLKYKVVR DPPLQMDVAS 900
ILHLNRKFVD MDLNLGSVYQ YWVITISGTE ESEPSPAVTV IHGRGYCGDG IIQKDQGEQC 960
DDMNKINGDG CSLFRCQEV S FNCIDEPSRC YFHDGDGVC EFEQKTSIKD CGVYTPQGFL 1020
DQWASNASVS HQDQCCPGWV IIGQPAASQV CRTKVIDLSE GISQHAWYPC TISYPYSQLA 1080
QTTFWLRA YF SQPMVA AAVI VHLVTDGTY Y GDQKQETISV QLLDTKDQSH DLGLHVLSCR 1140
NNPLIIPVH DLSQFFYHSQ AVRVSFSSPL VAISGVALRS FDNFDPVTL SQRGETYSP 1200
AEQSCVHFAC EKTDCPELAV ENASLNCSSS DRYHGAQCTV SCRTGYVLQI RRDELKISQ 1260
TGPSVTVTCT EGKWNKQVAC EPVDCSIPDH HQVYAAAFSC PEGTTFGSQC SFQCRHPAQL 1320
KGNNSLLTCM EDGLWSFPEA LCELMCLAPP PVPNADLQTA RCRENKHVKG SFCKYKCKPG 1380
YHVPSSSRK KRAFKTQCT QDGSWQEGAC VPVTCDDPPP KFHLGYQCTN GFQFNSECR 1440
KCEDSDASQG LGSNVIHCRK DGTWNGSFHV CQEMQGCQSV PNELSNLSKL QCPDGYAIGS 1500
ECATSCLDHN SESILPMNV TVRDIPHWLN PTRVERVCT AGLKWYHPA LIHCVKGCPE 1560
FMGDNYCDAI NNRAFCNYDG GDCCTSTVKT KKVTFPPMSC DLQGDACARD PQAQEHRSKD 1620
LRGYSHG

```

Seq ID NO: B30 DNA sequence  
Nucleic Acid Accession #: NM\_032808.1  
Coding sequence: 61..1008

80

```

1 11 21 31 41 51
CTAGTCTATC TCCGCTTCTT CAACCTCTCC TACAACCCCA TCAGCACCAT TGAGGGCTCC 60
ATGTTGCATG AGCTGCTCCG GCTGCAGGAG ATCCAGCTGG TGGGCGGCA GCTGCGCTG 120

```



GTGGAGCCCT ATGCGCTCCG CGGCGCTCAAC TACCTGCGCG TGCTCAATGT CTCTGGCAAC 180  
 CAGCTGACCA CACTGGAGGA ATTAGTCTTC CACTCGGTGG GCAACCTGGA GACACTCATC 240  
 CTGGACTCCA ACCCGCTGGC CTGCGACTGT CGGCTCCTGT GGGTGTTCG GCGCGCGTGG 300  
 CGGCTCAACT TCAACCGGCA GCAGCCACGC TGCGCCACGC CCGAGTTTGT CCAGGGCAAG 360  
 GAGTTCAAGG ACTTCCCTGA TGTGCTACTG CCCAACTACT TCACCTGCCG CCGCGCCCGC 420  
 ATCCGGGACC GCAAGGCCCA GCAGGTGTTT GTGGACGAGG GCCACACGGT GCAGTTTGTG 480  
 TGCCGGGCGG ATGGCGACCC GCGCGCCGCC ATCCTCTGGC TCTCACCCCG AAAGCACCTG 540  
 GTCTCAGCA AGAGCAATGG GCGGCTCACA GTCTTCCCTG ATGGCACGCT GGAGGTGCGC 600  
 TACGCCAGG TACAGGACAA CGGCACGTAC CTGTGCATCG CGGCCAACGC GGGCGGCAAC 660  
 GACTCCATGC CCGCCACCTT GCATGTGCGC AGCTACTCGC CCGACTGGCC CCATCAGCCC 720  
 AACAGACCT TCGCTTTCAT CTCCAACAG CCGGGCGAGG GAGAGGCCAA CAGCACCCGC 780  
 GCCACTGTGC TTTTCCCTT GCACATCAAG ACCCTCATCA TCGCCACCAC CATGGGCTTC 840  
 ATCTCTTTC TGGGCGTCGT CCTCTCTGC CTGGTGTGCT TGTCTCTCTG GAGCCGGGGC 900  
 AAGGGCAACA CAAAGCACAA CATCGAGATC GAGTATGTGC CCCGAAAGTC GGACGCGAGC 960  
 ATCAGTCTCG CCGACGCGCC CCGCAAGTTC AACATGAAGA TGATATGAGG CCGGGGCGGG 1020  
 GGGCAGGGAC CCGCGGCGG CCGGGCAGGG GAAGGGGCGT GGCCGCCACC TGCTCACTCT 1080  
 CCAGTCTTTC CCACCTCTTC CTACCTCTTC TACACACGTT CTCTTCTCTC CTCCCGCTTC 1140  
 CGTCCCTGTC TGCCCCCGC CAGCCCTCAC CACCTGCCCT CCTTCTACCA GGACCTCAGA 1200  
 AGCCAGAGAC TGGGGAGCCC ACCTACACAG GGGCATTTGAC AGACTGGAGT TGAAGGCCGA 1260  
 CGAACCGACA CCGCGGAGAG TCAATAATTC AATAAAAAAG TTACGAACTT TCTCTGTAA 1320  
 TTGGGTTTCA ATAATTATGG ATTTTATGA AACTTTGAAA TAATAAAAA AGAAAAAAAC 1380  
 TATTTCTAT AGCTAGTCGG AATGCAAACT TTTGACGTCC TGATTGCTCC AGGGCCCTCT 1440  
 TCCAACCTAG TTTCTTGTTC TTCTCTTCTT CCTCTCTCTC TTCTTCTCTC TTTCTCTTCT 1500  
 TTTCCCAAGT GGGGAGGGAT CACTCAGGAA AACAGGAAAG GAGGTTCCAG CCCCACCCAC 1560  
 CTGCCACCCC CGCCCGAGGC ACCATCAGGA GCAGGCTAGG GGGCAGGCCT GGGCCAGCT 1620  
 CCGGGCTGGC TTTTTCGAGG GCGCAGGTGG AGGGACAGG TCTGCCGATG GGGGTGGAG 1680  
 CCTGTCTGCT GGGCTGCCAG GCGGCACCCAC TGCAAGGGGT GGGAGCCTGG CTTGGGTGTG 1740  
 GCTGAGACTC TGGACAGAGG CTGGGGTCTT CTGGGGGAC AGCACAGTCA GTGGAGAGAG 1800  
 CCAGGGGTCT GCGATGGGGC CCACCCAGC CTCTGTCTCC AGCTCTGCTG CTCACCTGCT 1860  
 GTGTGGCTC AAGCAGGTCA CTGGCCTCTC TGGGCTCAG TCTCCACATC TGTACAAATG 1920  
 GGAACATTAC CCCTGCCCCT GCCTACCTCA CAGGGCTGTT GTGAGGAATT GATGAGATGA 1980  
 TGTATGTGAA ACACCTTGTG ACCTGTAAAG CGCTGTGCAC ACCTG

Seq ID NO: B31 Protein sequence  
 Protein Accession #: NP\_116197.1

1 11 21 31 41 51  
 MLHELLRLQE IQLVGGQLAV VEPYAFRGLN YLRVLNVSGN QLTLEELVF HSVGNLETLI 60  
 LDSNPLACDC RLWVFRRRW RLNFNRQOPT CATPEFVQVK EFKDFPDVLL PNYFTCRRAR 120  
 IRDRKAQQVF VDEGHTVQFV CRADGDPPEA ILWLSPRKHL VSAKSNGLRT VFPDGTLEVR 180  
 YAQVDNGTY LCIAANAGGN DSMPAHLHVR SYSPDWP HQP NKTFAFISNQ PGEGEANSTR 240  
 ATVPFPFDIK TLIIATTMGF ISFLGVVLF LVLFLWSRG KGNTKHNI EI BYVPRKSDAG 300  
 ISSADAPRK NMKMI

Seq ID NO: B32 DNA sequence  
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51  
 CAGCACATAC AAGAAACATA CAGTGTACCT CAAAGGGGCG CCTTGAAATG TCATCAAAGG 60  
 GTAATAACCT AGTGAGTGAG TTGTGATGTC ATCTGGAACA TAGGAAATGG GGCTCTTAGC 120  
 GTATTGCGTA CGAAGGAAGC CAGGCTGGTC CTGGCAGGAA GTAATGATA ATCTTTGGGA 180  
 AACCAGGACC CTGCCTCCCA GCCCAGAGGT GGAGGAGGGC GGTCAAGGTG GGGCTACAG 240  
 TGGCAGACA CTGACAAAGG TAGAGGAAA TGAATAGCA CATCTACGCT GCAGTCTGGT 300  
 GAAAGTGGCC GGGGTGGTCC TTGGAACA GTTGGGCTGT TCTTGGCAGG AATTAGTGAC 360  
 AGCCTTTCG TCACGGGCGG GGACGCTTG ATTTAAAAA AATAAATAA TAAACGTCT 420  
 GGGTATAGAA A

Seq ID NO: B33 DNA sequence  
 Nucleic Acid Accession #: NM\_006174.1  
 Coding sequence: 71..1408

1 11 21 31 41 51  
 GAAAGGCTAT CGGTAACAAC TGACCTGCCA CAAAGTTAGA AGAAAGGATT GATTCAAGAA 60  
 AGACTATAAT ATGGATTAG AGCTCGACGA GTATTATAAC AAGACACTTG CCACAGAGAA 120  
 TAATACTGCT GCCACTCGGA ATTCTGATTT CCCAGTCTGG GATGACTATA AAAGCAGTGT 180  
 AGATGACTTA CAGTATTTTC TGATTGGGCT CTATACATTT GTAAGTCTTC TTGGCTTTAT 240  
 GGGGAATCTA CTATTATTAA TGGCTCTCAT GAAAAAGCGT AATCAGAAGA CTACGGTAAA 300  
 CTTCCTCATA GCGAATCTGG CCTTTCTGA TATCTGGTT GTGCTGTTT GCTCACTTT 360  
 CACACTGACG TCTGTCTGTC TGGATCAGTG GATGTTGGC AAAGTCATGT GCCATATTAT 420  
 GCCTTTTCTT CAATGTGTGT CAGTTTGGT TTCAACTTTA ATTTTAATAT CAATTGCCAT 480  
 TGTCAAGTAT CATATGATAA AACATCCCAT ATCTAATAAT TTAACAGCAA ACCATGGCTA 540  
 CTTTCTGATA GCTACTGTCT GGACACTAGG TTTTGCCATC TGTCTCTCCC TTCCAGTGT 600  
 TCACAGTCTT GTGGAATTC AAGAAACATT TGGTTCAGCA TTGCTGAGCA GCAGGTATT 660  
 ATGTGTTGAG TCATGGCCAT CTGATTGATA CAGAATTGCC TTTACTATCT CTTTATTGCT 720  
 AGTTCAGTAT ATTCTGCCCC TAGTTTGTCT TACTGTAAGT CATAAAGTG TCTGCAGAAG 780  
 TATAAGCTGT GGAATTGCTA ACAAGAAAA CAGACTTGAA GAAAATGAGA TGATCAACT 840  
 AACTCTTCAT CCATCCAAAA AGAGTGGGCC TCAGGTGAAA CTCTCTGGCA GCCATAAATG 900  
 GAGTTATTCA TTCAACAAAA AACACAGAAG AAGATATAGC AAGAAGACAG CATGTGTGTT 960  
 ACCGTCTCCA GAAAGACCTT CTCAAGAGAA CCACTCCAGA ATACTTCCAG AAAACTTTGG 1020  
 CTCTGTAAGA AGTCAGTCT CTTATCCAG TAAGTTCATA CCAGGGGTCC CCACTTGCTT 1080  
 TGAGATAAAA CCTGAAGAAA ATTCAGATGT TCATGAATTG AGAGTAAAC GTTCTGTATC 1140

AAGAATAAAA AAGAGATCTC GAAGTGT TTT CTACAGACTG ACCATACTGA TATTAGTATT 1200  
 TGCTGTAGT TGGATGCCAC TACACCTTTT CCATGTGGTA ACTGATTTTA ATGACAATCT 1260  
 TATTTCAAAT AGGCATTTCA AGTTGGTGTA TTGCATTTGT CATTTGTTGG GCATGATGTC 1320  
 CTGTTGTCTT AATCCAATTC TATATGGGTT TCTTAATAAT GGGATTAAAG CTGATTTAGT 1380  
 GTCCCTTATA CACTGTCTTC ATATGTAATA ATTCTCACTG TTT

Seq ID NO: B34 Protein sequence  
 Protein Accession #: NP\_006165.1

1 11 21 31 41 51  
 MDLEDEYYN KTLATENNTA ATRNSDFPVW DDYKSSVDDL QYFLIGLYTF VSLLGFMGNL 60  
 LILMALMKKR NQKTTVNFLI GNLAFS DILV VLFCSPTFLT SVLLDQWMFG KVMCHIMPFL 120  
 QCVSVLVSTL ILISIAIVRY HMIKHPISNN LTANHGYFLI ATVWTLGFAL CSPLPVFHSN 180  
 VELQETFGSA LLSRYLCVE SWPDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240  
 GLSNKENRLE ENEMINLT LH PSKSGPQVK LSGSHKWSYS FIKHRRRYS KKTACVLPA 300  
 ERPSQENHSR ILPENFGSVR SQLSSSKFI PGVPTCFEIK PEENSVDVHEL RVKRSVTRIK 360  
 KRSRSVFYRL TILILVFAVS WMLPLHFHV TDFNDNLISN RHFKLVYCIC HLLGMMSCCL 420  
 NPILYGLFNN GIKADLVSLI HCLHM

Seq ID NO: B35 DNA sequence  
 Nucleic Acid Accession #: NM\_014279.1  
 Coding sequence: 286..1689

1 11 21 31 41 51  
 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60  
 CCTGCCACGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120  
 CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGTCTGA TCCAGGCGTG 180  
 GGGACACGAG CCAGGCGCGG CCGCGCGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240  
 TCCGCGTCCA CGCAGCGCGC GCGCGGCCAG CACCCAGGCG CCTGCATGCC AGGTCGTG 300  
 AGGTGGCAGC GAGACATGCA CCCGCGCGG AAGCTCCTCA GCCTCCTCTT CCTCATCTG 360  
 ATGGGCACTG AACTCACTCA AGTGCTGCC ACCAACCTG AGGAGAGCTG GCAGGTGTAC 420  
 AGCTCTGCC AGGACAGCGA GGCAGGTGT ATCTGCACAG TGGTCGCCCC ACAGCAGACC 480  
 ATGTGTTTCA GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540  
 ATGTCTCAAT CCATAGAGGT CTGAGCAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600  
 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660  
 AAGCAACACC TGGCCAGGCA GTTTAAGGCG ATAAAGCGA AAATGGATGA ACTTAGGCCT 720  
 TTGATACCTG TGTGGAAGA GTACAAGGCC GATGCCAAAT TGGTATTGCA GTTTAAAGAG 780  
 GAGGTCCAGA ATCTGACGTC AGTGCTTAAC GAGCTGCAAG AGGAAATGG CGCCTATGAC 840  
 TACGATGAAC TTCAGAGCAG AGTGTCCTAT CTGTAAGAAA GGCTCCGTGC ATGCATGCAA 900  
 AAACTAGCTT GCGGGAAGTT GACGGGCATC AGTGACCCCG TGACTGTCAA GACCTCCGGC 960  
 TCGAGGTTTC GATCCTGGAT GACAGACCTT CTCGCCCTG AAGGCGATAA CCGGCTGTGG 1020  
 TACATGGAGC GCTATCACAA CAACCGCTTC GTACGTGAGT ACAAGTCCAT GGTGACTTTC 1080  
 ATGAACACGG ACAATTTTCA CTCCCAACCG CTCCCAACCG CTGGTTCGG CACGGGGCAG 1140  
 GTGGTCTACA ACGGTTCTAT CTACTTCAAC AAGTTCAGG GCCACATCAT CATCAGGTTT 1200  
 GACCTGAAGA CAGAGACCAT CCTCAAGACC CGCAGCCTGG ACTATGCCGG TTACAACAAC 1260  
 ATGTACCACT ACGCTGGGG TGGCCACTCG GACATCGACC TCATGGTGA CGAGAGCGGG 1320  
 CTGTGGGCGG GTAGCGCCAC CAACCAAGAC GCTGGCAACA TCGTGGTCAG TAGGCTGGAC 1380  
 CCGTGTGCC TGCAGACCTT GCAGACCTGG AACACGAGCT ACCCAAGCG CAGCGCCGGG 1440  
 GAGGCCTTCA TCATCTGCGG CACGCTGTAC GTCAACCAAC GCTACTCAGG GGGTACCAAG 1500  
 GTCCACTATG CATACCAGAC CAATGCCTCC ACCTATGAAT ACATCGACAT CCCATTCCAG 1560  
 AACAAATACT CCCACATCTC CATGCTGGAC TACAACCCCA AGGACCGGGC CCGTATGTC 1620  
 TGGAAACAAC GCCACAGAT CCTCTACAAC GTGACCTCTT TCCACGTCAT CCGCTCCGAC 1680  
 GAGTTGTAGT TCCTCTCTCC TGGAGGCCAA GGGCCACGCT CCTCACCA CAAGGACTCC 1740  
 TGTGAAACTG CTGCCAAAAA GATACCAATA ACTATAACAA TACCGATCTT GAAAAATCAT 1800  
 CAGCAGTGCG GATTCTGACA TCGAGGGATG GCATTACCTC CGTGTCTTCT CCTTTCGAGC 1860  
 CGGCGGGCCA CAGACCTCGG AAGAAACTCC CGTATTGCA GCTGGAACTG CAGCCCAACG 1920  
 CGCCCCGGTT TTCTCCCGG CCTGTCCCT CTCTGGTCAA ACAACATACT AAAGAGGCGA 1980  
 GGCATGACT GTTGGCCAGT TCTCACCGGG GAAAAACCA CTGTTAGGAT GGCATGAACA 2040  
 TTTCTTAGA TCGTGGTCAG CTCGAGGAA TGTGGCGTCC AGGCTCTTTG AGAGCCATGG 2100  
 GCTGCACCGC GCCGTAGGCT AGTGTAATCT GCATCCCAT GCAGTGCCGT TTCTTGACTG 2160  
 TGTGTCTGTC TCTTAGATTA ACGTGCTGA GGCTCCACAT AGCTCCTGGA CCTGTGTCTA 2220  
 GTACATACTG AAGCGATGGT CAGAGTGTGT AGAGTGAAGT TGCTGTGCCC ACATTGTTT 2280  
 AACTCGCGTA CCCCGTAGAT ACATTGTGCA ACGTCTCTCT GTTATTCCCT TGAGGTGGTA 2340  
 ACTTCGTATG TTAGCTTTAT CGCATGATTG TTGTAAATGC AATGCCGTAG TTTGGATTAA 2400  
 TAAGTGGATG GTTTTTGTTT CTAATAAGAA AAAAAAATC AGTGTTCACC CTTATAGAGA 2460  
 CATAGTCAAG TTCATGTTGA TAATAATCAA AGGAATTACT CTCTCTTGT TAAATTAGCT 2520  
 AAATCATGTA ACCGCAGATA GGAAGGGCTC ACCTGGGGAA ACTCTGGTTT CCGATGGGAC 2580  
 AGGAAAGTCA TACGGGCAAC AGTATGCGGA AAGTACGTT TTTTAAGTAA AAAACAAAGG 2640  
 CAACTTTGT ACTATCCAGT TATCTAAGGA ACAATAAAAA CATTAGGAGA AAAAAAAGG 2700  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: B36 Protein sequence  
 Protein Accession #: NP\_055094.1

1 11 21 31 41 51  
 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TVLPNTPEE SWQVYSSAQD SEGRICITVV 60  
 APQQTMC SRD ARTKQLRQLL BKVNMSQSI EVLDRRTQD LQYVEKMEQ MKGLSKFKQ 120  
 VEESHKQHLA RQFKAIKAKM DELRLPIVL EBYKADAKLV LQFKEVQNL TSVLNLQEE 180  
 IGAYDYDELQ SRVNLLEERL RACMQKLACG KLTGISDPVT VKTSGSRFGS WMTDPLAPEG 240  
 DNRVWYMDGY HNNRFVREYK SMVDFMNTDN FTSHRLPHEW SGTGQVYVNG SIYFNKFQSH 300  
 IIRFDLKT E TILKTRSLDY AGYNNMYHYA WGGHSDIDL M VDESLWAVY ATNQNAGNIV 360

VSRLDPVSLQ TLQTNWNTSYP KRSAGEAFII CGTLYVTNGY SGGTKVHYAY QTNASTYEI 420  
DIPFQNKYSH ISMLDYNPKD RALYAWNNGH QILYNVTLPH VIRSDEL

Seq ID NO: B37 DNA sequence  
Nucleic Acid Accession #: NM\_006334.1  
Coding sequence: 286..693

```

1      11      21      31      41      51
|      |      |      |      |      |
10 GCGCGGGGGA GCCATTAGGA GGCGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
   CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
   CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGTCTGAA TCCAGGCGTG 180
   GGGACACGAG CCAGGCGCCG CCGCCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
   TCCGCGTCCA CGCAGCCGCC GGCCGGCCAG CACCCAGGGC CTGTCATGCC AGGTCTGTGG 300
15 AGGTGGCAGC GAGACATGCA CCCGGCCCCG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG 360
   ATGGGCACTG AACTCACTCA AGTGCTGCCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420
   AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTCGCCCC ACAGCAGACC 480
   ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
   ATGTCTCAAT CCATAGAGGT CTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600
20 AAGATGGAGA ACAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660
   AAGCAACACC TGGCCAGGCA GTTTAAGGGC TAACTTAAAA GAGTTTTCCT AATGCTGCAG 720
   TGAATGAAGA AGCAGTCCAC TCCCATGTAA CCATGAAAGA GAGCCAGAGA GCTTTTGTGA 780
   CCATGCAATT TTAATATTAT TTCCCAATAC TTAGCACCAT TTCATAAGG AACCTTGAAT 840
   ACAACCAAGA TCCTCCTTTG CATGCGACTG TAGCTGCATT TCATGAATAG TTTGAACCTT 900
25 TGTCATATGCA TTTTGTGAAA AAGAAAGAAA AAAAAAATT CGTGTATGTG ACTCAAAGCA 960
   TGTAACCTTA AGATGTTGCA TTCTAAACTG ACAATAAAGA CCTTTCCTCC

```

Seq ID NO: B38 Protein sequence  
Protein Accession #: NP\_006325.1

```

1      11      21      31      41      51
|      |      |      |      |      |
30 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQVLPTNPEE SWQVYSSAQD SEGRICITVV 60
   APQQTMCSSD ARTKQLRQLL EKQVNMSQSI EVLDRRTQRD LQYVEKMENQ MKGLESKFKQ 120
35 VEESHKQHLA RQPKG

```

Seq ID NO: B39 DNA sequence  
Nucleic Acid Accession #: NM\_058199.1  
Coding sequence: 286..795

```

1      11      21      31      41      51
|      |      |      |      |      |
45 GCGCGGGGGA GCCATTAGGA GGCGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
   CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
   CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGTCTGAA TCCAGGCGTG 180
   GGGACACGAG CCAGGCGCCG CCGCCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
   TCCGCGTCCA CGCAGCCGCC GGCCGGCCAG CACCCAGGGC CTGTCATGCC AGGTCTGTGG 300
   AGGTGGCAGC GAGACATGCA CCCGGCCCCG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG 360
   ATGGGCACTG AACTCACTCA AAATAAAAGA GAAAACAAAG CAGAGAAGAT GGGAGGGCCA 420
50 GAGAGCGAGA GGAAGACCA AGGAGAGAAG ACACTGAACG AGCTTCCCTT GTTTTGCCTG 480
   GAAGCCACG CTGGCTCCCT GGCTCTGCCG AGGATGTGCA GTCCAAATCC CAATCCAGCA 540
   GTGGGGTTAT GTGCTCCCGC TTACCTCTAG AGCCCTTCTC CTGGTGCTGC CCAGACGATC 600
   AGCCAGTCCC TCCTGGAGAG GTTCTGCATG GCCTCTAGGA GAGAAGTTT CTGGGCCCA 660
   GGAAGGCTTG GTGGAGGGTG GTGGTGTGTC ACTGTGTGTC GACAGATGCA TTCATTCTATG 720
55 TGCACACACA CACACACACA TGCACACACA GGGGAGCAGA TACCTGAGA GAAGAGCCAA 780
   CCAGTCTCTG ATTATGGGCA AGCTGCCCCA CAAAGGGCTA TGCCTGTGTC TTATTGAGAC 840
   ACCTTGGCAA AGAGATGGCT GATTCTGGGT GGTCTCTGGC ATGGCCGCAC CCAAGGGCCC 900
   TCCAAGCCTT AATGGCACCC TGAAGCCTCC ATGCCCAGGC CAAAAGATGC TTTTCTCTCC 960
60 TAAAAAATAA AAAAAAATAA

```

Seq ID NO: B40 Protein sequence  
Protein Accession #: NP\_478106.1

```

1      11      21      31      41      51
|      |      |      |      |      |
65 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQNKRENKAE KMGGPESERK TTGEKTLNEL 60
   PLFCLEAHAG SLALPRMCSP NPNPAVGLCR PAYPQSPSPG AAQTISQSL ERFCMASRRE 120
   VFLAPGRPGG GWWLCTVAGQ MHSFMTHTH THAHTGBQIP AEKSQPGPD

```

Seq ID NO: B41 DNA sequence  
Nucleic Acid Accession #: AY038071.1  
Coding sequence: 1..1686

```

1      11      21      31      41      51
|      |      |      |      |      |
75 ATGAGCAATC AGTACCAGGA GGAGGGCTGC TCCGAGAGGC CCGAGTGCAA AAGTAAATCT 60
   CCAACTTTGC TCTCCTCTCA CTGCATCGAC AGCATCCTGG GCCGAGGAG CCCGTGCAAA 120
   ATGCGGTGTC TGGGAGCGCG GCAGAGCTTG CCTGCTCCGC TGACACAGCCG CGCCGACCCG 180
   GAAAAGGCCG TGCAAGGCTC CCCTAAGAGC AGCAGCGCCC CGTTCGAGGC CGAGCTGCAC 240
80 CTGCCGCCCA AGCTGCGCGC CCTGTACGGC CCGGGCGGGG GCCGCCTCCT TCAGGGTGGC 300
   GCAGCGGCGG CGGCGGCGGC GCGGCGGCGC GCGGCAGCGG CCGCCACGGC CACGGCGGGT 360
   CCACGCGGGG AGGCCCCCTC GCCGCCACCG CCAACCGCGC GGGCCGGGGA ACGGCCGGAC 420
   GGCAGAGGGG CCGCGCGCGC AGCCGCGGCC GCGGCGCGCG CGGCCTGGGA CACGCTCAAG 480
   ATCAGCCAGG CGCCGAGGT GAGCATCAGC CGCAGCAAGT CGTACCAGCA GAACGGGGCG 540

```

5  
10  
15  
20

```

CCCTTCGTGC CGCCGCCGCC CGCGCTGGAC GAGCTGGGCG GCCCGGGGGG CGTCACGCAC 600
CCGGAGGAGC GCCTCGGCGT GGCCGGCGGC CCGGGCAGCG CCCCGGCTGC GGGTGGTGGC 660
ACCGGCACCG AGGACGACGA GGAGGAGCTG CTGGAGGACG AAGAAGATGA GGACGAGGAA 720
GAGGAACCTGC TGGAGGACGA CGAGGAGGAG CTGCTGGAGG ACGACGCCCG CGCGCTGCTC 780
AAGGAGCCCC GCGCTGTTC TGTGGCCGCC ACTGGCGCGG TGGCCGCAGC AGCTGCCGCT 840
GCAGTGGCCA CAGAGGGCGG GGAGCTGTCA CCCAAGGAGG AGCTGCTGCT GCACCCGGAA 900
GACGCTGAGG GCAAGGACGG CGAGGACAGC GTGTGCCTCT CTGCGGGCAG CGACTCGGAG 960
GAGGGGCTGC TGAACGCAAA ACAGAGGCGC TACCGCACCA CGTTACCAG CTACCAGCTG 1020
GAGGAACCTGC AGCGGGCCTT CCAGAAGACG CACTACCCGG ACGTCTTAC CAGGAGGAA 1080
CTGGCCATGA GGCTGGACTT GACCGAGGCC CGAGTCCAGG TCTGGTTCCA GAACCGTCGG 1140
GCCAAGTGGC GCAAGCGGGA GAAGGCAGGC GCGCAGACCC ACCCCCTGG GCTGCCCTTC 1200
CCGGGGCCGC TCTCCGCCAC CCACCCGCTC AGCCCCTACC TGGACGCCAG CCCCTCCCT 1260
CCGCACCACC CGCGCTCGA CTCGCTTGG ACTGCGCTG CCGCGCCGC CGCGCCGCC 1320
TTCCCGAGCC TACCTCGCC TCCGGGCTCG GCCAGCCTGC CGCCACGCGG GCGCGCGCTG 1380
GGCCTGAGCA CTTTCTCGG AGCGGCAGTG TTCCGACACC CAGCTTTCAT CAGCCCGGCA 1440
TTCCGGCAGC TTTTTCAC AATGGCCCC CTGACACGCG CGTCGACCGC GGCGCGCTC 1500
CTGAGACAGC CCACACCCGC CGTGGAGGGC GCAGTGGCAT CGGGCGCCCT GGCCGACCCG 1560
GCCACGGCGG CCGCAGACAG ACGCGCCTCT AGCATAGCCG CGCTGAGGCT CAAGGCCAAG 1620
GAGCAGCGG CCGAGCTCAC GCAGCTCAAC ATCTGCCCG GCACAGCAC GGGCAAGGAG 1680
GTGTGC

```

Seq ID NO: B42 Protein sequence  
Protein Accession #: AAK93901.1

25  
30  
35

```

1 11 21 31 41 51
| | | | |
MSNQYQEEGC SERPECKSKS PTLSSYCID SILGRRSPCK MRLLGAAQSL PAPLTSRADP 60
EKAVQSGSPKS SSAPFPAELH LPFKLRRLYG PGGGRLLQGA AAAAAAAAAA AAAAAATATAG 120
PRGEAPFPFP PTPARPERPD GAGAAAAAAA AAAAAMDTLK ISQAPQVSIS RSKSYRENGA 180
PFVPPPALD ELGGPGGVTH PEERLGVAGG PGSAPAAGGG TGTEDDEEEL LEDEEDEDEE 240
EELLEDEEEE LLEDDARALL KEPRRCPVAA TGAVAAAAAA AVATEGGELS PKEELLLHPE 300
DAEGKDGEDS VCLSGSDSE EGLLKRKQRR YRTTFTSYQL EELEAFQKT HYPDVFTRFE 360
LAMRLDLTEA RVQVWFQNRK AKWRKREKAG AQTHPPGLPF PGPLSATHPL SPYLDASFPF 420
PHHPALDSAW TAAAAAATAA FPLPPPPGS ASLPPSGAPL GLSTFLGA AV FRHPAFISPA 480
FGRLFSTMAP LTSASTAAAL LRQPTPAVEG AVASGALADP ATAAADRRAS SIAALRLKAK 540
EHAAQLTQLN ILPGTSTGKE VC

```

Seq ID NO: B43 DNA sequence  
Nucleic Acid Accession #: CAT cluster

40  
45  
50  
55  
60

```

1 11 21 31 41 51
| | | | |
CGCTGCCCC CCCGTTGCTT CTCTCTCTTC CCTTCTGCCT GCGTGCCTGC CCGTCTTTGG 60
TTCCGCCGGT TCCGTGCGCC CTCTCTGGGC TTCCGGCTTCA CCTCCGCTCT GGTGTGCTGC 120
CTGCTCTCCT CCGCTCTCAT GCCCCTTTC GCTCCTACTC TGGTGTGCTC CCCCTCCCTC 180
GCTCGTTTCT CTTGTTCTCT TCCTTCCCGG TTCTGTGTTCT GCTTCTTCTG GTTCCCTCTC 240
GTCGTGTGTT GTGGGTGCTC CTCTGCGTCC TGCGTCTTTC TCTTGCCTTT CCGCGCGCTT 300
CCTGTTTTGG TCCCCCTGGT TCTCGCGCGG TTCTGTGTGC GCGGGCGGCC CCGTCTTTTC 360
TTGGTGTGTT GCTCCTGCTC TCTGTCTGGT GTTCTCCGCC GTCTGTGTTCT TTCTCCTTTT 420
ATCTTCTGTT TCTCTTTTTT CTTGTTTCTT CTTGTTTTTT TTTGTCTTTG TTTTCTCTTA 480
GCTGAGGTTG GGGAGAGATA ACGCTGTAAA CTTTATTATT TCAGGAAATC TGGAAACCTA 540
CAGTCTCCAT CCTGTCTCAG CCAAGAAGGA GCTCACTGTG GGCACCAGAG ACAGGGACCC 600
AATGTGGAGA CCGTGAGACC TGTGTCCGGC CCGTGAACCT CAAGCAGAGG GCAGGCTTCC 660
TGAGCATTGA AGAGATATCA TGGGAGAAAC AAACAGAAAC TGAAGAATA TGCAAGGTGT 720
CTTTCTTGA TGTATTCCA TGATAGTAG TAGGGGACAG AGTGAGAGAG GCTGACTAGG 780
TCTGGACATG TCCCTGTGAA GAGTCAGGGT GTGATTCCGA GAGGCGCATG AGAAGGAAGG 840
TGGATTTTAA GGCTGGAAT CTGAGGGTCA GTGTCCAG TCACCTCAGAG ACAGAATCAC 900
AGCATAGCCC TTGCTGATGG CAA

```

Seq ID NO: B44 DNA sequence  
Nucleic Acid Accession #: NM\_014421.1  
Coding sequence: 718..1497

65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
CCACGCGTCC GCGGGAGACC CGCGCGAGC GTAGCGCAAG TCCGCTCCCT AGGCATCGCT 60
GCGCTGGCAG CGATTGCTG TCTCTGTGA GTACGGGAC AACGCTTCGG GGCAACTGTG 120
AGTGC CGCTG TGGGGACCT CGATTCTCT CAGATCTCGA GGATTGCTC CGGGGACGTC 180
TCTGATCCC CTAATAAAGC GCCTGCTAAC TTGAAAAAGG AGCACTGTGT CCTGCAAGT 240
TTGACACATA AAGGATAGGA AAAGAGAGGA GAGAAAGCA ACTGAGTTGA AGGAGAAAGGA 300
GCTGATGCGG GCTCTCTGAT CAATTAAGAG GAGAGTTAAA CCGCGGAGAT CCCGGCGGGA 360
CCAAGGAGGT GCGGGGCAAG AAGGAACGGA AGCGGTGCGA TCCACAGGGC TGGGTTTTCT 420
TGACACCTGG GTACACGCTC CTGCGGAGA AAGCGCTCG CATTGTGATT CTTCAGTTA 480
TTGCAAGAAT TCCGTGCTCG GTGGAGAAGC GGGTCTCGCT TGGGTTCCGC TAATTCTGT 540
CCTGAGGCGT GAGACTGAGT TCATAGGGTC CTGGGTCCCC GAACCAAGGA GGGTTGAGGG 600
AACACAATCT GCAAGCCCC GCGACCCAAG TGAGGGGCC CGTGTGGGG TCTCCCTCC 660
CTTTGATTC CCACCCCTCC GGGCTTTGCG TCTTCTGGG GACCCCTCG CCGGAGATG 720
CGCGGCTTGA TCGGAGCAA GGATTCGTCC TGCTGCTGCT TCCTACTGGC CGCGGTGCTG 780
ATGGTGGAGA GCTCACAGAT CGGCAGTTCG CGGGCCAAAC TCAACTCCAT CAAGTCTCT 840
CTGGCGGGG AGACGCTCG TCAGGCCGCC AATCGATCTG CGGGCATGTA CCAAGGACTG 900
GCATTCGGCG GCAGTAAGAA GGGCAAAAC CTGGGGCAGG CCTACCTTG TAGCAGTGAT 960
AAGGAGTGTG AAGTTGGGAG GTATTGCCAC AGTCCCCACC AAGGATCATC GCGCTGCATG 1020
GTGTGTCGGA GAAAAAGAA GCGCTGCCAC CGAGATGGCA TGTGTGCCC CAGTACCCGC 1080
TGCAATAATG GCATCTGTAT CCCAGTTACT GAAAGCATCT TAACCCCTCA CATCCCGGCT 1140

```

5 CTGGATGGTA CTCGGCACAG AGATCGAAAC CACGGTCATT ACTCAAACCA TGACTTGGGA 1200  
 TGGCAGAAATC TAGGAAGACC ACACACTAAG ATGTCACATA TAAAAGGGCA TGAAGGAGAC 1260  
 CCTGCCTAC GATCATCAGA CTGCATTGAA GGGTTTTGCT GTGCTCGTCA TTTCTGGACC 1320  
 AAAATCTGCA AACCAGTCGT CCATCAGGGG GAAGTCTGTA CCAAACAACG CAAGAAGGGT 1380  
 10 TCTCATGGGC TGGAAATTTT CCAGCGTTGC GACTGTGCGA AGGCCTGTCT TTGCAAAGTA 1440  
 TGGAAAGATG CCACCTACTC CTCCAAAGCC AGACTCCATG TGTGTCAGAA AATTTGATCA 1500  
 CCATTGAGGA ACATCATCAA TTGCAGACTG TGAAGTTGTG TATTTAATGC ATTATAGCAT 1560  
 GGTGGAATAA AAGGTTTCAGA TGCAGAAGAA TGGCTAAAAT AAGAAACGTG ATAAGAATAT 1620  
 AGATGATCAC AAAAAGGGAG AAAGAAAACA TGAAGTGAAT AGATTAGAAT GGGTGACAAA 1680  
 TGCAGTGCGC CCAGTGTTC CATTATGCAA CTGTCTATG TAAATAATGT ACACATTGT 1740  
 GGAAATGCT ATTATTAAGA GAACAAGCAC ACAGTGGAAA TTACTGATGA GTAGCATGTG 1800  
 ACTTTCCAAAG AGTTTAGGTT GTGCTGGAGG AGAGGTTTCC TTCAGATTGC TGATTGCTTA 1860  
 15 TACAAATAAC CTACATGCCA GATTTCTATT CAACGTTAGA GTTTAACAAA ATACTCCTAG 1920  
 AATAACTTGT TATACAATAG GTTCTAAAAA TAAAATTGCT AAACAAGAAA TGAAACATG 1980  
 GAGCATTGTT AATTACAAAC AGAAAAATAC CTTTGTGATT GTAACACTAC TTCTGCTGTT 2040  
 CAATCAAGAG TCTTGGTAGA TAAGAAAAAA ATCAGTCAAT ATTTCCAAAT AATTGCAAAA 2100  
 TAATGGCCAG TTGTTTAGGA AGGCCTTTAG GAAGACAAAT AAATAACAAA CAAACAGCCA 2160  
 CAAATACTTT TTTTCAAAA TTTTAGTTTT ACCTGTAATT AATAAGAACT GATACAAGAC 2220  
 20 AAAAACAGTT CCTTCAGATT CTACGGAATG ACAGTATATC TCTCTTTATC CTATGTGATT 2280  
 CCTGCTCTGA ATGCATTATA TTTTCCAAAG TATACCCATA AATTGTGACT AGTAAAAATC 2340  
 TTACACAGAG CAGAAATTTT ACAGATGGCA AAAAAATTTA AAGATGTCCA ATATATGTGG 2400  
 GAAAAGAGCT AACAGAGAGA TCATTATTTC TTAAGATTG GCCATAACCT GTATTTTGAT 2460  
 AGAATTAGAT TGGTAAATAC ATGTATTCAAT ACATACTCTG TGGTAATAGA GACTTGAGCT 2520  
 25 GGATCTGTAC TGCACCTGGAG TAAGCAAGAA AATTGGGAAA ACTTTTTCGT TTGTTGAGGT 2580  
 TTTGGCAACA CATAGATCAT ATGCTGAGG CACAAGTTGG CTGTTCATCT TTGAAACAG 2640  
 GGGATGCACA GTCTAAATGA ATATCTGCAT GGGATTGTCT ATCATAATNT TTCCTATGCN 2700  
 GNTGAATTCT GTGTGAGGTC CTGTGCTCGT CCTATCCTCA AATTATTTAT TTTATAGTGC 2760  
 TGAGATCCTC AAATAATCTC AATTTCGGAG GTTTCACAAA ATGGACTCCT GAAGTAGACA 2820  
 GAGTAGTGAG TTTTCATTGC CCTCTATAAG CTCTGACTA GCCAATGGCA TCATCCAATT 2880  
 30 TTCTTCCCAA ACCTCTGCAG CATCTGCTTT ATTGCCAAAG GGCTAGTTTC GGTTCCTGTC 2940  
 CAGCCATTGC GGTAAAAAAA TATAAGTAGG ATAACCTGTA AAACCTGCAT ATTGCTAATC 3000  
 TATAGACACC ACAGTTTCTA AATTCTTTGA AACCCTTTA CTACTTTTTT TAAACTTAAC 3060  
 TCAGTTCTAA ATACTTTGTC TGGAGCACAA AACAATAAAA GGTATCTTTA TAGTTGTGAC 3120  
 35 TTTAACTTT TGTAGACCAC AATTCACTTT TTAGTTTTCT TTTACTTAAA TCCCATCTGC 3180  
 AGTCTCAAAAT TTAAGTTCTC CCAGTAGAGA TTGAGTTTGA GCCTGTATAT CTATTAATAA 3240  
 TTTCAACTTC CCACATATAT TTAATAAGAT GATTAAAGCT TACATTTTCT GCACAGGTCT 3300  
 GCAAAACACA AAATTATATA CTAGTCCATC CAAGAACCAG AGTTTGTATA AACAGGTTGC 3360  
 TATAAGCTTG GTGAAATGAA AATGGAACAT TTCAATCAAA CATTTCTTAT ATAACAATTA 3420  
 40 TTATATTTAC AATTGGTTTT CTGCAATATT TTTCTTATGT CCACCCTTTT AAAAATTATT 3480  
 ATTTGAAGTA ATTTATTTAC AGGAAATGTT AATGAGATGT ATTTTCTTAT AGAGATATTT 3540  
 CTTACAGAAA GCTTTGTAGC AGAATATATT TGCAGCTATT GACTTTGTAA TTAGGAAAA 3600  
 ATGTATAATA AGATAAATC TATTAATTT TTCTCCTCTA AAAACTGAAA AAAAAAATAA 3660  
 AAAAAAATAA A

Seq ID NO: B45 Protein sequence  
 Protein Accession #: NP\_055236.1

50 1 11 21 31 41 51  
 MAALMRSKDS SCCLLLLLAAV LMVESSQIGS SRALKNSIKS SLGGETPGQA ANRSAGMYQG 60  
 LAFGGSKKKG NLGQAYPCSS DKECEVGRYC HSPHQGSSAC MVRRRKKKRC HRDGMCCPST 120  
 RCNNGICIPV TESILTPHIP ALDGRHRDR NHGHYSNHD L GWQNLGRPH KMSHIKGHEG 180  
 DPLRSSDCI EGFCCARHFV TKICKPVLHQ GEVCTKQRKK GSHGLEIFQR CDCAKGLSCK 240  
 VWKDATYSSK ARLHVCQKI

Seq ID NO: 46 DNA sequence  
 Nucleic Acid Accession #: NM\_019885.1  
 Coding sequence: 1..1539

60 1 11 21 31 41 51  
 ATGCTCTTTG AGGGCTTGGA TCTGGTGTG GCGCTGGCCA CCTCGCCGCG GTGCCTGGTG 60  
 TCCGTGACGC CGTGTGCGCAG CAGCTGTGGC AGCTGCGCTG GGCGCCCACT 120  
 65 CGCGACAAGA GCTGCAAGCT GCCCATCCCC AAGGGATCCA TGGGCTTCCC GCTCATCGGA 180  
 GAGACCGGCC ACTGGCTGCT GCAGGGTTCT GGCTTCCAGT CGTGCAGGAG GGAGAAGTAT 240  
 GGCAACGTGT TCAAGACGCA TTTGTTGGGG CGGCCGCTGA TACGCGTGAC CGGCGCGGAG 300  
 AACGTGCGCA AGATCCTCAT GGGCGAGCAC CACCTCGTGA GCACCGAGTG GCCTCGCAGC 360  
 ACCCGCATGT TGCTGGGCCC CAACACGGTG TCCAATTCCA TTGGCGACAT CCACCGCAAC 420  
 70 AAGCGCAAGG TCTTCTCCAA GATCTTCAGC CACGAGGCCC TGGAGAGTTA CCTGCCCAAG 480  
 ATCCAGCTGG TGATCCAGAA CACACTGCGC GCCTGGAGCA GCCACCCCGA GGCCATCAAC 540  
 GTGTACAGG AGGCGCAGAA GCTGACCTTC CGCATGGCCA TCCGGGTGCT GCTGGGCTTC 600  
 AGCATCCCTG AGGAGGACCT TGGGCACCTC TTTGAGGTCT ACCAGCAGTT TGTGGACAAT 660  
 GTCTTCTCCC TGCCCTGTGCA CCTGCCCTTC AGTGGCTACC GGCAGGGCAT TCAGGCTCGG 720  
 75 CAGATCCTGC AGAAGGGGCT GGAGAAGGCC ATCCGGGAGA AGCTGCAGTG CACACAGGGC 780  
 AAGGACTACT TGGAGCCCTT GGACCTCCTC ATTGAGAGCA GCAAGGAGCA CGGGAAGGAG 840  
 ATGACCATGC AGGAGCTGAA GGACGGGACC CTGGAGCTGA TCTTTGCGGC CTATGCCACC 900  
 ACGGCCAGCG CCAGCACCTC ACTCATATG CAGCTGCTGA AGCACCCAC TGTGCTGGAG 960  
 AAGCTGCGGG ATGAGCTGCG GGCTCATGGC ATCCTGCACA GTGGCGGCTG CCCCTGCGAG 1020  
 80 GGCACACTGC GCGCTGACAC GCTCAGTGGG CTGCGCTACC TGGACTGCGT CATCAAGGAG 1080  
 GTCATGCGCC TGTTCACGCC CATTTCCGGC GGCTACCGCA CTGTGCTGCA GACCTTCGAG 1140  
 CTTGATGGTT TCCAGTATCC CAAAGGCTGG AGTGTATGAT ATAGCATCCG GGACACCCAT 1200  
 GACACAGCGC CGGTGTTCAA AGACGTGAAC GTGTTGAGCC CCGATCGCTT CAGCCAGGCG 1260  
 CGGAGCGAGG ACAAGGATGG CCGCTTCCAT TACCTCCCGT TCGGTGGCGG TGTCCGGACC 1320  
 TGCCTGGGCA AGCACCTGGC CAAGCTGTTT CTGAAGGTGC TGGCGGTGGA GCTGGCTAGC 1380

5  
10  
15  
20  
25  
30  
35  
40  
45  
50

ACCAGCCGCT TTGAGCTGGC TACACGGACC TTCCCCCGCA TCACCTTGGT CCCCCTCCTG 1440  
 CACCCCGTGG ATGGCCTCAG CGTCAAGTTC TTGGCCCTGG ACTCCAACCA GAACGAGATC 1500  
 CTGCCGGAGA CGGAGGCCAT GCTGAGCGCC ACAGTCTAAC CCAAGACCCA CCCCCTCAG 1560  
 CCCAGCCGAG CGACGCGGGT GGTGGTTGTG GGAGGTAGAA ACCTGTGTGT GGGAGGGGGC 1620  
 CGGAACGGGG AGGGCGAGTG GCCCCCATAC TTGCCCTCCC TTGCTCCCCC TCCCTGGCAA 1680  
 ACCCTACCCA AAGCCAGTGG GCCCATTCC TAGGGCTGGG CTCCCTTCT GGCTCCAGCT 1740  
 TCCCTCCAGC CACTCCCAT TTACCATCAG CTCAGCCCTT GGAAGGGCG TGGCAGGGGC 1800  
 TCTGCATGCC CGTGACAGTG TTAGGTGTCA GCGCGTGCTA CAGTGTTTT GTGATGTTCT 1860  
 GAACGTCTCC CTTCCTCCG TTCTTTCCG ACCCTTTTAG CTGGGGTTGG GGGACGGGAA 1920  
 GAGCGGTGCC CCCTTGGGGC CACTCTTCAG CGTCTCCTCC TCCTGCGCCC CCACTGCGTC 1980  
 TGCCCCAGGA CAGCATCCTG GGTAGCAGAA CAGGAGTCAA CCTTGGCGGG GCGGGGGCTG 2040  
 CGTCCAACCT GGAGATTGCC CTTCCTTATG CCACGGTTCC CACCTCCCT CACCAAGTTG 2100  
 GACAATTGA AATTACCTAT TGCTGCTACT TGTCTGTCC TCTGACCTTG GGGCAAAGGA 2160  
 GCCCAGGGCC CTGTCTCCCC AGCATCCTCC CTGGTGGCCC TGGGCAGGTG CACTGACACC 2220  
 CCCACCTTCC CATCCCTGTC TGAACCAGGC CCTGTTACAC ACAGCCGCTT AAGGCCCGCG 2280  
 GCTCATGTGC TCCCGCCCT CATATTTAT CACTGATAGA GAATCTTGGG GATGCTGGGG 2340  
 TCTGGAGTGA ACATCTCCTC CCCTTCATGC CTTAGCCTGT GTTCTAGCTG TCCTGGCGAG 2400  
 ACTTCTGTGA GTGAAGAGGA AGGGGTCTCT GGTCAAACCC AGCCCCAGG GCCTAGGGTT 2460  
 GAAAGCCTTC CCGGCTCCG GGCATTATTT GGGTTTAATC TCGAGCCTC ACTCTGGAC 2520  
 TGAAGTCCCG TGCCCTCTGC TTATCCCTGG TGGAGATGGA ATGTGGCCCA TTGCCTCCTC 2580  
 CCTCTCCTGT CAAAAACCTT GATCAGGTAG ATTTGGAGGC GGCCACGATT TCCTGTTTGG 2640  
 CCCTGTTTCA CCCCAGTGCA CTGGCCCTGA CTCAGGCGT GAGTATGGGG AAGGATACGG 2700  
 GTTCTTCTGA CCGGGAGCAA GGGCCTCCGT CTTCCTTCC TTAACCTCC CCCTTGGCCC 2760  
 TCCGCCCTGA AAAAGGTGTC CTTGAAGTCC CTTCACCTC TATGCCACTG TCTGCTTAGC 2820  
 CCAGCTCAGG GGTGGGGAAG AGGCGAAAGC GTGGGGGAGG TGAGCGCAGC GGCAGTTCTG 2880  
 CCTCGGAGCT GATTGCAAGG CCCTGTGTGG TCTCCGACA GCTGCGGAA GGCTGCCGCA 2940  
 GCTGAAGCTG AAGAGCGGC TACGTGCGGT TTGTACGGGG GATTGGGTTG AAACTGGCC 3000  
 AGTCGGGATG ACTGGGTGAA AGAGGAGTAG CTCCTGCCAC TGGCGTTTGT AGTGTGGCA 3060  
 ATTTGGGATG CCTCCTGGGG AAGGTTTCCG GCGGTTTGGT GAGTCTCTAG ATTTTCTCTT 3120  
 GCTTTCTGTG TTTATTGGTT TTTGATGTTG TAAAAGCAAT GAATCCCTT TACAAGAAAA 3180  
 TCGAAAACAC AGAAGAATGA AGGACATGCC AGTCCCGAT CGTGCTGTG AGCACTCAG 3240  
 TGGCTCCCTC AGACCAGATC CCGTAGGCAG CCCACAGAC CGACCCTGAC CCCACTACA 3300  
 GCCACCTGAG AGATAGACTA TAGGAACGGG CCCATACCAC ACAGACTGCT CTCCAATCCC 3360  
 TGAGTCTCAG ATGTCTCATT TATTCTTAC TTTTCCAATA CTAAGAAAAA GTGTGGAATA 3420  
 GACATTATTG GCAAAATTGC TCATCCCTAA TCCTGAAAAA CAGGCCAGAA TGGGTAAAGA 3480  
 CTGTGCAAG CTGTCAACAT AGTACATGG TGCACCGGA CCTGTACCCC CTCCCCCCAA 3540  
 CACAAAACCA GTGTCTGGGA GGTTCATTTT CCTTAAACT GATCCAGCTG GCCCTGAACC 3600  
 AATTTGTTTT GACTGAGTAT CTAGGAGAGC AGTAAAGTGA ACTTCAGACA AGCCCACTGG 3660  
 GTCTGGTCCA GGTGAGGGG AGGGGGCATG GGGCTGGGAG GTCTCAGGGG CCTTCCCTGG 3720  
 GGGTGGCCAG CCTGGTAGGG GGCAGAGAAG GAAAAGCTGA GGGGGGTCCC TGTAGGGAG 3780  
 GAAAGAAGGA TCATTTGCCCC CGCTGGGTCT CAAAGGCAGT GAGAAGAGAG CTGAAGAAAG 3840  
 CTCTGGCTGG CTGACAGGAT CCCTGTGTGG TAATTGGTCC CTCTTTCAG CTCTCTAGTG 3900  
 AGATGCCCGT GTCTGTGCGT GTGCGTGTGT GTTTCATACA GCTAGCATTG GATGGGTGAT 3960  
 GTTCTTACT TATCATCCCT AACTATTGCA ACTTGACCTT AAAAGACAA AACCCACAA 4020  
 AACTCTTCTT GCCACGGCT TGCAGATTGA AGCACTTTCG ATGTTGGGCG CTGGCGTTTG 4080  
 TGTCTGGGCG AACCCGTGA CCCTGCCAG ATGGCTATAA TATTATTTTA TACACAAACC 4140  
 TTTTTTTCA TAAATGTTAT AATTTGTGT CTGTCTTTAT AAATAATTAT AAGTACTATT 4200  
 TTTGTTATAA TTCAAATAG ATATTAGTA TAAAGTTTTT GCTGTTAAAT ATTTGTTATT 4260  
 TAGTAAAAATA TGAATTTTGC TCTATTGTAA ACATGGTTCA AAATATTAAT ATGTTTTTAT 4320  
 CACAGTCGTT TTAATATTGA AAAAGCACTT GTGTGTTTGG TTTTGATATG AAACCTGGTAC 4380  
 CGTGTAGTGT TTTTGTCTGT CGTGGTTTTA ATCTGTATAT AATATTCCAT GTTGCAATT 4440  
 AAAAA

Seq ID NO: B47 Protein sequence  
 Protein Accession #: NP\_063938.1

60  
65

1 11 21 31 41 51  
 | | | | |  
 MLFEGLDLVS ALATLAACLV SVTLLLAVSQ QLWQLRWAAT RDKSCKLPIK KSGMGFPLIG 60  
 ETGHWLLQGS GFQSSRRKGY GNVFKTHLLG RPLIRVTGAE NVRKILMGEH HLVSTEWPRS 120  
 TRMLLGPNTV SNSIGDIHRN KRKVFSKIPS HEALESYLPK IQLVIQDTRL AWSSHPEAIN 180  
 VYQEAQKLTF RMAIRVLLGF SIPEEDLGHF FEVYQQFVDN VFSLPVDLPF SGYRRGIQAR 240  
 QILQKGLEKA IREKLQCTQG KDYLDALELL IESSKEHGKE MTMQELKDGT LELIFAAYAT 300  
 TASASTSLIM QLLKHPTVLE KLRDELRAHG ILHSGGCPCE GTLRLDLSG LRYLDCVIKE 360  
 VMRLFTPISG GYRTVLQTFE LDGFQIPKGV SVMYSIRDTH DTAPVFKDKN VFDPDFRSQA 420  
 RSEDKDGRFH YLPFGGGVRT CLGKHLAKLF LKVLAVELAS TSFELATRT FPRITLVFVL 480  
 HPVDGLSVKF FGLDSNQNEI LPETEAAMLSA TV

Seq ID NO: B48 DNA sequence  
 Nucleic Acid Accession #: AB040527.1; AL136582.1  
 Coding sequence: 94..2319

75  
80

1 11 21 31 41 51  
 | | | | |  
 GCGGCTGCGG GGTTCCTGGT GCTGAGGACG GACGCCATTG GAGTTCCCGA GAAGCATGGC 60  
 TGAGGGAAGC TTCAGCGTGC AATCGGAAAG CTACAGTGTG GAAGACATGG ATGAGGGTAG 120  
 CGACGAAGTC GGGGAGGAAG AGATGGTTGA AGGCAACGAC TATGAAGAAT TCGGTGCGTT 180  
 TGGTGGCTAT GGCACCTTCA CCAGCTTTGA CATCCATATC CTCAGAGCCT TCGGAAGCTT 240  
 GGGTCAGGC CTTCGCACTT TATCGAATGA GCCCTGGGAA CTGGAAAAAC CTGTGCTGGC 300  
 CCAGACCTGT GTGGAGGCAT TGCAGCTGGA TCCGGAACA CTGCGCAATG AGACGGCCGC 360  
 CCGTGCTGCC AACGTAGCCC GCGCCGCCGC CTCCAACCGT GCGGCTCGGG CCGCTGCCGC 420  
 CGCTGCCCGT ACCGCTTCA GTCAAGTGGT CGCTAGCCAC CGGGTGGCCA CGCCGAGGT 480  
 CTAGGAGAGG GATACCCAGC CCACGACCTA CGCCGCGGAG GCTCAGGGGC CCACCCCTGA 540  
 GCCACCCCTT GCTTCTCCCG AGACCTCCCA GATGTTAGTC ACCAGTAAGA TGGCTGCCCC 600

5  
10  
15  
20  
25  
30

```

CGAGGCTCCG GCAACCTCCG CACAGTCCCA GACAGGCTCC CCGGCCCAGG AGGCTGCTAC 660
TGAGGGCCCT AGTAGCGCCT GTGCTTTCTC TCAGGCTCCG TGTGCCAGGG AGGTGGACGC 720
CAACCGGCCC AGCAGAGCCT TCCTGGGCCA GAATGATGTC TTCGATTTC A CTCAGCCGCG 780
AGGTGTCACT GGCATGGCCT TCCCGCGCCC CAAGAGACCT GCCCAGAGCC AAGAGGCTGC 840
CACAGAGGGC CCCAGTGCCT CCTCTGGTGT GCCCAGAGCG GGACCTGGCA GGGAGGTGGC 900
AGCCACCCCG CCCAAGACCA CCAAGTCGGG GAAGGCGCTG GCCAAGACTC GGTGGGTGGA 960
GCCTCAGAAT GTTGTGGCAG CAGCTGCTGC CAAGGCCAAG ATGGCCACGA GCATCCCTGA 1020
GCCGGAGGGT GCAGCTGCTG CCACTGCTCA GCACAGTGCT GAGCCCTGGG CCAGGATGGG 1080
AGGCAAGAGG ACCAAGAAGT CCAAGCACCT GGATGATGAG TATGAGAGCA GCGAGGAGGA 1140
GAGAGAGACT CCCGCGGTCC CACCCACCTG GAGAGCATCA CAGCCCTCAT TGACGGTGCG 1200
GGCTCAGTTG GCCCCCTCGG CCCCAGTGGC CCGGAGGTCC CAGATACCCT CAAGGCACGT 1260
ACTGTGCCTG CCCCCCGCCA ACGTGACCCT TCTGCAGGAG AGGGCAAATA AGTTGGTGAA 1320
ATACCTGATG ATTAAGGACT ACAAGAAGAT CCCCATCAAG CGCGCAGACA TGCTGAAGGA 1380
TGTCAATCAGA GAATATGATG AACATTTCCT TGAGATCATT GAACGAGCAA CGTACACCCT 1440
GGAAAAGAAG TTTGGGATCC ACCTGAAGGA GATCGACAAG GAAGAACCAC TGTATATTCT 1500
TGTCTGCACA CGGACTCCTC CAGCTCGCCT CTTGGAAAA ACCAAGGACA CTCCCAGGCT 1560
GAGTCTCTCT TGGGTGATTC TGGGCGTCAT CTTATGAAT GGCAACCGTG CCAGCGAGGC 1620
TGTCTCTCTG GAGGCTAGG GCAAGATGGG ACTGCGCCTT GGGGTGAGGC ACCCATTCCT 1680
CGGCGATCTG AGGAAGCTCA TCACAGATGA CTTTGTGAAG CAGAAGTACC TGGAAATACAA 1740
GAAGATCCCC AACAGCAACC CAGCTGAGTA TGAATTCTCT TGGGGCCTGC GAGCCCCGCCA 1800
TGAGACCAGC AAGATGAGGG TCTGAGATT CATCGCCAG AATCAGAACC GAGACCCCGG 1860
GGAATGGAAG GCTCATTTCT TGGAGGCTGT GGATGATGCT TTCAAGACAA TGGATGTGGA 1920
TATGGCCGAG GAACATGCCA GGGCCACAGT GAGGCCACAG ATGAATATCG GGGATGAAGC 1980
GCTGATTGGA CGGTGGAGCT GGGATGACAT ACAAGTCGAG CTCTGACCT GGGATGAGGA 2040
CGGAGATTTT GGGGATGCCT GGGCCAGGAT CCCCTTTGCT TTCTGGGCCA GATACCATCA 2100
GTACATTCTG AATAGCAACC GTGCCAACAG GAGGGCCACG TGGAGAGCTG GCCTCAGCAG 2160
TGGCACCAAT GGAGGGGCCA GCACCAGCGT CCTAGATGGC CCCAGCACCA GCTCCACCAT 2220
CCGACACAGA AATGCTGCCA GAGCTGGCGC CAGCTTCTTC TCCTGGATCC AGCACCCTTG 2280
ACGAACCTGA CGCATCTTAC TGGCCAAGCC AGAGCGCCTC CTCTCAGATT CCTTCTCGAC 2340
ACAGCACCTT AGGCGGCTTC TTCTGTCTAG TCGGAGGTGG CATGCAAGAT GAAGCTCTCT 2400
TTGCTCTTCC TGTCTTCATT TTGTGCTTTT CCTGTGTGTT TCATGTTTTG GGTATCAGTG 2460
TTACATTAAA GTTGCAAAAT TAAA

```

Seq ID NO: B49 Protein sequence  
Protein Accession #: BAB33378.1; CAB66517.1

35  
40  
45  
50

```

1 11 21 31 41 51
MAEGSFSVQS ESYSVEDMDE GSDEVGEEEM VEGNDYEEFG AFGGYGLTSL FDIHILRAFG 60
SLGPGRLRLS NEPWELNPV LAQTLVEALQ LDPETLANET AARAANVARA AASNRAARAA 120
AAAARTAFSQ VVASHRVATP QVSGEDTQPT TYAAEAQGPT PEPPLASPTQ SQMLVTSKMA 180
APEAPATSAQ SQTGSPAQEA ATEGPSSACA FSQAPCAREV DANRPSTAFI QNDVDFDTQ 240
PAGVSGMAFP RPKRPAPAE AATEGPSAAS GVPQTGPGRV VAATRPKTK SGKALAKTRW 300
VEPQNVVAAA AAKAKMATSI PEPEGAAAA AQHSAEPWAR MGGKRKKKSK HLDDEYESSE 360
BERETPAVPP TWASQPSLT VRAQLAPRPP MAPRSQIPSR HVLCLPPRNV TLLQERANKL 420
VLKLMIKDYK KIPKIRADML KDVIREFDEH FPEIIERATY TLEKKFGIHL KEIDKEEHL 480
ILVCTRSSA RLLGKTKDTP RLSLLVLILG VIFMNGNRAS EAVLWEALRK MGLRPGVRHP 540
FLGLRLKLT DDFVQKQYLE YKKIPNSNPP EYEFWLGLRA RHETSKMRVL RFIAQNQRD 600
PREWKAHFL EAVDDAFKTM DMMAEEHARA QMRAQMNIGD EALIGRNSWD DIQVELLTWD 660
EDGDFGDARA RIPPAFWARY HQYILNSNRA NRRATWRAGV SSGTNGGAST SVLDGPSTSS 720
TIRTRNAARA GASFFSWIQH R

```

Seq ID NO: B50 DNA sequence  
Nucleic Acid Accession #: XM\_084965.1  
Coding sequence: 356..2014

55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
GACCTAGCGT GTGCTCAGCT CTGGACAAGA CATGGATGTA GGCAGACATG CTTCTGCCT 60
GCTGGGCTTA GTGCACCAAT GCTAAGGACA GACATGAAGG GCTTGGGAAA GGCATGAAGA 120
TGCAGGGAGT CTAGGAGAGA GGATAAGAAA AACAAGCATT TTGTGGTGGG TTGAATTGCG 180
TTGTGCTTTT TAGAGGCATT TCGTGATCCA TGGTTGCGCT CCCGTGAAGA GCGAGTCTAG 240
AGAAGGAATC CGAAGCGGCG GCGGCGAGCG CGGCTCAGGT TGATTTAGAA TACGGGTGAC 300
AGTGGCCTGG CCGAGGCCCA CTGCTGACGA AAGCGGCTTA TCCCGCGCGG TTCCATGGA 360
GACGAGCCGG AGCCGCGGCG GCGGCGGGGC TGTACGCGAG CGCGGCGGAG CTGGCGCGTC 420
CGTGGGGGTC TGCAGGAGGA AGCGGAGGCG CGGGGCGGGG ACCGGGACCC TCGCGGCAGA 480
CATGGACTTG CATTTGTACT GTGCCGCCGA AACGCCGGCC GCCGAGCCGC CGTCCGGGAA 540
GATTATAAAA GCTGCCCTTA AATTATTCAA GAAGAGGAAA TCGGGTGGCA CCATGCCAG 600
CATTTTGGG GTCAAAAACA AAGGGGACGG GAAAAGCTCG GGTCCGACGG GGCTGGTGAG 660
GAGCAGGACC CAGCAGCGAC TTGCCGAGGT GCTGGTGCTG GAGAGCGGCA GGAAGGAGGA 720
GCCGCGCGCG GGGGCGGACA GCGGCGGGGG CGGCGGGGGG CGGCCGAACC CGGGGCCCCC 780
CAGAGCCGCA GGGCCCGGCG GGGGCTCCTT CGCCAGCAGC TCGGTGGCCA AGTCGCACAG 840
CTTCTTCTCG CTGCTGAAGA AGAACGGGCG CTCGGAAGAG GGCAGGAGAG AGCTGTGGA 900
CGCGAGCAAG CGCGGCGGCA AACAAAAGCG GGGGCTGCGG GGGCTGTTC A GCGGCATGCG 960
CTGGCAGAG AAAGACAAGC GGGCCAAGGC GGAGGCCGCG GAGGGGCGCG CGCCCCGGGG 1020
CGGCTTGATC TCACCCCGCT CGCTCACCGC CAGCCTGGAG TGCCTCAAG AGGAGACGCC 1080
CAGAGCCGCG CGCGAGCCGG AGGAGCCCGC CCAGGACGCC CCGCGAGACC CAGCAGGCTG 1140
TGGAGATATT ATTGCAGACC AAGAGGAAGA GGCAGGTCCC AGCTGTGACA AGCATGTCCC 1200
CGGGCCAGGC AAGCCCGGCT TGTCTAAAAA GAACCCCGGC GTGGTGGCCT ACCAAGGAGG 1260
CGGGGAAGAG ATGGCCAGCC CGGACGAGGT GGACGACACC TATCTACAGG AGTCTCGGGA 1320
CATGCTCTCC CAGACCGAGG AGCAGGGACC CGAGCCCCAG GAGGGCGCGG CTAAGGTGGC 1380
AGCTGCGCTG GAAACCAAGG TGGTGCCCGA GACCCCAAAA GACACCAGGT GTGTGGAAGC 1440
GGCCAAGGAC GCGTCTCGG TCAAGCGCAG GAGGCTCAAC CGGATTCCCA TCGAGCCCCA 1500
TCCTAAGGAG GAGCCCAAGC ACCCGGAGAA GGAGCAGCAG GAAGGCGTCC CCAAGCAGCA 1560

```

CGAGGGCTAC TGGGACTCCA CCACGCCAGG CCCAGAGGAA GACAGCTCGA GCAGCGGGAA 1620  
 GAAGGCGGGC ATCCCCCGGG ATAGCTACAG CGGGGACGCG CTCTATGATC TCTATGCTGA 1680  
 CCGGGACGGA AGTCCAGCAA CCCTTCCTGG AGGGAAGGAC AACGAGGAGA CGTCCCTCCCT 1740  
 GTCCCGGTAA AAGCCCCGAT CTCCAGGCAC CATCACCTGT CCACTGCGAA CACCAGGCAG 1800  
 CTTGCTGAAG GACTCTAAGA TCCCTATTAG CATCAAGCAC CTGACCAACC TTCCATCTAG 1860  
 CCATCCCGTG GTGCACCAGC AACCTCCAGG GAGTGAGATG CCCAGAACA AAATCCCGGT 1920  
 TTCAAAGTG CTGCTCCGCA GAGTCAGCAA CCGGGGCTTG GCTGGGACCA CCATCAGAGC 1980  
 AACGGCCTGC CACGACAGTG CCAAAAAGTT GTGAGGTCTT CCAGGCCAAG GTGGATGGGC 2040  
 CCCATGCCAA GGAATACAAC TTTTCCCTGG AAACCACTAA AGTAAGTTT GCTTTTCCTA 2100  
 AAGAAAGTCT TTTAGGACAC CACCCGTCCT CCGCCCTGCT CCAGAGCGTG GACCGAGGAG 2160  
 GTCTTTGTGC CCTGAGCAGG GACCGGATAA CACCAGAAAG AGGGATGCTA CACGGGGGTT 2220  
 TCTCTCTCA AGATAAGTCC CTGAGAATTA TTTTCAAGCA CTTTTTCTT TTTTACCTTT 2280  
 AAGTTTTTCT TCCTTTTCT TTAATATACT GAACACTTGG AAGTCACCTT TACTTGCCTT 2340  
 TGCAGAAAAC AGAACTTAGC CAAACCTAAG TAAGAGTCAT GCCTGGATAT TGGGATAAGC 2400  
 CAGTGTCTAG AGGCCTGAAG GAACCGCTGA AGAACCAGAG GAGATCTCCT CTTCGAAGAC 2460  
 ACGTTTCCTT CCTTCCCTTC TTTCTCTTT CCTTCCAGT T

Seq ID NO: B51 Protein sequence  
 Protein Accession #: XP\_084965.1

1 11 21 31 41 51  
 METSRSRGGG GAVSERGGAG ASVGVCRRA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60  
 GKINKAAPFL FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120  
 EEPRGGGDSG GGGGGRPNFG PPRAAGPGGG SLASSSVAKS HSFFSLKKN GRSENGKGE 180  
 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGGLILPGSL TASLECVKEE 240  
 TPRAAREPEE PSQDAPRDPF GCGDIIADQE EEAGPSCDKH VPGPGKPLS KKNPGVVAYQ 300  
 GGGEEMASDV EVDDTYLQEF WDMLSQTEEQ GPPEQEGAAK VAAALETKVV PETPKDTRCV 360  
 EAAKDASSVK RRRLLNRPIE PHPKEEPKHP EKEQEGVFN SDEGYWDSST GPPEEDSSSS 420  
 GKKGAGIPRDS YSGDALYDLY ADPDGSPATL PGGKDNEETS SLSRLKPVSP GTITCPLRTP 480  
 GSLKDSKIP ISIKHLTNLP SSHPVVHQPF SRSEMPRTKI PVSKVLVRRV SNRGLAGTTI 540  
 RATACHDSAK KL

Seq ID NO: B52 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..2016

1 11 21 31 41 51  
 ATGGAGACGA GCCGGAGCCG CGGCGGCGGC GGGGCTGTCA GCGAGCGCGG CGGAGCTGGC 60  
 GCGTCCGTGG GGGTCTGCAG GAGGAAGGCG GAGGCCGGGG CCGGGACCGG GACCCCTCGG 120  
 GCAGACATGG ACTTGCAATG TGACTGTGCC GCCGAAACGC CGGCCGCCGA GCCGCCGTGC 180  
 GGAAGATTA ATAAAGCTGC CTTCAAATTA TTCAAGAAGA GGAATTCGGG TGGCACCATG 240  
 CCCAGCATTT TTGGGGTCAA AAACAAAGGG GACGGGAAAA GCTCGGGTCC GACGGGGCTG 300  
 GTGAGAGCA GGACCCACGA CGGACTTGCC GAGGTGCTGG TGTGAGAGAG CGGCAGGAAG 360  
 GAGGAGCCGC GCGGCGGGGG CGACAGCGGC GGGGGCGGCG GGGGGCGGCC GAACCCGGGG 420  
 CCCCCAGAG CCGCAGGGCC CGGCGGGGCC TCCCTCGCCA CGAGCTCGGT GGCCAAGTCG 480  
 CACAGCTTCT TCTCGTGCT GAAGAAGAAC GGGCGCTCGG AAAACGGCAA GGGAGAGCCT 540  
 GTGGACCGCA GCAAGGCGCG CGGCAACAA AAGCGGGGGC TCGGGGGGCT GTTCAGCGGC 600  
 ATGCGCTGGC ACAGGAAAGA CAAGCGGGCC AAGCGGAGG CCGCGGAGG GCGCGCGCCC 660  
 GGGGGCGGCT TGATCCTACC CGGCTCGCTC ACCGCCAGCC TGGAGTGCCT CAAGGAGGAG 720  
 ACGCCCAGAG CCGCGCGCGA GCGGAGGAG CCCAGCCAGG ACGCCCCCGC AGACCCAGCA 780  
 GGTGAGCCCG CAGGGGGGAG GGAGGTGCCC GCCCCCGCCG ACCCGGCCCC AGCGCGGAGC 840  
 TGCCGAGAGG CAGAGGGCCT CGCGCACCCC GCGCACACCG GCGCCCGGGG AGAGGACGCC 900  
 GCGGGGCATC GCGCGCGCGA CCGGGGGGCC GGGGAGGTCC GCACGGCAGA GGACGCTTCC 960  
 AGGACGGGG CCGTTCCTCG AAAGACGGTC CCCCTTGTCT ACTCCGAAGG CGGCAGCGGC 1020  
 CGGGCGCCCG CCGCCCCAGA CCTTGCCTCT GTCGATCCAC CCTCAGACCC GTCGGCAGAT 1080  
 CGTATTGTGT TGATGTTTTC TGACGTGACT TCACTGAAAA GCTTTGACTC TCTTACAGGC 1140  
 TGTGGAGATA TTATTGAGA CCAAGAGGAA GAGGCAGGTC CCAGCTGTGA CAAGCATGTC 1200  
 CCCGGGCCAG GCAAGCCGGC TCTGTCTAAA AAGAACCCTG GCGTGTGGC CTACCAAGGA 1260  
 GGGGGGGAAG AGATGGCCAG CCGGACGAG GTGGACGACA CCTATCTACA GGAGTTCTGG 1320  
 GACATGCTCT CCCAGACCGA GGAGCAGGGA CCCGAGCCCC AGGAGGGCGC GGTAAAGGTG 1380  
 GCAGCTGCGC TGGAAACCAA GGTGTGCCCC GAGACCCCCA AAGACACCAG GTGTGTGGAA 1440  
 GCGGCCAAGG ACGCGTCTC GGTCAAGCGC AGGAGGCTCA ACCGGATTC CATCGAGCCC 1500  
 CATCTAAGG ACTAGCCCAA GCACCCGGAG AAGGAGCAGC AGGAAGGCGT CCCCAACAGC 1560  
 GACGAGGGCT ACTGGGACTC CACACGCGCA GGCCAGAGG AAGACAGCTC GAGCAGCGGG 1620  
 AAGAGGGCGG GCATCCCCCG GATAGCTAC AGCGGGGACG CGCTCTATGA TCTCTATGCT 1680  
 GACCCGACG GAAGTCCAGC AACCTTCTT GGAGGGAAGG ACAACGAGGA GACGTCTCTC 1740  
 CTGTCCCGGT TAAAGCCCGT ATCTCCAGGC ACCATCACCT GTCCACTGCG AACACCAGGC 1800  
 AGCTTGCTGA AGGACTCTAA GATCCCTATT AGCATCAAGC ACTTGACCAA CCTTCCATCT 1860  
 AGCATCCCG TGGTGACCA GCAACCTTCC AGGAGTGAGA TGCCCAAGAA AAAAATCCCG 1920  
 GTTTCCAAAG TGCTGGTCCG CAGAGTCAGC AACGGGGGCT TGGCTGGGAC CACCATCAGA 1980  
 GCAACGGCCT GCCACGACAG TGCCAAAAAG TTGTGA

Seq ID NO: B53 Protein sequence  
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
 METSRSRGGG GAVSERGGAG ASVGVCRRA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60  
 GKINKAAPFL FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120  
 EEPRGGGDSG GGGGGRPNFG PPRAAGPGGG SLASSSVAKS HSFFSLKKN GRSENGKGE 180  
 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGGLILPGSL TASLECVKEE 240  
 TPRAAREPEE PSQDAPRDPF GPAGGEEVP APADRAPARS CREAEGLAHP GDTGARGEDA 300



AGHRRRAEPGP GEVTRTAEDAS RTGAVPVKTV PLVDSEGGSG RAPAAPDPAS VDPPSDPSAD 360  
 RICLMFSDVT SLKSFDSLTV CGDIIADQEE EAGPSCDKHV PGPGKPALSK KNPGVVAYQG 420  
 GGEEMASPDV VDDTYLQEFW DMLSQTTEEQ PEPQEGAAGV AAALETKVVF ETPKDRTRCVE 480  
 AAKDASSVKR RRLNRIPIEP HPKEEPKHPK KEQQEGVPSN DEGYWDSTTP GPEEDSSSSG 540  
 5 KAGIPRDSY SGDALVDLYA DPDGSPTLP GGKDNREETSS LSRLKPVSPG TITCPLRTPG 600  
 SLLKDSKIPI SIKHLTNLPS SHPVVHQQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR 660  
 ATACHDSAKK L

Seq ID NO: B54 DNA sequence  
 Nucleic Acid Accession #: NM\_014138.1  
 Coding sequence: 60..854

1 11 21 31 41 51  
 15 CTGCAGAGAC TTCCCAGGAA GTTCCAGCGC CCTCTCAGCC TTCGTACTCA GAACAGCCGA 60  
 TGATGGGCCT CAGTAACCTG AGCCCCGCTC CTGGCCCCAG CCAGGCCGTG CCTCTCCCAG 120  
 AGGGGCTGCT CCGCCAGCGG TACAGAGAGG AGAAGACCCT GGAAGAGCGG CGGTGGGAGA 180  
 GGCTGGAGTT CCTTCAGAGG AAGAAAGCAT TCCTGCGGCA TGTGAGGAGG AGACACCGCG 240  
 20 ATCACAATGGC CCCCTATGCT GTTGGGAGGG AAGCCAGAAT CTCCCCATTA GGTGACAGAA 300  
 GTCAAGATCG ATTCCGATGT GAATGTCGAT ACTGCCAGAG CCACAGGCCG AATCTTTCTG 360  
 GGATCCCTGG GGAGAGTAAC AGGGCCCCAC ATCCCTCCTC CTGGGAGACG CTGGTGACAG 420  
 GCCTCAGTGG CTTGACTCTC AGCCTAGGCA CCAACCAGCC CGGCCCTCTG CCTGAAGCGG 480  
 CACTCCAGCC ACAGGAGACA GAGGAGAAGC GCCAGCGAGA GAGGCAGCAG GAGAGCAAAA 540  
 TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTG CACCCCCATG 600  
 25 GGATGGAGAC CCGAAGGGAC TCAGACGGAG CCGCCGTGTT GGCAGCGCCT GGGTGTGGGC 660  
 CCATTTTGGG GACCAACAG CAAGCTGTGG TCGGATGAGT GCCAGGACCT GTGTACCGGG 720  
 ACACGTGGGA GTCTCTCCAG CATGATGCTT GACTGACCCG AGGAAGGTCC TCATGTTTCG 780  
 TGCTGTGATC TCTCGATGG CTGTGAGGCA TTCCTTGGCA AGGGACGCTG CGTACCAGCG 840  
 GTCCTCACCG CATCTACAT GGCTCCTGTG ATGCATGTTG TCGCTTTCCC ACCCGGGATC 900  
 30 TCCATCTCTC TTCCTTCTCT GCTGTCACTA AGAGATCACA TGCTGTGTGA GTGTGAATGC 960  
 CTTGTGCGTG TCCTGTGCTT TTGCACCATT GAGTTGACTG CCTCTGAGAA GCAGCACTAG 1020  
 GCCTGTTGAA ATGCAATGTG CTGCCCTGAG ATCCAGTTTC AAGAATGGGC AGGTAAACGC 1080  
 ATGTGGGAAA AGGAATGTGG AATGAGAACT TGGTGGTTCA CCGCTGTACT ATTTGTGTAA 1140  
 35 ATGTTTACGT ATGTGATAAG CTACATGTAT GTAAATGTTG CAATACCCCT AACAGTCGAG 1200  
 TAGTAGTCTC CCTTACAGGA ATTTTGTGACG GGGTTCCTCA TCATCAATAC CAAATAAATA 1260  
 TATGTAGGAA TGGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1320  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

Seq ID NO: B55 Protein sequence  
 Protein Accession #: NP\_054857.1

1 11 21 31 41 51  
 45 MMGLSNLSPG PGPSQAVPLP EGLLRQRYRE EKTLEERRWE RLEFLQRKKA FLRHVRRRHR 60  
 DHMAPYAVGR EARISPLGDR SQNRFRCECR YCQSHRPNLS GIPGESNRAP HPSSWETLVQ 120  
 GLSGLTSLSG TNQPGPLPEA ALQPQETEEK RQRERQQESK IMFQRLKQW LLEN

Seq ID NO: B56 DNA sequence  
 Nucleic Acid Accession #: NM\_000025.1  
 Coding sequence: 198..1424

1 11 21 31 41 51  
 55 GCTACTCCTC CCCAAGAGC GGTGGCACCG AGGGAGTTGG GGTGGGGGGA GGCTGAGCGC 60  
 TCTGGCTGGG ACAGCTAGAG AAGATGGCCC AGGCTGGGGA AGTCGCTCTC ATGCCCTTGT 120  
 GTCCCCCTCC CTGAGCCAGG TGATTTGGGA GACCCCTCTC TTCCTTCTTT CCTTACCGCC 180  
 CCACGCGCGA CCGCGGGATG GCTCCGTGGC CTCACGAGAA CAGCTCTCTT GCCCATGGC 240  
 CGGACCTCCC CACCCTGGCG CCCAATACCG CCAACACCAG TGGGCTGCCA GGGGTTCCGT 300  
 60 GGGAGGCGGC CCTAGCCGGG GCCCTGCTGG CGCTGGCGGT GCTGGCCACC GTGGAGGCA 360  
 ACCTGCTGGT CATCGTGGCC ATCGCCTGGA CTCCGAGACT CCAGACCATG ACCAACGTGT 420  
 TCGTACTTTC GCTGGCCGCA GCCGACCTGG TGATGGGACT CCTGGTGGTG CCGCCGCGCG 480  
 CCACCTTGGC GCTGACTGGC CACTGGCCGT TGGGCGCCAC TGGCTGCGAG CTGTGGACCT 540  
 CGGTGGACGT GCTGTGTGTG ACCGCCAGCA TCGAAACCCT GTGCGCCTG GCCGTGGACC 600  
 65 GCTACCTGGC TGTGACCAAC CCGCTGCGTT ACGGCGCACT GGTCAACAAG CGCTGCGCCC 660  
 GGACAGCTGT GGTCTCTGTG TGGTCTGTGT CGGCGCGCGT GTCGTTTGGC CCATCATGA 720  
 GCCAGTGGTG GCGCGTAGGG GCCGACGCGG AGGCGCAGCG CTGCCACTCC AACCCGCGCT 780  
 GCTGTGCTCT CGCCTCCAAC ATGCCCTACG TGCTGCTGTC CTCCTCCGTC TCCTTCTACC 840  
 70 TTCCTCTTCT CGTGATGCTC TTCGTTACG CGCGGCTTTT CGTGGTGGCT ACGCGCCAGC 900  
 TCGCTTGTCT GCGCGGGGAG CTGGGCGGCT TTCGCCCCGA GGAGTCTCCG CCGGCGCGCT 960  
 CGCGCTCTCT GCCCCCGGCC CCGGTGGGGA CGTGCGCTCC GCCCGAAGGG GTGCCCGCCT 1020  
 GCGGCGCGCG GCCCGCGCGC CTCCTGCTCT TCCGGGAACA CCGGCGCCTG TGACCTTGG 1080  
 GTCTCATCAT GGGCACCTTC ACTCTCTGCT GGTGGCCCTT CTTTCTGGCC AACGTGCTGC 1140  
 GCGCCCTGGG GGGCCCTCTC CTAGTCCCAG GCCCGGCTTT CTTTCCCTG AACTGGCTAG 1200  
 75 GTTATGCCAA TTCTGCTTTC AACCCGCTCA TCTACTGCGG CAGCCCGGAC TTTGCGAGCG 1260  
 CCTTCCGCGG TCTTCTGTGC CGCTGCGGCC GTGCGCTGCC TCCGAGAGCC TGCGCCCGCG 1320  
 CCGGCGCGGC CCTCTTCCCC TCGGGCGGTC CTGCGGCCCG GAGCAGCCCA GCGCAGCCCA 1380  
 80 GGCTTTGCCA ACGGCTCGAC GGGGCTTCTT GGGGAGTTTC TTAGGCTTGA AGGACAAGAA 1440  
 GCAACAACTC TGTGTATCAG AACCTGTGGA AAACCTCTGG CCTCTGTTCA GAATGAGTCC 1500  
 CATGGGATTC CCGGCTGTG AACTCTACCT CTCCAGAAC TGACGACTGG GCCATGTGAC 1560  
 CCAAGGAGGG ATCCTTACCA AGTGGGTTTT CACCATCCTC TTGCTCTCTG TCTGAGAGAT 1620  
 GTTTTCTAAA CCCCAGCCTT GAACCTCACT CCTCCCTCAG TGGTAGTGTC CAGGTGCGCT 1680  
 GGAGCAGCAG GCTGGCTTTG GTAGGGGAC CATCACCCG GCTTGCCTGT GCAGTCAGTG 1740  
 AGTGCTTAGG GCAAGAGAG CTCCCTGCTT TCCATTCTCT CTGCCACCCA AACCTGATG 1800

5 AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGGT AGAAAAGACC 1860  
 AAGATTTGGG GTTTTATCTC TGGTTCCCTT ATTACTGCTC TCAAGCAGTG GCCTCTCTCA 1920  
 CTTTAGCCAT GGAATGGCTC CGATCTACCT CACAGCAGTG TCAGAAGGAC TTCGCCAGGG 1980  
 TTTTGGGAGC TCCAGGGTTC ATAAGAAGGT GAACCATTAG AACAGATCCC TTCTTTTCTT 2040  
 TTTGCAATCA GATAAATAAA TATCACTGAA TGCAGTTCAT CCTCGGCCCA CTTCCCTCC 2100  
 GTTTGTTTTT TTTTCATAAT CCACTTACTC CCTTCCCTTC TACTCTGCGC TGGCTTTTGA 2160  
 CAGAGGCAGT AAATTAGGCC TAATCCTCAC TCTTTTCTTC CTAATCTTCA TCAACAAAA 2220  
 AATGAAAAGT CTGTCTGGAC GAAGGGGAGT GAGCTTGAGC CTTTGATATC TTGCTCCCCC 2280  
 10 ACCCTTCTGT AAATCTCTGA AATCCAGTTG CCATTGAGTA GCAAAGCCAC GCTCCCCACA 2340  
 GGACTTGGAC AGAGGGCCCA CAGGGGGATG GGCTGGCTGT GGCCAGGTTT AGGGCAGGGG 2400  
 GCATTTGTCC CCTCCATGCT ATAATCCAGT GGTGCCCTAC ATGGTGTGTG TGTGTGTGTG 2460  
 TCGCTGTGTG TGTGTGTGTG TGTGTCTGGA GGCACAGGCA CAAAGCATTG CTTGGGTTGG 2520  
 TCAAATGTCT TGTGTCTATA ATATATTCTG ATGTTTCCCA GCCTTCCAC AACCTCTACC 2580  
 15 TTCCCACTCA CCTTCCCCAG CTACAAAAAT CTGTATTATC CTCTTAAAGT AAAACTGGAG 2640  
 TTAC

Seq ID NO: B57 Protein sequence  
 Protein Accession #: NP\_000016.1

20 1 11 21 31 41 51  
 MAPWPHENSS LAPWPDLPPL APNTANTSGL PGVPWEAALA GALLALAVLA TVGNNLLVIV 60  
 AIAWTPRLQT MTNVFVTSIA AADLVMLLV VPPAATLALT GHWPLGATGC ELWTSVDVLC 120  
 VTASIEITLCA LAVDRYLAVT NPLRYGALVT KRCARTAVVL VVVVSAAVSF APIMSQWVRV 180  
 25 GADAEARQCH SNPRCCAFAS NMPYVLLSSS VSFYLLPLVM LFVYARVFFV ATRQLRLLRG 240  
 ELGRFPPEES PAPRSRLAP APVGTCAPE GVPACGRRPA RLLPLREHRA LCTLGLIMGT 300  
 FTLCWLPPFL ANVLRALGGP SLVPGPAFLA LNWLYANSA FNPLIYCRSP DFRSAFRRL 360  
 CRCGRRLPPE PCAARPALE PSGVPAARSS PAQPRLCQRL DGASWGV

30 Seq ID NO: B58 DNA sequence  
 Nucleic Acid Accession #: NM\_032553.1  
 Coding sequence: 37..1038

35 1 11 21 31 41 51  
 CACCATTAGG CAAAGATAGT TTCTCTAGAG AGAATCATGC CTGCTAATTA CACGTGTACC 60  
 AGGCCAGATG GAGACAATAC AGATTTTCGA TACTTTATTT ATGCAGTGAC ATACACTGTC 120  
 ATTCTTGTGC CAGGTCTCAT AGGGAATATA TTAGCCCTGT GGGTATTCTA TGGTTATATG 180  
 40 AAAGAAACAA AACGAGCTGT GATATTTATG ATAACTTAG CCATTGCTGA CTTACTACAA 240  
 GTTCTTTCTT TGCCACTGAG GATCTTCTAC TACTTGAATC ATGACTGGCC ATTTGGGCCT 300  
 GGTCTCTGCA TGTCTGTTT CTACCTGAAG TATGTCAACA TGTATGCAAG CATCTACTTC 360  
 TTGGTCTGCA TCACTGTGCG ACGATTTTGG TTTCTCATGT ACCCCTTTCG CTTCCATGAC 420  
 TGCAACAGCA AATATGACCT GTACATCAGC ATTGCTGGCT GGCTGATCAT CTGCCTTGCC 480  
 45 TGTGTACTCT TTCCACTCCT CAGAACCAGT GATGATACCT CTGGCAATAG GACCAAATGC 540  
 TTTGTGGATC TTCTTACCAG GAATGTCAAC CTGGCCAGT CCGTTGTTAT GATGACCATT 600  
 GGCAGTTTGA TTGGGTTTGT AACTCCGCTT CTGATTGTCC TATATTGTAC CTGGAAGACG 660  
 GTTTTATCAC TCGAAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC 720  
 TTGAAGATGA TTCTAACCTG TGCAGGGGTA TTCTTAATTT GCTTTGCACC TTATCATTTT 780  
 50 AGTTTTCTCT TAGATTTCTT GGTGAAGTCC AATGAAATTA AAAGCTGCCT AGCCAGAAGG 840  
 GTGATTCTAA TATTTCTTCT TGTGGCATTG TGTCTTGCTA GCTGGAATTC ATGTCTTGAC 900  
 CCAGTCTATAT ACTACTTTTC CACTAATGAG TTCCGAAGAC GGCTTTCAAG ACAAGATTG 960  
 CATGACAGCA TCCAATCTCA TGCAAAATCC TTTGTGAGTA ACCATACAGC TTCCACCATG 1020  
 ACACCTGAAT TATGCTAAAA CAAAAAACA AACTGAATGT GACCTGAAAT GCAAGTACAT 1080  
 CAGAACATAT TCTCAATACC CAAGCCACAG GGAAGAACTT GCAAAACAAC ACAGCTTTTC 1140  
 55 AGTTCGTCTC TATCTTACTG CTATGGGGAA TTCCTTCTT CAAAGCAGGA CCTATTTGGA 1200  
 GCATTACGAT CCACGATTAT TGATGTTGAC ATGTCCATGT AGTAATTTTT CTTCAGT

Seq ID NO: B59 Protein sequence  
 Protein Accession #: NP\_115942.1

60 1 11 21 31 41 51  
 MPANYTCTRP DGDNTDFRYF IYAVTYTVIL VPGLIGNILA LWVFGYMKKE TKRAVIFMIN 60  
 LAIADLLQVL SLPLRIFYYL NHDWPFPGPL CMFCFYLYV NMYASIVFLV CISVRRFWFL 120  
 65 MYPPRFHDCQ QKYDLYISIA GWLIICLACV LFPLLRSTDD TSGNRTKCFV DLPTRNVNLA 180  
 QSVVMMTIGE LIGFVTPLLI VLYCTWKTIV SLQDKYPMAQ DLGEKQKALK MILTCAGVFL 240  
 ICFAPYHFSF PLDFLVKSNE IKSCLARRVI LIFHSVALCL ASLNSCLDEP IYYFSTNEFR 300  
 RRLSRQDLHD SIQLHAKSFV SNHTASTMTF ELC

70 Seq ID NO: B60 DNA sequence  
 Nucleic Acid Accession #: CAT cluster

75 1 11 21 31 41 51  
 GATTCGGATT TTAATCCGAC TCACTATAGG GAATTTTGGC CCTCGAGGCC AAGAATTCGG 60  
 CCGAGGGT AGACATTTAA CTGAGTCTT TTCATATCAC GGTATGCTT TATTTTACCC 120  
 TCATATATAA TTAATTTTCA TCTGGGCATA TATTTCCAGA TTAGAAATCA TTCTTTTCA 180  
 TACATTTTAA GGAATTTATA CATTTGCATC TGAATTTGTA TTCATTATCT TCTAGAAACC 240  
 80 AAGAGTGGAC TTGGTATCCG TCTGATTATA TTTTCTTTGT TGGTAAAGAG CCTCTTTT 300  
 CCCTTTTAT TTTCACTCTC TCTTCTCTA GTGTTTATAA TCTTATTTT ATGAATGTAG 360  
 TCTAATTATT TAGAACACTG TCTCCAGTA TGTGTTTATT TGGGTTGTG TTTTGAACAT 420  
 TGCTCCAGG TCGAGTTTAT TGTGTGTTA TGTTCCTAT TTGAGGTTGG ACACTTAGAA 480  
 AATTTTCTCA ATTCGAAAC TATTTTCTCT CAGCACTCAG AATTTTAT CAAAGATTAT 540  
 TTCCACGATT ATTTCTGTCT CTGTTTCTT CGTGTCTTA ACCTAGAATT CAATTGTTA 600

ATGTTAGACC TTACACATCT TCAATGTATC ATATATATTT CACTCATATT ATTTATTGTC 660  
 ATATCTTTTG GACTATTGTG TGAAAGCAAT AAATGTATAT TACTTTAAAA AAAAAAAAAA 720  
 AAAACTHCAAT TTTCAAATTT AATACACACA AATTGTGCAT ACCCACACAC ATATACCACA 780  
 GATATATTCA TTTTCAGGAT TTCTTAAAGT GTTATTTTAA AAATAATCAT ATTCTTATTT 840  
 TGTGAACGTG GGGATTCTCT GAAACTTTT GAAAACTCTC ATTAGTCTGT GTTTGTGTGG 900  
 TTTCTTTAAA TTATCTCTTC CTTCAGAATT ACTTTTGTGT TTTGAATTG AGTCTTTGCC 960  
 ATTCATAAGG CGGGCTTTCC TTGAATACCA GATAACTCTG AGTTTCTGT TCATATTTAA 1020  
 GAATAAATAA CCTAATTTGA AAAAAAAAAA AAAAA

10 Seq ID NO: B61 DNA sequence  
 Nucleic Acid Accession #: NM\_014522.1  
 Coding sequence: 846..3911

15 1 11 21 31 41 51  
 | | | | |  
 CTGGTGGTCC AGTACCTCCA AAGATATGGA ATACACTCCT GAAATATCCT GAAAACTTTT 60  
 TTTTTCAGCA ATCCTTTAAT AAGCAGTTAT GTCAATCTGA AAGTTGCTTA CTGTACTCTT 120  
 ATATTAATAG CTATTCCTGT TTTCTTATC CAAAGAAAAA TCCTCTAATC CCCTTTTCAC 180  
 ATGATAGTTG TTACCATGTT TAGGCATTAG TCACATCAAC CCCTCTCCTC TCCCAAACCT 240  
 CTCTTCTTCA AATCAAACTT TATTAGTCCC TCCTTTTATA TGATTCCTTG CCTCGTTTTA 300  
 TCCAGATCAA TTTTTTTTC CTTTGATGCC CAGAGCTGAA GAAATGGACT ACTGTATAAA 360  
 TTATTCATTG CCAAGAGAAT AATTGCATTT TAAACCCATA TTATAACAAA GAATAATGAT 420  
 TATATTTTGT GATTGTGAAC AAATACCCCT TATTTTCCCT TAACATTTGA ATTAAATATT 480  
 TTAATTATTT GTATTCTCTT TAACATCTCT GGTATATTAA AGTATTATCT TTTATATATT 540  
 25 TATCAATGGT GGACACTTTT ATAGGTACTC TGTGTCAATT TTGATACGT AGGTATCTTA 600  
 TTTCAATTAT CTTTATCTTT AATGTACGAA TTCATAATAT TTGATTGAGA ACAAAATTAT 660  
 CACTAATTAA CAGAGTGTCA ATTTATGCTAA CATCTCATT ACTGATTTTA ATTTAAACAA 720  
 GTTTTGTGTA ACATGCATGT TTAGGGTTGG CTTCTTAATA ATTTCTTCTT CCTCTTCTCT 780  
 CTCTCCTCTT CTTTGGTCCA GTGTGTGCGG GGTTAATACA ACAAACTGTA ACAAGTGTAC 840  
 30 CTGGTATGGA CTTGTGTGCC GGGACGTACA TTTTCGCGGT CCTGCTAGCA TGCGTGGTGT 900  
 TCCACTCTGG CGCCCAGGAG AAAAAGTACA CCATCCGAGA AGAAATGCCA GAAAACGTCC 960  
 TGATAGGCGA CTTGTGTAAG GACCTTAAC TGTGCTGAT TCCAAACAG TCCTTGACAA 1020  
 CTGCTATGCA GTTCAAGCTA GTGTACAAGA CCGGAGATGT GCCACTGATT CGAATTGAAG 1080  
 AGGATACCTG TGAGATCTTC ACTACTGGCG CTCGCATTGA TCGTGAGAAA TTATGTGCTG 1140  
 35 GTATCCCAAG GGATGAGCAT TGCTTTTATG AAGTGGAGGT TGCCATTTTG CCGGATGAAA 1200  
 TATTTAGACT GGTTAAGATA CGTTTCTTGA TAGAAGATAT AAATGATAAT GCACCATTGT 1260  
 TCCAGCAAC AGTTATCAAC ATATCAATTC CAGAGAACTC GCCTATAAAC TCTAAATATA 1320  
 CTCTCCAGC GGCTGTTGAT CCTGACGTAG GAATAAACGG AGTTCAAAAC TACGAACATA 1380  
 TTAAGAGTCA AAACATTTT GGCCTCGATG TCATTGAAAC ACCAGAAGGA GACAAGATGC 1440  
 40 CACAACGTAT TGTTCAAAAG GAGTTAGATA GGGAAAGAGAA GGATACCTAC GTGATGAAAG 1500  
 TAAAGGTGTA AGATGGTGGC TTTCTTCAA GATCCAGTAC TGCTATTTTG CAAGTGAGTG 1560  
 TTACTGATAC AAATGACAA CACCCAGTCT TTAAGGAGAG AGAGATTGAA GTCAGTATAC 1620  
 CAGAAAATGC TCCTGTAGGC ACTTCAGTGA CACAGCTCCA TGCCACAGAT GCTGACATAG 1680  
 GTGAAAATGC CAAGATCCAC TTCTCTTTCA GCAATCTAGT CTCCAACATT GCCAGGAGAT 1740  
 45 TATTTCACTT CAATGCCACC ACTGGACTTA TCACAATCAA AGAACCCTG GATAGGGAAG 1800  
 AAACACCAA CCACAGTTA CTGGTTTGG CAAGTGATGG TGGATTGATG CCAGCAAGAG 1860  
 CAATGGTGCT GGTAAATGTT ACAGATGTCA ATGATAATGT CCCATCCATT GACATAAGAT 1920  
 ACATCGTCAA TCCTGTCAAT GACACAGTTG TTCTTTCAGA AAATATTCCA CTCAACACCA 1980  
 AAATTGCTCT CATAACTGTG ACGGATAAGG ATCGCGACCA TAATGGCAGG GTGACATGCT 2040  
 50 TCACAGATCA TGAATCCCTT TTCAGATTAA GGCCAGTATT CAGTAATCAG TTCTCTCTGG 2100  
 AGACTGCAGC ATATCTTGAC TATGAGTCCA CAAAAGAATA TGCCATTAAA TTAAGTGGCTG 2160  
 CAGATGCTGG CAAACCTCCT TTGAATCAGT CAGCAATGCT CTTCATCAA GTGAAGATG 2220  
 AAAATGACAA TGTCTCAGTT TTCACCCAGT CTTTCGTAA TGTGTTCTAT CTGAGAATA 2280  
 55 ACTCTCTGCG CATCCAGTTG AGGAAAGTAA GTGCAATGGA TGCAGACAGT GGGCCTAATG 2340  
 CTAAGATCAA TTACCTGTGA GGCCTGATG CTCACCTGA ATTCAGCCTG GATTGTCTGA 2400  
 CAGGCATGCT GACTGTAGTG AAGAACTAG ATAGAGAAAA AGAGGATAAA TATTTATTTCA 2460  
 CAATTCCTGGC AAAAGATAAC GGGGTACCAC CCTTAACCAG CAATGTCAAC GTCTTTGTAA 2520  
 GCATTATTGA TCAGAAATGAC AATAGCCAGG TTTTCACTCA CAATGAATAC AACTTCTATG 2580  
 60 TCCAGAAAA CCTTCCAGG CATGGTACAG TAGGACTAAT CACTGTAACT GATCCTGATT 2640  
 ATGGAGACAA TTTGTCAGTT ACGCTCTCCA TTTTAGATGA GAATGATGAC TTCAACATTG 2700  
 ATTACAAAC TGGTGTATC CGACCAATA TTTCAATTGA TAGAGAAAA CAAGAATCTT 2760  
 ACACCTTTCTA TGTAAAGGCT GAGGATGGTG GTAGAGTATC ACGTCTTCTA AGTGCCAAAG 2820  
 TAACCATAAA TGTTGGTTGAT GTCATGACA ACAAAACAGT TTTCAATTGTC CCTCCTTCCA 2880  
 65 ACTGTTCTTA TGAATTGGTT CTACCGTCCA CTAATCCAGG CACAGTGGTC TTTGAGTTAA 2940  
 TTGCTGTGTA CAATGACACT GGCATGAATG CAGAGGTTCTG TTACAGCATT GTAGGAGGAA 3000  
 ACACAAGAGA TCTGTTTGA ATCCGACCAAG AAACAGGCAA CATAACATTG ATGGAGAAAT 3060  
 GTGATGTTAC AGACCTTGGT TTACACAGAG TGTGGTCAA AGCTAATGAC TTAGGACAGC 3120  
 CTGATTCCTT CTTCAGTGTG GTAATTGTCA ATCTGTTCTG GAATGAGTCTG GTGACCAATG 3180  
 70 CTACACTGAT TAATGAACCT GTGCGCAAAA GCACCTGAAGC ACCAGTGACC CCAAACTCTG 3240  
 AGATAGCTGA TGTATCTCTA CCAACTAGTG ACTATGTCAA GATCCTGGTT GCAGCTGTTG 3300  
 CTGGCACCAT AACTGTCGTT GTAGTTATTT TCATCACTGC TGTAGTAAGA TGTGCGCCAG 3360  
 CACCACACCT TAAGGCTGCT CAGAAAAACA AGCAGAATTC TGAATGGGCT ACCCCAAACC 3420  
 CAGAAAAACG GCAGATGATA ATGATGAAGA AAAAGAAAA GAAGAAGAAG CATTCCCCTA 3480  
 75 AGAATCTGCT GCTTAATTTT GTCATATTG AAGAACTAA GGCAGATGAT GTTGACAGTG 3540  
 ATGGAACAG AGTCACACTA GACCTTCTTA TTGATCTAGA AGAGCAACA ATGGGAAAGT 3600  
 ACAATTGGGT AACTACACCT ACTACTTTCA AGCCGACAG CCCTGATTG GCCCGACACT 3660  
 80 ACAATCTGC CTCTCCACAG CCGCTCTCC AAATTCAGCC TGAACCTCCC CTGAATTCGA 3720  
 AGCACCACAT CATCAAGAA CTGCTCTCG ATAACACCTT TGTGGCCTGT GACTCTATCT 3780  
 CCAAGTGTTC CTCAAGCAGT TCAGATCCCT ACAGCGTTTC TGAAGTGGC TATCCAGTGA 3840  
 CGACCTTCGA GGTACCTGTG TCCGTACACA CCAGACCGGT AGGTATCCAA GTTCTAACA 3900  
 CACTTTCTA ACTATTTTTT TATTATTATT TTCAGTTGAT GTAGAATTT ACAAACTCTA 3960  
 TTGACTTCAA AGAGGATGTA AAACAATCAT ATTCTACAGA TGTACCCAAT AGATATATGG 4020  
 ATTCATTTAA GTTTGGTAGA AGATGAGAAC AAAATAACTA CTGATTTAGG AAAATGGAT 4080  
 GCAGAATAAT AATTATAGTA GGGGCAATTT TGTCTGTAGA TGGCAGTATG ACAATCTTG 4140

CTAGAGAATA TATTGAAAAA AACTTCAACA CAAAGGGTTG TAGCACTGTC CTCAGTACCA 4200  
 TTGTGTGCAT GAGGATCAGA ATAGTCTGGG CTAGATACAT CACATTAAAG CTTTTCAGAA 4260  
 TCTGATAAAT AGCTCTAAAT ACTAATGATA TTGACAAGCC TAGCTTCACT TGGGAAAATC 4320  
 TGTGGCTGTT CACAGAAATT CAGCACCAAG TTATTCCCC CATACTCTAC CAGGCTTCA 4380  
 GGTCTCATA AAGAAAAGTG TCGTTTTAG ATTAGGAAC CAAAATTATT TTGGTGATC 4440  
 AAATCTACAG TCACACAATA TAACAAGAA GGGATTAGAA AAATGAAAGC CTAATCATTC 4500  
 TCATCTTTAA GCCAGAGAA GAAATATATA TGAGGTCTCT GGATAGCTAT TTAATATATT 4560  
 GCATATTTAT GCAAGGTATT TTGAGCCCTT CAGAAGACAT TCT

Seq ID NO: B62 Protein sequence  
 Protein Accession #: NP\_055337.1

1 11 21 31 41 51  
 15 MDLLSGTYIF AVLLACVVFH SGAQEKNYTI REEMPENVLI GDLLKDLNLS LI PNKSLTTA 60  
 MQFKLVYKTG DVPLIRIEED TGEIFTTGAR IDREKLCAGI PRDEHCFYEV EVAILPDEIF 120  
 RLVKIRFLIE DINDNAPLEFP ATVINISIEP NSAINSKYTL PAAVDPDVGI NGVQNYELIK 180  
 SQNIFGLDVI ETPEDGKMPQ LIVQKELDRE EKDTYVMKVK VEDGGFPQRS STAILQVSVT 240  
 20 DTNDNHPVFK ETEIEVSIPE NAPVGTSTVQ LHATDADIGE NAKIHFSFSN LVSNIARRLF 300  
 HLNATTGLIT IKEPLDREET PNHKLVLVAS DGGLMPARAM VLVNVDVDND NVPSIDIRYI 360  
 VNPVNDTVVL SENIPLNTKI ALITVTDKDA DHNGRVTCTF DHEIFPRLRP VFSNQFLLT 420  
 AAYLDYESTK EYAIKLLAAD AGKPLPNQSA MLFIKVDEN DNAPVFTQSF VTSVIPENNS 480  
 PGIQLTKVSA MDADSGPNK INYLLGPDAP PEFSLDCRTG MLTVVKKLDK EKEDKYLFTI 540  
 25 LAKDNGVPLP TSNVTVFVSI IDQNDNSPVF THNEYNFYVP ENLPRHGTVG LITVTDPDYD 600  
 DNSAVTSLIL DENDDFTIDS QTGVIRPNIS PDREKQESYT FYVKAEDGGR VSRSSSAKVT 660  
 INVVDVNDNK PVFIIVPPSN SYELVLPSIN PGTVVQVIA VDNDTGMNAE VRSIVGGNT 720  
 RDLFAIDQET GNITLMEKCD VTDLGLHRLV VKANDLGQPD SLFVSVIVNL FVNESVTNAT 780  
 30 LINELVKRSK EAPVTPNTEI ADVSPTSDY VKILVAAVAG TITVVVVIPI TAVVRCRQAP 840  
 HLKAAQKNKQ NSEWATPNPE NRQMIMMKKK KKKKKHSPKN LLLNFVTIEE TKADDVSDG 900  
 NRVTLDLPID LEEQTMGKYN WVTTPPTFKP DSPDLARHYK SASPQPAFQI QPETPLNSKH 960  
 HIIQELPLDN TFAVCDISIK CSSSSSDPYS VSDCGYPVTT FEVPVSVHTR PVGIQVSNIT 1020  
 F

Seq ID NO: B63 DNA sequence  
 Nucleic Acid Accession #: XM\_059180.2  
 Coding sequence: 276..3740

1 11 21 31 41 51  
 40 GCGGCGGCCG CGGAGTATCC TGGAGCTGCA GACAGTGC GGCTGCGCCC AGTCCCGGCT 60  
 GTCTCTGCGC CGACCCCTCC TCAGCCCTGG GCGCGGCGAC GCTGGGGCCC CGCGGGGCTG 120  
 GCGCGCTAGC GAGCCTGCGG GTGCAACCCA GCCAGCGCAG CGACGGGGCG CTGCGCTGGC 180  
 CAGGCGGCACA CGGAAGTGCG CTCTCTGTA GTAGCTTTGG AAGTAGAGA AGAAAATCCA 240  
 45 GTTGTCTTCT TGGAGAACAC TGGACAGCTG AATAAATGCA GTATCTAAAT ATAAAAGAGG 300  
 ACTGCAATGC CATGGCTTTC TGTGCTAAAA TGAGGAGCTC CAAGAAGACT GAGGTGAACC 360  
 TGGAGGCCCC TGAGCCAGGG GTGGAAGTGA TCTTCTATCT GTCGGACAGG GAGCCCTCC 420  
 GGTGGGCGAC TGGAGCATAC ACAGCAGAGG AACTGTGCAT CAGGGCTGCA CAGGCATGCC 480  
 GTATCTCTCC TCTTTGTGAC AACCTCTTTG CCTGTATGA CGAAGAACACC AAGCTCTGGT 540  
 50 ATGCTCCAAA TCGCACCATC ACCGTTGATG ACAAGATGTC CCTCCGGCTC CACTACCGGA 600  
 TGAGGTCTTA TTTACCAAT TGGCATGGAA CCAACGACAA TGAGCAGTCA GTGTGGCGTC 660  
 ATTCTCCTAA GAAGCAGAAA AATGGCTACG AGAAAAAAA GATTCCAGAT GCAACCCCTC 720  
 TCCTTGATGC CAGCTCACTG GAGTATCTGT TTGCTCAGGG ACAGTATGAT TTGGTGAAAT 780  
 GCCTGGCTCC TATTCGAGAC CCCAAGACCG AGCAGGATGG ACATGATATT GAGAACGAGT 840  
 55 GTCTAGGGAT GGCTGTCTGT GCCATCTCAC ACTATGCCAT GATGAAGAAG ATGCAGTTGC 900  
 CAGAACTGCC CAAGGACATC AGCTACAAGC GATATATTCC AGAAACATTG AATAAGTCCA 960  
 TCAGACAGAG GAACCTTCTC ACCAGGATGC GGATAAATAA TGTTTTCAAG GATTTCTCTA 1020  
 AGGAATTTAA CAACAAGACC ATTTGTGACA GCAGCGTGTC CACGCATGAC CTGAAGGTGA 1080  
 AATACTTGGC TACCTTGGAA ACTTTGACAA AACATTACGG TGCTGAAATA TTTGAGACTT 1140  
 60 CCATGTTACT GATTTTATCA GAAAATGAGA TGAATTGGTT TCATTCGAAT GACGGTGGAA 1200  
 ACGTTCTCTA CTACGAAGTG ATGGTGACTG GGAATCTTGG AATCCAGTGG AGGCATAAAC 1260  
 CAAATGTTGT TTTCTGTTGA AAGGAAAAAA ATAACTGAA GCGGAAAAAA CTGAAAAATA 1320  
 AACACAAGAA GGATGAGGAG AAAACAAGA TCCGGGAAGA GTGGAACAAT TTTTCTTACT 1380  
 TCCCTGAAAT CACTCAGATT GTAATAAAGG AGTCTGTGGT CAGCATTAAC AAGCAGGACA 1440  
 65 ACAAGAAAAT GGAAGTGAAG CTCTCTTCCC ACGAGGAGGC CTTGTCTCTT GTGTCCCTGG 1500  
 TAGATGGCTA CTTCCGGCTC ACAGCAGATG CCCATCATT CCTCTGCACC GAGTGGCCCC 1560  
 CCGGTTGAT CGTCCACAAC ATACAGAATG GCTGTCATGG TCCAATCTGT ACAGAATACG 1620  
 CCATCAATAA ATTGCGGCAA GAAGGAAGCG AGGAGGGGAT GTACGTGCTG AGGTGGAGCT 1680  
 70 GCACCGACTT TGACAACATC CTCATGACCG TCACCTGCTT TGAGAAGTCT GAGCAGGTGC 1740  
 AGGGTGCCCA GAAGCAGTTC AAGAACTTTC AGATCGAGGT GCAGAAGGGC CGTACAGTC 1800  
 TGCACGGTTC GGACCGCAGC TTCCCAGCT TGGGAGACCT CATGAGCCAC CTCAAGAAGC 1860  
 AGATCTGCG CACGGATAAC ATCAGCTTCA TGCTAAACCG CTGCTGCCAG CCAAGCCCC 1920  
 GAGAAATCTC CAACCTGCTG GTGGCTACTA AGAAGCCCA GGAGTGGCAG CCCGTCTACC 1980  
 75 CCATGAGCCA GCTGAGTTTC GATCGGATCC TCAAGAAGGA TCTGGTGACG GCGGAGCACC 2040  
 TTGGGAGAGG CACGAGAACA CACATCTATT CTGGGACCCT GATGGATTAC AAGGATGACG 2100  
 AAGGAACCTC TGAAGAGAG AAGATAAAG TGATCCTCAA AGTCTTAGAC CCCAGCCACA 2160  
 GGGATATTCT CTTGGCCCTC TTCGAGGCAG CCAGCATGAT GAGACAGGTC TCCCAACAAC 2220  
 ACATCGTGTA CCTCTATGGC GTCTGTGTCC GCGACGTGGA GAATATCATG GTGGAAGAGT 2280  
 TTGTGGAAGG GGGTCCCTCT GATCTCTTCA TGCACCGGAA AAGCGATGTC CTTACCACAC 2340  
 80 CATGGAATTT CAAAGTTGCC AAACAGCTGG CCAAGTCCCT GAGCTACTTG GAGGATAAAG 2400  
 ACCTGGTCCA TGGAAATGTG TGTACTAAAA ACCTCCTCCT GGCCCGTGAG GGCATCGACA 2460  
 GTGAGTGTGG CCCATCTATC AAGCTCAGTG ACCCGGCAT CCCATTACG GTGCTGTCTA 2520  
 GGCAAGAATG CATTGAACGA ATCCCATGGA TTGCTCCTGA GTGTGTTGAG GACTCCAAGA 2580  
 ACCTGAGTGT GGCTGCTGAC AAGTGGAGCT TTGGAACAC GCTCTGGGAA ATCTGTACA 2640  
 ATGGCGAGAT CCCCTTGAAA GACAAGACGC TGATTGAGAA AGAGAGATT TATGAAAGCC 2700

5  
10  
15  
20  
25  
30  
35  
40

```

GGTGCAGGCC AGTGACACCA TCATGTAAGG AGCTGGCTGA CCTCATGACC CGCTGCATGA 2760
ACTATGACCC CAATCAGAGG CCTTTCTTCC GAGCCATCAT GAGAGACATT AATAAGCTTG 2820
AAGAGCAGAA TCCAGATATT GTTTCAGAAA AAAAACCCAGC AACTGAAGTG GACCCACAC 2880
ATTTTGAATA GCGCTTCCCTA AAGAGGATCC GTGACTTGGG AGAGGGCCAC TTTGGGAAGG 2940
TTGAGCTCTG CAGGTATGAC CCGAAGGGG ACAATACAGG GGAGCAGGTG GCTGTTAAAT 3000
CTCTGAAGCC TGAGAGTGGA GGTAAACCACA TAGCTGATCT GAAAAAGGAA ATCGAGATCT 3060
TAAGGAACCT CTATCATGAG AACATTGTGA AGTACAAAGG AATCTGCACA GAAGACGGAG 3120
GAAATGGTAT TAAGCTCATC ATGGAATTTT TGCCTTCGGG AAGCCTTAAG GAATATCTTC 3180
CAAGAATAAA GAACAAATAA AACCTCAAAC AGCAGCTAAA ATATGCCGTT CAGATTGTGA 3240
AGGGGATGGA CTATTTGGGT TCTCGGCAAT ACGTTACCGG GGACTTGGCA GCAAGAAATG 3300
TCCTTGTGTA GAGTGAACAC CAAGTAAAAA TTGGAGACTT CGGTTTAACC AAAGCAATTG 3360
AAACCGATAA GGAGTATTAC ACCGTCAAGG ATGACCGGGA CAGCCCTGTG TTTTGGTATG 3420
CTCCAGAATG TTTAATGCAA TCTAAATTTT ATATTGCCCT TGACGCTCTG TCTTTTGGAG 3480
TCACTCTGCA TGAGCTGCTG ACTTACTGTG ATTCAAGATC TAGTCCCATG GCTTTGTTC 3540
TGAAAATGAT AGGCCCAACC CATGGCCAGA TGACAGTCAC AAGACTTGTG AATACGTTAA 3600
AAGAAGGAAA ACCGCTGCCG TGCCCACTTA ACTGTCCAGA TGAGGTTTAT CAACTTATGA 3660
GGAAATGCTG GGAATTCCTA CCATCCCAATC GGACAAGCTT TCAGAACCTT ATTGAAGGAT 3720
TTGAAGCACT TTTAAAAATA GAAGCATGAA TAACATTTAA ATTTCCACAGA TTATCAAGTC 3780
CTTCTCCTGC AACAAATGCC CAAGTCATTT TTTAAAAATT TCTAATGAAA GAAGTTTGTG 3840
TTCTGTCCAA AAAGTCACTG AACTCATACT TCAGTACATA TACATGTATA AGGCACACTG 3900
TAGTGCTTAA TAGTGTAAG GACTTCCTCT TTAATTTGG TACCAGTAAC TTAGTGACAC 3960
ATAATGACAA CCAAATATT TGAAAGCACT TAAGCACTCC TCCTTGTGGA AAGAAATATAC 4020
CACCATTTC TCTGGCTAGT TCACCATCAC AACTGCATTA CCAAAGGGG ATTTTGTGAA 4080
ACGAGGAGTT GACCAAAATA ATATCTGAAG ATGATTGCTT TTCCCTGCTG CCAGCTGATC 4140
TGAAATGTTT TGCTGGCACA TTAATCATAG ATAAAGAAAG ATTGATGGAC TTAGCCCTCA 4200
AATTTAGTA TCTATACAGT ACTAGACCAT GCATTCCTAA AATATTAGAT ACCAGGTAGT 4260
ATATATTGTT TCTGTACAAA AATGACTGTA TTCTCTCACC AGTAGGACTT AAACCTTGT 4320
TCTCCAGTGG CTTAGCTCCT GTTCCTTTGG GTGATCACTA GCACCCATTT TTGAGAAAGC 4380
TGGTCTTACA TGGGGGGATA GCTGTGGAAT AGATAATTG CTGCATGTTA ATTTCTAAGA 4440
ACTAAGCCTG TGCCAGTGCT TTCTTAAGCA GTATACCTTT AATCAGAACT CATTTCCAGA 4500
ACCTGGATGC TATTACACAT GCTTTAAGA AACGTCAATG TATATCCTTT TATAACTCTA 4560
CCACTTTGGG GCAAGCTATT CCAGCACTGG TTTTGAATGC TGTATGCAAC CAGTCTGAAT 4620
ACCACATACG CTGCACTGTT CTTAGAGGGT TTCCATACCT ACCACCGATC TACAAGGGTT 4680
GATCCCTGTT TTTACCATCA ATCATCACCC TGTGGTGCAA CACTTGAAAG ACCCGGCTAG 4740
AGGCACTATG GACTTCAGGA TCCACTAGAC AGTTTTCAGT TTGCTTGGAG GTAGCTGGGT 4800
AATCAAAAAA GTTTAGTCAT TGATTCAATG TGAACGATTA CGGTCTTTAT GACCAAGAGT 4860
CTGAAAAATC TTTTGTATG CTGTTTAGTA TTCGTTTGTG ATTGTTACTT TTCACCTGTT 4920
GAGCCCAATC TCAGGATTGG TTCAGTGCCA GCAATGAAGT TGCCATTAA ATTTGTTTCAT 4980
AGCCTACATC ACCAAGGTC CTGTGTCAA CCTGTGGCCA CTCTATATGC ACTTTGTTTA 5040
CTCTTTATAC AAATAAATAT ACTAAAGACT TT

```

Seq ID NO: B64 Protein sequence

Protein Accession #: A39577

45  
50  
55  
60  
65

```

1 11 21 31 41 51
MQYLNLIKEDC NAMAFCAKMR SSKKTEVNLE APEPGVEVIF YLSDREPLRL GSGEYTADEL 60
CIRAAQACRI SPLCHNLFAL YDENTKLWYA PNRTITVDDK MSLRLHYRMR FYFTNWHGTN 120
DNEQSVWRHS PKKQKNGYEK KKIIPDATPLL DASSLEYLFA QQGYDLVKCL APIRDPKTEQ 180
DGHDIENECL GMAVLAISHY AMMKMQLPE LPKDISYKRY IPETLNKSIR QRNLTRMRI 240
NNVFKDFLKE FNNKTI CDSS VSTHDLKVKY LATLETTLKH YGAEIFETSM LLISSENMEN 300
WFHSNDGGNV LYEVMTGN LGIQWRHKPN VVSVEKEKNK LKRKKLENKD KKDEEKNKIR 360
EEWNNFSFFP EITHIVIKES VVSINKQDNK KMEKLSSHE EALSFSVSLVD GYFRLTADAH 420
HYLCTDVAPP LIVHNQNGC HGPICTEYAI NKLRQEGSEE GMYVLRWST DFDNILMTVT 480
CFEKSEBQVQ AOKQFNFIQ EVQKGRYSLH GSDRSFSLG DLMSHLKKQI LRTDNISFML 540
KRCCQPKPRE ISNLLVATKK AQEWQPVYPM SLSFDRILK KDLVQGEHLG RGTRTHIYSG 600
TLMDDYKDEG TSEKKIKVI LKVLDPShRD ISLAFPEAAS MMRQVSHKHI VYLGVVCVRD 660
VENIMVEEFV EGGPLDLFMH RKSDVLTTPW KFKVAKQLAS ALSYLEDKDL VHGNVCTKNL 720
LLAREGIDSE CGPFIKLSDP GIPITVLSRQ ECIERIPWIA PECVEDSKNL SVAADKWSFG 780
TTLWEICYNG EIPLDKTLI EKERFYESRC RPTVPSCKEL ADLMTRCMNY DPNQRPFFRA 840
IMRDINKLEE QNPDIIVSRK NQPTVEVDPTH FEKRFLLKIR DLGEGHFGKV ELCRYDPEDN 900
TGEQVAVKSL KPESGGNHIA DLKKEIEILR NLYHENIVKY KGICTEDGGN GIKLIMEFLP 960
SGSLKEYLPK NKNKINKLQQ LKYAVQICKG MDYLGSRQYV HRDLAARNVL VESEHQVKIG 1020
DFGLTKAIET DKEYYTVKDD RDSFVFWYAP ECLMQSKFYI ASDVWSFGVT LHELLTYCDS 1080
DSSPMALFLK MIGPTHGQMT VTRLVNLTKE GKRLPCPPNC PDEVYQLMRK CWEFQPSNRT 1140
SFQNLIEGFE ALLK

```

Seq ID NO: B65 DNA sequence

Nucleic Acid Accession #: NM\_004867.1

Coding sequence: 140..931

75  
80

```

1 11 21 31 41 51
GATCCAGAC CTCGGCTTGC AGTAGTGTTA GACTGAAGAT AAAGTAAGTG CTGTTTGGGC 60
TAACAGGATC TCCTCTTGCA GTCTGCAGCC CAGGACGCTG ATTCCAGCAG CGCCTTACCG 120
CGCAGCCCGA AGATTACACTA TGGTGAAAAT CGCCTTCAAT ACCCCTACCG CCGTGCAAAA 180
GGAGGAGGCG CGGCAAGACG TGGAGGCCCT CCTGAGCCGC ACGGTCAGAA CTCAGATACT 240
GACCGGCAAG GAGCTCCGAG TTGCCACCCA GGA AAAAGAG GGCCTCTCTG GGAGATGTAT 300
GCTTACTCTC TTAGGCCTTT CATTCTCTT GGCAGGACTT ATTGTTGGTG GAGCCTGCAT 360
TTACAAGTAC TTCATGCCA AGAGCACCAT TTACCGTGGG GAGATGTGCT TTTTGTATTC 420
TGAGGATCCT GCAAAATCCC TTCGTGGAGG AGAGCCTAAC TTCCTGCCTG TGACTGAGGA 480
GGCTGACATT CGTGAGGATG ACAACATTGC AATCATTTGAT GTGCCTGTCC CCAGTTTCTC 540
TGATAGTGAC CCTGCAGCAA TTATTCATGA CTTTGAAAAG GGAATGACTG CTTACCTGGA 600
CTTGTGCTG GGAACATCT ATCTGATGCC CCTCAATACT TCTATTGTTA TGCCTCCAAA 660

```

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

AAATCTGGTA GAGCTCTTTG GCAACTGGC GAGTGGCAGA TATCTGCCTC AAACCTATGT 720
GGTTCGAGAA GACCTAGTTG CTGTGGAGGA AATTCGTGAT GTTAGTAACC TTGGCATCTT 780
TATTTACCAA CTTTGCATAA ACAGAAAGTC CTTCCGCCTT CGTCGCAGAG ACCTCTTGCT 840
GGGTTTCAAC AAACGTGCCA TTGATAAATG CTGGAAGATT AGACACTTCC CCAACGAATT 900
TATTTGTTGAG ACCAAGATCT GTCAAGAGTA AGAGGCAACA GATAGAGTGT CCTTGGTAAT 960
AGAAGTCAG AGATTTACAA TATGACTTTA ACATTAAGGT TTATGGGATA CTCAAGATAT 1020
TTACTCATGC ATTTACTCTA TTGCTTATGC CGTAAAAAAA AAAAAAAAAA AAAAAAAAAA 1080
AA
  
```

Seq ID NO: B66 Protein sequence  
 Protein Accession #: NP\_004858.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MVKIAFNTPT AVQKEEARQD VEALLSRTVR TQILTGKELR VATQEKEGSS GRCMLTLGL 60
SFILAGLIVG GACIYKYFMP KSTIYRGEMC FFDSEDPANS LRGGEPNPLP VTEADIRE 120
DNIAIIVDVFV PSFSDSDPAA ITHDFEKGMT AYLDLLLGNC YLMLPNTSIV MPPKNLVLF 180
GKLASGRYLP QTYVREDELV AVEEIRDVS N LGIFYQLCN NRKSFRLRRR DLLLGFNKRA 240
IDKCKIRHF PNEFIVETKI CQE
  
```

Seq ID NO: B67 DNA sequence  
 Nucleic Acid Accession #: XM\_083862.1  
 Coding sequence: 121..813

```

1      11      21      31      41      51
|      |      |      |      |      |
ACGCGGGGAGG TCTGAGCTGT GGGCTGAGGC AGCGCAGCCG CTGCGCCAGG GTGCGCGATG 60
CCTTGAACCT GGGAAACTAT GTGAAGCAAC ACTCTGGATT TTGAAAGACA TCTTTTCATC 120
ATGGGACAGC AAATTTCCGA TCAGACACAG TTGGTTATTA ACAAGTTACC AGAAAAAGTA 180
GCAAAACATG TTACGTGTGT TCGAGAGAGT GGCTCCTTAA CTTATGAAGA ATTTCTCGGG 240
AGAGTAGCTG AGCTTAATGA TGTAAACGGCT AAAGTGGCTT CTGGCCAGGA AAAACATCTT 300
CTCTTTGAGG TACAACCTGG GTCTGATTCC TCTGCTTTTT GGAAGTGGT TGTACGGGTG 360
GTCTGTACCA AGATTAAACA AAGCAGTGGC ATTGTGGAGG CATCACGGAT CATGAATTTA 420
TACCAGTTTA TTCAACTTTA TAAAGATATC ACAAGTCAAG CAGCAGGAGT ATCGGCACAG 480
AGCTCCACCT CTGAAGAACC TGATGAAAC TCATCCTCTG TAACATCTTG TCAGGCTAGT 540
CTTTGGATGG GAAGGGTGAA GCAGCTGACC GATGAGGAGG AGTGTGTGAT CTGTATGGAT 600
GGGCGGGCTG ACCTCATCCT GCCTTGTGCT CACAGCTTTT GTCAGAAGTG TATTGATAAA 660
TGGAGTGATC GACACAGGAA TTGCCCTATT TGTGCGCTAC AGATGACTGG AGCAAATGAA 720
TCTTGGGTGG TATCAGATGC ACCCACTGAA GATGATATGG CTAACATAT TCTTAACATG 780
GCTGATGAGG CAGGCCAGCC CCACAGGCCA TGACCTTGAA GTGAAAGTCT TCTGTTGCTA 840
TTGTGGGCTC AAATATTGTT TCATGGGGGA AGAATGTAGG GTTGTGGCAC TGGCACAGAG 900
ACAGGAAAAA CCATTTTCCC CACTCTTTTA TTTTGTCTAT TCTGATCATT TGTCCTCCCT 960
TTAAAAATAA ACTTCCCATG TCTTCCAAA AAAAAAAAAA AAAAA
  
```

Seq ID NO: B68 Protein sequence  
 Protein Accession #: XP\_083862.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MGQQISDQIQ LVINKLPKPV AKHVTILVRES GSLTYEEFLG RVAELNDVTA KVASGQEKHL 60
LFEVQPGSDS SAFKVVVVRV VCTKINKSSG IVEASRIMNL YQFIQLYKDI TSQAAGVLAQ 120
SSTSEEPDEN SSVVTSQAS LWMGRVKQLT DEBECCICMD GRADLILFCA HSFQCKCIDK 180
WSDRHRNCPI CRLQMTGANE SWVVSADAPTE DDMANYILNM ADEAGQPHRP
  
```

Seq ID NO: B69 DNA sequence  
 Nucleic Acid Accession #: NM\_002975.1  
 Coding sequence: 180..1151

```

1      11      21      31      41      51
|      |      |      |      |      |
CGACCAACGG ACCGGACAGA GACGAGGAGA GGAACAGGAA GAGAGAAGCT GGGAGAATCG 60
GGAACCTGGG GGCTAGTGAC CTGCACACAG GGCAGGGGCA CTCGGCAGTT CCCAGAGGCC 120
ACCCCTCCCA CCCAGACAT CCAGACATCT GGAACCTTGG GTGCCAAGAG TCCAGCTTAA 180
TGCAGGCAGC CTGGCTTTTG GGGGCTTTGG TGGTCCCCCA GCTCTTGGGC TTTGGCCATG 240
GGGCTCGGGG AGCAGAGAGG GAGTGGGAGG GAGGCTGGGG AGGTGCCAG GAGGAGGAGC 300
GGGAGAGGGA GGCCCTGATG CTGAAGCATC TGCAGGAAGC CCTAGGACTG CCTGCTGGGA 360
GGGGGGATGA GAATCCTGCC GGAACCTGTG AGGGAAAAAG GGAAGTGGAG ATGAGGAGG 420
ACCAGGGGGA GGAAGAGGAG GAGGAAGCAA CGCCAACCCC ATCTCCGGC CCCAGCCCCT 480
CTCCCAACCC TGAGGACATC GTCACTTACA TCCTGGGCGG CCTGGCCGGC CTGGACGCAG 540
GCCTGCACCA GCTGCACGTC CGTCTGCACG CGTTGGACAC CCGCTGGGTC GAGCTGACCC 600
AGGGGCTGCG GCAGCTGCGG AACGCGGCAG GCGACACCCG CGATGCCGTG CAAGCCCTGC 660
AGGAGGCGCA GGGTCGCGCC GAGCGCGAGC ACGGCGGCTT GGAGGGCTGC CTGAAGGGGC 720
TGCGCCTGGG CCACAAGTGC TTCCTGCTCT CGCGCGACTT CGAAGCTCAG GCGGCGGCGC 780
AGGCGCGGTG CACGCGCGCG GGCGGGAGCC TGGCGCAGCC GGCAGACCCG CAGCAGATGG 840
AGGCGCTCAC TCGGTACCTG CGCGCGGCGC TCGCTCCCTA CAACTGGCCC GTGTGGCTGG 900
GCGTGACAGG TCGGCGCGCC GAGGGCCTCT ACCTCTTCCA AAACGGCCAG CGCGTGTCTT 960
TCTTCGCTG GCATCGCTCA CCCC GCCCGG AGCTCGGCGC CCAGCCCAGC GCCTCGCCGC 1020
ATCCGCTCAG CCCGAGCCAG CCCAAGCGTG GCACGCTCGA GAACTGCGTG GCGCAGGCC 1080
CTGACGACGG CTCTGGTGG GACCAAGACT GCCAGCGGCG TCTCTACTAC GTCTGCGAGT 1140
TCCCCCTCTA GCGGGGCCGG TACCCGCGCT CTTGCCCCAT CCCACACCC GGCCTTTCCC 1200
TGCGCCGTGC CCACCTCTCT CCGGAATCGC CTTTCCCTTC CTGGCCACGA ATGGCAGCGT 1260
CCTCCCCGAC CCCAGTCTG GCGGCTTCTG GGAGGGCTCT TGCGGTGCCG GCACTCCTCC 1320
TTGTTAGTGT CTTCTCTTGA AGGGGCGGGC ACCAGGCTAG GTCCGGTGCC AATAAATCCT 1380
TGTGGAATCT GAAAAAAA AAAAAA
  
```

Seq ID NO: B70 Protein sequence  
Protein Accession #: NP\_002966.1

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
MQAAWLLGAL VVPQLLGFCH GARGAEREWE GVGWGAQESEE REREALMLKH LQEALGLPAG    60
RGDENPAGTV EGKEDWEMEE DQEEEEEEEA TPTPSSGGPSP SPTPEDIVTY ILGRLAGLDA    120
10     LRLGHLHVRLL ALDTRVVELT QGLRQLRNAA GDTRDAVQAL QEAQGRAERE HGRLEGCLKG    180
      LRLGHKCFLL SRDFEAQAAA QARCTARGGS LAQPADRQQM EALTRYLRAA LAPYNWPEVWL    240
      GVHRRRAEGL YLPENGQRVS FFAWHRSRPR ELGAQPSASP HPLSPDQPNG GTLENCVAQA    300
      SDDGSWWDHD CQRRLLYVCE FPF

```

Seq ID NO: B71 DNA sequence  
Nucleic Acid Accession #: BC000839.1

```

15     1      11      21      31      41      51
      |      |      |      |      |      |
CTGGCCAGGG CGACTGGCGG ATAAGGTCTT GTGCGTGGCC TCGAGGCTTA AAAGTAGCAG    60
20     TGGGGCTTTG TGAAGGACAA AATGGCGATG GCGGGCCGTG TAGGTCCCCC TTCCTATGAT    120
      GAGGACCTTT TCACAGACCT GTACTGAGCT CCGTGAGGAT AAGTAACTCT GAGGAGATGG    180
      GCCCTGCAAG CCTCCTTCTT AGCCGTCTGT TCAGAAAATA GCGTTTTCGA AATGCCCTGA    240
      GTTGACCTAA TGTCTTATTG GGCTCCTGTC TGCAGGATT ACGCCACGT TGAACCGGAA    300
      GAGAGCTCTG TTGTTGCAAT GTTCAGCCCA CAAGAGCTTA CTGGTGAAGG AATGGGACAA    360
25     GACCCATCTT TATGCAAAAG CAGCGTTACA GTAATGTTC AGCATCTCAT AATCTATCCT    420
      GGGGAATTCA GCTGCCTCCC AGGGTGAATA CAGGTATTCC TGATGACAGT CTGCCTCTAT    480
      CTTACAGAGC AGCTTGTGTC TATATACCAT TGAAAAGCCT TCAGAGCTGA GAGGTACTAC    540
      TAACCAATAA CCTGCTTGGC TCAAAGGGCC AGCACCTTCT CTCTAAAGCC CAAGAGGAGT    600
      TTGAGGAAAA CTAGTGTGCT GTGTTCACTC CAGGCTGAAG TTACAGGTCT GAGCAAAATA    660
30     GGTGTATAAA AATGGAATC TGTCTTGGAG GACATCAGAA GGTGAATTTT CCAAGTTCTT    720
      GGACAACCTA GCTGTTGAAA AGCTTCTTGG GTTTGGGGGG TATTTACAGT GTACCTTAAA    780
      GTGTTAGCAG ATACAGATTA AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGGTTTGCT    840
      GTGTATCACA TTCTCTGTAAT TTATCACCCC CTTCCTGCAA CATTATTAT CTGGAATCTA    900
      CCTGCCCTTT TTTCTTTTAG ATACAAGGGC TTGGTTTTGT TACCCAGGCT GGTTCACAGG    960
35     CCATAGCTTT AAGAGATCCT CTCACCACAG ATTTCCAAAG TGCTGGGATT GCAGGTGTGA    1020
      TTCATGGCAC CCAGACTTTG CTGCTTTTCT TACATGATCC AGGCCACAGAA CCCAAACTCA    1080
      GGCACGTGAT AGATGACCAC TTTCGTAAAC TACTGACCTA AGTTGTTGCC AATTGTTGAT    1140
      TGAACCTCCC ATAACCTCCAC TTCGTGTCTG TTCTCTGTA TACAGCCACC TTCTGTTCCT    1200
      GTCATGAGCC TTTAGTCTCT CATTGTCATA TTGCAAATAC TATGTTCCAT GTAGGTAGCT    1260
40     CATTACAGGC CTTGCTCTTC ACTTCAAAAA AGGTTCCCTT GAGGACTGGC TGTCATTTTG    1320
      GTTGTCTGTG TTGGTTGTTG ATGAAAATAA TAAATGATT GATTACATAA AAAAAAAAAA    1380
      AAAAAAA

```

Seq ID NO: B72 DNA sequence  
Nucleic Acid Accession #: CAT cluster

```

45     1      11      21      31      41      51
      |      |      |      |      |      |
TGCTAGTAGG GCCTGGGTTA ATCGGCCGAG GGTGGCTTCG TGGTCTTTAT AGCTGTTACT    60
50     CTTTGTACTT GTCTTTTCT TTTATTTCT TTTGAGCGAT TGTGCGAACA TAGCATAGCA    120
      CGCACTATGG CAGCAGGCTC GTGCTGCTCG GCCAGGGCGA CTGGCGGATA AGGTCTTTGT    180
      CGTGGCCTCG AGGCTTAAAA GTAGCAGTGG GGCTTTGTGA AGGACAAAAA GCGGATGGCG    240
      GGCCGTGTAG GTCCCCCTTC CTATGATGAG GACCTTTTCA CAGACCTGTA CTGAGCTCCG    300
      TGAGGATAAA TAACTCTGAG GAGATGGGCC CTGCAAGCCT CTTGCTTAGC CGTCTGTTC    360
55     GAAAATAGCG TTTTCGAAAT GCCCTGAGTT GACCTAATGT CTTATTGGGC TCCTGTCTGC    420
      AGGATTTACG CGCACGTGGG AACCGAAGAG AGCTCTGTTG TTGCAATGTT CAGCCACAAA    480
      GAGCTTACTG GTGAAGGAAT GGGACAAGAC CCATCTTTAT GCAAGCCAG CGTTACAGTA    540
      ATGTTCCAGC ATCTCATAAAT CTATCCTGGG GAATTCAGT GCCTCCGAGG GTGAATACAG    600
      GTATCTCTGA TGACAGTCTG CCTCTATCTT ACAGAGCAGC TTGTTGCTAT ATACCATTGA    660
      AAAGCCTTCA GAGCTGAGAG GTACTACTAA CCAATAACCT GCTTGGCTCA AAGGGCCAGC    720
60     ACCTTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAAC TA GGTGCTGTG TTAACCTCCG    780
      GCTGAAAGTA CAGGTCTGAG CAAATAAGGT GTATAAAAAA TGGAACTGTT CTTGGAGGAC    840
      ATCAGAAGGT GAATTTTCCA AGTTCTTGGG CAACCTAGCT GTTGAAAAGC TTTCTGGGTT    900
      TGGGGGGTAT TTCAGATGTA CCTTAAAGTG TTAGCAGACA CAGATTAAGA CACTGGGAGC    960
65     CAATGAAACA GCAGTTGAGG GTTTGCTGTG TATCACATTT CTGTATTTTA TCACCCCTTT    1020
      CCTGCAACAT TATTATCTG GAATCTACCT GCCCTTTTGT TTTTATGATA CAAGGGCTTG    1080
      GTTTTGTGTT CCAGGCTGGT TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGATT    1140
      TCCAAAGTGC TGGGATTGCA GGTGTGATTC ATGGCACCCA GACTTTGCTG CCTTCTTAC    1200
      ATGATCCAGG CCCAGAACCC AAACCTCAGC ACTGTATAGA TGACCACTTT CGTAAACTAC    1260
70     TGACCTAGCT TGTTGCCAAT TGTTGATTGA ACTTCCCAT ACTCCACTTC GTGTCTGTTT    1320
      CTCTGTATAC AGCCACCTTC TGTTCCCGTC ATGAGCCTTT AGGTCTCCAT TTGCATATTG    1380
      CAAATACTAT GTTCCATGTA GGTAGCTCAT TCAGGGCCTT GCTCTTCACT TCAAAAAAGG    1440
      TTCCCTTGAG GACTGGCTGT CAATTGTGTG TGCTGTGTTG GTTGTGTATG AAAATAATAA    1500
      AATGATTGAT TACATAAAAA AAAAAAAAAA AAAAAACAAA CACAAAAAAC    1560
75     CGCCGCGCTT TTTCCCGGGC GCACAAAGTT ATAAAACGCC GTCCATC

```

Seq ID NO: B73 sequence  
Nucleic Acid Accession #: NM\_000222.1  
Coding sequence: 22..2952

```

80     1      11      21      31      41      51
      |      |      |      |      |      |
GATCCCATCG CAGCTACCGC GATGAGAGGC GCTCGCGGCG CCTGGGATTT TCTCTGCGTT    60
      CTGCTCTTAC TGCTTACCGT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA    120

```

	CCGTCTCCAC	CATCCATCCA	TCCAGGAAAA	TCAGACTTAA	TAGTCCCGGT	GGGCGACGAG	180
	ATTAGGCTGT	TATGCACTGA	TCCGGGCTTT	GTCAAATGGA	CTTTTGAGAT	CCTGGATGAA	240
	ACGAATGAGA	ATAAGCAGAA	TGAATGGATC	ACGGAAGG	CAGAAGCCAC	CAACACCGGC	300
5	AAATACACGT	GCACCAACAA	ACACGGCTTA	AGCAATTCCA	TTTATGTGTT	TGTTAGAGAT	360
	CCTGCCAAGC	TTTTTCTTGT	TGACCGCTCC	TTGTATGGGA	AAGAAGACAA	CGACACGCTG	420
	GTCCGCTGTC	CTCTCAGAGA	CCCAAGAGTG	ACCAATTATT	CCCTCAAGGG	GTGCCAGGGG	480
	AAGCCTCTTC	CCAAGGACTT	GAGGTTTATT	CCTGACCCCA	AGGCGGGCAT	CATGATCAAA	540
	AGTGTGAAAC	GCGCCTACCA	TCGGCTCTGT	CTGCATTGTT	CTGTGGACCA	GGAGGGCAAG	600
10	TCAGTGTCTG	CGGAAAAATT	CATCCTGAAA	GTGAGGCCAG	CCTTCAAGGC	TGTGCCTGTT	660
	GTGTCTGTGT	CCAAAGCAAG	CTATCTTCTT	AGGGAAGGGG	AAGAATTAC	AGTGACGTGC	720
	ACAATAAAAG	ATGTGTCTAG	TTCTGTGTAC	TCAACGTGGA	AAAGAGAAAA	CAGTCAGACT	780
	AAACTACAGG	AGAAATATAA	TAGCTGGCAT	CACGGTGACT	TCAATTATGA	ACGTCAGGCA	840
	ACGTTGACTA	TCAGTTTACG	GAGAGTTAAT	GATTCTGGAG	TGTTTCATGTG	TTATGCCAAT	900
15	AATACTTTTG	GATCAGCAAA	TGTCAACAAC	ACCTTGGGAG	TAGTAGATAA	AGGATTCAAT	960
	AATATCTTCC	CCATGATAAA	CACTACAGTA	TTTGTAAACG	ATGGAGAAAA	TGTAGATTG	1020
	ATTGTTGAAT	ATGAAGCATT	CCCCAAACCT	GAACACCAGC	AGTGGATCTA	TATGAACAGA	1080
	ACCTTCACTG	ATAAATGGGA	AGATTATCCC	AAGTCTGAGA	ATGAAAGTAA	TATCAGATAC	1140
	GTAAGTGAA	TTTCTCTAAC	GAGATTAAAA	GGCACCAGAG	GAGGCACTTA	CACATTCCCTA	1200
20	GTGTCCAATT	CTGACGTCAA	TGCTGCCATA	GCATTTAATG	TTTATGTGAA	TACAAAACCA	1260
	GAAATCTCTG	CTTACGACAG	GCTCGTGAAT	GGCATGCTCC	AATGTGTGGC	AGCAGGATTC	1320
	CCAGAGCCCA	CAATAGATTG	GTATTTTTGT	CCAGGAACCTG	AGCAGAGATG	CTCTGCTTCT	1380
	GTACTGCCAG	TGGATGTGCA	GACACTAAAC	TCATCTGGGC	CACCGTTTGG	AAAGCTAGTG	1440
	GTTCAGAGTT	CTATAGATTG	TATGTCATTG	AAGCACAATG	GCACGGTTGA	ATGTAAGGCT	1500
25	TACAACGATG	TGGGCAAGAC	TTCTGCCTAT	TTTAACTTTG	CATTTAAAGG	TAACAACAAA	1560
	GAGCAAAATC	ATCCCCACAC	CCTGTTCACT	CCTTTGCTGA	TGTTTTCGT	AATCGTAGCT	1620
	GGCATGATGT	GCAATTATTG	GATGATCTG	ACCTACAAAT	ATTACAGAAA	ACCCATGTAT	1680
	GAAGTACAGT	GGAAAGTTGT	TGAGGAGATA	AATGGAAACA	ATTATGTTTA	CATAGACCCA	1740
	ACACAACCTC	CTTATGATCA	CAAAATGGAG	TTTCCCAGAA	ACAGGCTGAG	TTTTGGGAAA	1800
30	ACCTTGGGTG	CTGGAGCTTT	CGGGAAGGTT	GTGAGGCAAA	CTGCTTATGG	CTTAATTAAG	1860
	TCAGATGCGG	CCATGACTGT	CGCTGTAAAG	ATGCTCAAGC	CGAGTGCCCA	TTTGACAGAA	1920
	CGGGAAGCCC	TCATGTCTGA	ACTCAAAGTC	CTGAGTTACC	TGTTTAATCA	CATGAATATT	1980
	GTGAATCTAC	TTGGAGCCTG	CACCATTGGA	GGGCCCACCC	TGGTCATTAC	AGAATATTGT	2040
	TGCTATGGTG	ATCTTTTGAA	TTTTTTTGAA	AGAAAACGTG	ATTCATTAT	TGTTTCAAAG	2100
35	CAGGAAGATC	ATGCAGAAAG	TGCACCTTAT	AAGAATCTTC	TGCATTCAAA	GGAGTCTTCC	2160
	TGCAGCGATA	GTACTAATGA	GTACATGGAC	ATGAAACCTG	GAGTTTCTTA	TGTTGTCCCA	2220
	ACCAAGGCCG	ACAAAAGGAG	ATCTGTGAGA	ATAGGCTCAT	ACATAGAAAG	AGATGTGACT	2280
	CCGCCATCA	TGGAGGATGA	CGAGTTGGCC	CTAGACTTAG	AAGACTTGCT	GAGCTTTTCT	2340
	TACCAGGTGG	CAAAAGGGCAT	GGCTTTCTCT	GCCTCCAAGA	ATTGTATTCA	CAGAGACTTG	2400
40	GCAGCCAGAA	ATATCTCTCT	TACTCATGGT	CGGATCACAA	AGATTGTGTA	TTTTGGTCTA	2460
	GCCAGAGACA	TCAAGAATGA	TTCTAATTAT	GTGGTTAAAG	GAAACGCTCG	ACTACTCTGT	2520
	AAGTGGATGG	CCCTGAAAG	CATTTTCAAC	TGTGTATACA	CGTTTGAAG	TGACGTCTGG	2580
	TCCTATGGGA	TTTTTCTTTG	GGAGCTGTTT	TCCTTAGGAA	GCAGCCCCCTA	TCCTGGAATG	2640
	CCGGTCGATT	CTAAGTTCTA	CAAGATGATC	AAGGAAGGCT	TCCGGATGCT	CAGCCCTGAA	2700
45	CACGCACCTG	CTGAAATGTA	TGACATAATG	AAGACTTGCT	GGGATGCAGA	TCCCCTAAAA	2760
	AGACCAACAT	TCAAGCAAA	TGTTTCAAGT	ATTGAGAAAG	AGATTTCAGA	GAGCACCAAT	2820
	CATATTACTT	CCAACCTAGC	AAACTGCAGC	CCCAACCGAC	AGAAGCCCGT	GGTAGACCAT	2880
	TCGTGTGGGA	TCAATCTCTG	CGGCAGCACC	GCTTCTCTCT	CCGACCTCTT	GCTTGTGCAC	2940
	GACGATGTCT	GAGCAGAATC	AGTGTTTGGG	TCACCCCTCC	AGGAATGATC	TCTTCTTTTG	3000
50	GCTTCCATGA	TGGTTATTTT	CTTTTCTTTC	AACTTGCATC	CAACTCCAGG	ATAGTGGGCA	3060
	CCCCACTGCA	ATCTGTCTTT	TCTGAGCACA	CTTAGTGGC	CGATGATTTT	TGTCATCAGC	3120
	CACCATCCTA	TTGCAAAAGT	TCCAACCTGA	TATATTCCCA	ATAGCAACGT	AGCTTCTACC	3180
	ATGAACAGAA	AACATTCTGA	TTTGGAAAAA	GAGAGGGAGG	TATGGACTGG	GGGCCAGAGT	3240
	CCTTTCCAAAG	GCTTCTCCAA	TTCTGCCCAA	AAATATGGTT	GATAGTTTAC	CTGAATAAAT	3300
55	GGTAGTAATC	ACAGTTGGCC	TTTCAAGACCA	TCCATAGTAG	TATGATGATA	CAAGATTAGA	3360
	AGCTGAAAAAC	CTAAGTCTCT	TATGTGAAAA	ACAGAACATC	ATTAGAACAA	AGGACAGAGT	3420
	ATGAACACCT	GGGCTTAAAG	AATCTAGTAT	TTTATGCTGG	GAATGAGACA	TAGGCCATGA	3480
	AAAAAATGAT	CCCCAAGTGT	GAACAAAAGA	TGCTTCTCTG	TGGACCACTG	CATGAGCTTT	3540
	TATACTACCG	ACCTGGTTTT	TAAATAGAGT	TTGCTATTAG	AGCATTGAAT	TGGAGAGAAG	3600
60	GCCTCCCTAG	CCAGCACTTG	TATATACGCA	TCTATAAATT	GTCCTGTGTT	ATACATTGTA	3660
	GGGGAAAAAC	CCATAAGTTA	TCGTTTCTGT	ATACAACCTT	GGCATTATGT	CCACTGTGTA	3720
	TAGAAGTAGA	TTAAGAGCCA	TATAAGTTTG	AAGGAAACAG	TTAATACCAT	TTTTTAAGGA	3780
	AACAATATAA	CCACAAAGCA	CAGTTTGAAC	AAAATCTCCT	CTTTTAGCTG	ATGAACCTTAT	3840
	TCTGTAGATT	CTGTGGAACA	AGCCTATCAG	CTTCAGAAATG	GCATTGTACT	CAATGGATTT	3900
65	GATGCTGTTT	GACAAAGTTA	CTGATTCAC	GCATGGCTCC	CACAGGAGTG	GGAAAAACAT	3960
	GCCATCTTAG	TTTGGATTCT	TATGTAGCAG	GAAATAAAGT	ATAGGTTTAG	CCTCCTTCGC	4020
	AGGCATGTCC	TGGACACCGG	GCCAGTATCT	ATATATGTGT	ATGTACGTTT	GTATGTGTGT	4080
	AGACAAATAT	TTGGAGGGGT	ATTTTGGCCC	TGAGTCCAAG	AGGGTCTCTT	AGTACCTGAA	4140
	AAGTAACCTG	GCTTTCATTA	TTAGTACTGC	TCTTGTCTCT	TTTACATAG	CTGTCTAGAG	4200
70	TAGCTTACCA	GAAGCTTCCA	TAGTGGTGCA	GAGGAAGTGG	AAGGCATCAG	TCCCTATGTA	4260
	TTTGCAGTTC	ACCTGCACCT	AAGGCACCTT	GTTATTTAGA	CTCATCTTAC	TGTACCTGTT	4320
	CCTTAGACCT	TCCATAATGC	TACTGTCTCA	CTGAAACATT	TAAATTTTAC	CCTTTAGACT	4380
	GTAGCCTGGA	TATTATCTCT	GTAGTTTACC	TCTTTAAAAA	CAAAACAAAA	CAAAACAAAA	4440
	AACTCCCTTT	CCTCACTGCC	CAATATAAAA	GGCAAATGTG	TACATGGCAG	AGTTTGTGTG	4500
75	TGTCTTGAA	AGATTACAGT	ATGTTGCCTT	TATGGTTTCC	CCCTTCTACA	TTTCTTAGAC	4560
	TACATTTAGA	GAACGTGTGC	CGTTATCTGG	AAGTAACCAT	TTGCACTGGA	GTTCTATGCT	4620
	CTCGCACCTT	TCCAAGTTTA	ACAGATTTTG	GGGTTGTGTT	GTCACCCAG	AGATTGTTGT	4680
	TTGCCATACT	TGTCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4740
	AAGTGGTTGT	TAGTTATAGA	TGTCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTG	4800
80	TGCGCATACT	TGTCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4860
	AAGTGGTTGT	TAGTTATAGA	TGTCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTG	4920
	AATGCTCTTT	GAATATTCCC	AAGCCCATGA	GTCCTTGAAA	ATATTTTATA	TATATACAGT	4980
	AACTTTATGT	GTAAATACAT	AAGCGGCGTA	AGTTTAAAGG	ATGTTGGTGT	TCCACGTGTT	5040
	TTATTCCTGT	ATGTTGTCCA	ATTGTTGACA	GTTCTGAAGA	ATTC		



Seq ID NO: B74 protein sequence  
Protein Accession #: NP\_000213.1

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
MRGARGAWDF LCVLLLLLRV QTGSSQPSVS PGEPSPPSIH PGKSDLIVRV GDEIRLLCTD 60
PGFVKWTFEI LDETENKQON EWITEKAEAT NTGKYTCTNK HGLSNSIYVF VRDPAKFLV 120
DRSLYGKEDN DTLVRCPLTD PEVTNYSLKG CQKPLPKDL RFIPDPKAGI MIKSVKRAYH 180
RLCLHCSVDQ EGKSVLSEKF ILKVRPAFKA VPVSVSKAS YLLREGEEFT VTCTIKDVSS 240
10     SVYSTWKREN SQTLQEKYN SWHHGDFNYE RQATLTISSA RVNDSGVFMC YANNTFGSAN 300
VTTTLEVVVK GFNIFPFIN TTVFVNDGEN VDLIVEYEF PKPEHQWIY MNRTFTDKWE 360
DYPKSENESEN IRYVSELHLT RLKGTGEGTY TFLVNSNDVN AAIAFNVYVN TKPEILTYDR 420
LVNGLMLQVVA AGFPEPTIDW YFCPGTEQRC SASVLPVDVQ TLNSSGPPFG KLVVQSSIDS 480
15     SAFKHNGTVE CKAYNDVGKT SAYFNFAFKG NNKEQIHPHT LFTPLLIGFV IVAGMMCIIV 540
MILTYKYLQK PMYEVQWKVV BEINGNNYVY IDPTQLPYDH KWEFFRNRLS FGKTLGAGAF 600
CKVVEATAYG LIKSDAAMTV AVKMLKPSAH LTEREALMSE LKVLVSYLGNH MNIVNLLGAC 660
TIGGPTLVIT EYCCYGDLLN FLRRKRDSFI CSKQEDHAEA ALYKNLLHKS ESSCSDSSTNE 720
20     YMDMKPGVSY VVPTKADKRR SVRIGSYIER DVTPAIMEDD ELALDLEDLL SFSYQVAKGM 780
AFLASKNCIH RDLAARNILL THGRITKICD FGLARDIKND SNYVVKGNAR LPVKWMAPEP 840
IFNCVYTFES DVWSYGIPLW ELFSLGSSPY PGMPVDSKFY KMIKEGFRML SPEHAPAEMY 900
DIMKTCWDAD PLKRPTFKQI VQLIEKQISE STNHIYSNLA NCSPNRQKPV VDHSVRINSV 960
GSTASSQPL LVHDDV

```

Seq ID NO: B75 DNA sequence  
Nucleic Acid Accession #: NM\_004456  
Coding sequence: 58..2298

```

30     1      11      21      31      41      51
      |      |      |      |      |      |
GAATTCGGGG CGACGCGCGG GAACAACGCG AGTCGCGCGG CGGGACGAAG AATAATCATG 60
GGCCAGACTG GGAAGAAATC TGAGAAGGGA CCAGTTGTGT GGCGGAAGCG TGTAAAATCA 120
GAGTACATGC GACTGAGACA GCTCAAGAGG TTCAGACGAG CTGATGAAGT AAAGAGTATG 180
TTTAGTTCCTA ATCGTCAGAA AATTTTGGAA AGAACGGAAA TCTTAAACCA AGAATGGAAA 240
35     CAGCGAAGGA TACAGCTGTG GCACATCCTG ACTTCTGTGA GCTCATGTGC CGGGACTAGG 300
GAGTGTTCGG TGACCACTGA CTTGGATTTT CCAACACAAG TCATCCCATI AAAGACTCTG 360
AATGCAGTTG CTTTCAGTACC CATAATGTAT TCTTGGTCTC CCCTACAGCA GAATTTTATG 420
GTGGAAGATG AAATCTTTT ACATAACATT CCTTATATGG GAGATGAAGT TTAGATCAG 480
GATGGTACTT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAAGTACA CGGGGATAGA 540
40     GAATGTGGGT TTATAAATGA TGAATTTTTT GTGGAGTTGG TGAATGCCCT TGGTCAATAT 600
AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAAGCAGAAA 660
GATCTGGAGG ATCACCAGGA TGATAAGAAA AGCCGCCCAC CTCGGAATTT TCCTTCTGAT 720
AAAATTTTGG AGGCCATTTT CTCAATGTTT CCAGATAAAG GCACAGCAGA AGAAGTAAAG 780
GAAAAATATA AAGAACTCAC CGAACAGCAG CTCCAGGCG CACTTCTCTC TGAATGTACC 840
45     CCCAACATAG ATGGACCAAA TGCTAAATCT GTTCAGAGAG AGCAAAGCTT AACTCTCTTT 900
CATACGCTTT TCTGTAGCGG ATGTTTTTAA TATGACTGCT TCCTACATCC TTTTCATGCA 960
ACACCCAAACA CTTATAAGCG GAAGAACACA GAAACAGCTC TAGACAACAA ACCTTGTGGA 1020
CCACAGTGTT ACCAGCATTT GGAGGGAGCA AAGGAGTTTG CTGTCTCTCT CACCGCTGAG 1080
CGGATAAAGA CCCCAACAAA ACGTCCAGGA GGCAGCAGAA GAGGACGGCT TCCCAATAAC 1140
50     AGTAGCAGGC CCAGCACCCC CACCATTAAT GTGCTGGAAT CAAAGGATAC AGACAGTGAT 1200
AGGGAAGCAG GGACTGAAAC GGGGGGAGAG AACAATGATA AAGAAGAAGA AGAGAAGAAA 1260
GATGAAACTT CGAGCTCCTC TGAAGCAAAT TCTCGGTGTC AAACACCAAT AAAGATGAAG 1320
CCAAATATTG AACCTCCTGA GAATGTGGAG TGGAGTGGTG CTGAAGCCTC AATGTTTAGA 1380
GTCCTCATTT GCATCTACTA TGACAATTTT TGTGCCATTG CTAGGTTAAT TGGGACCAAA 1440
55     ACATGTAGAC AGGTGTATGA GTTTAGAGTC AAAGAATCTA GCATCATAGC TCCAGCTCCC 1500
GCTGAGGATG TGGTACTTCC TCCAAGGAAA AAGAAGAGGA AACACCGGTT GTGGGCTGCA 1560
CACTGCAGAA AGATACAGCT GAAAAAGGAC GGCTCCTCTA ACCATGTTTA CAATATCAA 1620
CCCTGTGATC ATCCACGGCA GCCTTGTGAC AGTTCGTGCC CTTGTGTGAT AGCACAATAA 1680
60     TTTTGTGAAA AGTTTTGTCA ATGTAGTTCA GAGTGTCAAA ACCGCTTTCC GGGATGCCGC 1740
TGCAAAGCAC AGTGCAACAC CAAGCAGTGC CCGTGCTACC TGGCTGTCCG AGAGTGTGAC 1800
CCTGACCTCT GTCCTACTTG TGGAGCCGCT GACCATGGG ACAGTAAAAA TGTGTCTGTC 1860
AAGAACTGCA GTATTACAGG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGACGTG 1920
GCAGGCTGGG GTATTTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC 1980
70     TGTGGAGAGA TTATTCTCTA AGATGAAGCT GACAGAAGAG GGAAGTGTGA TGATAAATAC 2040
ATGTGCAGCT TTCTGTTCAA CTTGAACAAAT GATTTTGTGG TGGATGCAAC CCGCAAGGGT 2100
AACAAAATTC GTTTTGCAAA TCATTCCGTA AATCCAAACT GCTATGCAAA AGTTATGATG 2160
GTTAACGGTG ATCAGAGGAT AGGTATTTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
CTGTTTGTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCCG CATCGAAAGA 2280
75     GAAATGGAAA TCCCTTGACA TCTGCTACCT CTTCCCTCTC CTCTGAAACA GCTGCCTTAG 2340
CTTCAGGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAATTCTG 2400
AATTTGCAAA GTACTGTAG AATAATTTAT AGTAATGAGT TTAATAATCA ACTTTTATT 2460
GCCTTCTCAC CAGCTGCAAA GTGTTTGTGA CCAGTGAATT TTTGCAATAA TGCAGTATGG 2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAACCTTGA AAAAAAATAA AAAAAA

```

Seq ID NO: B76 Protein sequence  
Protein Accession #: NP\_004447

```

80     1      11      21      31      41      51
      |      |      |      |      |      |
MGQTGKSKSE GPVCRWRKVK SEYMRLRLQL RFRRADDEVKS MFSSNRQKIL ERTEILNQEW 60
KQRRIQPVHI LTVSVSLRGT RECSVTSDDL FPTQVIPLKT LNAVASVPIM YSWSPLQONF 120
MVEDETVLHN IPYMGDEVLD QDGTFFIELI KNYDGKVVHD RECGFINDEI FVELVNALGO 180
YNDDDDDDDG DDPEEREKQK KDLEDHRDDK ESRPPKFPFS DKILEAISSM FPDKGTAERL 240
KEKYKELTEQ QLEFALPPEC TPNIDGPNAK SVQREQSLHS FHTLFCRRCF KYDCFLHPFH 300
ATPNTYKRKN TETALDNKPC GPQCYQHLEG AKEFAAALTA ERIKTPPKRP GGRRRGRPLN 360

```

NSSRPSTPTI NVLESKDIDS DREAGTETGG ENNDKEEEK KDETSSSSEA NSRCQTPIM 420  
 KPNIEPPENV EWSGAEASMF RVLIGTYIDN FCAIARLIGT KTCRQVYEFV VKESSIIAPA 480  
 PAEDVDTPPR KKKRKHRLWA AHCRIQLKK DGSSNHVYNY QPCDHPRQPC DSSCPVIAQ 540  
 NFCEKFCQCS SECQNRFFPG RCKAQCNQTKQ CPCYLAVREC DPDLCLTCGA ADHWDSKNVS 600  
 CKNCISIQRGS KKHLLAPSD VAGWGIFIKD PVQKNEFISE YCCEIISQDE ADRRRGVYDK 660  
 YMCSEFLNLFN NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720  
 ELFVDYRYSQ ADALKYVGIE REMEIP

Seq ID NO: B77 DNA sequence  
 Nucleic Acid Accession #: NM\_007015  
 Coding sequence: 1..1005

1 11 21 31 41 51  
 15 ATGACAGAGA ACTCCGACAA AGTTCCCAT T GCCCTGGTGG GACCTGATGA CGTGGGAATTC 60  
 TGCAGCCCC CGGCGTAGCG TACGCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC 120  
 AAGGTGGGAG CCGTGGTCCCT CATTTGCGGA GCTGTGCTGC TGCTCTTTGG GGCATCGGG 180  
 GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240  
 ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC 300  
 20 TTTAAAAATGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCCTA GAATGGCATC 360  
 ACAGGAATTC GTTTTGCTGG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420  
 ATTCCTGAGG TGGGCGCCGT GACCAACAG AGCATCTCCT CCAAACTGGA AGGCAAGATC 480  
 ATGCCAGTCA AATATGAAGA AAATCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540  
 25 GACAACAGCT TCTTGAGTTC TAAGGTGTTA GAATCTGCG GTGACCTTCC TATTTCTGG 600  
 CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAAGAA GAGAAGTGGT AAGAAAAATT 660  
 GTTCCAACCTA CCACAAAAG ACCACACAGT GGACACGGA GCAACCCAGG CGCTGGAAGA 720  
 CTGAATAATG AAACAGACC CAGTGTCAA GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780  
 CCTTATCATC AGCAGGAAGG GGAAGCATG ACATTCGACC CTAGACTGGA TCACGAAGGA 840  
 30 ATCTGTTGTA TAGAATGTAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900  
 GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCTG CAGAGTCATC 960  
 ATGCCATGTA GCTGTGGTGT GCGCCGTATC TTGGGCATGG TGTGAAATCA CTTCATATAT 1020  
 CACGTGCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATTA AGGCAGGTTG 1080  
 ATGCTGATGG GACCATAAAA TATTTTACA CGCAGCCTGA GCGGTTATTC TTGACACTCT 1140  
 35 TAACAGAAAT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAAAATGCA CTGAAAGGGT 1200  
 AGTTCAAGTC TAAATGCCA TAACCCCGTT ATTTGTTATT TTTTATTGTC ATTGATTTGC 1260  
 CATAAGTCTT CCCTTGCTTG CATCTTCAA AGCTATTTCG AAATAAACAC GAAAATTTAC 1320  
 AGTTTGCC

Seq ID NO: B78 Protein sequence  
 Protein Accession #: NP\_008946

1 11 21 31 41 51  
 45 MTENDSKVPI ALVGPDDVEF CSFPAYATLT VKPSSPARLL KVGAVVLISG AVLLLLFGAIG 60  
 AFYFWKGS DS HIYNHYTMS INGKLQDGS EIDAGNNLET FKMGSAGEEA IAVNDFQNGI 120  
 TGIRFAGGEK CYIKAQVKAR IPEVGAVTKQ SISKLEGI MPVKYEENSL IWVAVDQPVK 180  
 DNSFLSSKVL ELCGDLPIFW LKPTYPKEIQ RERREVRKI VPTTTKRPHS GPRSNFAGR 240  
 50 LNNETRPSVQ EDSQAFNPDN FYHQEGESM TFDPRLDHEG ICCIECRSY THCQKICEPL 300  
 GGYYPWPYNY QGCRSACRVI MPCSWWVARI LGMV

Seq ID NO: B79 DNA sequence  
 Nucleic Acid Accession #: NM\_012449.1  
 Coding sequence: 66..1085

1 11 21 31 41 51  
 55 CCGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60  
 AATTAAATGGA AAGCAGAAAA GACATCACAA ACCAAGAAGA ACTTTGGAAG ATGAAGCCTA 120  
 60 GGAGAAATTT AGAAGAAGAC GATTATTGTC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180  
 AAAGACCTGT GCTTTTGATC TTGCACCAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240  
 CAGAACTTCA GCACACACAG GAACTCTTTC CACAGTGGCA CTGCCAATT AAAATAGCTG 300  
 CTATTATAGC ATCTCTGACT TTTCTTACA CTCTTCTGAG GGAAGTAATT CACCCTTTAG 360  
 CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAAGTCTTG 420  
 65 CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG 480  
 TCCAACCTCA TAATGGAAC AGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540  
 TAACAAGAAA GCAGTTTGGG CTTCTCAGTT TCTTTTGTG TGTACTGCAT GCAATTTATA 600  
 GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAACTGG GCATATCAAC 660  
 70 AGGTCCAACA AAATAAAGAA GATGCCTGGA TTGAGCATGA TGTGAGGAGA ATGGAGATTT 720  
 ATGTGTCTCT GGAATTTGTG GGATTTGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC 780  
 CATCTGTGAG TGAATCTTTG ACATGGAGAG AATTTCACTA TATTCAGAGC AAGCTAGGAA 840  
 TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCTGGAAT AAGTGGATAG 900  
 ATATAAAACA ATTTGTATGG TATACACCTC CAACTTTTAT GATAGCTGTT TTCCTTCAA 960  
 75 TTGTTGTCTT GATATTTAAA AGCACTACTAT TCCTGCCATG CTTGAGGAAG AAGATACTGA 1020  
 AGATTAGACA TGGTTGGGAA GACGTCACCA AAATTAACAA AACTGAGATA TGTTCACAGT 1080  
 TGTAAGATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140  
 TCAAGTTTGT ATTTGTTAAT AAAATGATTA TCAAGGAAA AAAAAAAAAA AAAAA

Seq ID NO: B80 Protein sequence  
 Protein Accession #: NP\_036581.1

1 11 21 31 41 51  
 80 MESRKDITNQ EELWKMPPRR NLEEDDYLHK DTGETSMLKR PVLLHLHQTA HADEFDPCSE 60  
 LQHTQELFPQ WHLPKIAAI IASLTFLYTL LREVIHPLAT SHQQVYKIP ILVINKVLEPM 120

VSITLLALVY LPGAIAIVQ LHNKTKYKFF PHWLDKWMLT RKQFGLLSFF FAVLHAIYSL 180  
 SYPMRRSYRY KLLNWAYQV QONKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240  
 VSDSLTWREF HYIQSKLGIV SLLLGTHAL IFAWNKWIID KQFVWYTPPT FMIAVFLPIV 300  
 VLIFKSILFL PCLRKKILKI RHGWEDVTKI NKTEICSQL

Seq ID NO: B81 DNA sequence  
 Nucleic Acid Accession #: NM\_000684  
 Coding sequence: 87..1520

10 1 11 21 31 41 51  
 | | | | | |  
 TGCTACCCGC GCCCGGGCTT CTGGGGTGTT CCCCAACCAC GGCCAGCCG TGCCACACCC 60  
 CCCGCCCCCG GCCTCCGCAG CTCGGCATGG GCGCGGGGT GCTCGTCTTG GCGCCTCCG 120  
 AGCCCGGTAA CCGTCTGCTG GCCGCACCG TCCCGACCG GCGCGCCACC GCGCGCGGGC 180  
 15 TGCTGGTGCC CGCGTCGCG CCCGCCCTCGT TGCTGCCTCC CGCCAGCGAA AGCCCGGAGC 240  
 GCCTGTCTCA GCAGTGGACA GCGGGCATGG GTCTGTGTAT GCGGCTCATC GTGCTGCTCA 300  
 TCGTGGCGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCCCGGG CTGCAGACGC 360  
 TCACCAACCT CTTTCATCATG TCCCTGGCCA GCGCCGACCT GGTTCATGGGG CTGCTGGTGG 420  
 TGCCGTTTCGG GGCCACCATC GTGGTGTGGG GCGGCTGGGA GTACGGCTCC TTCTCTGCG 480  
 20 AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540  
 TTGCCCTGGA CCGGTACCTC GCCATCACCT CGCCCTTCCG CTACCAGAGC CTGCTGACGC 600  
 GCGCGCGGGC GCGGGGCTC GTGTGACCGG TGTGGGCCAT CTCGGCCCTG GTGTCTCTCC 660  
 TGCCCATCCT CATGCACCTG TGGCGGGCGG AGAGCGACGA GGCGCGCCG TGCTACAACG 720  
 25 ACCCAAGTGC CTGCGACTTC GTACCAACC GGGCCTACGC CATCGCCTCG TCCGTAGTCT 780  
 CCTTCTACGT GCCCCTGTGC ATCATGGCCT TCGTGTACCT GCGGGTGTTC CGCAGAGGCC 840  
 AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCCGTTT CCTCGCGCGC GCAGCGCGGC 900  
 CGCCCTCGCC CTCGCCCTCG CCCGTCCCGG CGCCCGCGCC GCGCGCCGGA CCCCGCGGCC 960  
 CGCGCGCCGC CGCGGCCACC GCGCGCTGG CCAACGGGCG TGCGGGTAAG CGCGGGCCCT 1020  
 CGCGCCTCGT GCGCCTACGC GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG 1080  
 30 TCTTCAACGT CTGCTGGGCTG CCCCTCTTCC TGGCCAAAGT GGTGAAGGCC TTCCACCGCG 1140  
 AGCTGGTGCC CGACCGCTC TTCGTCTTCT TCAACTGGCT GGGCTACGCC AACTCGGCCT 1200  
 TCAACCCCAT CATCTACTGC CGCAGCCCCG ACTTCCGCAA GGCCTTCCAG GGAATGCTCT 1260  
 GCTGCGCGCG CAGGCTGCTC CGCCGGCGCC ACAGCAGCCA CGGAGACCGG CCGCGCGCCT 1320  
 CGGGCTGTCT GCGCCGCGCC GGACCCCGCG CATCGCCCGG GCGCGCCTCG GACGACGACG 1380  
 35 ACGACGATGT CGTCGGGGCC ACGCGCCCGG CGCGCCTGCT GGAGCCCTGG GCGCGCTGCA 1440  
 ACGCGGGGGC GCGCGCGGAC AGCGACTCGA GCCTGACGA GCGGTGCCG CCGGCTTCCG 1500  
 CCTCGGAATC CAAGGTGTAG GCGCGCGCGG GCGCGCGGAC CTCCGGGCGC GGCTTCCCAG 1560  
 GGGAAAGAGG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAATCGA AGCCCAACAAT 1620  
 40 CCTCGTCTGA ATCATCCGAG GCAAGAGAA AAGCCACGGA CCGTTGCACA AAAAGGAAG 1680  
 TTTGGGAAGG GATGGGAGAG TGGCTTGCTG ATGTTCTTTC TTG

Seq ID NO: B82 Protein sequence  
 Protein Accession #: NP\_000675.1

45 1 11 21 31 41 51  
 | | | | | |  
 MGAGVLVLGA SEPNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQWTAG 60  
 MGLLMALIVL LIVAGNVLVI VAIKTPRLQ TLNLFIMSL ASADLVMGLL VVFPFATIVV 120  
 WGRWEYGSFF CELWTSVDVL CVTASITELC VIALDRYLAI TSPFRYQSLR TRARARGLVC 180  
 50 TVWAISALVS FLPLMHWRW AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM 240  
 AFVYLRVFRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RPAATAATAP 300  
 LANGRAGKRR PSRLVALREG KALKTLGIIM GVFTLCWLPF FLANVVKAFH RELVDPDLFV 360  
 FFWNLGYANS AFNPILYCRS PDFRKAFOGL LCCARRAARR RHATHGDRPR ASGCLARPGP 420  
 55 PPSFGAASDD DDDVDVGATP PARLLEPWAG CNGGAADSD SSDLDEPCRPG FASESKV

Seq ID NO: B83 DNA sequence  
 Nucleic Acid Accession #: NM\_000729.2  
 Coding sequence: 2..421

60 1 11 21 31 41 51  
 | | | | | |  
 GGCTCAGCTG CCGGGCTGCT CCGGTTGGAA ACGCCAAGCC AGCTGCCGTC CTAATCCAAA 60  
 AGCCATGAAC AGCGGCGTGT GCCTGTGCGT GCTGATGGCG GTACTGGCGG CTGGCGCCCT 120  
 65 GACGCAGCCG GTGCCTCCCG CAGATCCCGC GGGCTCCGGG CTGCAGCGGG CAGAGGAGGC 180  
 GCCCCGTAGG CAGCTGAGGG TATCGCAGAG AACGGATGGC GAGTCCCGAG CGCACCTGGG 240  
 CGCCCTGCTG GCAAGATACA TCCAGCAGGC CCGGAAAGCT CCTTCTGGAC GAATGTCCAT 300  
 CGTTAAGAAC CTGCAGAACC TGGACCCAG CCACAGGATA AGTGACCGGG ACTACATGGG 360  
 CTGATGGGAT TTTGGCCGTC GCAGTGCCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420  
 70 GCCGCCATCA GCCCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAAT AAGACAACAA 480  
 TCACACTCAT AACTCATTGT CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540  
 TCAATGTGAA AATTGTGCTC GTAAGATTGT CCAGTGCAAC CACACACGCT CACAGAGAGT 600  
 TGTGCAAACT GAAGCAAAA CTGTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT 660  
 TATGCTATTA AAGTGATTTC ATTCTGCC

Seq ID NO: B84 Protein sequence  
 Protein Accession #: NP\_000720.1

80 1 11 21 31 41 51  
 | | | | | |  
 MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEEAP RQLRVLSQRT DGESEHLGA 60  
 LLARYIQQAR KAPSGRMSIV KNLQNLDP SH RISDRYMGW MDFGRSAE YEYPS

TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis

5	<u>A1 DNA SEQUENCE</u>	
	Gene name:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Unigene number:	Hs.154210
	Probeset Accession #:	M31210
10	Nucleic Acid Accession #:	M31210
	Coding sequence:	251-1396
15	TCTAAGGTC GGGGGCAGCA GCAAGATGCG AAGCGAGCCG TACAGATCCC GGGCTCTCCG 60 AACGCAACTT CGCCCTGCTT GAGCGAGGCT GCGGTTTCCG AGGCCCTCTC CAGCCAAGGA 120 AAAGCTACAC AAAAAGCCTG GATCACTCAT CGAACCACCC CTGAAGCCAG TGAAGGCTCT 180 CTCGCTCGC CCTCTAGGCT TCGTCTGGAG TAGCGCCACC CCGGCTTCTT GGGGACACAG 240 GGTGCGCACC ATGGGGCCCA CCAGCGTCCC GCTGGTCAAG GCCCACCACA GCTCGGTCTC 300 TGACTACGCT AACTATGATA TCATCGTCCG GCATTACAAC TACACGGGAA AGCTGAATAT 360 CAGGCGGAC AAGGAGAACA GCATTAACT GACCTCGGTG GTGTTCATT TCATCTGCTG 420 CTTTATCATC CTGGAGAACA TCTTTGTCTT GCTGACCATT TGGAAAACCA AGAAATTCCA 480 CCGACCCATG TACTATTTTA TTGGCAATCT GGCCCTCTCA GACCTGTGG CAGGAGTAGC 540 CTACACAGCT AACCTGCTCT TGCTGCGGCG CACCACCTAC AAGCTCACTC CCGCCAGTGT 600 GTTTCTGCGG GAAGGGAGTA TGTTTGTGGC CCTGTCAGCC TCCGTGTTC GTCTCCTCGC 660 CATCGCCATT AGCGGTATA TCACAATGCT GAAATGAAA CTCACACACG GGAGCAATAA 720 CTTCGCGCTC TTCTGCTTAA TCAGCGCTG CTGGGTCATC TCCCTCATCC TGGGTGGCCT 780 GCCTATCATG GGCTGGAATC GCATCAGTGC GCTGTCCAGC TGCTCCACCG TGCTGCCGCT 840 CTACACAAG CACTATATCC TCTTCTGCAC CACGGTCTTC ACTCTGCTTC TGCTCTCCAT 900 CGTCATTCTG TACTGCAGAA TCTACTCCTT GGTCAAGGACT CGGAGCCGCC GCCTGACGTT 960 CCGCAAGAAC ATTTCCAAGG CCAGCCGCGC CTCTGAGAAT GTGGCGCTGC TCAAGACCGT 1020 AATTATCGTC CTGAGCGTCT TCATCGCCTG CTGGGCACCG CTCTTCATCC TGCTCCTGCT 1080 GGATGTGGCG TGCAAGGTGA AGACCTGTGA CATCCTCTTC AGAGCGGAGT ACTTCTGGT 1140 GTTAGCTGTG CTCACCTCCG GCACCAACCC CATCATTTAC ACTCTGACCA ACAAGGAGAT 1200 GCGTCGGGCC TTCATCCGGA TCATGTCTTG CTGCAAGTGC CCGAGCGGAG ACTCTGCTGG 1260 CAAATTCAGC CGACCCATCA TCGCCGGCAT GGAATTCAGC CGCAGCAAT CGGACAATTC 1320 CTCCACCCCC CAGAAAAGAC AAGGGGACAA CCCAGAGACC ATTATGTCTT CTGGAACCGT 1380 CAACTCTTCT TCCTAGAACT GGAAGCTGTC CACCCACCCG AAGCGCTCTT TACTTGGTCG 1440 CTGGCCACCC CAGTGTGTTG AAAAAATCT CTGGGCTTCG ACTGCTGCCA GGGAGGAGCT 1500 GCTGCAAGCC AGAGGGAGGA AGGGGGAGAA TACGAACAGC CTGGTGGTGT CGGGTGTG 1560 TGGGTAGAGT TAGTCTCTGT GAACAATGCA CTGGGAAGGG TGGAGATCAG GTCCCGGCCT 1620 GGAATATATA TTCTACCCCT CTGGAGCTTT GATTTTGAC TGAGCCAAAG GTCTAGCATT 1680 GTCAAGCTCC TAAAGGGTTC ATTTGGCCCC TCCTCAAAGA CTAATGTCCC CATGTGAAAG 1740 CGTCTCTTTG TCTGGAGCTT TGAGGAGATG TTTTCTTCA CTTTAGTTTC AAACCCAAGT 1800 GAGTGTGTGC ACTTCTGCTT CTTTAGGGAT GCCCTGTACA TCCACACCC CACCTCCCT 1860 TCCCTTATA CCCTCTCTCA ACCTTCTTTT ACTTTATACT TTAACCTACCT GAGAGTTATC 1920 AGAGCTGGGG TTGTGGAATG ATCGATCATC TATAGCAAAAT AGGCTATGTT GAGTACGTAG 1980 GCTGTGGGAA GATGAAGATG GTTTGGAGGT GTAAAACAAT GTCCTTCGCT GAGGCCAAAG 2040 TTTCCATGTA AGCGGGATCC GTTTTTTGA ATTTGGTTGA AGTCACTTTG ATTTCTTTAA 2100 AAAACATCTT TTCAATGAAA TGTGTTACCA TTTTATATCC ATTGAAGCCG AAATCTGCAT 2160 AAGGAAGCCC ACTTTATCTA AATGATATTA GCCAGGATCC TTGGTGTCTT AGGAGAAACA 2220 GACAAGCAAA ACRAAGTGAA AACCGAATGG ATTAACTTTT GCAAACCAAG GGAGATTCT 2280 TAGCAAAATGA GTCTAAACAA TATGACATCC GTCTTTCCCA CTTTGTGTTA TGTTTATTTT 2340 AGAATCTTGT GTGATTGTAT TCAAGCAACA ACATGTTGTA TTTTGTGTTG TTAAGAGTAC 2400 TTTTCTTGAT TTTTGAATGT ATTTGTTTCA GGAAGAAGTC ATTTATGGA TTTTCTAAC 2460 CCGTGTTAAC TTTTCTAGAA TCCACCTCTT TGTGCCCTTA AGCATTACTT TAACTGGTAG 2520 GGAACGCCAG AACTTTTAAG TCCAGCTATT CATTAGATAG TAATTGAAGA TATGTATAAA 2580 TATTACAAAG AATAAAATA TATTACTGTC TCTTTAGTAT GGTTTTCAGT GCAATTAAAC 2640 CGAGAGATGT CTTGTTTTTT TAAAAAAGAT AGTATTTAAT AGGTTTCTGA CTTTGTGGA 2700 TCATTTTGCA CATAGCTTTA TCACTTTTA AACATTAATA AACTGATTTT TTTAAAG	
60	<u>A2 Protein sequence:</u>	
	Gene name:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Unigene number:	Hs.154210
	Probeset Accession #:	M31210
65	Protein Accession #:	AAA52336
	Signal sequence:	none found
	Transmembrane domains:	50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301
	Cellular Localization:	plasma membrane
70	1 11 21 31 41 51           MGPTSVPLVK AHRSSVSDYV NYDIIVRHYN YTGKLNISAD KENSIKLTSV VFILICCFII 60 LENIFVLLTI WKTKKPHRPM YFIGNLALS DLLAGVAYTA NLLLSGATTY KLTPAQWFLR 120 EGSMFVALSA SVFSLAIAI ERYITMLMKM LHNGSNNFRL FLLISACWVI SLILGGLPIM 180 GWNCISALSS CSTVLPYHK HYILFCTTVF TLLLLSIVIL YCRIYSLVRT RSRRLTFRKN 240 ISKASRSSEN VALLKTVIIV LSVFIACWAP LFILLLLDVG CKVKTCIDILF RAEYFLVLAV 300 LNSGTNPPIY TLINKEMRRA FIRIMSCCK PSQDSAGKFK RPIIAGMEFS RSKSDNSSHP 360 QKDEGDNPET IMSSGNVNSS S	
80	<u>A3 DNA SEQUENCE</u>	
	Gene name:	G protein-coupled receptor 51
	Unigene number:	Hs.198612
	Probeset Accession #:	AA452928
	Nucleic Acid Accession #:	NM_004624.1

1-2826 (underlined sequences correspond to start and stop codons)

**55**     A4 Protein sequence:  
          Gene name:                         G protein-coupled receptor 51  
          Unigene number:                  Hs.198612  
          Probeset Accession #:           AA452928  
**60**     Protein Accession #:              NP\_005449.1  
          Signal sequence:                1-42  
          Pfam domains:                    7tm\_3 [481-754], ANF\_receptor [130-204]  
          Transmembrane domains:        22-44, 477-499, 517-539, 552-574, 595-617, 653-675, 692-713, 722-744  
          Cellular Localization:          plasma membrane

	1	11	21	31	41	51	
	MASPRRSQGP	GRPPPPPPPP	ARLLLLLLLL	LLLPLAPGAW	GWARGAPRPP	PSSPPLSIMG.	60
	LMPLTKKEVAK	GSIGIRGVLPA	VELATEIQIRN	ESLLRPYFILD	LRLYLDETCDN	AKGLKAFYDA	120
70	IKYGPNNHLMV	FQGVCPVSU	IIAESLQGNW	LVQLSFAATT	PVLADKKKYP	YFKFTVPSDN	180
	AVNPAILKLL	KGYQWKRVGT	LTQDVQRFSE	VRNDLTGVLY	GEDIEISDTE	SFSNDPCTSV	240
	KCLKGNVDRI	ILGQPDQMA	AKVFCCKAYE	MMNGSKYQWI	IPGWYEPSW	EQVHTEANSS	300
	RRLKNLLAA	MELYIGVDFE	PLSSQKIKIT	SGKTPQQYER	EYNNKRSGVG	PSKFHGAYAD	360
75	GIWVIAKTILQ	RAMEITLHASS	RHQRIQDFNY	TDHTLTGRIIL	NAMNETNFFG	VTGQVVFNRG	420
	ERMGTIKFTQ	FQDSREVKVG	EYNVAADTLE	IINDTIRFQG	SEPPDKTKII	LEQLRKISLP	480
	LYSILSALT	LGMIMASAPL	FFNIKNRNQK	LIKMSPPYMN	NLIILGGMLS	YASIFLEGD	540
	GSFVEKTFPE	TLCTVTRTWL	TGUYTITAFGA	MPAKTWRVHA	IPKNVMKKKK	IIKDQKLLVI	600
	VGMMLIDLC	LIICQAVDPL	LRRITVEKYS	EPDPAGRDIS	IRPLEHCEN	THMTIWLGTI	660
80	YAYKGLMLMF	GCFLAWETRN	VSPALNDSK	YIGMSYVNVG	IMCIIGAASV	FLTRDQPNVQ	720
	FCIVALVIIIF	CSITITCLFV	VPKLITLRTN	PDAATONRRF	QFTQNQKKED	SKTSTSTSVS	780
	NQASTSRLEG	LQSENHRLRM	KITELDKDLE	EVTMQLQDTP	EKTTYIKQNH	YQELNDIILN	840
	GNFTSTDDGG	KAILKNHLDP	NPQLQWNTWE	PSRTCKDPIE	DINSPEHIQR	RLSLQLPILH	900
	HAYLPSIGGV	DASCSPCVS	PTASPRHRHV	PPSFRVMVSG	L		

A5 DNA SEQUENCE

Gene name:

ESTs

Unigene number:

Hs.293616

Probeset Accession #:

AW043782

Nucleic Acid Accession #:

none found

Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

10 1 11 21 31 41 51  
 | | | | | |  
 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG 60  
 CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCC GGGAACTACT TCACCAATGA 120  
 GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA 180  
 GTGTGACGGG CTGCCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240  
 15 GTCGAAATGT GGCCCAACCT TCTTCCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTCTG 300  
 CTTCCGGTGG AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360  
 AAACCCCTCTG CTTTGTCTCA CCGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA 420  
 GAGCTTCATC TGGCATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480  
 20 AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540  
 TTACCCAGCG ATCACCCTAT CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600  
 CCTGCTGGCA CTGCTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGTGCCCGT 660  
 GCACCGGGTG CAGCACCTCT TGCTGCTGTC CCGCCTGGTG GTCTTGAGCC ACCCCACCA 720  
 CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780  
 25 GAATGCGTCG GAAGTAGGCT CCCCACCTTC CTACTCCGAG GCCTTGCTGG ACCAGAGGCC 840  
 TCGGTGGTAT GACCTTCCTC CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900  
 CGACCTGCCC CCTTACCGCT CCGGTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960  
 CAGCAGCCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020  
 GGGCACTGCT GAGCCAGGAG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080  
 30 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTC TAACAATTG 1140  
 TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
 AACTATCTCT GACTTCCCCT CCTCCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260  
 TGACATGATC TGTGTGCGT CTTTCTGTGC AGGTCACTCT TCCCTTGGGA CCCGAGATCA 1320  
 CACCTCATTT TTTCACATTA TTCTGTTTCT GTTGAGAGAG CAGCATATAA AACAGTATTG 1380  
 35 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440  
 CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500  
 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAATT CCATTTGAGC 1560  
 ATCAAAACCT GCTTTGCACA ATCCTATTG ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620  
 AAGAAACCTT TGGACGTGAG TAACACCTTT CAGCAGTCGC AACGTATTTT TGGTTTGTG 1680  
 40 AAGCACTCTG AAACCATCTA CCCTGTATAA ATTCTGGCTT TAGAATTTG CCCAAGAATG 1740  
 CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800  
 GAGCCCTCTC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860  
 TACACCTCTG CTGGCTCTAC AGCCACTTAC CTGGTTCTG GACTGTCAAC CTCACAGCTG 1920  
 ACCTGCCCCG AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980  
 45 GTATGTCCTT GTGGCCCAAC CCCAGCCTGT CTGTCTCATT CATGCAGCCT CAACACTGGC 2040  
 CTCCAAAGTT CCGTTAACAC TTGCAAAAGTC CTTTATACCT GTGCATTTGG ACTTGAGGAC 2100  
 ACTGTTTCTC ATCAGAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160  
 CTGCACTGTG CACGCTCCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220  
 GGTCAAGGTC AGGCCCTCTC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280  
 50 AGACAATTG GAGTCAAGAT TTTCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340  
 TGAACAGTGT TGTGTTGTTT TTCCCTCTA GTTAAGGGAC TATTATATG TGTATAGGAA 2400  
 AGCTGTCTCT TTTTGTGTTT TTCTTTAAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC 2460  
 ACACCTCTGC CCCGCTGAGC CCCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520  
 ACATTGTGTC ATTGTGTCAC TTTGAGTTA TTATTATCA AGTTCTTGAA GGAAGCAGAA 2580  
 55 AGAGGAGACT CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTCTTTTCTT 2640  
 TTCTCTGTGT CAGTCTCAGC ACAGGGCCCG CTCTCCCTGCA GGAATAAGGG GTAAAAACGTT 2700  
 AAGGTGTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGAA CCAGGTAGAG 2760  
 CCACTCCGGG CAGCTGTAC CCATTGAGAA CTCTTTCCG CAGCTGAAAG AATGTTTCACT 2820  
 AACCTGTTT ACCTATAATT AAACAGAGCC TGCAAGAAAG GGGGCTAAAG TGGCATTCAG 2880  
 60 TGATCTGTT CTGTAGACTT TTCTTCTTT TTTTAACCAA ATCCAAAGGA TGTACAGAA 2940  
 AAGCTAGCCA CTGCTATTTT GTTTTGTGTT AAAAAAAGAA GAAAGAAAGA AAGAAAGAAA 3000  
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060  
 CTGAGTAATC CAATAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120  
 CATTTTCACT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTTCTTC 3180  
 65 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAA TGGTTTATG 3300  
 AGATAAGGGA TGCTACTATA TGCTTTTATA AAACAACAG GGACATTTT ATTATAGATT 3360  
 TGATTTTCTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGC GGCAGGGTTT 3420  
 TTTTGGGGG GAGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CAGCAATAT 3480  
 70 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCA 3540  
 AAAATAGTCT CATCTCTTTT TTTCTCAAA GAGATCCGTG TTTTATTTA GCATTAAAT 3600  
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660  
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720  
 GAAAGTTGT GTGCTGTTGC TTTTGTGTTT TTGGTTAGGC TTGGTTTGT TTTTAAATTT 3780  
 75 TTATACTTTC TAATAAATT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG WNMCTAMARM 3840  
 AAMMAAAAC AWYWTGGGG GGGCTTGGG CTGGAAGAAA GTTTTAAACA CCACTTCGGG 3900  
 TGGGGCGGG GGGCCACGT AGGTACGGCG ACCACGCGG CCCAAACGGG ACCCCAGAG 3960  
 GAAACCTCTG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCGCCGGG 4020  
 GGAACCCGCA GAGTGTGCG TAAACACAC CCGAAGAGAG AACTCAGAG CACACAAGCG 4080  
 80 GGACTCAACC AGGAGGACCC AAGGAACCC GATAGAGTAC G

A6 Protein sequence:

Gene name:

ESTs

Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51  
 MWLLGFLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60  
 EKECPKAKSK CGPTFFPCAS GIHICIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 15 KNGLCIDKSF ICDGQNNQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180  
 VIFVLVVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHCN VTYNVNNGIQ 240  
 YVASQAEQNA SEVGSPPSYS EALLDQRPAP YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PQPGPQEGT AEPRDSEPSQ GTEEV

20 A7 DNA SEQUENCE  
 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)

Unigene number: Hs.149609  
 Probeset Accession #: X06256  
 Nucleic Acid Accession #: NM\_002205  
 25 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51  
 ATGGGGAGCC GGAGCCAGCA GTCCCTCTC CACGCCGTGC AGCTGCGCTG GGGCCCCCGG 60  
 CGCCGACCCC CGCTSSSTGCC GCTGCTGTGT CTGCTSSSTGC CGCCGCCACC CAGGGTCGGG 120  
 GGCTTCAACT TAGACGCGGA GGGCCACGCA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 180  
 GGATTCTCAG TGGAGTTTTA CCGGCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240  
 35 CCCAAGGCTA ATACAGCCA GCCAGGAGTG CTGCAGGGTG GTGCTGTCTA CCTCTGTCTC 300  
 TGGGGTGCCA GCGCCACACA GTGCACCCCT ATTGAATTG ACAGCAAAGG CTCTCGGCTC 360  
 CTGGAGTCCT CACTGTCCAG CTCAGAGGGA GAGGAGCCTG TGGAGTACAA GTCCTTGACG 420  
 TGGTTCGGGG CAACAGTTCG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC 480  
 AGCTGGCGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA 540  
 GATAACTTCA CCCGAATTCT GGAGTATGCA CCCTGCCGCT CAGATTTCAG CTGGGCAGCA 600  
 40 GGACAGGGTT ACTGCCAAGG AGGCCTCAGT GCCGAGTTCA CCAAGACTGG CCGTGTGGTT 660  
 TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720  
 ATTGCAAGAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780  
 CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGTGGTAA 840  
 45 TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGTGTGTC CCAAGGGGAA CCTCACTTAC 900  
 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCGATCCC TCTACAACCT CTCAGGGGAA 960  
 CAGATGGCCT CTTACTTTGG CTATGCAGTG GCCGCCACAG ACGTCAATGG GAGACGGCTG 1020  
 GATGACTTGC TGGTGGGGGC ACCCTGTGTC ATGGATCGGA CCCTGACGG GCGGCTCAG 1080  
 GAGGTGGGCA GGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCACC 1140  
 50 CTTACCTTCA CTGGCCATGA TGAGTTTGGC CGATTGGCA GCTCCTTGAC CCCCTGGGG 1200  
 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC 1260  
 CAGCAGGGAG TAGTGTTTGT ATTCTCTGGG GGGCCAGGAG GGCTGGGCTC TAAGCCTTCC 1320  
 CAGGTCTGTC AGCCCTGTG GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380  
 CGAGGAGGCC GAGACCTTGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCTTTGGT 1440  
 55 GTGGACAAGG CTGTGGTATA CAGGGGCCGC CCATCGTGT CCGCTAGTGC CTCCCTCACC 1500  
 ATCTTCCCCG CCAATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1560  
 GCCTGCATCA ACCTTAGCTT CTGCCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT 1620  
 GGTTCACAG TGGAACCTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGCGGGGCA 1680  
 CTGTTCTTGG CCTCCAGGCA GGCACCCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740  
 60 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAATT TCGAGACAAA 1800  
 CTCTCGCCGA TTCACATGCG TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1860  
 CACGGCCTCA GGCAGCCCTT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920  
 ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGTG 1980  
 GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCC TGAACCTCAC TTTCCATGCC 2040  
 65 CAGAACTTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCCTCCAGAG 2100  
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2160  
 TTTGCCGTGA ACCAGAGCCG CCTGTGTTG TGTGACCTGG GCAACCCCAT GAAGCAGGA 2220  
 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC 2280  
 70 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGAGCTGGTT 2340  
 TCCTTTCCGC TCTCCGTGGA GGCTCAGGCC CAGTCAACCC TGAACGGTGT CTCCAAGCCT 2400  
 GAGGCACTGC TATTCCAGT AAGCGACTGG CATCCCCGAG ACCAGCCTCA GAAGGAGGAG 2460  
 GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520  
 AGCCAGGGTG TGCTGGAAC TCGCTGTCCC CAGGCTCTGG AAGGTCAGCA GCTCCTATAT 2580  
 75 GTGACCAGAG TTACGGGACT CAACTGCACC ACCAATCACC CCATTAAACC AAAGGGCCTG 2640  
 GAGTTGGATC CCGAGGGTTC CTGCAACCAC CAGCAAAAAC GGGAAAGTCC AAGCCGACG 2700  
 CTGCTTCTCT CGGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGTG CAGGCTGCGC 2760  
 TGTGAGCTCG GGGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAAGTTGA TTTCCAGATC 2820  
 TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCCTGCAGTG TGAGGCTGTG 2880  
 80 TACAAGGCC TGAAGATGCC CTACCGAATC CTGCCTCGGC AGCTGCCCA AAAAGAGCGT 2940  
 CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGCGT CCCACTGTGG 3000  
 ATCATCATCC TACATFCTCT GTTTGGCCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060  
 TACAAGCTTG GATTCTTCAA ACGTCTCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG 3120  
 CTCAGCCTC CAGCCACCTC TGATGCCCTGA

A8 Protein sequence:

Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)  
 Unigene number: Hs.149609  
 Probeset Accession #: X06256  
 Protein Accession #: NP\_002196  
 Signal sequence: 1-42  
 Transmembrane domains: 998-1020  
 Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036  
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MGSRTPE SPL	HAVQLRWGPR	RRPPLPL LLL	LLLPPPPRVG	GFNLDAEAPA	VLSGPPGSFF	60
GFSVEFYRPG	TDGVSVLVGA	PKANTSQPGV	LQGGAVYLCF	WGASPTQCTP	IEFDSKGSRL	120
LESSLSSESG	EEPVEYKSLQ	WFGATVRAHG	SSILACAPLY	SWRTEKEPLS	DPVGTCTYLS	180
DNFTRILEYA	PCRSDFSWAA	QGGYCQGGFS	AEFTTKTRVV	LGGPGSYFWQ	GQILSATQEQ	240
IAESYYPEYL	INLVQQLQQT	RQASSIYDDS	YLGYSVAVGE	FSGDDTDFV	AGVPGKNLTY	300
GYVTILNGSD	IRSLYNSFGE	QMASYFGYAV	AATDVNGDGL	DDLVLGAPLL	MDRTPDGRPQ	360
EVGRVYVYLQ	HPAGIEPTPT	LTLTGHDEFG	RFGSSLTPLG	DLDQDGYNDV	AIGAPFGGET	420
QQGVVVFVPG	GPGLGSKSPS	QVLQPLWAAS	HTPDFFGSAL	RGGRLDLDNG	YPDLIVGSFG	480
VDKAVVYRGR	PIVSASASLT	IFPAMFNPEE	RSCSLEGNPV	ACINLSFCLN	ASGKHVADSI	540
GFTVELQLDW	QKQKGGVRRR	LFLASRQATL	TQTLLIQNGA	REDCREMKIY	LRNESEFRDK	600
LSPHIALNLF	SLDPQAPVDS	HGLRPLALHYQ	SKSRIEDKAQ	ILLDCGEDNI	CVFDLQLEVF	660
GEQNHVYLG	KNALNLTFFHA	QNVGEGGAYE	AELRVTPAPE	AEYSGLVRHP	GNFSSLSCDY	720
FAVNQSRLLV	CDLGNPMKAG	ASLWGGRLRFT	VPHLRDTKKT	IQDFDQILSK	NLNNSQSDVV	780
SFRLSVEAQA	QVTILNGVSKP	EAVLFPVSDW	HPRDQPQKEE	DLGPAVHHVY	ELINQGFSSI	840
SQGVLELSCP	QALEGQQLLY	VTRVTGLNCT	TNHPINPKGL	ELDPEGLSHH	QQKREAPSR	900
SASSGPQILK	CPAECEFRRL	CBLGPHLQHE	SQSLQLHFRV	WAKTFLQREH	QPFSLQCEAV	960
YKALKMPYRI	LPRQLPQKER	QVATAVQWTK	AEYSYGVPLW	IIILAILFLG	LLGLLIYIIL	1020
YKLGFFKRSL	PYGTAMEKAQ	LKPPATSDA				

A9 DNA SEQUENCE

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)  
 Unigene number: Hs.287797  
 Probeset Accession #: X07979  
 Nucleic Acid Accession #: NM\_002211.1  
 Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
<u>ATGAATTTAC</u>	<u>AAACCAATTTT</u>	<u>CTGGATTGGA</u>	<u>CTGATCAGTT</u>	<u>CAGTTTGCTG</u>	<u>TGTGTTTGCT</u>	60
CAAAACAGATG	AAAATAGATG	TTTAAAGCA	AATGCCAAAT	CATGTGGAGA	ATGTATACAA	120
GCAGGGCCAA	ATTGTGGGTG	GTGCACAAAT	TCAACATTTT	TACAGGAAGG	AATGCCTACT	180
TCTGCACGAT	GTGATGATT	AGAAGCCTTA	AAAAAGAAGG	GTTGCCCTCC	AGATGACATA	240
GAAAAATCCCA	GAGGCTCCAA	AGATATAAAG	AAAAATAAAA	ATGTAACCAA	CCGTAGCATA	300
GGAACAGCAG	AGAAGCTCAA	GCCAGAGGAT	ATTACTCAGA	TCCAACCACA	GCAGTTGGTT	360
TTGCGATTAA	GATCAGGGGA	GCCACAGACA	TTTACATTAA	AATTCAAGAG	AGCTGAAGAC	420
TATCCCATTTG	ACCTTACTAA	CCTTATGGAC	CTGTCTTACT	CAATGAAAGA	CGATTGGAG	480
AATGTAAAAA	GTCTTGGAAC	AGATCTGATG	AATGAAATGA	GGAGGATTAC	TTCGGACTTC	540
AGAATTGGAT	TTGGCTCATT	TGTGGAAAAAG	ACTGTGATGC	CTTACATTAG	CACAACACCA	600
GCTAAGCTCA	GGAAACCTTG	CACAAGTGAA	CAGAACTGCA	CCAGCCCATT	TAGCTACAAA	660
AATGTGCTCA	GTCTTACTAA	TAAAGGAGAA	GTATTTAATG	AACCTGTTGG	AAAACAGCGC	720
ATATCTGGAA	ATTTGGATTG	TCCAGAAGGT	GGTTTCGATG	CCATCATGCA	AGTTGCAGTT	780
TGTGGATCAC	TGATTGGCTG	GAGGAATGTT	ACACGGCTGC	TGGTGTTC	CACAGATGCC	840
GGTTTTCAC	TTGCTGGAGA	TGGGAAACTT	GGTGGCATTG	TTTTACCAA	TGATGGACAA	900
TGTCACTGCG	AAAATAATAT	GTACACAAAT	AGCCATTATT	ATGATTATCC	TTCTATTGCT	960
CACCTTGTC	AGAAACTGAG	TGAAAATAAT	ATTACAGCAA	TTTTTGCACT	TACTGAAGAA	1020
TTTCAGCCTG	TTTACAAGGA	GCTGAAAAAC	TTGATCCCTA	AGTCAGCAGT	AGGAACATTA	1080
TCTGCAAAAT	CTAGCAATGT	AATTCAGTTG	ATCATGTATG	CATACAATTC	CCTTTCCTCA	1140
GAAGTCATT	TGGAAAACGG	CAAAATGTCA	GAAGGAGTAA	CAATAAGTTA	CAAACTTTAC	1200
TGCAAGAACG	GGGTGAATGG	AACAGGGGAA	AATGGAAGAA	AATGTTCCAA	TATTTCCATT	1260
GGAGATGAGG	TTCAATTTGA	AATTAGCATA	ACTTCAAATA	AGTGTCCAAA	AAAGGATTCT	1320
GACAGCTTTA	AAATTAGGCC	TCTGGGCTTT	ACGGAGGAAG	TAGAGGTTAT	TCTTCAGTAC	1380
ATCTGTGAAT	GTGAATGCCA	AAGCGAAGGC	ATCCCTGAAA	GTCCCAAGTG	TCATGAAGGA	1440
AATGGGACAT	TTGAGTGTGG	CGCGTGCAGG	TGCAATGAAG	AGCGTGTGG	TAGACATTGT	1500
GAATGCAGCA	CAGATGAAGT	TAACAGTGAA	GACATGGATG	CTTACTGCAG	GAAAGAAAAC	1560
AGTTTCAGAAA	TCTGCAGTAA	CAATGGAGAG	TGCGTCTGCG	GACAGTGTGT	TTGTAGGAAG	1620
AGGGATAATA	CAAAATGAAT	TTATTCTGGC	AAATTCTGCG	AGTGTGATAA	TTTCAACTGT	1680
GATAGATCCA	ATGGCTTAAT	TTGTGGAGGA	AATGGTGTGT	GCAAGTGTG	TGTGTGTGAG	1740
TGCAACCCCA	ACTACACTGG	CAGTGCATGT	GACTGTTCTT	TGGATACTAG	TACTTGTGAA	1800
GCCAGCAACG	GACAGCATCTG	CAATGGCCGG	GGCATCTGCG	AGTGTGGTGT	CTGTAAAGTGT	1860
ACAGATCCGA	AGTTTCAAGG	GCAAAACGTGT	GAGATGTGTC	AGACCTGCCT	TGGTGTCTGT	1920
GCTGAGCATA	AGAATGTGT	TCAGTGCAGA	GCCTTCAATA	AAGGAGAAAA	GAAAGACACA	1980
TGCACACAGG	AATGTTCCCTA	TTTAAACATT	ACCAAGGTAG	AAAGTCGGGA	CAAATTACCC	2040
CAGCCGGTCC	AACTGATGCC	TGTGTCCCAT	TGTAAGGAGA	AGGATGTTGA	CGACTGTTGG	2100
TTCTATTATTA	CGATATTTCAGT	GAATGGGAAC	AACGAGGTCA	TGGTTCATGT	TGTGGAGAAT	2160
CCAGAGTGTC	CCACTGGTCC	AGACATCAT	CCAATTGTAG	CTGGTGTGTT	TGCTGGAATT	2220



GTTCTATTG GCCTTGCATT ACTGCTGATA TGGAAGCTTT TAATGATAAT TCATGACAGA 2280  
 AGGGAGTTTG CTAATTTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAAT 2340  
 CCTATTATA AGAGTGCCCT AACAACCTGTG GTCAATCCGA AGTATGAGGG AAAATGA

**A10 Protein sequence:**

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)  
 Unigene number: Hs.287797  
 Probeset Accession #: X07979  
 Protein Accession #: NP\_002202.1  
 Signal sequence: 1-21  
 Transmembrane domains: 732-754  
 INB domain: 34-464  
 PSI domain: 26-76  
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MNLQPIFWIG	LISSVCCVFA	QTDENRCLKA	NAKSCGECIQ	AGPNCGWCTN	STFLQEGMPT	60
SARCDLEAL	KKKGCPDDI	ENPRGSKDIK	KNKNVTNRSK	GTAELKLPED	ITQIQPQQLV	120
LRRLSGEPQT	FTLKFKRAED	YPIDLYYLMD	LSYSMKDDLE	NVKSGLTDLM	NEMRRITSDF	180
RIGFGSFVEK	TVMPYISTTP	AKLRNPCTSE	QNCTSPFSYK	NVLSLTNKGE	VFNELVGKQR	240
ISGNLDSPEG	GFDAIMQVAV	CGSLIGWRNV	TRLVVFSTDA	GFHFAGDGKL	GGIVLPNDGQ	300
CHLENNMYTM	SHYDYPSIA	HLVQKLSENN	IQTIFAVTEE	FQPVYKELKN	LIPKSAVGTL	360
SANSSNVIQL	IIDAYNSLSS	EVILENGKLS	EGVTISYKSY	CKNGVNGTGE	NGRKCSNISI	420
GDEVQFEISI	TSNKCPKIDS	DSFKIRPLGF	TEEVEVILQY	ICECEQSEGE	IPESPKCHEG	480
NGTFECGACR	CNEGRVGRHC	ECSTDEVNSE	DMDAYCRKEN	SSEICSNNGE	CVCQCVCVRK	540
RDNTNEIYSG	KFCECDNFNC	DRSNGLICGG	NGVCKCRVCE	CNPNTYGSAC	DCSLDTSTCE	600
ASNGQICNGR	GICECGVCKC	TDPKFQQTCC	EMCQTCLGVC	AEHKECVQCR	AFNKGEKKDT	660
CTQECSEYFNI	TKVESRDKLP	QPVQPDVPSH	CKEKDVDCCW	FYFTYSVNGN	NEVMVHVVEN	720
PECPTGPDII	PIVAGVVAGI	VLIGLALLLI	WKLMIIHDR	REFAKFEKEK	MNAKWDGTEN	780
PIYKSAVTTV	VNPKYEGK					

**A11 DNA SEQUENCE**

Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
ATGATTGCTT	CACAGTTTCT	CTCAGCTCTC	ACTTTGGTGC	TTCTCATTA	AGAGAGTGGA	60
GCCTGGTCTT	ACAACACCTC	CACGGAAGCT	ATGACTTATG	ATGAGGCCAG	TGCTTATTGT	120
CAGCAAAAGT	ACACACACCT	GGTTGCAATT	CAAAACAAAG	AAGAGATTGA	GTACCTAAAC	180
TCCATATTGA	GCTATTACCC	AAGTTATTAC	TGGATTGGAA	TCAGAAAAGT	CAACAATGTG	240
TGGGTCTGGG	TAGGAACCCA	GAAACCTCTG	ACAGAAGAAG	CCAAGAAGCT	GGTCCAGGT	300
GAACCCAAAC	ATAGGCAAAA	AGATGAGGAC	TGCGTGGAGA	TCTACATCAA	GAGAGAAAAA	360
GATGTGGGCA	TGTGGAATGA	TGAGAGGTGC	AGCAAGAAGA	AGCTTGCCCT	ATGCTACACA	420
GCTGCCTGTA	CCAATACATC	CTGCAGTGGC	CACGGTGAAT	GTGTAGAGAC	CATCAATAAT	480
TACACTTGCA	AGTGTGACCC	TGGCTTCAGT	GGACTCAAGT	GTGAGCAAAT	TGTGAAGTGT	540
ACAGCCCTGG	AATCCCTGGA	GCATGGAAGC	CTGGTTTGCA	GTCACCCACT	GGGAACTTC	600
AGCTACAATT	CTTCTGTCTC	TATCAGCTGT	GATAGGGGTT	ACCTGCCAAG	CAGCATGGAG	660
ACCATGTCAGT	GTATGTCTCT	TGGAGAATGG	AGTGTCTCTA	TTCAGCCTCG	CAATGTGGTT	720
GAGTGTGATG	CTGTGACAAA	TCCAGCCAAT	GGGTTCTGTG	AATGTTTCCA	AAACCCTGGA	780
AGCTTCCCAT	GGAAACACAC	CTGTACATTT	GACTGTGAAG	AAGGATTGTA	ACTAATGGGA	840
GCCCAGAGCC	TTCAGTGTAC	CTCATCTGGG	AATTGGGACA	ACGAGAAGCC	AACGTGTAAA	900
GCTGTGACAT	GCAGGCCCGT	CCGCCAGCCT	CAGAATGGCT	CTGTGAGGTG	CAGCCATTCC	960
CCTGTCTGGAG	AGTTACACCT	CAAATCATCC	TGCAACTTCA	CCTGTGAGGA	AGGCTTCATG	1020
TTGCAGGGAC	CAGCCAGGTT	TGAATGCACC	ACTCAAGGGC	AGTGGACACA	GCAAAATCCCA	1080
GTTTGTGAAG	CTTTCCAGTG	CACAGCCTTG	TCCAACCCCG	AGCGAGGCTA	CATGAATTGT	1140
CTTCCTAGTG	CTTCTGGCAG	TTTCGGTTAT	GGGTCCAGCT	GTGAGTTCTC	CTGTGAGCAG	1200
GGTTTTGTGT	TGAAGGGATC	CAAAAGGCTC	CAATGTGGCC	CCACAGGGGA	GTGGGACAAC	1260
GAGAAGCCCA	CATGTGAAGC	TGTGAGATGC	GATGCTGTCC	ACCAGCCCCC	GAAGGGTTTG	1320
GTGAGGTGTG	CTCATTCCCC	TATTGGAGAA	TTCACCTACA	AGTCTCTCTG	TGCCTTCAGC	1380
TGTGAGGAGG	GATTTGAATT	ATATGGATCA	ACTCAACTTG	AGTGACATC	TCAGGGACAA	1440
TGGACAGAAG	AGTTTCTCTC	CTGCCAAGTG	GTAAATGTGT	CAAGCCTGGC	AGTTCCGGGA	1500
AAGATCAACA	TGAGCTGCAG	TGGGGAGCCC	GTGTTTGGCA	CTGTGTGCAA	GTTCGCCTGT	1560
CCTGAAGGAT	GGACGCTCAA	TGGCTCTGCA	GCTCGGACAT	GTGGAGCCAC	AGGACACTGG	1620
TCTGGCCTGC	TACCTACCTG	TGAAGCTCCC	ACTGAGTCCA	ACATTCCCTT	GGTAGCTGGA	1680
CTTCTGCTG	CTGGACTCTC	CCTCCTGACA	TTAGCACCAT	TTCTCCTCTG	GCTTCGGAAA	1740
TGCTTACGGA	AAGCAAGAAA	ATTGTCTCCT	GCCAGCAGCT	GCCAAAGCCT	TGAATCAGAC	1800
GGAAGCTACC	AAAAGCCTTC	TTACATCCTT	<u>TAA</u>			

**A12 Protein sequence:**

Gene name: Selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Protein Accession #: NP\_000441  
 Signal sequence: 1-22  
 Transmembrane domains: 555-573  
 C-lectin domain: 23-139

Cellular Localization: plasma membrane

5 1 11 21 31 41 51  
 | | | | |  
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRythlVAI QNKEEIEYLN 60  
 SILSYSPSY WIGIRKVN NV WVVVGTKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120  
 DVGWMDNERC SKKKLALCYT AACTNTSCSG HGEVETINN YTCKCDPGFS GLKCEQIVNC 180  
 10 TALESPHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIACNVV 240  
 ECDVNTNPAN GFVFCFQNP G SFPWNTTCTF DCEEGFELMG AQLQCTSSG NWDNEKPTCK 300  
 AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEFGM LQGPQAVECT TQGWTTQIP 360  
 VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGTGEWDN 420  
 EKPTCEAVRC DAVHQPPKGL VRCASPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480  
 15 WTEVPSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540  
 SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLLWLRL CLRKAKKFVP ASSCQSLESD 600  
 GSYQKPSYIL

A13 DNA SEQUENCE

20 Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Nucleic Acid Accession #: NM\_001508  
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 | | | | |  
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60  
 CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCCTTA TTCTGGTGTA CCTGATCATC 120  
 30 TTCGTGATGG GCCTTCTGGG GAACAGCGCC ACCATTCCGG TCACCCAGGT GCTGCAGAAG 180  
 AAAGGATAC TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGCACATC 240  
 TTGGTGTTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACCC 300  
 ACGTCCAGCT ACACCTGTGTC CTGCAAGCTG CACACTTTC TCTTCGAGGC CTGCAGCTAC 360  
 GCTACGCTGC TGCACGTGCT GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTACCCCC 420  
 35 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TCTGATTGG CTTCGTCTGG 480  
 GTCACCTCCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTCG 540  
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG 600  
 CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660  
 CAGTCCAGCA TCTTCGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720  
 40 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 780  
 ACCGCGCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840  
 ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACAG 900  
 ATTGGAGGA TCATGGCTGC GGCCAACCC AAGCAGGACT GGACGAGGTC CTACTTCCCG 960  
 GCGTACATGA TCCTCCTCCC CTTCCTCGAG ACGTTTCTCT ACCTCAGCTC GGTTCATCAAC 1020  
 45 CCCTCTCTGT ACACGGTGTG CTGCGAGCAG TTTCGGCGGG TGTTCTGTGA GGTGCTGTGC 1080  
 TGCCGCTGTG CGCTGCAGCA CGCCAACAC GAGAAGCGCC TGCGCGTACA TGCGCACTCC 1140  
 ACCACCGACA GCGCCCGCTT TGTGCGAGCG CCGTTGCTCT TCGGCTCCCG GCGCCAGTCC 1200  
 TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260  
 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACAGGCC 1320  
 50 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

A14 Protein sequence:

55 Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Protein Accession #: NM\_001508, NP\_001409  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [72-172, 224-344]  
 60 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342  
 Cellular Localization: plasma membrane

65 1 11 21 31 41 51  
 | | | | |  
 MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTQVLQK 60  
 KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120  
 ATLLHVLTL FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALFL LFAMGTEYPL 180  
 VNVPSHRGLT CNRSSTRHHE QPETSNSMIC TNLSSRWTVF QSSIFGAFVV YLVVLLSVAF 240  
 70 MCWNMMQVLM KSQKGLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLLIV TLAVCWMPNQ 300  
 IRRIMAAKVP KHDWTSRYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC 360  
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEFQ 420  
 SKSQSLSLES LEPNSGAKPA NSAAENGFBQ HEV

AI ProstateA15 DNA sequence

80 Gene name: CEGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Nucleic Acid Accession #: AJ400877  
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	GGCGTCCGCG	CACACCTCCC	CGCGCCGCGC	CCGCCACCGC	CCGCACTCCG	CCGCCCTCTGC	60
	CCGCAACCCG	TGAGCCATCC	ATGGGGGTCG	CGGGCCGCAA	CCGTCCCAGG	GCGGCCCTGGG	120
5	CGGTGCTGCT	GCTGCTGCTG	CTGCTGCCGC	CACTGCTGCT	GCTGGCGGGG	GCCGTCCCAG	180
	CGGGTCCGGG	CCGTGCCGCG	GGGCCGCGAG	AGGATGTAGA	TGAGTGTGCC	CAAGGGCTAG	240
	ATGACTGCCA	TGCCGACGCC	CTGTGTGAGA	ACACACCCAC	CTCCTACAAG	TGCTCCTGCA	300
	AGCTGGGCTA	CCAAGGGGAA	GGCAGGCAGT	GTGAGGACAT	CGATGAATGT	GGAAATGAGC	360
	TCAATGGAGG	CTGTGTCCAT	GACTGTTTGA	ATATTCCAGG	CAATTATCGT	TGCACTTGTT	420
10	TTGATGGCTT	CATGTTGGCT	CATGACGGTC	ATAATTGTCT	TGATGTGGAC	GAGTGCCTGG	480
	AGAACAATGG	CGGCTGCCAG	CATACCTGTG	TCAACGTCAT	GGGGAGCTAT	GAGTGTCTGT	540
	GCAAGGAGGG	GTTTTTCTCT	AGTGACAATC	AGCACACCTG	CATTACCCGC	TGGAAGAGGG	600
	GCCTGAGCTG	CATGAATAAG	GATCACGGCT	GTAGTCACAT	CTGCAAGGAG	GCCCCAAGGG	660
	GCAGCGTCGC	CTGTGAGTGC	AGGCCTGGTT	TTGAGCTGGC	CAAGAACCAG	AGAGACTGCA	720
15	TCTTGACCTG	TAACCATGGG	AACGGTGGGT	GCCAGCACTC	CTGTGACGAT	ACAGCCGATG	780
	GCCAGAGGTG	CAGCTGCCAT	CCACAGTACA	AGATGCACAC	AGATGGGAGG	AGTGCCTTGG	840
	AGCGAGAGGA	CAGTGTCTGT	GAGGTGACAG	AGAGCAACAC	CACATCAGTG	GTGGATGGGG	900
	ATAACCGGGT	GAACCGGCGG	CTGCTCATGG	AAACGTGTGC	TGCTAACCAAT	GGAGGCTGTG	960
	ACCGCACCTG	TAAGGATACT	TCGACAGGTG	TCCACTGCAG	TTGTCTCTGT	GGATTCACTC	1020
20	TCCAGTTGGA	TGGGAAGACA	TGTAAGATA	TTGATGAGTG	CCAGACCCGC	AATGGAGGTT	1080
	GTGATCATT	CTGCAAAAAC	ATCGTGGGCA	GTTTTGACTG	CGGCTGCAAG	AAAGGATTTA	1140
	AATTTATTAAC	AGATGAGAAG	TCTTGCCAAG	ATGTGGATGA	GTGCTCTTTG	GATAGGACCT	1200
	GTGACCAACAG	CTGCATCAAC	CACCTGGCA	CATTGTCTTG	TGCTTGCAAC	CGAGGGTACA	1260
	CCCTGTATGG	CTTCAACCCAC	TGTGGAGACA	CCAATGAGTG	CAGCATCAAC	AACGGAGGCT	1320
	GTGACAGAGT	CTGTGTGAAC	ACAGTGGGCA	GCTATGAATG	CCAGTGCCAC	CCTGGGTACA	1380
25	AGTCCCACTG	GAATAAAGAA	GACTGTGTGG	AAGTGAAGGG	GCTCCTGCCC	ACAAGTGTGT	1440
	CACCCCGTGT	GTCCCTGCAC	TGCGGTAAGA	GTGGTGGAGG	AGACGGGTGC	TTCTCTCAGAT	1500
	GTCACTCTGG	CATTCACTCT	TCTTCAGATG	TCACCACCAT	CAGGACAAGT	GTAACCTTTA	1560
	AGCTAAATGA	AGGCAAGTGT	AGTTTGAAAA	ATGCTGAGCT	GTTCCTCGAG	GGTCTGCGAC	1620
30	CAGCACTACC	AGAGAAGCAC	AGCTCAGTAA	AAGAGAGCTT	CCGCTACGTA	AACCTTACAT	1680
	GCAGCTCTGG	CAAGCAAGAT	CCAGGAGCCC	CTGGCCGACC	AAGCACCCCT	AAGGAAATGT	1740
	TTATCACTGT	TGAGTTTGAG	CTTGAAACTA	ACCAAAAGGA	GGTGACAGCT	TCTTGTGACC	1800
	TGAGCTGCAT	CGTAAAGCGA	ACCGAGAAGC	GGCTCCGTAA	AGCCATCCGC	ACGCTCAGAA	1860
	AGGCCGTCCA	CAGGAGGAGC	TTTCACTTCC	AGCTCTCAGG	CATGAACCTC	GACGTGGCTA	1920
35	AAAAGCCTCC	CAGAACATCT	GAACGCCAGG	CAGAGTCCTG	TGAGTGGGCG	CAGGGTCATG	1980
	CAGAAAACCA	ATGTGTCTAG	TGCAGGGCTG	GGACCTATTA	TGATGGAGCA	CGAGAACGCT	2040
	GCATTTTATG	TCCAAATGGA	ACCTTCCAAA	ATGAGGAAGG	ACAAATGACT	TGTGAACCAT	2100
	GCCCAAGACC	AGGAAATTCT	GGGGCCCTGA	AGACCCCAAG	AGCTTGGAA	ATGTCTGAAT	2160
	GTGGAGGTCT	GTGTCAACCT	GGTGAATATT	CTGCAGATGG	CTTTGCACCT	TGCCAGCTCT	2220
40	GTGCCCTGGG	CACGTTCCAG	CCTGAAGCTG	GTCGAACCTC	CTGCTTCCCC	TGTGGAGGAG	2280
	GCCTTGCCAC	CAACATCAG	GGAGCTACTT	CCTTTCAGGA	CTGTGAAACC	AGAGTTCAAT	2340
	GTTCACTGGG	ACATTTCTAC	AACACCAACA	CTCACCGATG	TATTCGTGCG	CCAGTGGGAA	2400
	CATACCAGCC	TGAATTTGGA	AAAAATAATT	GTGTTCTCTG	CCCAGGAAAT	ACTACGACTG	2460
	ACTTTGATGG	CTCCACAAAC	ATAACCCAGT	GTAAAAACAG	AAGATGTGGA	GGGGAGCTGG	2520
45	GAGATTTTAC	TGGGTACATT	GAATCCCAAA	ACTACCCAGG	CAATTACCCA	GCCAAACCCG	2580
	AGTGTACCTG	GACCATCAAC	CCACCCCAAC	AGCGCCGCGT	CCTGATCGTG	GTCCCTGAGA	2640
	TCTTCTCTGC	CATAGAGGAC	GACTGTGGGG	ACTATCTGGT	GATGCGGAAA	ACCTCTTCAT	2700
	CCAATTTCTG	GACAAATAT	GAAACCTGCC	AGACCTACGA	ACGCCCCATC	GCCTTCACCT	2760
	CCAGGTCAAA	GAAGCTGTGG	ATTCAGTTCA	AGTCCAATGA	AGGGAAACAG	GCTAGAGGGT	2820
50	TCCAGGTCCC	ATACGTGACA	TATGATGAGG	ACTACCAAGG	ACTCATTGAA	GACATAGTTC	2880
	GAGATGGCAG	GCTCTATGCA	TCTGAGAAC	ATCAGGAAT	ACTTAAGGAT	AAGAACTTAA	2940
	TCAAGGCTCT	GTTTGTGTCT	CTGGCCCATC	CCCAGAACTA	TTTCAAGTAC	ACAGCCCAAG	3000
	AGTCCCGAGA	GATGTTTCCA	AGATCGTTCA	TCCGATTGCT	ACGTTCCAAA	GTGTCCAGGT	3060
	TTTTGAGACC	TTACAAATGA	CTCAGCCAC	GTGCCACTCA	ATACAAATGT	TCTGCTATAG	3120
55	GGTTGGTGGG	ACAGAGCTGT	CTTCTTCTG	CATGTCAGCA	CAGTCGGGTA	TGTGCTGCTC	3180
	CCGTATCAGT	GACTCATTTG	AGTTCAATTT	TTATAGATAA	TACAGATATT	TTGGTAAATT	3240
	GAACCTGGTT	TTTCTTTCCC	AGCATCGTGG	ATGTAGACTG	AGAATGGCTT	TGAGTGGCAT	3300
	CAGCTTCTCA	CTGCTGTGGG	CGGATGTCTT	GGATAGATCA	CGGGCTGGCT	GAGCTGGACT	3360
	TTGGTCAGCG	TAGGTGAGAC	TCACTGTGCC	TTCTGGGGTC	TTACTCTCTC	TCAAGGAGTC	3420
60	TGTAGTGGAA	AGGAGGCCAC	AGAATAAGCT	GCTTATTCTG	AAACTTCAGC	TTCTCTAGC	3480
	CGGCCCTCT	CTAAGGGAGC	CCTCTGCACT	CGTGTGCAGG	CTCTGACCAG	GCAGAACAGG	3540
	CAAGAGGGGA	GGGAAGGAGA	CCCCTGCAGG	CTCCCTCCAC	CCACCTTGAG	ACCTGGGAGG	3600
	ACTCAGTTTC	TCCACAGCCT	TCTCCAGCCT	GTGTGATACA	AGTTTGATCC	CAGGAACCTG	3660
	AGTCTTAAGC	AGTGTCTCGT	AAAAAATAAA	GCAGAAAGAA	TTAGAAATAA	ATAAAACTAA	3720
65	AGCACTTCTG	GAGACAT					
	<u>A16 Protein sequence</u>						
	Gene name: CEGP1						
	Unigene number: Hs.222399						
70	Probeset Accession #: AA256485						
	Protein Accession #: CAB92285						
	Signal sequence: 1-31						
	Transmembrane domains: none						
	PFAM domains: EGF-like_domains [49-84,132-167,177-213,286-321,407-442]						
	CUB_domain [809-918]						
75	Cellular Localization: may be secreted						

	1	11	21	31	41	51	
80	MGVAGRNRPG	AAWAVLLLLL	LLPPLLLLAG	AVPPGRGAA	GPQEDVDECA	QGLDDCHADA	60
	LCQNTPTSYK	CSCKPGYQGE	GRQCEDIDEC	GNELNGGCVH	DCLNIPGNYR	CTCFDGFMLA	120
	HDGHNCLDLD	ECLENNGGCQ	HTCVNVMGSG	ECCKEGFFFL	SDNQHTCIHR	SEGLSCMNK	180
	DHGCSHICKE	APRGSVACEC	RPGFELAKNQ	RDCILTCHNG	NGGCQHSQDD	TADGPECSCH	240
	PQYKMHDTGR	SCLEREDTVL	EVTESNTTSV	VDGDKRVKRR	LLMETCAVNN	GGCDRTCKDT	300

STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK 360  
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCQQVCVN 420  
 TVGSYECQCH PGYKHLHNNKK DCVEVKLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480  
 SSDVTTTIRTS VTFKLNKGKC SLKNAELFPE GLRPALPEKH SSVKESFRYV NLTCSSGKQV 540  
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600  
 FHLQLSGMNL DVAKKPPRTS ERQAESCQVG QGHAENQCVS CRAGTYDGA RERCILCPNG 660  
 TFQNEEGQMT CEP CPRPGNS GALKTPPEAWN MSECGLCQP GEYSADGFAP CQLCALGTFQ 720  
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHFY NTTTHRCIRC PVGTYYQPEFG 780  
 KNNCVSCPGN TTDFDGGSTN ITQCKNRRCG GELGDFGTGYI ESPNYPGNYP ANTECTWTIN 840  
 PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSNSVTTY ETCQTYERPI AFTSRSKKLW 900  
 IQFKSNEGNS ARGFQVPYVT YDEBYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960  
 LAHPQNYFKY TAQESREMFP RSFIRLLRSK VSRFLRPYK

**A17 DNA sequence**

Gene name: ESTs  
 Unigene number: Hs.293102  
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-489 (entire sequence is an open-reading-frame)

1 11 21 31 41 51  
 | | | | |  
 CAAAAAGAAA TAGATAAAAT AAATGGAAAA TTAGAAGAGT CTCCTGATAA TGATGGTTTT 60  
 CTGAAGGCTC CCTGCAGAAT GAAAGTTTCT ATTCCAACCTA AAGCCTTAGA ATTGATGGAC 120  
 ATGCAAACTT TCAAAGCAGA GCCTCCCGAG AAGCCATCTG CCTTCGAGCC TGCCATGAA 180  
 ATGCAAAAGT CTGTTCCAAA TAAAGCCTTG GAATTGAAGA ATGAACAAAC ATTGAGAGCA 240  
 GATCAGATGT TCCTCTCAGA ATCAAAACAA AAGAAGTTG AAGAAAATTC TTGGGATTCCT 300  
 GAGAGTCTCC GTGAGACTGT TTCACAGAAG GATGTGTGTG TACCCAAGGC TACACATCAA 360  
 AAAGAAATGG ATAAATAAAG TGGAAAATTA GAAGATTCAA CTAGCCTATC AAAAATCTTG 420  
 GATACAGTTC ATTCTTGTGA AAGAACAAGG GAACCTTCAA AAGACCCCTG TGACCCACGT 480  
 TCAGGAAAA

**A18 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.293102  
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272  
 Protein Accession #: none found  
 Signal sequence: none  
 Transmembrane domains: none  
 Cellular Localization: nuclear

1 11 21 31 41 51  
 | | | | |  
 QKEIDKINGK LEESPDNDGF LKAPCRMKVS IPTKALELMD MQTFKAEPPE KPSAFEPAPAE 60  
 MQKSVPNKAL ELKNEQTLRA DQMFPSSESKQ KXVEENSWDS ESLRETVSQK DVCVPKATHQ 120  
 KEMDKISGKL EDSTSLSKIL DTVHSCERTR ELQKDPDPR SGK

**Breast****A19 DNA SEQUENCE**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ACCGGGCACC GGACGGCTCG GGTACTTTTCG TTCTTAATTA GGTATGCCC GTGTGAGCCA 60  
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA AACTGTGGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180  
 AGAGGTCTCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCTCTGTGC ACCAGATGCA 300  
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTCTG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAGA CCATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACGCAATGTG TGCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT AAGGGAGGGA 780  
 TGTGCTCTG GCCACGTGCT TACCTTGCA GTCACAGCCT GTGGTCATAG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900  
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTTGTA CTCCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCA 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140  
 CTCAGTTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACCTCCCC 1200  
 GTGGAAAAAG TGTGCTGGAG GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCTGTCC TGAACACGCG GGCCGTCCCT TTGATTTCCA ACAAGATCTG CAACCCACAG 1320  
 GACGTGTACG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380

GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACCAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCGGTG TCACCTCCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA 1620  
 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCTTG GAGCTCTGAG 1680  
 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT 1740  
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800  
 AGTGCACTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860  
 TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCACACC CAACTAATTT 1920  
 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAAATGA TGTGCCTGCT TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040  
 ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 AGGGCGGCCT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCTCTG 2160  
 ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
 GCACCAAGCC AGAAGTCAG AACTGCAGTC ACTGCAGTT TTCACTCTTA GGGACCAGAA 2280  
 CCAAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCCTAT TTTCATGATT TCTTGTAGC ATTTGTGCT TGACGTATTA 2400  
 TTGTCTTTG ATTCCAATA ATATGTTTCC TTCCCTCAA AAAAATAAAA AAAAAATAA 2460  
 AAAAAATAA

**A20 Protein sequence:**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SpC domain: 216-444  
 Cellular Localization: not determined

1 11 21 31 41 51  
 | | | | |  
 MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIILI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF 120  
 TAAWKTMCSS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180  
 VTALHHSYV REGCASGHV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240  
 LCGGSVITPL WIITAACHVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFDPGKVCWT SGWGATEDGA GDASPVLNHA 360  
 AVPLISNKIC NHRDVGII SPSMLCAGYL TGGVDSCQGD SGGPLVCQER RLWLKLVGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

**A21 DNA SEQUENCE**

Gene name: ESTs; opposite strand to TRPS1  
 Unigene number: none  
 Probeset Accession #: AA428090  
 Nucleic Acid Accession #: AA428090  
 Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGAAGCCCA GTTTGAAACA CTGGGCTGAT ATAAAAATGT TTCTGAAAT AGACCAAAGG 60  
 CAAGTTGTTG GAGAAGAAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAAAC 120  
 TTTTCAGACA CAGATGATCT TATGTCCATA GTGGAGGAAT CAGACAGCTG CTACAACCGT 180  
 GATTCTGTTG GGCTTCCTGG TAGAGCTGGA GACAGACTGC AACCCAAGAC AAAACCCAGA 240  
 GGAAAAACAA CTAACCTCAG CCATTGCCCC AATTTCCACC TTGCTAGTTA TCAGAGTTCA 300  
 CTATTGTTTA AGCTCCAGGG GTCATACTAT GGCAATCTAC TGGTGGAAAT TATTCIGAGC 360  
 AAGTGTTTTG TTCAGCTTGC AGTATTAAAA CAAAAAATC ATTGCCTCCA GCTGCAAAGC 420  
 AAGGGCATTG CCATTATGAA AGCCCCCTCA AGACTCTCTG CTATTTTCAA AACATGGAAA 480  
 GAAAAAGGGA AAAAAAGAAA AAAATAATA ATTAGAAGGA TTTGTTCCCT AATTTGGGCT 540  
 CCCAAAAATG AGAAATGAAG ATGTGATAAT GAGGGGAGAT ACTAATTATT TTAACCTCTC 600  
 CAAGCAAATC TTCTGAAGCA ATCAATTATT TATATACTTT ATGTTCTGTC TTTTGTAT 660  
 TTTCTCTCTG GTTAAAAACA TGCAGGTGAG TCTTGCCAAC GTCCTTTCCT ATCTGGATCT 720  
 GTTCTGCCTC ATTTCTCTTT CAAAGTCATC TTTCAGGGAA CTGCGCTTGA TTAATTTGAT 780  
 TTTAAACAAA CAAATAAGAT ATTIGATATA TTAATTTAAA CTTTTGTAGA TGATTGATTA 840  
 GGAATTGCAT CATGTTTACA TGAGTATACC GAATTCAAAG TTAACCTTCA TAAGCAGGAG 900  
 TTTTACACA TCGTAACATA ATCATTACCC AATACTCGAC ACTCAATATT TGATACTCAA 960  
 CTGAATGTTT TTGAAATAAA CACATTTTTA TGTATCTCT CTGGAGAAAG TAGTATATAT 1020  
 CTTTTCATAC AAAATATATC AGTGAGAGAG TGTGTTGTTA AGAAAAAAA TCAAAGCACA 1080  
 ACAAGTTGAG AGAGTCCAGG CTTTATCAAT ATAAGTAATA ATTTTGTAGA ATGGTGATT 1140  
 GATTTCACCA TTTCAATTCA GCAGAGCCTG TATATATATA TATATATATA TATATATATA 1200  
 TATATATATA TATATATATA TATATATATA TGATCTGTAT TTCTATTGCT TAGAAGGATG 1260  
 AAAGTGAATC CATATAAACC ATACCAACGC CGTTATGTGT AACTGGTGGT AAAACTTTAT 1320  
 TATTCAGATT TAGATGTAAC AGACATCTTT GCTGCCTGAA GATGTTTTCG ATAAGAAATA 1380  
 CACCAAGAAC ATGTTTGTGA GTAGAAATGA ACATGCACTA TGAAAACAAA ATAAAAATAA 1440  
 ACCGAAAAAT TTTATGTGTT GTAAGAACAG AACTATTATA GCCAACATTC TAGTATTCAA 1500  
 ATCAGGACTA CAAATGGAAT TCTTTTCTTT AGCAACATGA AATCATTTCA TATGAAAGAC 1560  
 ATTTCTGCTT GGTGAATATT GCTGTAAGTT AAATTTTACA TTGGCATTTT GAGATGTTCC 1620  
 CCCCTCATGC CTCCCCCAA GTTTTCCATG TGGTTGTCAA ATAGTCCGC

**A22 Protein sequence:**

Gene name: ESTs; opposite strand to TRPS1  
 Unigene number: none  
 Probeset Accession #: AA428090  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 113-129  
 Cellular Localization: not determined

10 1 11 21 31 41 51  
 | | | | |  
 MKPSLKHWAD IKMFSEIDQR QVVGEIEHLQ VVSVSYLVEN FSDTDDLMSI VEESDSCYNR 60  
 DSVGLPGRAG DRLQPKTKPR GKTNNLSHLP NFHLASYQSS LLFKLQGSYY GNLLVEFILS 120  
 KCFVQLAVLK QKKHCLQLQS KGIAIMKAPQ RLSAIFKTKW EKGKKEKKII IRRICSLIWA 180  
 15 PKNEK

#### A23 DNA SEQUENCE

20 Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Nucleic Acid Accession #: AL133619  
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 | | | | |  
 ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCCA GCTCGCGGAC CCCGGGCTCT 60  
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCGCGA GAGCCCGCAG 120  
 30 CTCAGGCAGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180  
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240  
 GAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCCCTCCCA GGCACACTCA 300  
 AACTGCGCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CTGGGGCTCA 360  
 GGGGGAACAC AGGACGGGGA GCCCTCCAG ACTGTCTCTG CCCACCTGGC TGCACCTGGC 420  
 CCTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGTACCTCT 480  
 35 AGCGTGGGCT GGACGATGTT ATGCAGCCAA GCACAGCACG TGCTGCTCTC GGAAGCCCA 540  
 GGGCCTGAGG TCATTGTCAGG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCCT 600  
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CTGCGCTGCG TAGATCTTTG 660  
 CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720  
 ATGCTGGGGG CCAGGGGATG ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
 40 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTGTG TTCCTTGCCA CTGTGCAAG 840  
 GCATTTCCCC ATCTCTGACG CGGCCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900  
 GCTCACTTCC CATATCTTTT GGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGA 960  
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TTCCAGGGA 1020  
 45 GACATGGAGA AGGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCAGTGAG 1080  
 CTGTTCTGGG CAAAGTGTGG CCAAGTTCGG CAGCCCCAGC CTGCGATGCG TGGGGACGCT 1140  
 GACAGGACAC GGAAGAGGCG CATGCTTTCC CTCGGGACCT GCTGTTCCAT GTGTCCCAAG 1200  
 CCTCCTGCT TTCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGGCCTC TGCTCCCTTG 1260  
 GGCCTCTGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320  
 50 AGGCTGAAGG AGGCTCTCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGGC 1380  
 GGGCGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440  
 TCTGTCAAGT CCACTCTTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500  
 TCCTTCAACA AGCAAGATTG AAAAGCTGAC GTCTCCCAGA AGGCGGACCT GGAAGAGGAG 1560  
 CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTTGGG TACAAGGGCA GGCCAGAAAG 1620  
 55 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAAGGC 1680  
 AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCCTGC CCCTTCCCTT GCGAAAGCCC 1740  
 ACCACACTTA GGCAGTGCAG AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCCTGCAG 1800  
 ACCCAAGAGC TCGGCGACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860  
 CCGGAGGAAG CCGGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCCAA GGTCTCCACC 1920  
 60 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CTGCCCGCA 1980  
 CTGAAGCAGA CCCCAGAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040  
 AAACGGCGCC TGCATCGCTC AGTGCTTTGA

#### A24 Protein sequence:

65 Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Protein Accession #: T43457  
 Signal sequence: none found  
 Transmembrane domains: 303-322  
 70 Cellular Localization: not determined

75 1 11 21 31 41 51  
 | | | | |  
 MSGAGVAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60  
 QQQHSEMLAK LHEEIEHLKR ENKGEFARGP RPALPPQAH S TLPLPQHRNT AINSSTRLGS 120  
 GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWDAATS SRGWTMLCSQ AQHVLLSGSP 180  
 GPEVIAGRQV ATGCPDLPF PSRAEMGRNP WDSPPARSL PQIAAVARPR ISSPMALSPH 240  
 80 MLGAQGIWTH SIQGSPLPAIW AATMGTKGGS RVLFPCHLSK ALPHPDGSPH PAQDPGLWSQ 300  
 AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVGGP FPSRCGNSS 360  
 LFWAKCGPSR WQPCPSAGDA DRTREEMLS LGTCCSMCPK PSCFPDGPSP NHLSRASAPL 420  
 GARWVCINGV VPEPGGSPA RLKEGSSRTH RFGGKRGRLA GGSADTVRSP ADSLSMSSFO 480  
 SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGGARK 540

EKAEASNAGA ACMGNSQHQG RQMAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600  
 TQELRHLKSL LEGSQRPQAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA 660  
 LKQTPKNNFA ERQKRLQAMQ KRRLHRSVL

**A25 DNA SEQUENCE**

Gene name: ESTs; prolactin receptor  
 Unigene number: Hs.25252  
 Probeset Accession #: AA057193  
 Nucleic Acid Accession #: NM\_000949  
 Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
15  GGAGGCTGAA ATCCCCAGAC GCCGGTTTTC TGGGCTGGGC TTCTGCTTA CTCACCTCTT 60
    CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTCCACACA ATGGAGCTTC 120
    ATGTCCTCGT GCAGGAAGTA CTCATCGACT GATGTGGCAG ACTTTGCTCC CTGACAAAAA 180
    TAAAGAACTC TCCTATTTCAT GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAACCCCTGAA 240
    GTGAACCTCT GATACATTTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAATGTGG 300
    CATCTGCAAC CGTTTTCACT CTGCTACTTT TTCTCAACAC CTGCCTCTCG AATGGACAGT 360
    TACCTCCTGG AAAACCTGAG ATCTTTAAAT GTCGTTCTCC CAATAAGGAA ACATTACACT 420
    GCTGGTGGAG GCCTGGGACA GATGGAGGAC TTCTTACCAA TTATTCACCTG ACTTACCACA 480
    GGGAAAGGAGA GACACTCATG CATGAATGTC CAGACTACAT AACCCTGGGC CCAACTCCT 540
    GCCACTTTGG CAAGCAGTAG ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600
    CTAACCCAGT GGAAGCAGT TTCTCGGATG AACTTTATGT GGACGTGACT TACATAGTTC 660
    AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAACAA GCCAGAAGAC AGAAAACCCCT 720
    ACCGTGGATG TAAATGGTCT CCACCTACCC TGATTGACTT AAAAATCTGGT TGGTTTACGC 780
    TCCTGTATGA AATTGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGCTG 840
    GGCAGCAAAC AGAGTTTAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG 900
    TTGCTGCAA ACCAGACCAT GGATCTGGA GTGCATGGAG TCCAGCGACC TTCATTGAGA 960
    TACCTAGTGA TTCCACCATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCCTTCTG 1020
    CTGTCTCTG TTTGATTATT GTCTGGGCGG TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080
    GCATCTTTCC GCCAGTTTCT GGGCCAAAAA TAAAAGGATT TGATGCTCAT CTGTTGAGGA 1140
    AGGGCAAGTC TGAAGAACTA CTGAGTGCTT TGGGATGCCA AGACTTTCCT CCCACTTCTG 1200
    ACTATGAGGA TTGCTGGTGG GAGTATTTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA 1260
    TGTCACTCCA TTCAAAAGAA CACCCAAGTC AAGGTATGAA ACCCAATAC CTGGATCCTG 1320
    AACTGACTC AGGCCGGGGG AGCTGTGACA GCCCTTCCCT TTTGTCTGAA AAGTGTGAGG 1380
    AATCCAGGC CAATCCCTCC ACATTCTATG ATCCTGAGGT CATTTGAGAAG CCAGAGAATC 1440
    CTGAAACAAC CCACACCTGG GACCCCGAGT GCATAAGCAT GGAAGGCAAA ATCCCTTATT 1500
    TTTATGCTGG TGGATCCAAA TGTTCACAT GGCCTTACC ACAGCCAGC CAGCACAACC 1560
    CCAGATCCTC TTACCAAT ATTAATGATG TGTGTGAGCT GGCTGTGGGC CTTGCAGGTG 1620
    CACCGGCCAC TCTGTTGAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAAACCATTA 1680
    AGTCTAGAGA AGAGGGAAG GCAACCCAGC AGAGGGAGGT AGAAAGCTTC CATTTCTGAGA 1740
    CTGACCAAGA TACGCCCTGG CTGCTGCCCC AGGAGAAAAC CCCCTTTGGC TCCGCTAAAC 1800
    CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAGATGG TGCAATTATCA TTGCTACCAA 1860
    AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT 1920
    ATGCCAAGGT TCCCGGGGTC ATGGATAACA ACATCTGGT GTTGGTGCCA GATCCACATG 1980
    CTAAGAAAGT GGCCTGCTTT GAAGAATCAG CCAAGAGGC CCCACCATCA CTTGAACAGA 2040
    ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100
    TGGGTGGTTT GGATTACCTG GATCCCGCAT GTTTTACACA CTCCTTTCAC TGATAGCTTG 2160
    ACTAATGGAA TGATTGGTTA AAATGTGATT TTTCTTCAGG TAACACTACA GAGTACGTGA 2220
    AATGCTCAAG AAGTATGTTA GACTGACACT ACTAAAGCTC CCAGCTCCTT TCATGCTCCA 2280
    TTTTAAACCA CTGCTCTCT TCTCCAGCAG CTGATTCCAG AACAATCAT TATGTTTCTT 2340
    AACTGTGATT TGATAGTTTA CTTTTGCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400
    AAAAGCACAC TGTCTAGTAT TCCTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAAAG 2460
    GCTTTCATGA TTTGGCATGG GACAGACGGA AATGAAATTG TCAAAATGT TTACCATAGA 2520
    AAGATGACAA AAGAAAATTT TCCACATAGG AAAATGCCAT GAAAATGTCT TTTGAAAAC 2580
    AACTGCATAA CCTTACACT CCTCGTCCAT TTTATTAGGA TTACCCAAAT ATAACCATT 2640
    AAAAGAAAGAA TGCATTCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA 2700
    TTGCTGATAT GCAAGTAAGA AAT
  
```

**A26 Protein sequence:**

Gene name: ESTs; prolactin receptor  
 Unigene number: Hs.25252  
 Probeset Accession #: AA057193  
 Protein Accession #: NP\_000940  
 Signal sequence: 1-23  
 Transmembrane domains: 237-253  
 FN3 domains: 28-112, 127-215  
 Cellular Localization: plasma membrane

```

75  1      11      21      31      41      51
    |      |      |      |      |      |
    MKENVASATV FTLLFLNLTC LLNGQLPPGK PEIFKCRSPN KETFTCWWRP GTDGLPTNY 60
    SLTYHREGT LMHECPDYIT GGPNSCHFVK QYTSMWRTYI MMVNATNMQG SSFSDELYVD 120
    VTYIVQPDPP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAAEW 180
    80  EHFAGQQTE FKILSLHPGQ KYLVQVRCKP DHGYWSAWSP ATFIQIPSDF TMNDTTVWIS 240
    VAVLSAVICL IIVWVALKGG YSMVTCIFPP VPGPKIKGFD AHLEKKGKSE ELLSALGQD 300
    FPTSDEYDL LVEYLEVDGS EDQHLMSVHS KEHPSQGMKP TYLDPDTSRG RGCDSPSL 360
    SEKCEEPQAN PSTFYDPEVI EKPENPETTH TWDPQCISME GKIPYFHAGG SKCSTWPLPQ 420
  
```

PSQHNPRSSY HNIITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQQREVE 480  
 SFHSETDQDT PWLLPQEKTP FGSAPLDYV EIHKNVDGA LSLLPKQREN SGKPKKPGTP 540  
 ENNKEYAKVS GVMDNNILVL VPDPAKNVA CFESAKEAP PSLEQNQAEK ALANFTATSS 600  
 KCRLQLGGLD YLDPACFTHS FH

# A27 DNA SEQUENCE

Gene name: Human neuropeptide Y receptor Y1 (NPYY1)  
 Unigene number: Hs.169266  
 Probeset Accession #: L07615  
 Nucleic Acid Accession #: NM\_000909.1  
 Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CATTCCCACC CTTCCTTCTT TAATAAGCAG GAGCGAAAAA GACAAATTCC AAAGAGGATT 60  
 GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATTG CAATATCGGG 120  
 AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTAAA 180  
 20 ATAATCTATA ACAACCAAC CAATCAAAAT GAATTCACAA TTTATTTCCC AGGTTGAAAA 240  
 TCATTTCAGTC CACTCTAATT TCTCAGAGAA GAATGCCAG CTCTCGGCTT TTGAAAATGA 300  
 TGATTGTGCT CTGCCCCTTG CCATGATATT TACCTTAGCT CTGCTTATG GAGCTGTGAT 360  
 CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAC AAAAGGAGAT 420  
 25 GAGAAATGTT ACCAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTTGCCAT 480  
 CATGTGTCTC CCTTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC 540  
 GATGTGTAAG TTGAATCCTT TTGTGCAATG TGTTCGAATC ACTGTGTCCA TTTTCTCTCT 600  
 GGTTCCTCATT GCTGTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660  
 TAATAGACAT GCTTATGTAG GTATTGCTGT GATTGGGTC CTGCTGTGG CTCTTCTTT 720  
 30 GCCTTTCTCTG ATCTACCAAG TAATGACTGA TGAGCCGTTT CAAAATGTAA CACTTGATGC 780  
 GTACAAAGAC AAATACGTGT GCTTTGATCA ATTTCCATCG GACTCTCATA GGTGTCTTA 840  
 TACCCTCTC CTCTTGGTGC TGCAGTATT TGGTCCACTT TGTTTTATAT TTATTTGCTA 900  
 CTTCAAGATA TATATAGGCC TAAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA 960  
 TAAGTACAGG TCCAGTGAAA CAAAAGAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020  
 35 ATTTGCACTC TGCTGGCTCC CTCTTACCAT CTTTAACTG GTGTTTGATT GGAATCATCA 1080  
 GATCATTGCT ACCTGCAACC ACAATCTGTT ATTCCTGCTC TGCCACCTCA CAGCAATGAT 1140  
 ATCCACTTGT GTCAACCCCA TATTTTATGG GTTCTGAAC AAAAAGCTTC AGAGAGACTT 1200  
 GCAGTTCTTC TTCAACTTTT GTGATTTCCG GTCTCGGGAT GATGATTATG AAACAATAGC 1260  
 CATGTCCACG ATGCACACAG ATGTTTCCAA AACTTCTTTG AAGCAAGCAA GCCCAGTCGC 1320  
 40 ATTTAAAAAA ATCAACAACA ATGATGATAA TGAAAAAATC TGAAACTACT TATAGCCTAT 1380  
 GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT 1440  
 TCTCCCAAGG AATGGGGTTG AAATCATTTG AAAATGACTA AGATTTTCTT GTCTTGCTTT 1500  
 TTACTGCTTT TGTGTGATGT GTCATAATTA CATTTGAAC AAAAGGTGTG GGCCTTTGGGG 1560  
 TCTTCTGGAA ATAGTTTGA CCAGACATCT TTGAAGTGCT TTTTGTGAAT TTATGCATAT 1620  
 45 AATATAAGA CTTTATACT GTACTTATG GAATGAATT TCTTAAAGT ATTACGATGC 1680  
 GCTGACTTCA GAAGTACCTG CCATCCAATA CGGTCAATAG ATTGGGTCAT CTTGATTAGA 1740  
 TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800  
 TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860  
 GAAGTCATTC AGAAGTGGTT TGAGGTTTCT GTTTTGTGGT GGTTTTGTGTT TGTTTTGTGTT 1920  
 50 TTTTTCACC TTAAGGGAGG CTTTCATTTC CTCCGACTG ATTGTCACTT AAATCAAAAT 1980  
 TTAAAAATGA ATAAAAAGAC ATACTTCTCA GCTGCAATA TTATGGAGAA TTGGGCACCC 2040  
 ACAGGAATGA AGAGAGAAG CAGCTCCCA ACTTCAAAAC CATTTTGGTA CCTGACAACA 2100  
 AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT 2160  
 TATATTTATT TGAATTGATG GTCAAGAGAT TTTCCATTTT TTTTACAGAC TGTTCAGTGT 2220  
 55 TTGTCAAGCT TCTGGTCTAA TATGTACTCG AAAGACTTTC CGCTTACAAT TTGTAGAAAC 2280  
 ACAAATATCG TTTTCCATAC AGCAGTGCCT ATATAGTGAC TGATTTTAACT TTTCAATGTC 2340  
 CATCTTTCAA AGGAAGTAAC ACCAAGGTAC AATGTTAAAG GAATATTAC TTTACCTAGC 2400  
 AGGGAATAAT ACACAAAAAC TGCAGATACT TCATATAGCC CATTTTAACT TGTATAAACT 2460  
 GTGTGACTTG TGGCGTCTTA TAAATAATGC ACTGTAAAGA TTACTGAATA GTTGTGTCACT 2520  
 60 GTTAATGTGC CTAATTTTCA GTATCTTGTA ATCATGATTG AGCCTCAGAA TCATTTGGAG 2580  
 AAACATATAT TTAAGAAACA AGACATACTT CAATGTATTA TACAGATAAA GTATTACATG 2640  
 TGTTTGATTT TAAAGGGCG GACATTTTAT TAAATCAAT ATTGTTTTTG CTTTCTCTGA 2700  
 GGAGTCTCTT TCAGTTTCAT TTTTCTCAT CCCATGACTT CCCTCCGATG GT

# A28 Protein sequence:

Gene name: Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds  
 Unigene number: Hs.169266  
 Probeset Accession #: L07615  
 Protein Accession #: NP\_000900.1  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [57-91]  
 Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286,  
 300-322  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MNSTLFSQVE NHSVHNSFSE KNAQLLAFEN DDCHLPLAMI FTLALAYGAV IILGVSGNLA 60  
 LIIILKQKE MRNVNIIIV NLSFSDLLVA IMCLPFTFVY TLMDDHVVFE AMCKLNPFVQ 120  
 CVSITVSIFS LVLIAVERHQ LIINPRGWRP NNRHAYVVGIA VIWVLAVASS LPFLIYQVMT 180  
 DEFPQNVTLTD AYKDKYVCFD QPPSDSHRLS YTTLLLVLYQ FGPLCFIFIC YFKIYIRLKR 240  
 RNNMMDKMRD NKYRSSETR INIMLLSIVV AFVVCWLPIT IFNTVFDWNH QIIATCNHNL 300  
 LFLLCHLTAM ISTCVNPIFY GFLNKNFQRD LQFFNFNCFDF RSRDDDDYETI AMSTMHTDVS 360



KTSCLKQASPV AFKKINNDD NEKI

A29 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)  
 Unigene number: Hs.208229  
 Probeset Accession #: AI819198  
 Nucleic Acid Accession #: NM\_032551.1  
 Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCCTGGG GGGCACCGGC CAACGCCTCC 60
GGCTGCCCGG GCTGTGGCGC CAACGCCTCG GACGGCCCGG TCCCTTCGCC GCGGGCCGTG 120
GACGCTGGCG TCGTACCGCT CTTCTTCGCG GCGCTGATGC TGTGCGGCTT GGTGGGGAAC 180
TCGCTGGTCA TCACGTCATC CTGCCGCCAC AAGCCGATGC GGACCGTGAC CAACCTCTAC 240
ATCGCCAACC TGGCGGCCAC GGACGTGACC TTCCTCCTGT GCTGCGTCCC CTTACGCGCC 300
CTGCTGTACC CGTGCCTCGG CTGGGTGCTG GCGCACTTCA TGTGCAAGTT CGTCAACTAC 360
ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420
TGGTACGTGA CGGTGTTCCC GTTGCGCGCC CTGCACCGCC GCACGCCCGG CCTGGCGCTG 480
GCTGTACAGC TCAGCATCTG GGTAGGCTCT CCGGCGGTGT CTGCGCCGGT GCTCGCCCTG 540
CACGCGCTGT CACCCGGGCG GCGCGCTTAC TGCACTGAGG CCTTCCCCAG CCGCGCCCTG 600
GAGCGCGCTT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGTGCGGCTT GCTCGCCACC 660
TGCCTGCTGT ATGCGGCCAT GCTGCGCCAC CTGGGCCGGG TCGCCGTGCG CCGCGCGCCC 720
GCCGATAGCG CCCTGACAGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGGCCAAG 780
GTCTCGCGCG TGGTGGCGCG CGTGGTCTCT CTCTTCGCGG CTGCTGGGGG CCCCATCCAG 840
CTGTTCTCTG TGCTGCAGGC GCTGGGCCCG GCGGGCTCCT GGCAACCCAG CAGCTACGCC 900
GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCCTACA GCAACTCCGC GCTGAACCCG 960
CTGCTCTACG CCTTCCTGGG CTCGCACTTC CGACAGGCCT TCCGCCGCGT CTGCCCTGTC 1020
GCGCGCGGCC GCCCGCGCGG CCGCGCGCGG CCGGACCCCT CGGACCCCGC AGCCCCACAC 1080
GCGGAGCTGC ACCGCTCTGG GTCCACCCG GCCCGGCCCA GGGCGCAGAA GCCAGGAGC 1140
AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA

```

A30 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA  
 Unigene number: Hs.208229  
 Protein Accession #: AI819198  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [59-323]  
 Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MHTVATSGEN ASWGAPANAS GCPGCGANAS DGPVPSRAV DAWLVPLFFA ALMLLGLVGN 60
SLVIYVICRH KPMRTVTNFI IANLAATDVT FLLCCVPFTA LLYPLPGWVL GDFMCKFVNY 120
IQQVSQVATC ATLTAMSVDR WYVTVFPLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180
HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240
ADSALQGQVL AERAGAVRAK VSRLVAAVVL LFAACWGPQI LFLVLQALGP AGSWHPRSYA 300
AYALKTWAKC MSYNSALNP LLYAFLGSHF RQAFRRVCPC APRRRRRPRR PGPSDPAAPH 360
AELHRLGSHP APARAQKPGS SGLAARGLCV LGEDNAPL

```

A31 DNA SEQUENCE

Gene name: CH22\_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)  
 Unigene number: Hs.252387  
 Probeset Accession #: NM\_014246  
 Nucleic Acid Accession #: NM\_014246  
 Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGCGCCGC CGCCGCCGCC CGTGCTGCCC GTGCTGCTGC TCCTGGCCGC GCGCGCCGCC 60
CTGCCGCCGA TGGGGCTGCG AGCGGCCGCC TGGGAGCCGC GCGTACCCGG CCGGACCCGC 120
GCCTTCGCCC TCCGGCCCGG CTGTACCTAC GCGGTGGGCG CCGCTTGACG GCCCGGGGCG 180
CCGCGGGAGC TGCTGGACGT GGGCCGCGAT GGGCGGCTGG CAGGACGTGC GCGGCTCTCG 240
GGCGCGGGGC GCCCGCTGCC GCTGCAAGTC CGCTTGGTGG CCGCAGTGC CCGGACGGCG 300
CTGAGCCGCC GCCTGCGGAC GCGCACGCAC CTTCCCGGCT GCGGAGCCCG TGCCCGGCTC 360
TGCGGAACCG GTGCCCGGCT CTGCGGGGCG CTCTGCTTCC CCGTCCCCGG CCGCTGCGCG 420
GCCGCGCAGC ATTCCGCGCT CGCAGCTCCG ACCACCTTAC CCGCTGCGCG CTGCCCGCCG 480
CGCCCCAGGC CCGCTGTGCC CCGCGCTCCC ATCTGCTTGC CGCCGGGCGG CTCGGTCCGC 540
CTGCGTCTGC TGTGCGCCCT GCGGCGCGCG GCTGGCGCCG TCCGGGTGGG ACTGGCGCTG 600
GAGGCGGCCA CCGCGGGGAC GCCCTCCGCG TCGCATCCCG CATCGCCGCC CCGTCCCGCG 660
AACTTGCCCG AAGCCCGGGC GGGGCCGGCG CGACGGGCCG GCGGGGCGAC GAGCGGCAGA 720
GGGAGCCTGA AGTTTCCGAT GCCCAACTAC CAGGTGGCGT TGTGTTGAGAA CGAACCGGCG 780
GGCACCTCA TCCTCCAGCT GCACGCGCAC TACACCATCG AGGGCGAGGA GGAGCGCGTG 840
AGCTATTACA TGGAGGGGCT GTTCGACGAG CGCTCCCGGG GCTACTTCCG AATCGACTCT 900
GCCACGGGCG CCGTGAGCAC GGACAGCGTA CTGGACCGCG AGACCAAGGA GACGACGCTC 960
CTCAGGGTGA AAGCGGTGGA CTACAGTACG CCGCCGCGCT CCGCCACCAC CTACATCACT 1020
GTCTTGGTCA AAGACACCAA CGACCACAGC CCGGTCTTCG AGCAGTCGGA GTACCGCGAG 1080
CGCGTGCGGG AGAACCTGGA GGTGGGCTAC GAGGTGCTGA CCATCCGCGC CAGCGACCCG 1140

```

	GACTCGCCCA	TCAACGCCAA	CTTGCGTTAC	CGCGTGTGG	GGGCGCGTG	GGACGTCTTC	1200
	CAGCTCAACG	AGAGCTCTGG	CGTGGTGAGC	ACACGGGCGG	TGCTGGACCG	GGAGGAGGCG	1260
	GCCGAGTACC	AGCTCCTGGT	GGAGGCCAAC	GACCAGGGGC	GCAATCCGGG	CCCGCTCAGT	1320
5	GCCACGGCCA	CCGTGTACAT	CGAGGTGGAG	GACGAGAACG	ACAACCTACC	CCAGTTTCAGC	1380
	GAGCAGAACT	ACGTGGTCCA	GGTGGCCGAG	GACGTGGGGC	TCAACACGGC	TGTGCTGCGA	1440
	GTGCAGGCCA	CGGACCGGGA	CCAGGGCCAG	AACGCGGCCA	TCACTACAG	CATCCTCAGC	1500
	GGGAACGTGG	CCGGCCAGTT	CTACCTGCAC	TCGCTGAGCG	GGATCCTGGA	TGTGATCAAC	1560
	CCCTTGGATT	TCGAGGATGT	CCAGAAATAC	TCGCTGAGCA	TTAAGGCCCA	GGATGGGGGC	1620
10	CGGCCCCCGC	TCATCAATTC	TTCAGGGGTG	GTGCTGTGTC	AGGTGCTGGA	TGTCAACGAC	1680
	AACGAGCCTA	TCTTTGTGAG	CAGCCCCCTC	CAGGCCACGG	TGCTGGAGAA	TGTGCCCTTG	1740
	GGCTACCCCG	TGGTGACAT	TCAGGCGGTG	GACGCGGACT	CTGGAGAGAA	CGCCCCGCTG	1800
	CACATATCGC	TGGTGGACAC	GGCCTCCACC	TTTCTGGGGG	GCGGCAGCGC	TGGGCCCTAAG	1860
	AATCCTGCC	CCACCCCTGA	CTTCCCTTTC	CAGATCCACA	ACAGCTCCGG	TTGGATCACA	1920
15	GTGTGTGCCG	AGCTGGACCG	CGAGGAGGTG	GAGCACTACA	GCTTCGGGGT	GGAGGCGGTG	1980
	GACCACGGCT	CGCCCCCAT	GAGCTCCTCC	ACCAGCGTGT	CCATCACGGT	GCTGGACGTG	2040
	AATGACAACG	ACCCGGTGT	CACGACGCCC	ACCTACGAGC	TTGCTCTGAA	TGAGGATGCG	2100
	GCCGTGGGGA	GACGCGTCT	GACCCTGCAG	GCCCGCGACC	GTGACGCCAA	CAGTGTGATT	2160
	ACCTACCAGC	TCACAGGGCG	CAACACCCGG	AACCGCTTTC	CACCTCAGCAG	CCAGAGAGGG	2220
20	GGCGGCCCTCA	TCACCCCTGGC	GCTACCTCTG	GACTACAAGC	AGGAGCAGCA	GTACGTGCTG	2280
	GCGGTGACAG	CATCCGACGG	CACACGGTCG	CACACTGCGC	ATGTCTTAAT	CAACGCTCACT	2340
	GATGCCAACA	CCACAGAGCC	TGTCTTTTCA	AGCTCCCAT	ACACAGTGAG	TGTCACTGAG	2400
	GACAGGCTGT	TGGGCACCTC	CATTGCTACC	CTCAGTGCCA	ACGATGAGGA	CACAGGAGAG	2460
	AATGCCCGCA	TCACCTACGT	GATTACAGAC	CCCGTGCCGC	AGTTCCGCAT	TGACCCCGAC	2520
25	AGTGGCACCA	TGTACACCAT	GATGGAGCTG	GACTATGAGA	ACCAGGTCCG	CTACACGCTG	2580
	ACCATCATGG	CCCAGGACAA	CGGCATCCCG	CAGAAATCAG	ACACCAACAC	CCTAGAGATC	2640
	CTCATCCTCG	ATGCCAATGA	CAATGCACCC	CAGTTCTTGT	GGGATTTCTA	CCAGGGTTCC	2700
	ATCTTTGAGG	ATGCTCCACC	CTCGACACAG	ATCCTCCAGG	TCTCTGCCAC	GGACCCGGAC	2760
	TCAGGTCCCA	ATGGGCGTCT	GCTGTACACC	TTCCAGGGTG	GGGACGACGG	CGATGGGGAC	2820
30	TTCTACATCG	AGCCCACTGT	CGGTGTGATT	CGCACCCAGC	GCCGGCTGGA	CCGGGAGAA	2880
	GTGGCCGTGT	ACAACCTTTG	GGCTCTGGCT	GTGGATCGGG	GCACTCCAC	TCCCTTAGC	2940
	GCCTCGGTAG	AAATCCAGGT	GACCATCTTG	GACATTAATG	ACAATGCCCC	CATGTTTGTG	3000
	AAGGACGAAC	TGGAGCTGTT	TGTTGAGGAG	AACAACCCAG	TGGGGTCCGT	GGTGGCAAG	3060
	ATTCGTGCTA	ACGACCTCTG	TGAAGGCCCT	AATGCCCAGA	TCATGTATCA	GATTGTGGAA	3120
35	GGGACATGCG	GGCATTTCTT	CCAGCTGGAC	CTGCTCAACG	GGGACCTCGG	TGCCATGGTG	3180
	GAGCTGGACT	TTGAGGTCCG	GCGGGAGTAT	GTGCTGTTGG	TGCAGGCCAC	GTCCGCTCCG	3240
	CTGGTGAGCC	GACCCACGGT	GCACATCCTT	CTCGTGGACC	AGAATGACAA	CCCCCTGTG	3300
	CTGCCCGACT	TCCAGATCCT	CTTCAACAAC	TATGTACCCA	ACAAGTCCAA	CAGTTTCCCC	3360
	ACCGGCGTGA	TCGGCTGAT	CCCGGCCCAT	GACCCCGACG	TGTGAGACAG	CCTCAACTAC	3420
40	ACCTTCGTGT	AGGGCAACGA	GCTGCGCCTG	TTGCTGCTGG	ACCCCGCCAC	GGGCGAACTG	3480
	CAGCTCAGCC	GCGACCTGGA	CAACAACCGG	CCGCTGGAGG	CGCTCATGGA	GGTGTCTGTG	3540
	TCTGATGGCA	TCCACAGCGT	CACGGCCTTC	TGCACCCCTG	GTGTCAACAT	CATCACGGAC	3600
	GACATGCTGA	GGCATTTCTT	CAGTGTCCGC	CTGGAGAACA	TGTCCCAGGA	GAAGTTCTCT	3660
	TCCCGCTGCG	TGGCCCTCTT	CGTGGAGGGG	GTGGCCGCGG	TGCTGTCCAC	CACCAAGGAC	3720
45	GACGTCTTCG	TCTTCAACGT	CCAGAACGAC	ACCGACGTCA	GCTCCAACAT	CCTGAACGTG	3780
	ACCTTCTCGG	CGCTGTGCTC	TGGCGGCGTC	CGCGGCCAGT	TCTTCCCGTC	GGAGGACCTG	3840
	CAGGAGCAGA	TCTACCTGAA	TCGGACGCTG	CTGACCACCA	TCTCCACGCA	GCGCGTGTCT	3900
	CCCTTCGACG	ACAACATCTG	CCTGCGCGAG	CCCTGCGAGA	ACTACATGAA	TGCGGTGTCT	3960
	GTTCTGCGAT	TCGACAGCTC	CGCGCCCTTC	CTCAGCTCCA	CCACCGTGCT	CTTCCGGCCC	4020
50	ATCCACCCCA	TCAACGGGCT	GCGCTGCCGC	TGCCCGCCCG	GCTTCAACCG	CGACTACTGC	4080
	GAGACGGAGA	TCGACCTCTG	CTACTCCGAC	CCGTGCGGCG	CCAACGGCCG	CTGCCGCGAG	4140
	CGCGAGGGCG	GCTACACCTG	CGAGTGCTTC	GAGGACTTCA	CTGGAGAGCA	CTGTGAGGTG	4200
	GATGCCCGCT	CAGGCGCTG	TGCCAACGGG	GTGTGCAAGA	ACGGGGGCAC	CTGCGTGAAC	4260
	CTGCTCATCG	GCGGCTTCCA	CTGCGTGTGT	CCTCTGCGCG	AGTATGAGAG	GCCCTACTGT	4320
55	GAGGTGACCA	CCAGGAGCTT	CCCCCCCCAG	TCCTTCGTCA	CCTTCCGGGG	CCTGAGACAG	4380
	CGTTTCCACT	TCACCATCTC	CCTCACGTTT	GCCACTCAGG	AAAGGAACGG	CTTGCTTCTC	4440
	TACAACGGCC	GCTTCAATGA	GAAGCACGAC	TTCATCGCCC	TGGAGATCGT	GGACGAGCAG	4500
	GTGCAGCTCA	CCTTCTCTGC	AGGCGAGACA	ACAACGACCG	TGGCACCGAA	GGTTCCCACT	4560
	GGTGTGAGTG	ACGGGCGGTG	GCACCTCTGT	CAGGTGCACT	ACTACAACAA	GCCCAATATT	4620
60	GGCCACCTGG	GCCTGCCCCA	TGGGCGGTCC	GGGGAAAAGA	TGGCGTGGT	GACAGTGGAT	4680
	GATTGTGACA	CAACCATGGC	TGTGCGCTTT	GGAAGGACA	TCGGGAACCTA	CAGCTGCGCT	4740
	GCCCAGGGCA	CTCAGACCGG	CTCCAAGAAG	TCCCTGGATC	TGACCGGCCC	TCTACTCTG	4800
	GGGGGTGTCC	CCAACCTGCC	AGAAGACTTC	CCAGTGACCA	ACCGGCGATT	CGTGGGCTGC	4860
	ATGCGGAACC	TGTGAGTGA	CGGCAAAAAT	GTGGACATGG	CCGGATTTCAT	GCCTCAACAT	4920
65	GGCACCCGGG	AAGGCTGCGC	TGCTCGGAGG	AACCTCTGCG	ATGGGAGGCG	GTGTGAGAA	4980
	GGAGGCACCT	GTGTCAACAG	GTGGAATATG	TATCTGTGTG	AGTGTCCACT	CCGATTCCGG	5040
	GGGAAGAACT	GTGAGCAAGC	CATGCCCTCAC	CCCCAGCTCT	TCAGCGGTGA	GAGCGTCTGT	5100
	TCCTGGAGTG	ACCTGAACAT	CATCATCTCT	GTGCCCTGGT	ACCTGGGGCT	CATGTTCCGG	5160
	ACCGGGAAGG	AGGACAGCGT	TCTGATGGAG	GCCACCACTG	GTGGGCCCA	CAGCTTTCAG	5220
70	CTCCAGATCC	TGAACAACCTA	CCTCCAGTTT	GAGGTGTCCC	ACGGCCCCCTC	CGATGTGGAG	5280
	TCCGTGATGC	TGTCCGGGTT	GCGGGTGACC	GACGGGGAGT	GGCACCACT	GCTGATCGAG	5340
	CTGAAGAATG	TTAAGGAGGA	CAGTGAGATG	AAGCACCTGG	TCACCATGAC	CTTGACTAT	5400
	GGGATGGACC	AGAACAAGGC	AGATATCGGG	GGCATGCTTC	CCGGGCTGAC	GGTAAGGAGC	5460
	GTGGTGGTGC	GAGGCGCTTC	TGAAGACAAG	GTCTCCGTGC	GCCGTGGATT	CCGAGGCTGC	5520
75	ATGCAGGGAG	TGAGGATGGG	GGGGACGCCC	ACCAACGTCG	CCACCTTGAA	CATGAACAAC	5580
	GCACCTCAAG	TCAGGGTGAA	GGACGGCTGT	GATGTGGACG	ACCCCTGTAC	CTCGAGCCCC	5640
	TGTCCCCCCA	ATAGCCGCTG	CCACGACGCC	TGGGAGGACT	ACAGCTGCGT	CTGTGACAAA	5700
	GGGTACCTTG	GAATAAATG	TGTGGATGCC	TGTCACTTGA	ACCCCTGCGA	GAACATGGGG	5760
	GCCTGCGTGC	GCTCCCCCGG	CTCCCCGAG	GGGTACGTGT	GCGAGTGTGG	GCCCACTGAC	5820
80	TACGGGCGGT	ACTGTGAGAA	CAAACTCGAC	CTTCCGTGCC	CCAGAGGCTG	TGGGGGAAAC	5880
	CCCGTCTGTG	GACCTTGCCA	CTGTGCCGTC	AGCAAAGGCT	TTGATCCCGA	CTGTAATAAG	5940
	ACCAACGGCC	AGTGCCAATG	CAAGGAGAAT	TACTACAAGC	TCCTAGCCCA	GGACACCTGT	6000
	CTGCCCTGCG	ACTGCTTCCC	CCATGGCTCC	CACAGCCGCA	CTTGGACAT	GGCCACGGGG	6060
	CAGTGTGCTT	GCAAGCCCGG	CGTCATCGGC	CGCCAGTGCA	ACCGCTGCGA	CAACCCGTTT	6120
	GCCGAGGTCA	CCACGCTCGG	CTGTGAAGTG	ATCTACAATG	GCTGTCCCAA	AGCATTGAG	6180

	GCCGGCATCT	GGTGGCCACA	GACCAAGTTC	GGGCAGCCGG	CTGCGGTGCC	ATGCCCTAAG	6240
	GGATCCGTTG	GAAATGCGGT	CCGACACTGC	AGCGGGGAGA	AGGGCTGGCT	GCCCCCAGAG	6300
	CTCTTTAACT	GTACCAACCA	CTCCTTCGTG	GACCTCAGGG	CCATGAATGA	GAAGCTGAGC	6360
5	CGCAATGAGA	CGCAGGTGGA	CGGCGCCAGG	GCCCTGCAGC	TGGTGAGGGC	GCTGCGCAGT	6420
	GCTACACAGC	ACACGGGCAC	GCTCTTTGGC	AATGACGTGC	GCACGGCCTA	CCAGCTGCTG	6480
	GGCCACGTCC	TTCAGCACGA	GAGCTGGCAG	CAGGGCTTCG	ACCTGGCAGC	CACGCAGGAC	6540
	GCCGACTTTC	ACGAGGACGT	CATCCACTCG	GGCAGCGCCC	TCCTGGCCCC	AGCCACCAGG	6600
	GCGGCGTGGG	AGCAGATCCA	GCGGAGCGAG	GGCGGCACGG	CACAGCTGCT	CCGGCGCCTC	6660
10	GAGGGCTACT	TCAGCAACGT	GGCAGCAAC	GTGCGGCGGA	CGTACCTGCG	GCCCTTCGTC	6720
	ATCGTCACCG	CCAACATGAT	TCTTGCTGTC	GACATCTTTG	ACAAGTTCAA	CTTTACGGGA	6780
	GCCAGGGTCC	CGCGATTTCGA	CACCATCCAT	GAAGAGTTCC	CCAGGGAGCT	GGAGTCTCTC	6840
	GTCTCCTTCC	CAGCCGACTT	CTTCAGACCA	CCTGAAGAAA	AAGAAGGCCC	CCTGCTGAGG	6900
	CCGGCTGGCC	GGAGGACCAC	CCCGCAGACC	ACGCGCCCGG	GGCTTGGCAC	CGAGAGGGAG	6960
15	GCCCCGATCA	GCAGGCGGAG	GCACACCCCT	GATGACGCTG	GCCAGTTCGC	CGTCGCTCTG	7020
	GTCACTATTT	ACCGCACCTT	GGGGCAGCTC	CTGCCCCGAGC	GCTACGACCC	CGACCGTCTG	7080
	AGCCTCCGGT	TGCCTCACCG	GCCCATCAT	AATACCCCGA	TGGTGAGCAC	GCTGGTGTAC	7140
	AGCGAGGGGG	CTCCGCTCCC	GAGACCCCTG	GAGAGGCCCG	TCCTGGTGGA	GTTCGCCCTG	7200
	CTGGAGGTGG	AGGAGCGAAG	CAAGCCTGTC	TGCGTGTCTT	GGAAACCACT	CCTGGCCGTT	7260
20	GGTGGGACGG	GAGGGTGGTC	TGCCCGGGGC	TGCGAGCTCC	TGTCCAGGAA	CCGGAACACAT	7320
	GTCCGCTGCC	AGTGCAGCCA	CACAGCCAGC	TTTGCGGTGC	TCATGGATAT	CTCCAGGCGT	7380
	GAGAACGGGG	AGGTCTTGCC	TCTGAAGATT	GTCACTATG	CCGCTGTGTC	CTTGTCACTG	7440
	GCAGCCCTGC	TGGTGGCCTT	CGTCTCCTG	AGCCTGTGTC	GCATGCTGCG	CTCCAACCTG	7500
	CACAGCATTC	ACAAGCACCT	CGCCGTGGCG	CTCTTCCTCT	CTCAGCTGGT	GTTCGTTGAT	7560
25	GGGATCAACC	AGACGGAAAA	CCCGTTTCTG	TGCACAGTGG	TTGCCATCCT	CCTCCACTAC	7620
	ATCTACATGA	GCACCTTTGC	CTGGACCCCT	GTGGAGAGCC	TGCATGTCTA	CCGCATGCTG	7680
	ACCGAGGTGC	GCAACATCGA	CACGGGGCCC	ATGCGGTTCT	ACTACGTCGT	GGGCTGGGGC	7740
	ATCCCGGCCA	TTGTACAGG	ACTGGCGGTC	GGCCTGGACC	CCCAGGGCTA	CGGGAACCCC	7800
	GACTTCTGCT	GGCTGTGCTC	TCAAGACACC	CTGATTTGGA	GCTTTGCGGG	GCCCATCGGA	7860
30	GCTGTTATAT	TGCTCAACAC	AGTCACTTCT	GTCTATCTGA	CAAAGGTTTC	CTGCCAAGA	7920
	AAGCACCATT	ATTATGGGAA	AAAAGGGATC	GTCTCCCTGC	TGAGGACCCG	ATTCTCTCTG	7980
	CTGCTGCTCA	TCAGCGCCAC	CTGGCTGCTG	GGGCTGCTGG	CTGTGAACCG	CGATGCACTG	8040
	AGCTTTCACT	ACCTCTTCGC	CATCTTCAGC	GGCTTACAGG	GCCCTTCGT	CCTCCTTTTC	8100
	CACCTGCGTG	TCAACCAGGA	GGTCCGGAAG	CACCTGAAGG	GCGTGCTCGG	CGGGAGGAAG	8160
35	CTGCACCTGG	AGGACTCCGC	CACCACCAGG	GCCACCCCTG	TGACGCGCTC	CCTCAACTGC	8220
	AACACCACCT	TCGGTGACGG	GCCTGACATG	CTGCGCACAG	ACTTGGGCGA	GTCCACCGCC	8280
	TCGCTGGACA	GCACTGCTCAG	GGATGAAGGG	ATCCAGAAGC	TCCGCGTGTC	CTCTGGGCTG	8340
	GTGAGGGGCA	GCCACGGAGA	GCCAGACCGG	TCCCTCATGC	CCAGGAGCTG	CAAGGATCCC	8400
	CCTGGCCACG	ATTCGACTC	AGATAGCGAG	CTGTCCCTGG	ATGAGCAGAG	CAGCTCTTAC	8460
40	GCCTCCTCAG	ACTCGTCAGA	CAGCGAGGAC	GATGGGGTGG	GAGCTGAGGA	AAAATGGGAC	8520
	CCGGCCAGGG	GCGCGCTCCA	CAGCACCCCC	AAAGGGGACG	CTGTGGCCAA	CCACGTTCCG	8580
	GCCGGCTGGC	CCGACCAGAG	CCTGGCTGAG	AGTGACAGTG	AGGACCCCG	CGGCAAGCCC	8640
	CGCCTGAAGG	TGGAGACCAA	GGTCAGCGTG	GAGCTGCACC	GCGAGGAGCA	GGGCAGTCAC	8700
	CGTGGAGAGT	ACCCCCCGGA	CCAGGAGAGC	GGGGGCGCAG	CCAGGCTTGC	TAGCAGCCAG	8760
45	CCCCCAGAGC	AGAGGAAAGG	CATCTTGAAG	AATAAAGTCA	CCTACCCGCC	GCCGCTGACG	8820
	CTGACGGAGC	AGACGCTGAA	GGGCGGCTC	CGGGAGAAGC	TGGCCGACTG	TGACAGAGC	8880
	CCCACATCCT	CGCGCACGTC	TTCCTTGGGC	TCTGGCGGCC	CCGACTGCGC	CATCACAGTC	8940
	AAGAGCCCTG	GGAGGGAGCC	GGGGCGTGAC	CACCTCAACG	GGGTGGCCAT	GAATGTGCGC	9000
	ACTGGGAGCG	CCCAGGCCGA	TGGCTCCGAC	TCTGAGAAAC	CGTGAGGCAA	GCCCGTCAAC	9060
50	CCACACAGGC	TGCGGCATCA	CCCTCAGACC	TTGAGGCCCA	AGGGGCCACT	GCCCTTGAAG	9120
	TGGAGTGGGC	CCAGGATGTG	GCGGTCCCCA	TGGTGGCAGC	CCCCGACTG	ATCATCCAGA	9180
	CACAAAGGTC	TTGGTTCTCC	CAGGAGCTCA	GGGCTGTCTA	GACCTGTGTA	CAAGTGCCAA	9240
	AGGCCACAGG	CATGAGGGAG	GCGTGGACCA	CTGGGCCAGC	ACCCTGAGT	CCTAAGACTG	9300
	CAGTCAAAGC	CAGAAGTGAG	AGGGGACCCC	AGACTGGGCG	CAGAGGCTGG	CCAGAGTTCA	9360
55	GGAAAGCCGG	GCACAGACCA	AAGACCCGGG	TCCAGCCCGG	CCCAGGCGGG	CATCTCATGG	9420
	CAGTGGGAGC	CCGTGGCTGG	CAGCCCGGGC	AGTCTTTTGC	AAAGGCACCC	CTTGTCTTAA	9480
	AATCACTTCC	CTATGTGGGA	AAGGTGGAGA	TACTTTTATA	TATTTGTATG	GGACTCTGAG	9540
	GAGGTGCAAC	CTGTATATAT	ATTGCAATTC	TGCTGACTTT	GTTATCCCGA	GAGATCCATG	9600
	CAATGATCTC	TTGCTGTCTT	CTCTGTCAAG	ATTGCACAGT	TGTACTTGAA	TCTGGCATGT	9660
60	GTTGACGAAA	CTGGTGCCCC	AGCAGATCAA	AGGTGGGAAA	TACGTACGCA	GTGGGGCTAA	9720
	AACCAAGCCG	CTAGAAGCCC	TACAGCTGCC	TTCCGCCAGG	AAGTGAGGAT	GGTGTGGGCG	9780
	CTCCCGCCCG	GCCCCCTGGG	TCCCCAGTGT	TCGCTGTGTG	TGCGTTTGTG	CTCTGCTGCC	9840
	ATCTGCCCCG	GCTGTGTGAA	TTCAAGACAG	GGCAGTGACG	CAC TAGGCAG	GTGTGAGGAG	9900
	CCCTGCTGAG	GTCACTGTGG	GGCAGGTTG	CCACACGGCT	GTCATTTTTC	ACCTGGTCACT	9960
65	TCTGTACCCA	CCACCCCTCT	CCCTCACCGC	CTCCAGGTG	GCCCCGGAGC	TGCAGGTGGG	10020
	GATGGCTTTG	TCCTTTGCTC	CTGCTCCCGG	TGGGACCTGG	GACCTTAAAG	CGTTGCAGGT	10080
	TCCTGATTTG	GACAGAGGTG	TGGGGCCTTC	CAGGCCGTTA	CATACCTCCT	GCCAAATCTC	10140
	TAACCTCTCT	AGACTGCGAG	GATCTCCAGG	CAGGGTTCTC	CCCTCTGGAG	TCTGACCAAT	10200
	TACTTCATTT	TGCTTCAAAT	GGCCAATTGT	GCAGAGGGAC	AAAGCCACAG	CCACACTCTT	10260
70	CAACGGTTAC	CAAACTGTTT	TTGGAAATTC	ACACCAAGGT	CGGGCCCACT	GCAGGCAGCT	10320
	GGCACAGCGT	GGCCCCAGGG	GCTGTGGAAC	GGGTCCCGCA	ACTGTGACAC	ATGTTTGATT	10380
	TTAGCGTTTC	CTTTGTCTCT	CAAAATCAGG	GCCCCAAATA	GTGATCAGCA	CAGCTGCTTC	10440
	CAAAATAGGAG	AAACCATATA	ATAGGATGAA	AATCAAGTAA	AATGCAAAGA	TGTCCACACT	10500
	GTTTTTAACT	TGACCTGTAT	GAAAATGTGA	GCACTGTTAG	CAGATGCCCTA	TGGGAGAGGA	10560
75	AAAGCGTATC	TGAAAATGGT	CCAGGACAGG	AGGATGAAAT	GAGATCCCCAG	AGTCTCTACA	10620
	CCTGAATGAA	TTATACATGT	GCCTTACCAG	GTGAGTGGTC	TTTCGAAGAT	AAAAAATCT	10680
	AGTCCCTTTA	AACGTTTGCC	CCTGGCGTTT	CCTAAGTACG	AAAAGGTTTT	TAAGTCTTCG	10740
	AACAGTCTCC	TTTCATGACT	TTAACAGGAT	TCTGCCCCCT	GAGGTGTAAT	TTTTTTGTTC	10800
	TATTTTTCCT	CACGTACTCC	ACAGCCAACA	TCACGAGGTG	TAATTTTATA	TTTGATCAGA	10860
80	ACTGTTACCA	AAAAACAAC	GTCAAGTTTA	TTGAGATGGG	AAAAATGTAA	ACCTATTTT	10920
	ATTACTTAAG	ACTTTATGGG	AGAGATTAGA	CACCTGGAGG	TTTTTAACAGA	ACGTGTATTT	10980
	ATTAATGTTT	AAAACACTGG	AATTACAAAT	GAGAAGAGTC	TACAATAAAT	TAAGATTTT	11040
	GAATTTGTAC	TTCTGCGGTG	CTGGTTTTC	TCCACAAACA	CCCCCGCCCC	TCCCCATGCC	11100
	CAGGGTGGCC	GTGGAAGGGA	CGGTTTACGG	ACGTGCAGCT	GAGCTGTCCG	TGTCCCATGC	11160
	TCCCTCAGCC	AGTGGAACGT	GCCGGAACCT	TTGTTCATT	CCCTAGTAGG	CCTGCCACAG	11220

CCTAGATGGG CAGTTTTTGT CTTTCACCAA ATTTGAGGAC TTTTTTTTTT TGCCATTATT 11280  
 TCTTCAGTTT TCTTTGTTTG CACTGATCTT TCTCCTCTCC TTCTGTGACT CCAGTGACTC 11340  
 AGACGTTAGA CCTCTTGATG TTTTCCCACT GGTCCCTGAG GCTCTGTTC

### 5 A32 Protein Sequence

Gene name: CH22\_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1), Hs.252387  
 Unigene number:  
 Protein Accession #: NP\_055061  
 Signal sequence: 1-20  
 Cadherin domains: 250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092, 1110-1199  
 Pfam domains: Laminin\_EGF [2003-2048], 7tm\_2 [2465-2708]  
 Latrophilin/GPS domains: 2407-2460  
 Transmembrane domains: 1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704  
 Cellular Localization: plasma membrane

20	1	11	21	31	41	51	
	MAPP	VLL	LPAM	WEPR	AFAL	AVGA	60
	PREL	LDV	GRLA	GRPL	PLQV	RLVAR	120
	CGTG	ARLC	GA	LCFV	PPGG	CA	180
25	LRLL	CAL	RRA	AGAV	RVLAL	EAAT	240
	GS	LKFP	MPNY	QVAL	FENEP	AGT	300
	ATGA	VSTDS	V	LDRET	KE	THV	360
	RVRE	NLE	VGY	EVLT	TIRAS	DR	420
	AEYQ	LLVE	AN	DQGR	NPGL	S	480
30	VQAT	DRD	QGG	NAAI	IHY	SIL	540
	RPPL	INS	SSGV	VSVQ	VLDV	ND	600
	HYRL	VD	TAST	FLGG	SGAG	PK	660
	DHGS	PPM	SSS	TSVS	ITVLD	V	720
	TYQL	TG	GNTR	NRFA	LS	SRG	780
35	DANT	HRP	VFQ	SSHY	TVSV	SE	840
	SGTM	YTM	MEL	DYEN	QVAY	TL	900
	IFED	APP	STS	ILQV	SATDR		960
	VAVY	NL	WALA	VDRG	SP	P	1020
	IRAN	DP	DEG	NAQI	MY	Q	1080
40	LVSRA	TVHIL	LVDQ	NDN	PPV		1140
	TFVQ	GNEL	RLL	LLDP	PAT	GEL	1200
	DMLT	NSIT	IVR	LENM	SQ	E	1260
	TFSA	LL	PGGV	RGQF	FP	SEDL	1320
	VLRE	DSS	APF	LSST	TVL	FRP	1380
45	REGG	YTCE	CEC	EDFT	GHE	CEV	1440
	EVTR	SFP	PPQ	SFVT	FR	LRQ	1500
	VQLT	FS	AGET	TTT	VAP	KVPS	1560
	DCDT	MA	VR	GKDI	GNYS	CA	1620
	MRNL	SVD	GKN	VDMA	GFI	ANN	1680
50	GKNC	EQA	MPH	PQ	FS	GES	1740
	LQIL	NNY	LQF	EVSH	GP	SDVE	1800
	GMDQ	NKAD	IG	GML	PGL	T	1860
	ALKV	RVK	DGC	DVDD	PCT	SSP	1920
	ACVR	SP	GP	GYVC	EC	GP	1980
55	TNGQ	CQ	CKEN	YYKL	LA	QDTC	2040
	AEVT	TLG	CEV	IYNG	CP	KAFE	2100
	LFNC	TTIS	FSV	DLRA	MNE	KLS	2160
	GHLV	Q	HES	WQ	Q	FDLA	2220
	EGYF	SN	VAR	N	VR	TR	2280
60	VSPF	AD	FFRP	PEEK	E	GPLLR	2340
	VIIY	RTL	Q	LP	ERY	DPDR	2400
	LEVE	ERT	KPV	CVF	WNH	SLAV	2460
	ENGE	VLP	LKI	VTYA	AV	SLSL	2520
	GINQ	TEN	PFL	CTV	VA	ILLHY	2580
65	IPAIV	TGL	AV	GLDP	Q	GYGNP	2640
	KHHY	Y	GKGI	VSLR	RTA	FL	2700
	HCVL	NQ	EV	RLK	GV	LG	2760
	SLDS	IV	DEG	IQKL	GV	SSGL	2820
	ASSH	SD	SDSE	DGVG	A	E	2880
70	RLKV	ETK	VSV	ELH	REE	Q	2940
	LTEQ	TLK	GRL	REKL	AD	CEQS	3000
	TGSA	QAD	GSD	SEK			

### 75 A33 DNA SEQUENCE

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3  
 Unigene number: Hs.198252  
 Probeset Accession #: X95876  
 Nucleic Acid Accession #: X95876  
 Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

80	1	11	21	31	41	51	
	CCA	ACCA	CAAG	AGAG	GGG	CAG	60
	GCC	ACCA	CCAT	GTG	AGT	GACC	120

5 CCCTCCTGGA GAACTTCAGC TCTTCCTATG ACTATGGAGA AAACGAGAGT GACTCGTGCT 180  
 GTACCTCCCC GCCCTGCCCA CAGGACTTCA GCCTGAACCT CGACCGGGCC TTCTTGCCAG 240  
 CCTCTACAG CCTCCTCTTT CTGCTGGGGC TGCTGGGCAA CGGCGCGGTG GCAGCCGTGC 300  
 TGCTGAGCCG GCGGACAGCC CTGAGCAGCA CCGACACCTT CCTGCTCCAC CTAGCTGTAG 360  
 CAGACACGCT GCTGGTGCTG ACACCTGCCG TCTGGGCAGT GGACGCTGCC GTCCAGTGGG 420  
 TCTTTGGCTC TGGCCTCTGC AAAGTGGCAG GTGCCCTCTT CAACATCAAC TTCTACGCAG 480  
 GAGCCCTCCT GCTGGCCTGC ATCAGCTTTG ACCGCTACCT GAACATAGTT CATGCCACCC 540  
 AGCTCTACCG CCGGGGGCCC CCGGCCCGCG TGACCCCTAC CTGCTGGCT GTCTGGGGGC 600  
 10 TCTGCCTGCT TTTGCGCCTC CCAGACTTCA TCTTCCTGTC GGCCACCCAC GACGAGCGCC 660  
 TCAACGCCAC CCACTGCCAA TACAACCTCC CACAGGTGGG CCGCACGGCT CTGCGGGTGC 720  
 TGCAGCTGGT GGTGCGCTTT CTGCTGCCCC TGCTGGTCAT GGCCTACTGC TATGCCACAC 780  
 TCCTGGCCGT GCTGCTGGTT TCCAGGGGCC AGCGGCGCCT GCGGGCCATG CGGCTGGTGG 840  
 TGGTGGTCGT GGTGGCCTTT GCCCTCTGCT GGACCCCTTA TCACCTGGTG GTGCTGGTGG 900  
 15 ACATCCTCAT GGACCTGGGC GCTTTGGCCC GCAACTGTGG CCGAGAAAGC AGGGTAGACG 960  
 TGGCCAAAGT GGTCACTCA GGCCTGGGCT ACATGCACTG CTGCCTCAAC CCGCTGCTCT 1020  
 ATGCCTTTGT AGGAGTCAAG TTCCGGGAGC GGATGTGGAT GCTGCTCTTG CGCTGGGCT 1080  
 GCCCAACCA GAGAGGGCTC CAGAGGCAGC CATCGTCTTC CCGCCGGGAT TCATCCTGGT 1140  
 CTGAGACCTC AGAGGCTCTC TACTCGGCT TGTGAGGCCG GAATCCGGGC TCCCTTTTCG 1200  
 20 CCCACAGTCT GACTTCCCCG CATTCAGGC TCCTCCCTCC CTCTGCCGGC TCTGGCTCTC 1260  
 CCCAATATCC TCGTCTCCGG GACTCACTGG CAGCCCCAGC ACCACCAAGT CTCCCGGGAA 1320  
 GCCACCTTCC CAGCTCTGAG GACTGCACCA TTGCTGCTCC TTAGCTGCCA AGCCCCATCC 1380  
 TGCCGCCCGA GGTGGCTGCC TGGAGCCCCA CTGCCCTTCT CATTTGAAAA CTAAACTTC 1440  
 ATCTTCCCCA AGTCCGGGGA GTACAAGGCA TGGCGTAGAG GGTGCTGCCC CATGAAGCCA 1500  
 CAGCCAGGC CTCAGCTCA GCAGTGACTG TGGCCATGGT CCCCAGACC TCTATATTTG 1560  
 25 CTCTTTTATT TTTATGTCTA AAATCCTGCT TAAACTTTT CAATAAACAA GATCGTCAGG 1620  
 ACCAAAAAAA AAAAAAAGAA AAAAAAAGAA AAAAAAAGAA AAAAAAAGAA BHLITERAT 1680  
 UREBHCBLAS TPBHCORHO LOGUESMOUS ECXCRMYLEV SERQVLDASD FAFLEENSTS 1740  
 PYDYGENESD FSDSPPCPD FSLNFDRTFL PALYSLLFLL GLLGNGAVAA VLLSQRTALS 1800  
 30 STDFTLLHLA VADVLLVLT PLWAVDAVQ WVFGPGLCKV AGALFNINFY AGAFLLACIS 1860  
 FDRYLSIVHA TQIYRRDPRV RVALTCIVVW GLCLLFALPD FIYLSANYDQ RLNATHCQYN 1920  
 FPQVGRFALR VLQLVAGFL PLVMAYCYA HILAVLLVSR QRRFRAMRL VVVVVAFAV 1980  
 CWTPLYHLVVL VDILMDVGV LARNCGRESHV DVAKSVTSGM GYMHCCLNPL LYAFVGVKFR 2040  
 EQMWMFLFRL GRSDQRGPQR QPSSSRRESS WSETTEASYL GL

**A34 Protein sequence**

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3  
 Unigene number: Hs.198252  
 Protein Accession #: P49682  
 40 Signal sequence: none found  
 Pfam domains: 7tm\_1 [70-318]  
 Transmembrane domains: 57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323  
 DRY box: 148-149  
 45 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 50 MVLEVS DHQV LNDAEVAALL ENFSSSYDYG ENESDSCCTS PPCPD FSLN PDRAFLPALY 60  
 SLLFLGLLG NGAVAALLS RRTALSSDT FLLHLAVADT LLVLTPLWA VDAAVQWVFG 120  
 SGLCKVAGAL FNINFYAGAL LLACISFDYR LNIHVATQLY RRGPPARVTL TCLAVWGLCL 180  
 LFALEPDFIFL SAHDERLNA THCQYNFPQV GRTALRVLQL VAGFLLPLLV MAYCYAHILA 240  
 VLLVSRGQRR LRAMRLVVVV VVAFALCWTP YHLVVLVDIL MDLGALARNC GRESRVDAK 300  
 55 SVTSGLGVMH CCLNPLLYAF VGVKFRERMW MLLRLGCPN QRLQRPSS SRRDSSWSET 360  
 SEASYSGL

**A35 DNA SEQUENCE**

Gene name: Differentially expressed C016 gene (clone MGC:5257)  
 Unigene number: Hs.69517  
 60 Probeset Accession #: AA447522  
 Nucleic Acid Accession #: BC001291  
 Coding sequence: 44-541 (start and stop codons are underlined)

65 1 11 21 31 41 51  
 | | | | |  
 GGGGGCGCCG CGCGCTGACC CTCCCTGGGC ACCGCTGGGG ACGATGGCGC TGCTCGCCTT 60  
 GCTGCTGGTC GTGGCCCTAC CGCGGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG 120  
 70 AGATCCAGAG GACTCCCAGC GAACGGACGA GGGTGACAAT AGAGTGTGGT GTCATGTTTG 180  
 TGAGAGAGAA AACACTTTTC AGTGCCAGAA CCCAAGGAGG TGCAAATGGA CAGAGCCATA 240  
 CTGCGTTATA GCGGCCGTGA AAATATTTCC ACGTTTTTTC ATGGTTGCGA AGCAGTGCTC 300  
 CGCTGGTTGT GCAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGAAGA 360  
 GCCCATGCCC TTCTTTTACC TCAAGTGTG TAAATTCGC TACTGCAATT TAGAGGGGGC 420  
 75 ACCTATCAAC TCATCAGTGT TCAAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG 480  
 GCTGTGGCTG GCCATCTCTC TGCTGCTGGC CTCCATTGCA GCCGGCCTCA GCCTGTCTTG 540  
 AGCCACGGGA CTGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTTGTC 600  
 ACCTGTTGCA TTAACCTTGT TTTCTGTGTA TTACCTCTTG GTTTGACTTC CCAGGGTCTT 660  
 GGGATGGGAG AGTGGGGATC AGGTGCAGTT GGCTCTTAAC CCTCAAGGGT TCTTTAATCT 720  
 80 ACATTCAAG GAAGTCCAGA TCTCCTGAGT AGTGATTTTG GTGACAAGTT TTTCTCTTTG 780  
 AAATCAAACC TTGTAACCTA TTTATTGCTG ATGGCCATCT TTTTCTTGA CTCCCTCTG 840  
 CCTCTGAGG GTTCACTATT GATGGGGAGG GAGGCCTAAG TACCCTCAT GGAGAGTATG 900  
 TGCTGAGATG CTTCCGACCT TTCAGGTGAC GCAGGAACAC TGGGGGAGTC TGAATGATTG 960  
 GGGTGAAGAC ATCCTGAGG TGAAGGACTC CTCAGCATGG GGGGCAGTGG GGCACACGTT 1020  
 AGGGCTGCCC CCATTCCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTTC TCAACCTTTT 1080

CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTTG AAGAACTTA GACTTCACCC 1140  
 ACCAGCTGGC ACAGGTGCAC AGATTCATAA ATTCCCACAC GTGTGTGTTT AACATCTGAA 1200  
 ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260  
 CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCACC AAAAACAAAT ACAAGGGGAC 1320  
 TTCAAAGTT CACGAAAAAA AAAAAA AAAA AAAA AAAA

A36 Protein sequence:

Gene name: Differentially expressed CO16 gene (clone MGC:5257)  
 Unigene number: Hs.69517  
 Probeset Accession #: AA447522  
 Protein Accession #: AAH01291  
 Signal sequence: 1-17 (first underlined sequence)  
 Transmembrane domain: 146 - 162  
 Cellular localization: plasma membrane

1 11 21 31 41 51  
 | | | | | |  
 MALLALLLVV ALPRVWTDAN LTARQRDPED SQRTDEGDNR VVCHVCEREN TFECQNPRRC 60  
 KWTEPYCVIA AVKIFPRFFM VAKQCSAGCA AMERPKPEEK RFLLEBPMPF FYLKCKCKIRY 120  
 CNLEGGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSLSL

A37 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51  
 | | | | | |  
 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCCGCTGTG 60  
 CCGTGTCTGT AGCAGGCGCG CGGAGAGCCA GCTGCTCCCC GGAACAACCT TCACCAATGA 120  
 GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCCG GCGCCTGGCA 180  
 GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240  
 GTCGAAATGT GGCCCAACCT TCTTCCCTG TGCCAGCGCG ATCCATGCA TCATTGGTCG 300  
 CTTCGGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360  
 AAACCCCTCT GTTGTCTCCA CCGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA 420  
 GAGCTTCATC TCGCATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480  
 AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540  
 TTACCCGAGC ATCACCTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGCG 600  
 CCTGCTGGCA CTGGTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCCG 660  
 GCACCGGCTG CAGCACCGCT TGCTGTCTGT CCGCTTGGTG GTCCCTGGAC ACCCCACCA 720  
 CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780  
 GAATGCGTCG GAAGTAGGCT CCCACCCCTC CTACTCCGAG GCCTTGTCTG ACCAGAGGCC 840  
 TGGGTGGTAT TTTCTTCTCT CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900  
 CGACCTGCCC CCTTACCGCT CCGGTCCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960  
 CAGCAGCTCT CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCCAGGA 1020  
 GGGCACTGCT GTGCCAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080  
 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTG TAACAATTG 1140  
 TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
 AACTATCTCT GCATTCCCTT CCTCCCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260  
 TGACATGATC TGTGTGCGT CTTTCTGTG AGGTCACTCT TCCCTTGGGA CCCGAGATCA 1320  
 CACCTCATTT TTTACATTA TTTGTGTTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380  
 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440  
 CGCTGGACCC AATCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500  
 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAATT CCATTGAGC 1560  
 ATCAAAACCT GCTTGCACA ATCTATTGTT ATGCCCCCAG TTCAGCAGAG TCAGTGGCCA 1620  
 AAGAAAACTT TGGACGTGAG TAACACCCCT CAGCAGTCGC AACGTTATTT TGGTTTGTG 1680  
 AAGGACTCTG AAACCATCTA CCTGTATATA ATTCTGGCTT TAGAAATTTG CCCAAGAATG 1740  
 CTCATTCTGA GAGCTTTCTT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800  
 GAGCCCTCC CATGAGTTTA TCCAAGTTCT CAGTCCTTAA AATGCAGGCT GCCAAGACCC 1860  
 TACACCTGCC CTGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCACC CTCCAGCTG 1920  
 ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980  
 GTATGTCCCT GTGGCCACCA CCCAGCCTGT CTTGCTCATT CATGCAGCCT CAACACTGGC 2040  
 CTCCAAAGTT CCCTAACAC TTGCAAAGTC CTTTTTACCT GTGCATTGAG ACTTGAGGAC 2100  
 ACTGGTTTCT ATCAGAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160  
 CTGCACTGTG CACGCTCCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220  
 GGTGAGGTC AGGCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280  
 AGACAATTG GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340  
 TGAAACAGTG TGTGTTGTTT TTCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA 2400  
 AGCTGTCTCT TTTTGTGTTT TTCCTTTAAC AAGTCCAAA GAAAGATGCA AAAGGAGATC 2460  
 ACACCTTTCG CCCCTGAGC CCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520  
 ACATTGTGTC ATTGTGACAC TTTGAGGTTA TTATTTATCA AGTCTTGAA GGAAGCAGAA 2580  
 AGAGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640  
 TTCTCTGTGT CAGCTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT 2700  
 AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGAA CCAGGTAGAG 2760  
 CCACCTCGGG CAGCTGTAC CATTTCAGAA CTTCTTTCCG CAGCTGAAGA AATGTTCACT 2820  
 AACCTGTTTG ACGTAATTA AACACAGACC TGCAGGAAGT GGGGCTAAAG TGGCATTGAG 2880  
 TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTACAGAA 2940  
 AAGCTAGCCA CTGTTATTTT GTTTGTTTAA AAAAAA GAAAGAAAGA AAGAAAGAAA 3000

AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060  
 CTGAGTAATC CAATAAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120  
 CATTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTTCTTC 3180  
 TTTCTGTGTC TCTGGAAGTT GTTTAGAGGA AAGAATCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTATG 3300  
 AGATAAGGGA TGCTACTATA TGCTTTTATA AAACAAACAG GGACATTTT ATTATAGATT 3360  
 TGATTTTAT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420  
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG 3540  
 AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT 3600  
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660  
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720  
 GAAAGGTTGT GTGTCTGTGC TTTTGTGTTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780  
 TTATACCTT TAATAAATTT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GWMCTAMARM 3840  
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCACTTCGGG 3900  
 TGGGGCGGCG GGGCCACGT AGGTACGGCG ACCACGGCG CCCAACGGG ACCCCAGAG 3960  
 GAAACCTCG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCGCCGG 4020  
 GGAACCGCA GAGTGTGCG TAAACACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

A38 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MWLLGPLCLL LSSAAESQLL PGNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60  
 EKECPKAKSK CGPTFFPCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 KNGLCIDKSF ICDGQNNCRD NSDEESCESS QEPGSGQVFW TSENQLVYYP SITYAIIGSS 180  
 VIFVLVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240  
 YVASQAEQNA SEVGSPPSYS EALLDQRPBW YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEFRDSEPSQ GTEEV

A39 DNA sequence

Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGCTGCTCG GCTTCTTGAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60  
 GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CTCCCGAGG GCGAGGCAGC 120  
 GACCCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240  
 CCGCGGCGGC CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCCCT 300  
 CGCTGCGCTC CTGGACGTTT CCGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360  
 TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCATC AGCGAGTGCA 420  
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 GCTCCTGGAC CTAGGGCCCG GCGTCGTCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGCG 540  
 CCGCGCGGAA AGCGCCGCGG GACAGTCAGT GACGAGGCCG GGGGGTCGCC GGGGCCACGA 600  
 CTTCTCGGAG ACCGTCCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660  
 TGTGGGGCGC TCGCGCTCG TCCGTCTCCT CATCCTGGAA CGCCGCTTCG CTCCTGCAGC 720  
 TGCTGCTGGC TGCGCTGCTG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780  
 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCCAGCGC 840  
 GGCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900  
 GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960  
 CGGGCGGACA AAGACGGGGC CGGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020  
 GGAGACGGCG AGGGTGCGCC CCCACCCGTG AGGGCTTGGC AGCGGTGCTC CCCTGAAGGC 1080  
 TCCCGGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCGG TGCCAGACGC 1140  
 CGCGGATTCC CATCTCTTCC ACGCGGCGGC CCCTCTCCCC TGCAGCGGCC CGCCTTGCCC 1200  
 ATCTACGTGC CGTTCCTCAT TGTGGGCTCC GTGTTTGTG CTTTATCAT CTTGGGGTCC 1260  
 CTGGTGGCAG CCGTGTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCA GACAGACCGA 1320  
 GCGCCAGGGG GTAAACCGCTT GATGGAGACC ATCCCATGA TCCCAAGTGC CAGCACCTCC 1380  
 CGGGGGTCTG CCTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440  
 GGGGCCCCGG CGCCCCCAAC AAGGTCACAG ACCAAGTGT GTTGCCTGGA AGGGACCATG 1500  
 AACACAGTGT ATGTCAACAT GCCCAGCAAT TTCTCTGTGC TGAACITGTA GCAGGCCACC 1560  
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGACG 1620  
 CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCCTGGCTAC 1680  
 AGGCAGATT AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740  
 ACTGTATAAC CGAGAGTCAAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTCGAG GTGGAAGTCC GCACATGTCT GTGGTATTTA TGGCACGATT CCTTTGGATG 1860  
 GCTTCATTG CCCCAGACT GTATGAAAC ATCTCCGAAT TAGCATTCTT GGATATGTTT 1920  
 CATCCAGGAT ATCATTGATT TATGATGGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040  
 AGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTATTAT TATTTCTTTT 2100

5 TTGTTGTGTA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160  
 TTTTITTTTT TTTTITTTAA TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG 2220  
 TGGTGCAGATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCCTGCCTC 2280  
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTTT 2340  
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400  
 TCTGCCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460  
 TGAGCCTTTT TTTTITTTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520  
 ATTCTAAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATTCACA 2580  
 10 GGCACACCTT AATTTTCATTG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640  
 GGGCTATTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700  
 TTA AAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACCTA ATGAAGACAT TTCAGAACTC 2760  
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCACTT CATCCCCTTC 2820  
 TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATCTTTT 2880  
 15 TATATTGAAA TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCCTG 2940  
 TGGTTATGGT TTGGCGTTTC CTTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCCT 3000  
 GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060  
 AAAAAATTTT TTGCTTACTT TATAAAATT CAAAGAAATG TGTTACAAAG ATACTTAGTA 3120  
 TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTT 3180  
 20 GCAGATCATA AGGCTTTTTA TACTCTTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240  
 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTTCTCCAC ACTGTTCTTG 3300  
 ATTTCTCTC TCCTTCAGGC CTCACAGGC ACTGTATTCA TTGCCAATGT TCCAAATAT 3360  
 CAAATTCAG TGAATTTAT TGTGTGTTCT TTACTTATAT AAAAAAGAT AACTTTAAGG 3420  
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTA ACAAATCGCT 3480  
 25 GTATGGTATG GTCTTCTACA CATTATGTC TATAGATATC TATCGATCAT CTTCTATTC 3540  
 TGTTTCATGA CTGAATAATG TAAACCACTG GTTGGCAATT GGTATCATCA ATGATACTCA 3600  
 TTTTAAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660  
 TGAAAAAAA AAAAAAAA AAAAAAAA

30 A40 Protein sequence  
 Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 35 Transmembrane domains: 402-424  
 Cellular localization: not determined

40 1 11 21 31 41 51  
 | | | | |  
 MLSGFLMSPS TQHRAYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60  
 GEAEKGNRGE PPWIRAAQQ PRPPAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPEA 120  
 SGRQPRGSPD CIPRFPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAEAGSG 180  
 45 PRGKRRGTVS DEARGSPGFR LLGDRPALSG DALSAFVVPV CGALAAARPS HPPTPLRSCS 240  
 CCWLRCWRRG RGPSEYCHG WLDAQGVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300  
 ARLDQGGGCDN DRQQGAGEFG RADKDGPRRL GRASCLRGTO GDGEGAPFPV RAWQRCSPG 360  
 SPKGRQLLRA FPGQLPRARR RGFPSPPRGG PSPLQRPALP IYVPFLIVGS VFVAFIILGS 420  
 LVAACCCRCRL RPKQDPQQSR APGGNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS 480  
 50 GARAPFTRSQ TNCLPEGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGGYL HPPVVGTVQ 540  
 HDSVPMTAVP PFMDGLQPGY RQIQSPFPHT NSEQMYPV TV

55 A41 DNA SEQUENCE:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51  
 | | | | |  
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60  
 CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTCACAG TTTCTTCCAA CTTGCCATT 120  
 65 GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180  
 ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
 ATGGTTATTC ATCACTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300  
 CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
 GAAACCCACTG ATAAGAATTT ATCACTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420  
 70 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
 TATGAGCCTC GGGATTATAC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540  
 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTCA 600  
 GAAGAAAACC TCTGCGACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660  
 75 TTACTATTTA GTTTTITTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTITTTAA 720  
 TCTGAAAAAA AAAAAAAA AAAAAAAA

80 A42 Protein sequence:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted



5  
1 | 11 | 21 | 31 | 41 | 51 |  
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60  
PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM 120  
FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

## A43 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1  
Unigene number: Hs.106778  
Probeset Accession #: N51919  
Nucleic Acid Accession #: AF189723  
Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

20  
1 | 11 | 21 | 31 | 41 | 51 |  
ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
TCTCAGTTTA AAAATCCCTT TATTATGCTG CTCTCTGGCT CTGCAGTCAT CAGTGTTTTA 240  
ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300  
25 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360  
CCAGAAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCC AGACTTGGTT 420  
CCAGGTGATA CAGTTTGCTT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTC 480  
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540  
AAGGTGACAG CTCTCAGGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600  
30 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCTT TGGAAACAGGA 660  
GAAAATTCTG AATTGGGGGA GGTTTTAAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780  
ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840  
ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTACAGTGT 900  
35 ACGCTAGCTC TTGGTGTATG GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960  
ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCAG ATAAACTGAG AACACTGACG 1020  
AAGAATGAAA TGACTGTATC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTACT 1080  
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTTGTTGATG GTGATGTTGT TCATGGATT 1140  
TATAACCCAG CTGTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200  
40 AGAACAATA CTCTAATGGG GAAGCCAAACA GAAGGGGCCCT TAATTGCTCT TGCAATGAAG 1260  
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAA CTGAATACCC TTTTAGCTCT 1320  
GAGCAAAAGT GGAATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380  
TGTTTTATGA AAGTGTCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440  
GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAGA GAAGGCACGC 1500  
45 ATGGGCTCAG CGGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCCTGAACCT GGGACAGCTG 1560  
ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620  
ACACACTCA TTGCTCAGG AGTATCAATA AAAATGATTA CTGGAGATT 1680  
GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCCAAAA CTTCACAGT AGTCTCAGGA 1740  
GAAGAAATAG ATGCAATGGA TGTTTCAGCAG CTTCACAAA TAGTACCAA GGTTCAGTA 1800  
50 TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860  
TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920  
ATTGGAGTTG CGATGGGCCA GACTGGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980  
CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040  
AATAACATTA AAAATTTTCT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTA 2100  
55 ATCTCATTTG CTACATTAAT GAACCTTCTC AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160  
ATCAATATTA TTATGGATGG ACCCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220  
GATGTCAATC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTGATA 2280  
CTTAAATATC TTGATTTTATC AATAATCATT GTTTGTGGGA CTCTGTTTGT CTCTGGCGT 2340  
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400  
60 TTTTGTGACA GTTCAATGAC ACTAAGTTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT 2460  
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520  
CTAGTTATTT ACTTCTCTCC GCTTCAGAA GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580  
GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640  
65 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700  
CTTGAAGTAT GA

## A44 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1  
Unigene number: Hs.106778  
Probeset Accession #: N51919  
Protein Accession #: AAF27813  
Signal sequence: none found  
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878  
Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]  
Cellular Localization: not determined

80  
1 | 11 | 21 | 31 | 41 | 51 |  
MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI 60  
SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQYEYRSEK SLEELSKLVP 120  
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS 180  
KVTAQPAAAT NGDLASRSNI AFMGTLVRGC KAKGVVIGTG ENSEFGEVFK MMQAEAPKT 240  
PLQKSMDDLK QLSFYISFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGLPFIVTV 300

TLALGVMRMV KKRAIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360  
 GVGYNQFGEV IVDGDDVVHGF YNPAVSRIE AGCVCNDAVI RNNTLMGKPT EGALIALAMK 420  
 MGLDGLQDDY IRKAIEYFSS EQKWMVAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480  
 5 GQTLTLTQQQ RDVYQKEKAR MGSAGLRVLA LASGPBLGQL TFLGLVGIID PPRTGVKEAV 540  
 TTLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG EEIDAMDVQQ LSQIVPKVAV 600  
 FYRASPRHKM KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMQGTGT DVCKEADAMI 660  
 LVDDDFQTIM SAIEBGKGIY NNIKNFVRFO LSTSI AALT ISLATLMNFP NPLNAMQILW 720  
 10 INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780  
 ELRDNVITPR DTTMTFTCFV FDFMFNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840  
 LVIIYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVERSREKIQ KHVSTSSSF 900  
 LEV

**A45 DNA sequence**

Gene name: ESTs  
 15 Unigene number: Hs.157601  
 Probeset Accession #: W07459  
 Nucleic Acid Accession #: AC005383  
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60  
 25 TTTTATTTCG AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120  
 CCTGGCGGTA GTTCTCCCGA CCTCAGCCGG GTCCGGTCTG GCCGCCCTCT CCCAGGAGAG 180  
 ACAAAACAGGT GTCCACCGTG GCAGCCGCGC CCCGGGCGCC CCTCTGTGA TCCCCTAGCG 240  
 CCCCTGGGCC CGAGCCGCGC CCGGTCTGT GAGTAGAGCC GCCCGGCAC CGAGCGCTGG 300  
 30 TCGCCGCTCT CCTTCCGTTA TATCAACATG CCCCTTTCC TGTGTCTGGA GGCCGTCTGT 360  
 GTTTTCTCTG TTTCCAGAGT GCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAGCAA 420  
 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480  
 ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCGGGAAGG GGAGCTTGA AAGGTCCAA 540  
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600  
 GCATTCCAGT TCAGTTCAC TCCTCATCTG GAATTCCTT TGGATTCTT TCAACCCAA 660  
 35 CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720  
 CTGTCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTCTGTGCCC 780  
 CAGATCCTCA TCATCGTCAC TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAAG 840  
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG 900  
 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAG TGCTGTTGGC TGAGCAGGTG 960  
 40 GAGGATGCCA CCAACGGCCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCCAGCGCC 1020  
 ACGCCAGACT GCAGGGTCGA GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGTTCCGG 1080  
 GAGTTCGCTG GCAATGCCCC ATGCTGGAGA GGATCGCGGC GGACCTTGC GGTGCTGGCT 1140  
 GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTGC CACTGCTAC 1200  
 AGGACCACTT GCCCAGGCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260  
 45 CCAGAAGGAC TGGACGGCTA CAGTGCCTC TGCCCGCTGG CCTTGGAGG GGAGGCTAAC 1320  
 TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCGACCTCC TCTTCTGCT GGACAGCTCT 1380  
 GCGGGCACCA CTCTGGACCG CTCTCTGCGG GCCAAAGTCT TCGTGAAGCG GTTGTGCGG 1440  
 GCGGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500  
 CTGTGGCGGG TGCCGTGTGG GGAGTACCAG GATGTGCTG ACCTGGTCTG GAGCTCGAT 1560  
 50 GGCATTCCCT TCCGTGGTGG CCCCACTCTG ACGGGCAGTG CCTTGCGGCA GGCGGCAGAG 1620  
 CGTGGCTTCG GGAGCGCCAC CAGGACGGGC CACGTAGAGT GGTGTTTGTG 1680  
 CTCACCTAGT CACACTCCGA GGATGAGGTT GCGGGCCAG CGCTCACGC AAGGGCGCGA 1740  
 GAGCTGCTCC TGCTGGGTGT AGGCACTGAG GCCGTGCGGG CAGAGCTGGA GGAGATCACA 1800  
 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAG ATCTGTTCAA CCAATCCCT 1860  
 55 GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCAGGGT GCCGACACA AGCCCTGGAC 1920  
 CTCGCTTCA TGTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980  
 AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTGCGC 2040  
 CTGGTGGTGT ATGGCAGCA GGTGCACTG GCCTTCGGGC TGGACACCAA ACCCAACCGG 2100  
 GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCCTACCTAG GTGGGGTGGG CTCAGCCGGC 2160  
 60 ACCGCCCTGC TGCACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCCTGGT 2220  
 GTCCCAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCCT 2280  
 GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGGTCG TGGGCGTGGG GCCTGTCCTA 2340  
 AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC CGGGATTCCC TGATCCACGT GGCAGCTTAC 2400  
 GCCGACCTGC GGTACCAACA GGACGTGCTC ATTGAGTGGC TGTGTGAGA AGCCAAGCAG 2460  
 65 CCAGTCAACC TCTGCAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAA 2520  
 GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGAG 2580  
 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATT TTAGAGAGCC CCTGAGGCAC 2640  
 ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT ACCCTCCCA GCAACTACAG AGAAGGCTGT 2700  
 70 GGCACTGAAA TGGTGCTTAC CTCTGGAAT GTCTGTGCCC CAGGTCTTAA GAATGTCTGC 2760  
 TTCCCGCCGT GGCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820  
 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCACCCACA AACGATGTTG TTGAAAAGTT 2880  
 TTGATGTGTA AGTAAATACC CACTTCTGT ACCTGCTGTG CCTGTTGAG GCTATGTCAT 2940  
 CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCTGAAG ACTTAAATTT AGCGGCCTGA 3000  
 CGTTCTTTTG CACACAATCA ATGCTGCCCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060  
 75 AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAGACA 3120  
 GCAGCTTTTC CACTTCCCCA GAGACATCTT GGATGCATTT GCATTGAGTC TGAAGGGGGG 3180  
 CTTGAGGAC GTTTGTGACT TCTTGGGAC TGCTTTTGT GTGTGGAAGA GACTTGGAAA 3240  
 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT 3300  
 80 TGTGATGGG CCCAGTCTG GAGGGCCACG TAAATCGTT CTGAGTCTG AGCAGTGTCC 3360  
 ACCTGAAGG TCTTC

**A45 Protein sequence**

Gene name: ESTs

Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGW domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPDLSFST QQEVKARIKR 120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180
FAVGVRFRPW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPCPCD 300
SQPCQNGGTC VPGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVFFVRFPV RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480
EAVRAELEEI TGSPKHMVYV SDPQDLFNQI PELQKGLCSR QRPGRCTQAL DLVFMMLDTSA 540
SVGPFNFAQM QSFVRSCALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLRRNGI 660
SVLVVGVGFPV LSEGLRLRLAG PRDSLHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP 720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP

```

COLONA47 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTACAG TTTCTTCCAA CCTTGCCATT 120
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCAA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCTTAGAAT CATGTTTGTA 420
GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
TATGAGCCTC GGGATTATACC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTCAT 600
GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAA 720
TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

```

A48 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLRSGWGD DITWVQTYEE GLFYAQKSKK 60
PLMVIHHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDQYVPRIM 120
FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

```

A49 DNA SEQUENCE

Gene name: G protein-coupled receptor 56  
 Unigene number: Hs.6527  
 Probeset Accession #: AA478599  
 Nucleic Acid Accession #: NM\_005682  
 Coding sequence: 163-2244 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
CGGCAGCAGG GTCTCGCTCT GTACACAGG CTGGAGTGCA GTGGTGTGAT CTTGGCTCAT 60
CGTAACCTCC ACCTCCCGGG TTCAAGTGAT TCTCATGCCT CAGCCTCCCG AGTAGCTGGG 120
ATTACAGGTG GTGACTTCCA AGAGTGACTC CGTCGGAGGA AAATGACTCC CCAGTCGCTG 180

```

5	CTGCAGACGA	CACTGTTCCT	GCTGAGTCTG	CTCTTCCTGG	TCCAAGGTGC	CCACGGCAGG	240
	GGCCACAGGG	AAGACTTTTC	CTTCTGCAGC	CAGCGGAACC	AGACACACAG	GAGCAGCCTC	300
	CACTACAAAC	CCACACACAG	CCTGCGCATC	TCCATCGAGA	ACTCCGAAGA	GGCCCTCACA	360
	GTCCATGCCC	CTTTCCTGTC	AGCCCCACCT	GCTTCCCGAT	CCTTCCCTGA	CCCCAGGGGC	420
	CTCTACCACT	TCTGCTCTTA	CTGGAACCGA	CATGCTGGGA	GATTACATCT	TCTCTATGGC	480
	AAGCGTGA	TCTTGCTGAG	TGACAAAGCC	TCTAGCCTCC	TCTGCTTCCA	GCACAGGAG	540
	GAGAGCTGG	CTCAGGGCCC	CCCGCTGTTA	GCCACTTCTG	TCACCTCCTG	GTGGAGCCCT	600
	CAGAACATCA	GCCTGCCACG	TGCCGCCAGC	TTCACTTCT	CCTTCCACAG	TCCTCCCCAC	660
10	ACGGCCGCTC	ACAATGCCTC	GGTGGACATG	TGCGAGCTCA	AAAGGGACCT	CCAGCTGCTC	720
	AGCCAGTTCC	TGAAGCATCC	CCAGAAGGCC	TCAAGGAGGC	CCTCGGCTGC	CCCCGCCAGC	780
	CAGCAGTTGC	AGAGCCTGGA	GTGAAACTG	ACCTCTGTGA	GATTCATGGG	GGACATGGTG	840
	TCCTTCGAGG	AGGACCGGAT	CAACGCCACG	GTATGGAAGC	TCCAGCCAC	AGCCGGCCTC	900
	CAGGACCTGC	ACATCCACTC	CCGGCAGGAG	GAGGAGCAGA	GCGAGATCAT	GGAGTACTCG	960
15	GTGCTGCTGC	CTCGAACACT	CTTCCAGAGG	ACGAAAGGCC	GGAGCGGGGA	GGCTGAGAAG	1020
	AGACTCCTCC	TGGTGGACTT	CAGCAGCCAA	GCCCTGTTCC	AGGACAAGAA	TTCAGCCCAA	1080
	GTCTGGGTG	AGAAGGTCTT	GGGGATTGTG	GTACAGAAAC	CCAAAGTAGC	CAACCTCACG	1140
	GAGCCCGTGG	TGCTCACTTT	CCAGCACCAG	CTACAGCCGA	AGAATGTGAC	TCTGCAATGT	1200
	GTGTTCTGGG	TTGAAGACCC	CACATTGAGC	AGCCCGGGGC	ATTGGAGCAG	TGCTGGGTGT	1260
20	GAGACCGTCA	GGAGAGAAAC	CCAAACATCC	TGCTTCTGCA	ACCATTGTAC	CTACTTTGCA	1320
	GTGCTGATGG	TCTCCTCGGT	GGAGGTGGAC	GCCGTGCACA	AGCACTACCT	GAGCCTCCTC	1380
	TCCTACGTGG	GCTGTGTCTG	CTCTGCCCTG	GCCTGCCTTG	TCACCATGTC	CGCCTACCTC	1440
	TGCTCCAGGG	TGCCCTGCCC	GTGCAGGAGG	AAACCTCGGG	ACTACACCAT	CAAGGTGCAC	1500
	ATGAACCTGC	TGCTGGCCGT	CTTCTGCTG	GACACGAGCT	TCTTGCTCAG	CGAGCCGGTG	1560
25	GCCTTGACAG	GCTCTGAGGC	TGGCTGCCGA	GCCAGTGCCA	TCTTCTGCA	CTTCTCCCTG	1620
	CTACCTGCC	TTTCTGGTAT	GGGCTCGAG	GGGTACAACC	TCTACCGACT	CGTGGTGGAG	1680
	GTCTTTGGCA	CCTATGTCCC	TGGCTACCTA	CTCAAGCTGA	GCGCCATGGG	CTGGGGCTTC	1740
	CCCATCTTTC	TGGTGACGCT	GGTGGCCCTG	GTGGATGTGG	ACAACATATG	CCCCATCATC	1800
	TTGGCTGTGC	ATAGGACTCC	AGAGGGCGTC	ATCTACCTTT	CCATGTGCTG	GATCCGGGAC	1860
30	TCCTGTGTCA	GCTACATCAC	CAACCTGGGC	CTCTTCAGCC	TGGTGTTCCT	GTCAACATG	1920
	GCCATGTAG	CCACCATGGT	GGTGACATC	CTGCGGCTGC	GCCCCACAC	CCAAAAGTGG	1980
	TCACATGTGC	TGACACTGCT	GGGCTCAGC	CTGGTCTTGG	GCCTGCCCTG	GGCCTTGATC	2040
	TTCTTCTCCT	TTGCTTCTGG	CACCTTCCAG	CTTGTGCTCC	TCTACCTTTT	CAGCATCATC	2100
	ACCTCCTTCC	AAGGCTTCC	CATCTTCATC	TGGTACTGGT	CCATGCGGCT	GCAGGCCCGG	2160
35	GGTGGCCCTC	CCCTCTGAA	GAGCAACTCA	GACTGCGCCA	GGCTCCCCAT	CAGCTCGGGC	2220
	AGCACCTCGT	CCAGCCGCAT	CTAGGCCTCC	AGCCACCTG	CCCATGTGAT	GAAGCAGAGA	2280
	TGGGGCTCG	TGCGACACTG	CCTGTGGCCC	CCGAGCCAGG	CCGAGCCCCA	GGCCAGTCAG	2340
	CCGAGACTT	TGGAAGGCC	AACGACCATG	GAGAGATGGG	CCGTGCGCAT	GGTGGACGGA	2400
	CTCCCGGGGC	TGGGGCTTTT	GAATTGCGCT	TGGGGACTAC	TCGGCTCTCA	CTCAGCTCCC	2460
40	ACGGGACTCA	GAAGTGCGCC	GCCATGTGTC	CTAGGGTACT	GTCCCCACAT	CTGTCCCAAC	2520
	CCAGCTGGAG	GCCTGTGCTC	TCCTTACAAC	CCCTGGGCCC	AGCCTCATTG	CTGGGGGCCA	2580
	GGCCTTGGAT	CTTGAGGGTC	TGGCACATCC	TTAATCTGT	GCCCTGCCT	GGGACAGAAA	2640
	TGTGGCTCCA	GTTGCTCTGT	CTCTCGTGGT	CACCTGAGG	GCACTCTGCA	TCCTCTGTCA	2700
	TTTTAACCTC	AGGTGGCACC	CAGGGCGAAT	GGGGCCAGG	GCAGACCTTC	AGGGCCAGAG	2760
45	CCCTGGCGGA	GGAGAGGCC	TTTGCCAGGA	GCACAGCAGC	AGCTCGCCTA	CCTCTGAGCC	2820

A50 Protein sequence

50	Gene name:	G protein-coupled receptor 56
	Unigene number:	Hs.6527
	Protein Accession #:	NM_005682.1
	Signal sequence:	1-26
	GPS domain:	342-394
55	Pfam domain:	7tm_2 [400-665]
	Transmembrane domains:	410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659
	Cellular Localization:	plasma membrane

60	1	11	21	31	41	51	
	MTPQSLQTT	LFLLSLLFLV	QGAHGRGHRE	DFRFSQRNQ	THRSSLHYKP	TPDLRISIEN	60
	SEEALTVHAP	FPAAPASRS	FDPGRGLYHF	CLYWNRHAGR	LHLLYGKRDF	LLSDKASSLL	120
	CFQHQEESLA	QGPPLLATSV	TSWNSPQNIS	LPSAASFIFS	FHSPHTAAH	NASVDMCELK	180
65	RDLQLLSQFL	KHPQKASRRP	SAAPASQQLQ	SLESKLTSVR	FMGDMVSFEE	DRINATVWKL	240
	QPTAGLQDLH	IHSRQEEEQS	EIMEYSVLLP	RTLFQRTKGR	SGEAEKRLLL	VDFSSQALFQ	300
	DKNSSQVLGE	KVLGIVVQNT	KVANLTPVV	LTFFHQQLQPK	NVTLCQVFWV	EDPTLSSPGH	360
	WSSAGCETVR	RETQTSFCFN	HLTYFAVLMV	SSVEVDAVHK	HYLSLLSVVG	CVVSALACL	420
	TIAAYLCSRV	PLPCRKPRD	YTIKVMHLL	LAVFLDTSF	LLSEPVALTG	SEAGCRASAI	480
70	FLHFSLLTCL	SWMGLLEGYNL	YRLVVEVFGT	YVPGYLLKLS	AMGWGFPFIFL	VTLVALVDVD	540
	NYGPIILAVH	RTPEGVIYPS	MCWIRDSLVS	YITNLGLFSL	VFLFNMAMLA	TMVVQILRLR	600
	PHTQKWSHVL	TLLGLSLVLG	LPWALIFFSF	ASGTFQLVVL	YLSIITSFQ	GFLIFIWYS	660
	MRLQARGGPS	PLKNSDCAR	LPISSGSTSS	SRI			

A51 DNA SEQUENCE

75	Gene name:	Hypothetical protein FLJ20063
	Unigene number:	Hs.5940
	Probeset Accession #:	AA053660
	Nucleic Acid Accession #:	AA053660
80	Coding sequence:	218-1360 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
CCCCCATGAC	TTTGTACAGC	TACTTCACTG	CTTCCCCCA	ATTAGTACAC	ATAGTTCTCTC	60

CACAATTCCT ACACCTGCTC CCCCCATAAT CAGTACACAT AGTTCCTCCA CAATTCCTAT 120  
 ACCTACTGCT GCAGACAGTG AGTCAACCAC AAATGTAAAT TCATTAGCTA CCTCTGACAT 180  
 AATCACCGCT TCATCTCCAA ATGATGGATT AATCACAAATG GTTCCTTCTG AAACACAAAG 240  
 5 TAACAATGAA ATGTCCCCCA CCACAGAAGA CAATCAATCA TCAGGGGCTC CCACTGGCAC 300  
 CGCTTTATTG GAGACCAGCA CCCTAAACAG CACAGGTCCC AGCAATCCTT GCCAAGATGA 360  
 TCCCTGTGCA GATAATTTCGT TATGTGTAA GCTGCATAAT ACAAGTTTTT GCCTGTGTTT 420  
 AGAAGGGTAT TACTACAACT CTTCTACATG TAAGAAAGGA AAGGTATTCC CTGGGAAGAT 480  
 TTCAGTGACA GTATCAGAAA CATTTGACCC AGAAGAGAAA CATTCCATGG CCTATCAAGA 540  
 10 CTTGCATAGT GAAATTACTA GCTTGTTTAA AGATGTATTT GGCACATCTG TTTATGGACA 600  
 GACTGTAATT CTTACTGTAA GCACATCTCT GTCAACAGA TCTGAAATGC GTGCTGATGA 660  
 CAAGTTTGTT GATGTAACAA TAGTAACAAT TTTGGCAGAA ACCACAAGTG ACAATGAGAA 720  
 GACTGTGACT GAGAAAATTA ATAAAGCAAT TAGAAGTAGC TCAAGCAACT TTCTAAACTA 780  
 TGATTTGACC CTTGGGTGTG ATTATTATGG CTGTAACCAG ACTGCGGATG ACTGCCTCAA 840  
 15 TGGTTTAGCA TGCAGATTGCA AATCTGACCT GCRAAGGCCT AACCCACAGA GCCCTTTCTG 900  
 CGTTGCTTCC AGTCTCAAGT GTCTGATGC CTGCAACGCA CAGCAACAAG AATGCTTAAT 960  
 AAAGAAGAGT GGTGGGGCCC CTGAGTGTGC GTGCGTGCCC GGCTACCAGG AAGATGCTAA 1020  
 TGGGAAGTGC CAAAAGTGTG CATTGTGCTA CAGTGGACTC GACTGTAAGG ACAAAATTCA 1080  
 GCTGATCCTC ACTATTGTGG GCACCATCGC TGGCATTGTC ATTCTCAGCA TGATAATTGC 1140  
 20 ATTGATTGTC ACAGCAAGAT CAAATAACAA AACGAAGCAT ATTGAAGAAG AGAACTTGAT 1200  
 TGACGAAGAC TTTCAAAATC TAAAACCTGC GTGACAGGC TTCACCAATC TTGGAGCAGA 1260  
 AGGGAGCGTC TTTCTAAGG TCAGGATAAC GGCCTCCAGA GACAGCCAGA TGCAAAATCC 1320  
 CTATTCAAGA CACAGCAGCA TGCCCCGCCC TGACTATTAG AATCATAAGA ATGTGGAACC 1380  
 CGCCATGGCC CCCAACCAAT GTACAAGCTA TTATTTAGAG TGTTTAGAAA GACTGATGGA 1440  
 25 GAAGTGAGCA CAGTAAAGA TCTGGCCTCC GGGGTTTTTC TTCCATCTGA CATCTGCCAG 1500  
 CCTCTCTGAA TGGAGTTGT GAATGTTTGC AACGAATCCA GCTCACTGCT TAAATAAGAA 1560  
 TCTATGACAT TAAATGTAGT AGATGCTATT AGCGCTTGTG AGAGAGGTGG TTTTCTTCAA 1620  
 TCAGTACAAA GTACTGAGAC AATGGTTAGG GTTGTCTTCT TAATCTTTT CCTGGTAGGG 1680  
 CAACAAGAAC CATTTCCAAT CTAGAGGAAA GCTCCCCAGC ATTGCTTGCT CTGGGGCAAA 1740  
 30 CATTGCTCTT GAGTTAAGTG ACCTAATTCC CCTGGGAGAC ATACGCATCA ACTGTGGAGG 1800  
 TCCGAGGGGA TGAGAAAGGA TACCCACCAT CTTTCAAGGG TCACAAGCTC ACTCTCTGAC 1860  
 AAGTCAGAA AGGGACACTG CTTCTATCCC TCCAATGGAG AGATTCTGGC AACCTTTGAA 1920  
 CAGCCCAGAG CTTGCAACCT AGCCTCACCC AAGAAGACTG GAAAGAGACA TATCTCTCAG 1980  
 CTTTTTCAGG AGGCGTGCCT GGGAAATCCAG GAACCTTTTG ATGCTAATTA GAAGGCCTGG 2040  
 35 ACTAAAAATG TCCACTATGG GGTGCACTCT ACAGTTTTTG AAATGCTAGG AGGCAGAAGG 2100  
 GGCAGAGAGT AAAAAACATG ACCTGGTAGA AGGAAGAGAG GCAAGAGAAA CTGGGTGGGG 2160  
 AGGATCAATT AGAGAGGAGG CACCTGGGAT CCACCTTCTT CTTAGGTGCC CCTCCTCCAT 2220  
 CAGCAAGGGA GCACTTCTCT AATCATGCCC TCCCGAAGAC TGGCTGGGAG AAGGTTTAAA 2280  
 AACAAAAAT CCAGGAGTAA GAGCCTTAGG TCAGTTTGAA ATTGGAGACA AACTGTCTGG 2340  
 40 CAAGGGTGC GAGAGGGAGC TTGTGCTCAG GAGTCCAGCC GTCCAGCCTC GGGGTGTAGG 2400  
 TTTCTGAGGT GTGCCATTGG GGCCTCAGCC TTCTCTGGTG ACAGAGGCTC AGCTGTGGCC 2460  
 ACCAACACAC AACACACAC ACACAACCAC ACACACAAAT GGGGGCAACC ACATCCAGTA 2520  
 CAAGCTTTTA CAAATGTTAT TAGTGTCTT TTTTATTCT AATGCCTTGT CCTCTTAAAA 2580  
 45 GTTATTTTAT TTGTATTAT TATTGTCTT TGACTGTTAA TTGTGAATGG TAATGCAATA 2640  
 AAGTGCCTTT GTTAGATGGT GAAAAAATA AAAAAAATA AAAAAAATA A

A52 Protein sequence:

Gene name: Hypothetical protein FLJ20063  
 Unigene number: Hs.5940  
 50 Probeset Accession #: AA053660  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 289-311  
 55 EGF domain: 45-74  
 SEA domain: 80-196  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 60 MVPSETQSN EMSPPTEDNQ SSGPPTGTAL LETSTLNSTG PSNPCQDDPC ADNSLCVKLH 60  
 NTSFCLCLEG YYNSSTCKK GKVPFGKISV TVSETFDPEE KHSMAQDLH SEITSLFKDV 120  
 FGTSVYQTV ILTVSTSLSP RSEMRADDFK VDVITVILA ETSDNEKTV TEKINKAIRS 180  
 65 SSSNFLNYDL TLRCDYYGCV QTADDCLNGL ACDCKSDLQR PNPQSPFCVA SSLKCPDACN 240  
 AQHKQCLIKK SSGAPECAV PGVQEDANGN CQKCAFYSG LDCKDKFQLI LTVIGTIAGI 300  
 VILSMIALI VTARSNNKTK HIEEENLIDE DFQNLKLRST GFTNLGAEGS VFPKVRITAS 360  
 RDSQMNPYS RHSSMPRPDY

A53 DNA SEQUENCE

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 75 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 80 ACCGGGCACC GGACGGCTCG GGTACTTTTC TTCTTAATTA GGTCAATGCC GTGTGAGCCA 60  
 GGAAGGGGCT GTGTTTATGG GAAGCCAGTA ACAGTGTGGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180  
 AGAGGTCTCT AATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240

TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCTGTTGC ACCAGATGCA 300  
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTGC CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAG CCATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACGCAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGAGGGA 780  
 TGTGCTCTG GCCAGTGGT TACCTTGCAG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900  
 CTTAGTTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTTGTAC TCCCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140  
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACTTCCCC 1200  
 GATGGAAGAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCTGTGCC TGAACACGCG GGCCGTCCCT TTGATTTCCT ACAAGATCTG CAACCAACAG 1320  
 GACGTGTAGC GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380  
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACACG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA 1620  
 TCCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680  
 TTCCGGCACC AGTAGCAGGC CCGAAGAGG CACCCTTCCA TCTGATTCCA GCACAACTT 1740  
 CAAGCTGCTT TTTGTTTTT GTTTTTTGA GGTGGAGTCT CGCTCTGTG CCCAGGCTGG 1800  
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860  
 TTGCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACACACC CAACTAATT 1920  
 TTGTATTTT AGTAGAGCA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAAATGA TGTGCTGCT TCAGCCTCCC ACAGTGTGCG GATTACAGGC ATGGGCCACC 2040  
 ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGCTCTGC AAAATTCTCT 2160  
 ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCATCTCTA GGGACCAAG 2280  
 CCAAAACCC CTTTCTTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCCTAT TTTTATGATT TCTTGTAGC ATTTGGTGTG TGACGTATTA 2400  
 TTGTCTTTG ATTCCAATA ATATGTTTCC TTCCCTCAA AAAAAAATA AAAAAAATA 2460  
 AAAAAA

**A54 Protein sequence:**

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SpC domain: 216-444  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFFP IIVIGIILI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLQVF 120  
 TAASWKTMCs DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180  
 VTALHHSYVY REGCASHVIV TLQCTACGHR RGYSSRIVGG NMSLLSQWVP QASLQFQGYH 240  
 LCGGSVITPL WITAAHCYV DLXLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSSE NFPDGKVCWT SGWGATEDGA GDASPVNLHA 360  
 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSQCGD SGGPLVCQER RLWKLVGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

**A55 DNA SEQUENCE**

Gene name: Putative G protein-coupled receptor GPCR150  
 Unigene number: Hs.97101  
 Probeset Accession #: AA215333  
 Nucleic Acid Accession #: NM\_014373  
 Coding sequence: 322-1338 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 GTGGCCTCGA GGTGGTGGCA GGGCCGCCCC CTGCAGTCCG GAGACGAACG CACGGACCGG 60  
 GCCTCCGGAG GCAGGTTTCG CTGGAAGGAA CCGCTCTCGC TTCGTCTTAC ACTTGCACAA 120  
 ATGTCTCCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180  
 AAATAACATA ATTGAAGGCA GTAAAGTGA AATTAATAG GAAGATCATC AGTCAAGGAA 240  
 GACCACTGAG AGAGGACAGA AAATGAAGCA GTGTTTATC ATGTGTATTT CAGCAGGTCT 300  
 TCTTGAAATT TAACTAAAAA TATGACTGCT CTCTCTTCAG AGAATGCTC TTTTCACTAT 360  
 CAGTTACGTC AAACAAACCA GCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT 420  
 GGGAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAAACAC CTGTCAAAAT 480  
 TTTATGGAAT ATTTTTCAT TTCACTAGCA TTCGTTGATC TTTTACTTTT GGTAACATT 540  
 TCCATTATAT TGTATTTTCA GGAATTTGTA CTTTAAAGCA TTAGGTTTCA TAAATACCAC 600  
 ATCTGCCTAT TTAATCAAA TATTTCTTTT ACTTATGGCT TTTTGCATTA TCCAGTTTTT 660  
 CTGACAGCTT GTATAGATTA TTGCTCGAAT TTCTCTAAAA CAACCAAGCT TTCAATTAG 720  
 TGTCAAAAAT TATTTTATTT CTTTACAGTA ATTTTAATTT GGATTTCAGT CCTTGCTTAT 780

GTTTTGGGAG ACCCAGCCAT CTACCAAGC CTGAAGGCAC AGAATGCTTA TTCTCGTCAC 840  
 TGTCTTTCT ATGTCAGCAT TCAGAGTTAC TGGCTGTCAT TTTTCATGGT GATGATTTTA 900  
 TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960  
 ACTTCCTATA TGAATGAAAC TATCTTATAT TTTCTTTTTC CATCCCACTC CAGTTATACT 1020  
 GTGAGATCTA AAAAATATT CTTATCCAAG CTCATTGTCT GTTTCTCTCAG TACCTGGTTA 1080  
 CCATTGTAC TACTTCAGGT AATCATTTGT TACTTTAAAG TTCAGATTCC AGCATATATT 1140  
 GAGATGAATA TTCCTGGTT ATACTTTGTC AATAGTTTTC TCATTGCTAC AGTGATTGG 1200  
 TTTAATTGTC ACAAGCTTAA TTTAAAGAC ATTGGATTAC CTTGGATCC ATTTGTCAAC 1260  
 TGGAGTGCT GCTTCATCC ACTTACAATT CCTAATCTTG AGCAAATGA AAAGCCTATA 1320  
 TCAATAATGA TTTGTTAATA TTATTAATTA AAAGTTACAG CTGTCATAAG ATCATAATT 1380  
 TATGAACAGA AAGAACTCAG GACATATTAA AAAATAAACT GAACTAAAAC AACTTTTGCC 1440  
 CCCTGACTGA TAGCATTTCA GAATGTGTCT TTTGAAGGCG TATACCACTT ATTAATAGT 1500  
 GTTTTATTTT AAAAACAATA TAATCCAAG AAGTTTTTAT AGTTATTTCAG GGACACTATA 1560  
 TTACAATAT TACTTTGTTA TTAACACAAA AAGTGATAAG AGTTAACATT TGGCTATACT 1620  
 GATGTTTGTG TTAATCAAAA AAACACTGCG ATGCAAACTG TTAGTAAAT CTGAGATTTC 1680  
 ACTGACAACT TTAAGATATC AACCTAAACA TTTTATTAAT ATGTTCAAAT GTAAGCAAGA 1740  
 AAAAAAAA

#### A56 Protein sequence

Gene name: Putative G protein-coupled receptor GPCR150  
 Unigene number: Hs.97101  
 Protein Accession #: NP\_055188  
 Signal sequence: none found  
 Transmembrane domains: 23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MTALSSSENS FQYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRKNT QCNFMEYFCI 60  
 SLAFVDLLLL VNISILYFR DFVLSIRFT KYHICLFTQI ISFTYGFHLY PVFLTACIDY 120  
 CLNFSKITKL SFKCQKLFYF FTVILIWISV LAYVLGDPAL YQSLKAQNAV SRHCPFYVSI 180  
 QSYNLSFFMV MILFVAFITC WEEVTTLVQA IRTSYMNET ILYPFFSSHS SYTVRSKKIF 240  
 LSKLIVCLFS TWLPFVLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN 300  
 LKDIGLPLDP FVNWKCCFIP LTIPNLEQIE KPISIMIC

#### A57 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60  
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120  
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180  
 CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240  
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC 300  
 TGTGCCAGCC GGGCCTTGCC CCGTCTCTCC TCCGGGCCCC CCGTGCCTGC CCGTGCAGTC 360  
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420  
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAAGTC 480  
 GCGCTCATTA AGCAGCTGTT TGAGGCCCCG GCCCTGAGCC AGCAGGACCG GGGACCTCTG 540  
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CTTGGCACTC 600  
 AGCCCTTCGA GGGTGGGCGC CCCATCGCAC CCACCTCTCT TGGCTGGAGA CCCCAGGCAG 660  
 GCCCAGCCAC AGTCCCGGAG TGGGCGCCTT CCTGCGCCCC TTGCCAGATG GGCTCCCCAG 720  
 GCCTGCCCCC GGTGCTGCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG 780  
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCAG CTACTACTGG CCGCTGTCAG 840  
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCG TTTCCAGCGG TGCCGCCCTG 900  
 GGTCCCCTCT TCAGGGAAG GCATGCCCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960  
 AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020  
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080  
 GTAAGCGGGG GGTGCTGTCC TGGCTGGGGA GCCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140  
 CTGGCCAAGG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200  
 GGCTGTCATG TGCCTCCAC AGACCTGGG GTGATGGCCT TCCCTCTCTT GGCCGGGACG 1260  
 TTGCCCCACG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA 1320  
 GACAGCTCCC AGGCACGCTA TAGGCAAAAG CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380  
 CTGGGGTCTC GCTCACCCCC CTTTGCTCTC ACGCCAGGCC TGTCCCCAGG TTTGAGCTGG 1440  
 GAGAGGCCAC CTCCTCAGC CAAGGAAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500  
 GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT 1560  
 GGGATACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTCACCA 1620  
 GAACCAAGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680  
 TCAGTGTGTG TGGGGCGCAG GGCCTCCGAT GCGGGGTGAG TGCGTGGGGG GCGCAGGGCC 1740  
 CCCGATGCGG GGTCACTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACTTTGGT 1800  
 ACATGTGCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAATCC 1860  
 CCTTCCGGAG CCCAGTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCT 1920  
 TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGCCCA GCATGCACT 1980  
 GCCCTCCTAC CTTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCTGG 2040  
 ACCTCCTGGG CAGGAAGAGG TGCAGGTCTT GAGGGCCTGT GCCCCACAGC CCCAGCACCC 2100  
 AGGTGGAAGT CAGCGCAGT GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCCCTCAGCA 2160  
 GGCTGCGGTC TGCCACCAAG GGCCTCCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCCC 2220

	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
	GGTGACTTCA	TCAGGAGACC	GCCACACATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCACCTCCG	GAAAACTGCG	CTTTCAGCCT	TGGTGTTCGG	TGCAAGGTGA	2400
5	AAAGAAATAG	GTCTCTCCAG	TTTACAGCTT	GAAATCAGGC	TAGTGAGTGG	CCCTGGAGAC	2460
	CACGAGGGGA	GAATTTAAAG	GCCCCGCTCG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCTCG	CCTGGAGCCT	GCCCTAGGAC	GCTGGGCGGG	TCAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CCTGGGCTCT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAGGT	ACATACACGT	2640
	GCGTGACAC	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
10	CAGAAGTGTG	CCCAGTTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTTGTGTTG	ATCAAGTTCC	AAGGAAAAGG	AACATCTCAG	CCGGGCGTGG	TGGTTCACGC	2820
	CTGGAATCCC	AGCACTTGAG	GCCAGGAGTT	CCAGAGCAGC	CTGGGCAACG	CAGTGAGAGA	2880
	CCCCATCTCT	ACAARAAAAA	AAAAAGAAAG	AAAGAAAATG	AGAGATCCAG	GTTTAAAAAT	2940
	TCATAAACAC	CACAAGGAAA	CAATACACTA	TGAGACCCAG	CAGAAGCAAC	AGATTGACTC	3000
15	TAGACCCAGA	TACTAGAATT	ATCAGAGAGA	ATATAAAGTA	ACAGTGTTTT	ATATATCTAA	3060
	AGAAATAAAA	GAGATTTCCTG	GAAACATGAA	AAAAAA			

A58 DNA sequence

	Gene name:	ESTs
	Unigene number:	Hs.157601
20	Probeset Accession #:	W07459
	Nucleic Acid Accession #:	AC005383
	Coding Sequence:	328-2751 (underlined sequences correspond to start and stop codons)

25	1	11	21	31	41	51	
	GACAGTGTTC	CGCGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGCGTAGAAG	TGAAGTACTT	60
	TTTTATTGTC	AGACCTGGGC	CGATGCCGCT	TTAAAAAACG	CGAGGGGCTC	TATGCACCTC	120
	CCTGGCGGTA	GTTCCTCCGA	CCTCAGCCGG	GTCCGGTTCGT	GCCGCCCTCT	CCCAGGAGAG	180
30	ACAAACAGGT	GTCCACAGTG	GCAGCCGCGC	CCCGGGCGCC	CCTCCTGTGA	TCCCGTAGCG	240
	CCCCCTGGCC	CGAGCCGCGC	CCGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG	300
	TCGCGGCTCT	CCTTCCGTTA	TATCAACATG	CCCCCTTTCC	TGTTGCTGGA	GGCCGCTCTGT	360
	GTTTCTCTGT	TTTCCAGAGT	GCCCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAGCAAA	420
	GAAACCATCG	GGAAGATTTT	AGCTGCCAGC	AAAATGATGT	GGTGCTCGGC	TGCAGTGGAC	480
35	ATCATGTTTC	TGTTAGATGG	GTCTAACAGC	GTCCGGAAAG	GGAGCTTTGA	AAGGTCCAAG	540
	CACTTTGCCA	TCACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600
	GCATTCAGT	TCAGTTCCAC	TCCTCATCTG	GAATTCCTCC	TGGATTCAAT	TTCAACCCAA	660
	CAGGAAGTGA	AGGCAAGAAT	CAAGAGGATG	GTTTTCAAAG	GAGGGCGCAC	GGAGACGGAA	720
	CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCCTGGAG	GCAGAAATGC	TTCTGTGCCC	780
40	CAGATCCTCA	TCATCGTCAC	TGATGGGAAG	TCCAGGGGGG	ATGTGGCACT	GCCATCCAAG	840
	CAGCTGAAGG	AAAGGGGTGT	CACGTGTGTT	GCTGTGGGGG	TCAGGTTTCC	CAGGTGGGAG	900
	GAGCTGCATG	CACCTGGCCAG	CGAGCCTAGA	GGGCAGCACG	TGCTGTGGC	TGAGCAGGTG	960
	GAGGATGCCA	CCAACGCCCT	CTTCAGCACC	CTCAGCAGCT	CGGCCATCTG	CTCCAGCGCC	1020
	ACGCCAGACT	GCAGGGTCTGA	GGCTCACCCC	TGTGAGCACA	GGACGCTGGA	GATGGTCCGG	1080
45	GAGTTTCGTG	GCAATGCCCC	ATGCTGGAGA	GGATCGCGGC	GGACCCCTGC	GGTGCTGGCT	1140
	GCACACTGTG	CCTTCTACAG	CTGGAAGAGA	GTGTTCTTAA	CCCAACCTGC	CACCTGCTAC	1200
	AGGACCACCT	GCCCAGGCCC	CTGTGACTCG	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT	1260
	CCAGAAGGAC	TGGACGGCTA	CCAGTGCCTC	TGCCCCGCTG	CCTTTGGAGG	GGAGGCTAAC	1320
50	TGTGCCCTGA	AGCTGAGCCT	GGAAATGCAGG	GTGCACTTCC	TCTTCTGCT	GGACAGCTCT	1380
	GCGGGCACCA	CTCTGGACGG	CTTCTGCGG	GCCAAAGTCT	TCGTGAAGCG	GTTTGTGCGG	1440
	GCCGTGCTGA	GCGAGGCTAG	TCGGGCCCGA	GTGGGTGTGG	CCACATACAG	CAGGGAGCTG	1500
	CTGGTGGCGG	TGCTGTGGGG	GGAGTACCA	GATGTGCCTG	ACCTGGTCTG	GAGCCTCGAT	1560
	GGCATTCCCT	TCCGTGGTGG	CCCCACCTTG	ACGGGCGAGT	CCTTGCAGCA	GGCGGCGAGG	1620
	CGTGGCTTCG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAGT	GGTGGTTTGT	1680
55	CTCACTGAGT	CACACTCCGA	GGATGAGGTT	GCGGGCCCGG	CGCGTCAAGC	AAGGGCGCGA	1740
	GAGCTGTCTC	TGCTGGGTGT	AGGCAGTGAG	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA	1800
	GGCAGCCCAA	AGCATGTGAT	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT	1860
	GAGCTGCAGG	GGAAGCTGTG	CAGCCGCGAG	CGGCCAGGGT	GCCGGACACA	AGCCCTGGAC	1920
	CTCGTCTTCA	TGTTGGACAC	CTCTGCCTCA	GTAGGGCCCG	AGAATTTTGC	TCAGATGCGA	1980
60	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGACGTGAC	ACAGGTTCGGC	2040
	CTGGTGGTGT	ATGGCAGCCA	GGTGACAGCT	GCCTTCGGGC	TGGACACCAA	ACCCACCCGG	2100
	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCCGG	2160
	ACCGCCCTGC	TGCACATCTA	TGACAAAGTG	ATGACCGTCC	AGAGGGGTGC	CCGGCCTGGT	2220
	GTCCCAAAAG	CTGTGGTGGT	GCTCACAGGC	GGGAGAGGCG	CAGAGGATGC	AGCCGTTTCT	2280
65	GCCCAAGAGC	TGAGGAACAA	TGGCATCTCT	GTCTTGGTGC	TGGGCGTGGG	GCCTGTCCTA	2340
	AGTGAGGGTC	TGCGGAGGCT	TGCAGGTCCC	CGGATTTCCC	TGATCCACGT	GGCAGCTTAC	2400
	GCCGACCTGC	GGTACCACCA	GGACGTGCTC	ATTGAGTGGC	TGTGTGAGAG	AGCCAAGCAG	2460
	CCAGTCAACC	TCTGCAAAAC	CAGCCCGTGC	ATGAATGAGG	GCAGCTGCGT	CCTGCAGAA	2520
	GGGAGCTACC	GCTGCAAGTG	TGCGGATGGC	TGGGAGGGCC	CCCACTGCGA	GAACCGTGAG	2580
70	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	GGATGGATTG	TTGAGACGCC	CCTGAGGCAC	2640
	ATGGCTCCCG	TGCAGGAGGG	CAGCAGCCGT	ACCCCTCCCA	GCAACTACAG	AGAAGGGCTG	2700
	GGCACTGAAA	TGGTGTCTAC	CTTCTGGAAT	GTCTGTGCC	CAGGTCTCTT	GAATGTCTGC	2760
	TTCCCGCCGT	GGCCAGGACC	ACTATTCTCA	CTGAGGGAGG	AGGATGTCCC	AACTGCAGCC	2820
	ATGCTGCTTA	GAGACAAGAA	AGCAGCTGAT	GTCAACCCAA	AACGATGTTG	TTGAAAAGTT	2880
75	TTGATGTGTA	AGTAAATACC	CACCTTCTGT	ACCTGCTGTG	CCTTGTGTAG	GCTATGTCTA	2940
	CTGCCACCTT	TCCTTGTAGG	ATAAACAAAG	GGTCTGGAAG	ACTTAAATTT	AGCGGCCTGA	3000
	CGTTCTCTTG	CACACAATCA	ATGCTCGCCA	GAATGTTGTT	GACACAGTAA	TGCCCAGCAG	3060
	AGGCCCTTAC	TAGAGCATCC	TTTGGACGGC	GAAGGCCACG	GCCTTTCAAG	ATGGAAAGCA	3120
	GCAGCTTTTC	CACCTTCCCA	GAGACATTCT	GGATGCATTT	GCATTGAGTC	TGAAAGGGGG	3180
80	CTTGAGGGAC	GTTTGTGACT	TCTTGGCGAC	TGCCTTTTGT	GTGTGGAAGA	GACTTGGAAA	3240
	GGTCTCAGAC	TGAATGTGAC	CAATTAACCA	GCTTGGTTGA	TGATGGGGGA	GGGGCTGAGT	3300
	TGTGCATGGG	CCCAGGTCTG	GAGGGCCACG	TAAATTCGTT	CTGAGTCTGT	AGCAGTGTCC	3360
	ACCTTGAAGG	TCTTTC					



A59 Protein sequence

Gene name: ESTs  
 Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGW domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

1	11	21	31	41	51	
MPPFLLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSSAAV	DIMFLLDGSN	60
SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPLDSFST	QQEVKARIKR	120
MVFKGGRTE	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
FAVGVRFPWR	BELHALASEP	RQGHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPGPCD	300
SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLLDS	SAGTTLDGFL	360
RAKVVFVKRFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPLVWVSL	DGIPFRGGPT	420
LTGSALRQAA	ERGFSGSATRT	GQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
EAVRAELEEI	TGSPKHVMVY	SDPQDLFNQI	PELQKGLCSR	QRPGCRTQAL	DLVFMLDTSA	540
SVGPENFAQM	QSFVRSALQV	FEVNPDTVQV	GLVVYGSQVQ	TAFGLDTPKT	RAAMLRAISQ	600
APYLGGVGSA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVL	T		
SVLVVGVGPV	LSEGLRRLAG	PRDSLIHVA	YADLRHYQDV	LIEWLCGEAK	QFVNLCKPSP	720
CMNEGSCVLQ	NGSYRCKCRD	GWEGPHCENR	EWSSCSVCVS	QGWILETPLR	HMAPVQEGSS	780
RTPPSNYREG	LGTEMVPTFW	NVCAPGP				

A60 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
ATGTTACAG	ATCCTGACAG	TGATCAACCT	CTGAACAGCC	TCGATGTCAA	ACCCCTGCGC	60
AAACCCCGTA	TCCCCATGGA	GACCTTCAGA	AAGGTGGGGA	TCCCCATCAT	CATAGCACTA	120
CTGAGCTGG	CGAGTATCAT	CATTGTGGTT	GTCCATCATCA	AGGTGATTCT	GGATAAATAC	180
TACTTCCTCT	CGCGGCAGCC	TCTCCACTTC	ATCCCGAGGA	AGCAGCTGTG	TGACGGAGAG	240
CTGGACTGTC	CCTTGGGGGA	GGACGAGGAG	CACTGTGTCA	AGAGCTTCCC	CGAAGGGCCT	300
CGAGTGGCAG	TCCGCTCTCT	CAAGGACCGA	TCCCACTGCG	AGGTGCTGGA	CTCGGCCACA	360
GGGAACCTGGT	TCTCTGCTCT	TTCGACAAC	TTCACAGAAG	CTCTCGCTGA	GACAGCCTGT	420
AGGCAGATGG	GCTACAGCAG	CAAACCCACT	TTCAGAGCTG	TGGAGATTGG	CCCAGACCAG	480
GATCTGGATG	TTGTTGAAAT	CACAGAAAAC	AGCCAGGAGC	TTCGATGCG	GAACTCAAGT	540
GGGCCCTGTC	TCTCAGGCTC	CCTGGTCTCC	CTGCACTGTC	TTGCCCTGTG	GAAAGCCCTG	600
AAGACCCCCC	GTGTGGTGGG	TGGGGAGGAG	GCCTCTGTGG	ATTCTTGGCC	TGGCAGGTG	660
AGCATCCAGT	ACGACAAACA	GCACGTCTGT	GGAGGGAGCA	TCCTGGACCC	CCACTGGGTC	720
CTCACGGCAG	CCCACTGCTT	CAGGAAACAT	ACCGATGTGT	TCAACTGGAA	GGTGCGGGCA	780
GGCTCAGACA	AACTGGGCAG	CTTCCCATCC	CTGGCTGTGG	CCAAGATCAT	CATCATTGAA	840
TTCAACCCCA	TGTACCCCAA	AGACAATGAC	ATCGCCCTCA	TGAAGCTGCA	GTTCCCACTC	900
ACTTTCTCAG	GCACAGTCAG	GCCCATCTGT	CTGCCCTTCT	TTGATGAGGA	GCTCACTCCA	960
GCCACCCAC	TCTGGATCAT	TGGATGGGGC	TTTACGAAGC	AGAATGGAGG	GAAGATGTCT	1020
GACATACTGC	TGCAGGCGTC	AGTCCAGGTC	ATTGACAGCA	CACGGTGCAA	TGCAGACGAT	1080
GCCTACACAG	GGGAAGTCAC	CGAGAAGATG	ATGTGTGCG	GCATCCCGGA	AGGGGGTGTG	1140
GACACCTGCC	AGGGTGACAG	TGGTGGGCCC	CTGATGTACC	AATCTGACCA	GTTGGCATGTG	1200
GTGGGCATCG	TTAGCTGGGG	CTATGGCTGC	GGGGGCCCGA	GCACCCAGG	AGTATACACC	1260
AAGGTCTCAG	CTCATCTCAA	CTGGATCTAC	AATGTCTGGA	AGGCTGAGCT	<u>GTAA</u>	

A61 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 LDLa domain: 54-94  
 Tryp\_SPC domain: 204-429  
 Cellular Localization: plasma membrane/ER

1	11	21	31	41	51	
MLQDPDSQDP	LNSLDVKPLR	KPRIPMETFR	KVGIPIIIAL	LSLASIIIVV	VLIKVILDKY	60
YFLCGQPLHF	IPRKQLCDGE	LDCPLGEDEE	HCVKSFPEGP	AVAVRLSKDR	STLQVLDSAT	120
GNWFSACFDN	FTEALAEFAC	RQMGYSSKPT	FRAVEIGPDQ	DLDVVEITEN	SQELMRNNS	180
GPCLSGSLVS	LHCLACGKSL	KTPRVVGEE	ASVDSWPWQV	SIQYDKQHVC	GGSIILDPHW	240
LTAACHFRKH	TDVFNWKVRA	GSDKLGSPFS	LAVAKIIIE	FNPMPKDN	IALMKLQFPL	300
TFSGTVRPIC	LPFFDEELTP	ATPLWIIIGW	FTKQNGGKMS	DILLQASVQV	IDSTRCNADD	360
AYQGEVTEKM	MCAGIPEGGV	DTQGDGSGGP	LMYQSDQWHV	VGVISWGYGC	GGPSTPGVYT	420
KVSAYLNWIY	NVWKAEAL					

**A62 DNA SEQUENCE**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Nucleic Acid Accession #: none found  
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
CCAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
CTGAGATCCT TGCAGTAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180
AGACCCAGCT GTGCTCCTGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240
AAGCTGAGGA ACTGGTCTGA TGCCGAGCTC GAGTGTCACT CTACGGAAA CGGAGCCAC 300
CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
CAGAGAAGCC AGCCGATATG GATTGGCCTG CACGACCCAC AGAAGAGGCA GCAGTGGCAG 420
TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480
AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTAA CTGGAGCAG CAACGAATGC 540
AACAGCGCC AACACTTCCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600
AACTCCTGCA CCAGCCCCGT CCTCTTCCTT TCTGTAGGCC TGGCTAAATC TGCTCATTAT 660
TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTTTA 720
GGCTTAGAGA CAGAACTTT AGCATTGGGC CCAGTAGTGG CTCTAGCTC TAAATGTTTG 780
CCCCGCCATC CCTTTCACA GTATCCTTCT TCCCTCCTCC CCGTCTCTCG GCTGCTCGA 840
GCAGTCTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAAT 900
AAAGATTGTA AGACAGAAGG AAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
ACACCTTCTC GCGCTCTCTC CATTGCTGCG ACCCCACCCC AGCCACTCAA CTCCTGCTTG 1020
TTTTCTCTTT GGCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA 1080
TACATTCTTT TAATAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA

```

**A63 Protein sequence:**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Protein Accession #: none found  
 Signal sequence: 1-22  
 Transmembrane domains: none found  
 C-type lectin domain: 47-156  
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWFYHKSX CYGYFRKLRLN WSDAELECSQ 60
YNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLYRSWSG 120
KSMGGNKHCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP

```

**A64 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

```

1      11      21      31      41      51
|      |      |      |      |      |
GCGGAACACC GGGCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
TCCCTCGTGG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGTGCGCTG CAGTGCOCGG 120
CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTTCAT GGGCTGCCCT GGGCAAGAGC 240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
TCTTTGGCCA CGCTGTGTCA GAGAAATGGT CCTCAGTGGG GGACCCCATG AACATCTCCA 660
TCATCGTGAC CGACCAGAA GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
AGGACCCACA CATAGTGCTC TTCACAATC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
CCAGTGGCCT GGACCGGGA AAAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
ACAAATGCTC CATGTTTGAC CCCCAGAGT ACGAGGCCCA TGTGCTGAG AATGCAGTGG 1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGAGCG CCCCAACTCA CCAGCGTGGC 1140
GTGCCACCTA CCTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
CTGAGAGCAA CCAGGCGATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
AGCACACCCT GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCTAACCT 1320
CCACAGCCAC CATAGTGCTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
CCTCAAAGT CGTTGAGGTC CAGGAGGGA TCCCACTGG GGAGCCTCTG TGTGCTTACA 1440
CTGCAGAAGA CCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCTGT AGAGACCCAG 1500

```

CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560  
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680  
 ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC 1740  
 ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCACAC CTCCCCTTTC CAGGCCACGC 1800  
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG 1920  
 ACCATGGCAA CAAAGACGAC CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
 ATGTGCAAAAC CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040  
 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100  
 TCAAGGAGCC CCTCCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160  
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 AGGCCAGGCC GGAGGTGTTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280  
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340  
 AGGCGGGTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TTCGACTATG 2400  
 AGGGCAGCGG CTCCGACGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460  
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520  
 ACCGTGGCGG GAGGAGCGAC TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AACGTACAGG 2580  
 CACAGAGCAT CTCGAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640  
 GGAAGTGGCC GTAGCAACTT GGCAGAGACA GGCATAGAGT CTGACGTTAG AGTGGTGTCT 2700  
 TCCTTAGCCT TTCAGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760  
 CACCTGGGCC AGGTTGCGCT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAATA 2820  
 TGCTCAACCC TGTGCTCTGG GCCTGGGCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880  
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940  
 TCAAAACGTT AGAGAAAGTT CTTCAAAGT GCAGCCAGA GCTGCTGGG CCACTGGCCG 3000  
 TCCTGCATT CTGTTTCCA GACCCCAATG CCTCCATTG GGATGGATCT CTGCGTTTTT 3060  
 ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CTGTGTGCGT TGCTATAGAT 3120  
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAAGCTTTT TATTAAAGAA A

**A65 Protein sequence:**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675 (second underlined sequence)  
 Cellular localization: plasma membrane

1 11 21 31 41 51  
 MGLPRGPLAS LLLQVQWLQ CAASEPCRAV FREAEVTLEA GGAQEPGQA LGKVFMGCPG 60  
 QEPALFSTDN DDFTVRNET VQERRSLKER NPLKIFPSKR ILRRHKRDV VAPISVPENG 120  
 KGPPFPRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLNN KPLDREEIAK 180  
 YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 DEDDAIYITN GVVAYSISQS EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TDMGDGSGST TAVAVVEILD ANDNAPMFDP QKYEAHVPEP AVGHEVQRLT VTDLDAPNSP 360  
 AWRATYILMG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTEGPVC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLAMPD DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540  
 VNDHGFVPEP RQITCNQSP VRHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600  
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFIFLVL 660  
 GAVLALLPLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVVF YGEBGGGEED QDYDITQLHR 720  
 GLEARPEVLL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEDED

**A66 DNA SEQUENCE**

Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Nucleic Acid Accession #: AF189723  
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGATTCCTG TATTGACATC AAAAAAGACA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
 ATTCCTCCAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
 TTTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTTCTGGCTT CTGCAGTCAT CAGTGTTTTA 240  
 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300  
 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360  
 CCAGAAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420  
 CCAGGTGATA CAGTTTGCCT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTC 480  
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540  
 AAGGTGACAG CTCTCTACGC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600  
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTTCAT TGGAAACAGGA 660  
 GAAAATTCCT AATTTGGGGA GGTTTTAAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
 CCTCTGATA AGAGCATGGA CCTCTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780  
 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840

5  
 10  
 15  
 20  
 25  
 30

```

ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTACAGTG 900
ACGCTAGCTC TTGGTGTTAT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960
ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCTG ATAAACTGG AACACTGACG 1020
AAGAAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTG 1140
TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAAATGCTCT TGCAATGAAG 1260
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320
GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
TGTTTTATGA AAGGTGCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAGA GAAGGCACGC 1500
ATGGGCTCAG CGGGACTCAG AGTTCCTGCT TTGGCTTCTG GTCCCTGAAC TGGACAGCTG 1560
ACATTTCTTG GCTTGGTGGG AATCATTTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
ACAACACTCA TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTG ACAGGAGACT 1680
GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTTCCAAA CTTCCTCAGT AGTCTCAGGA 1740
GAAGAAATAG ATGCAATGGA TGTTCCAGCAG CTTTCACAAA TAGTACCAA GGTTCAGTA 1800
TTTTACAGAG CTAGCCCAAG GCACAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860
TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920
ATTGGAGTTG GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTTAT 2040
AATAACATTA AAAATTTCGT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACTTTA 2100
ATCTCATTGG CTACATTAAT GAACCTTCCT AATCCTCTCA ATGCCATGCA GATTTTGTTG 2160
ATCAATATTA TTATGGATGG ACCCCAGCTG CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCATTG GTAAAGCTCG TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTGATA 2280
CTTAAATATC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTTG CTCTGGCGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
TTTTTTGACA TGTTCATATG ACTAAGTTCC AGATCCCAGA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTCTCTG GATCCATCAT GGGACAATTA 2520
CTAGTTATTT ACTTTCTCTC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTTGT TTTCTTTGGG TCTCAGCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTGA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT GA
  
```

#### A67 Protein sequence:

35  
 40  
 45

```

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: N51919
Protein Accession #: AAF27813
Signal sequence: none found
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
Cellular Localization: not determined
  
```

45  
 50  
 55  
 60

```

1 11 21 31 41 51
MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI 60
SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQEURSEK SLEELSCLVP 120
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLF EAVDLSIDES SLTGETTPCS 180
KVTAEPQPAAT NGDLASRSNI APMGTLVRCG KAKGVVIGTG ENSEFGEVFK MMQAEAPKT 240
PLQKSMDDLK QLSFYSPFI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGPLIVVTV 300
TLALGVMRMV KKRAIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360
GVGYNQFGEV IVDGDVHGF YNPAVSRIVE AGCVCNDAVI RNNITLMGKPT EGALIALAMK 420
MGLDGLQODY IRKAEYFPSS EQKWMVAVKCV HRTQQDREPI CFMKGAYEQV IKYCTTYQSK 480
GQTLTLTQQQ RDVYQOEKAR MGSAGLRVLA LASGPELGQL TFLGLVGIID PPRTVGKEAV 540
TTLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSVSG EEIDAMDVQQ LSQIVPKVAV 600
FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEADAMI 660
LVDDDFQTIM SAIEBGKGIY NNINKFVRFO LSTSLAALTL ISLATLMNFP NPLNAMQILW 720
INIMDGPFA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
ELRDNVITPR DTTMTFTCFV FDFMFNALSS RSQTSKVFEE GLCSNRMFCY AVLGSIIMGQL 840
LVIIYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVERSREKIQ KHVSTSTSSS 900
LEV
  
```

#### A68 DNA SEQUENCE

65  
 70

```

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
Unigene number: Hs.170195
Probeset Accession #: BE616633
Nucleic Acid Accession #: NM_001719
Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)
  
```

75  
 80

```

1 11 21 31 41 51
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCCGCTGC GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGCGC 120
CGATGCACGT GCGCTCAGT CGAGCTGCGG CGCCGCACAG CTTCTGCGCG CTCTGGGCAC 180
CCCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
GCTTCATCCA CCGGCGCCTC GCAGGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTGCCCCAC GCGCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGCGCGC GGGCCCGGCG 420
GCCAGGGCTT CTCTTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
GCCTGCAAGA TAGCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCGGGATC TACAAGGACT 660
  
```

ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720  
 AGCACTTGGG GCGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCCTCGG 780  
 AGGAGGGCTG GCTGGGTGTTT GACATCACAG CCACGAGCAA CCACTGGGTG GTCAATCCGC 840  
 GGCAACACCT GGGCCTGCAG CTCTCGGTGG AGACGTGGA TGGGCAGAGC ATCAACCCCA 900  
 AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACA GCAGCCCTTC ATGGTGGCTT 960  
 TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGAGC AAACAGCGCA 1020  
 GCCAGAACC GCTCAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080  
 AGAACAGCAG CAGCGACCCG AGGCAGGCCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140  
 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG 1200  
 AGGGGGAGTG TGCCTTCCCT CTGAATCCT ACATGAACGC CACCAACCAC GCCATCGTGC 1260  
 AGACGCTGGT CCACTTCATC AACCCGAAA CGGTGCCCAA GCCCTGCTGT GCGCCACGC 1320  
 AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380  
 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440  
 TTGGGGCCAA GTTTTTCTGG ATCCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500  
 CTGCCTTTTG TGAGACCTTC CCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560  
 AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620  
 TCCTACAAGC TGTGCAGGCA AAACCTAGCA GGAACCAACA ACAACGCATA AAGAAAAATG 1680  
 CCGGGGCCAG GTCATTGGCT GGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740  
 TTATGAGCGC CTACCAAGCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800  
 GGGCACATTG GTGTCTGTGC GAAAGGAAA TTGACCCGGA AGTTCTGTGA ATAAATGTCA 1860  
 CAATAAACG AATGAATG

A69 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number: Hs.170195

Probeset Accession #: BE616633

Protein Accession #: NP\_001710.1

Signal sequence: 1-30

Pfam domains: TGFb\_propeptide [37-281]

Transmembrane domains: none found

Cellular Localization: secreted

1 11 21 31 41 51  
 | | | | |  
 MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRRLRSQE RREMQREILS 60  
 ILGLPHRPRP HLQGHNSAP MFMLDLNAM AVEGGGGPGG QGFSYPYKAV FSTQGPPLAS 120  
 LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHRFRFDL SKIPEGEAVT AAEFRIYKDY 180  
 IRERFDNETF RISVYQLVQE HLGRESLFL LDRSLWASE EGWLVFDITA TSNHWVNP 240  
 HNLGLQLSVE TLDQSNINP LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300  
 QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAYYCE 360  
 GECAFFLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420  
 RNMVVRACGC H

CervicalA70 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)

Unigene number: Hs.87223

Probeset Accession #: AA250737

Nucleic Acid Accession #: NM\_001203

Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GGACGCGGCG AGTGC GGAGA CCGCGGCGCT 60  
 GAGGACGCGG GAGCCGGGAG CGCAGCGCGG GGGTGGAGTT CAGCTACTC TTTCTTAGAT 120  
 GTGAAAGGAA AGGAAGATCA TTTATGCCT TGTGATAAA GGTTCAGACT TCTGCTGATT 180  
 CATAACCAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240  
 TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300  
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGG TCCAAAGGTC 360  
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420  
 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCCTTGT GGTCACTTCT 480  
 GGTTCGCTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG AACTTCCCAT TCCTCATCAA 540  
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAGACCT ACACCTTACA 600  
 CTGCCTCCAT TGAAAACACG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660  
 ATATCTGTGA CTGTCTGTAG TTTGCTCTTG GTCTTATCA TATTATTTTG TTAATTCCGG 720  
 TATAAAGAC AAGAAACGAC ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC 780  
 ATTCCTCCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840  
 TCAGGCCTCC CTCTGCTGTG CCAAAGGACT ATAGCTAAGC AGATTTCAGAT GGTGAAACAG 900  
 ATTGGAAGAG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GCGGTGGCGA AAAGGTAGCT 960  
 GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020  
 ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATATG CTGCAGATAT CAAAGGGACA 1080  
 GGGTCTCTGA CCCAGTTGTA CTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140  
 TATCTGAAGT CCACCAACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200  
 AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAAACC AGCAATTGCC 1260  
 CATCGAGATC TGAAAAGTAA AAACATTTCT GTGAAGAAA ATGGAACCTG CTGTATTGCT 1320  
 GACCTGGGCC TGGCTGTTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380  
 ACTCGAGTTG GCACCAACAG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440  
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500  
 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560  
 CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGTCAT CAAGAAGTTA 1620

CGCCCCCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAACTC 1680  
 ATGACAGAAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740  
 ACACCTGCCA AAATGTCAGA GTCCCAGGAC ATTAAACTCT GATAGGAGAG GAAAAGTAAG 1800  
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860  
 TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAC 1920  
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980  
 TCTGTTTGTA GCGCGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT

**A71 Protein sequence**

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.72472 / Hs.87223  
 Probeset Accession #: AA250737 / U89326  
 Protein Accession #: NP\_001194  
 Signal sequence: 1-13  
 Transmembrane domains: 128-144  
 PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MLLRSAGKLN VGKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED 60  
 DSGLPVVTSGLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120  
 GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180  
 EQSQSSGSGS GLPLLQRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTEEAS 240  
 WPRETEIYQT VLMRHNILG FIAADIKGTG SWTQLVLITD YHENGSLYDY LKSTTLDAKS 300  
 MLKLAYSSVS GLCHLHTEIF STQKPAIAH RDLKSKNIVL KKNGTCCIAD LGLAVKFISD 360  
 TNEVDIPNT RVGTRKYMPP EVLDESLNRN HFQSYIMADM YSFGLLLWEV ARRCVSGGIV 420  
 EEYQLPYHDL VPSDFSYEDM REIVCIKKLR PSFPPNRWSSD ECLRQMGKLM TECWAHPAS 480  
 RLTAIRVKKLT LAKMSSESQDI KL

**Bladder****A72 DNA SEQUENCE**

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60  
 AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA 120  
 CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC 180  
 TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240  
 CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300  
 GCAGTGGCAG TCCGCCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360  
 GGGAACTGGT TCTCTGCTTG TTTGACAAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420  
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480  
 GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCATGCG GAACTCAAGT 540  
 GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG 600  
 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660  
 AGCATCCAGT ACACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720  
 CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780  
 GGCTCAGACA AACTGGGCGC CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840  
 TTCAACCCCA TGTACCCCAA AGACAATGAC ATGCCCTTCA TGAAGCTGCA GTTCCCACTC 900  
 ACTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960  
 GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020  
 GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080  
 GCGTACCAGG GGGAAAGTCAC CGAGAAGATG ATGTGTGCGA GCATCCCGGA AGGGGGTGTG 1140  
 GACACCTGCC AGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200  
 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260  
 AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGTGAGCT GTAA

**A73 Protein sequence:**

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 LDLa domain: 54-94  
 Tryp\_SpC domain: 204-429  
 Cellular Localization: plasma membrane/ER

1 11 21 31 41 51  
 | | | | |  
 MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPIIIAL LSLASIIIV VLIKVILDKY 60  
 YFLCGQLHF IPRQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT 120

GNWFSACFDN FTEALAEATAC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180  
 GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWFWQV SIQYDKQHVC GGSILDPHWV 240  
 LTAAHCFRKH TDVFNWKVRA GSDKLGSFPS LAVAKIIIE FNPMPKDNND IALMKLQFPL 300  
 TFSGTVRPIC LPFFDEELTP ATPLWIIIGW FTKQNGGKMS DILLQASVQV IDSTRCNADD 360  
 AYQGEVTEKM MCAGIPEGV DTCQDSSGGP LMYQSDQWHV VGIVSWGYGC GGFSTPGVYT 420  
 KVSAYLNWIY NVWKAEAL

## A74 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60  
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120  
 GCAGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180  
 CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCACTGGGG 240  
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCCTGG GGGAGCTGCT GGCTGCAGCC 300  
 TGTGCCAGCC GGGCCCTGCC CCCGTCCTCC TCCGGGCCCC CCTGCCCTGC CTGACGTCC 360  
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420  
 CTACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG 480  
 GCGCTCATT AGCAGCTGTT TGAGGCCGCG GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540  
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CCTGGCACTC 600  
 AGCCCTTCGA GGGTGGGCGC CCCATCGCAC CCACCTCTC TGCTGGAGA CCCCCGGCAG 660  
 GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CTTGCCGCC TGGCAGATG GGCTCCCCAG 720  
 GCCTGCCCCC GGTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG 780  
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCG CTACTACTGG CCGCTGTCAG 840  
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCGG TTTCCAGCG TGCCGCCCTG 900  
 GGTCCCATCT TCAGGGAAG GCACCTGCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960  
 AGAGGGCGCG GGGCGGCTCC GACGCGGCTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020  
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080  
 GTAAGCGGGG GGTGCCTGCC TGGCTGGGGA GCCCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140  
 CTGGCCAAAG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200  
 GGCTGTCATG TGCTCCAC AGACCTGGG GTGATGGCTT TCCCCCTCTT GGC CGGAGC 1260  
 TTGCCCCAGG TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA 1320  
 GACAGCTCCC AGGCACGTCA TAGGCAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGCG 1380  
 CTGGGGTCTT GCTCACCCTC CTTTGCTCTC ACGCCAGGCC TGTCCCCAGG TTTTCACTGG 1440  
 GAGAGGCCAC CTCCTCAGC CAAGGAAAAC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500  
 GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGGCCACTCC CGTGGTGTCT 1560  
 GGAGTACGCA CTGTTGGGGG GGGCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTACCA 1620  
 GAACACGGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680  
 TCAGTGTGTG TGGGGCGCAG GGCCTCCGAT GCGGGGTGAG TGCCTGGGGG GCGCAGGGCC 1740  
 CCCGATGCGG GGTGAGTGC TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACCTTTGGT 1800  
 ACAGTGTCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCACTC 1860  
 CCTTCCGAGG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920  
 TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980  
 GCCCTCCTAC CTTGAGATG GAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCTGG 2040  
 ACCTCCTGGG CAGGAAAGGG TGCAGGTCTT GAGGGCTGT GCCCCACAGC CCCAGCACCC 2100  
 AGGTGGACTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGTTCAGCA 2160  
 GGCTGGGGTC TGCCACACAG GGCCTCCCA CGTCTGCCCT TGAGGGTGGC TGCCATGCC 2220  
 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCAG 2280  
 GGTGACTTCA TCAGGAGACC GCCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340  
 GAGACAGGCT GGCACCTCCG GAAAAACTGC CTTTCAGCCT TGGTGTTCCG TGCAAGGTGA 2400  
 AAAGAAATAG GTCTCTCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAG 2460  
 CACGAGGGGA GAATTTAAAG GCCCGGCTG GCAGGGCTCA GGTGGCTGGC AGAGGCACAT 2520  
 GCAGACCTTG CCTGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580  
 GAGCAGCGTC CTTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACACGT 2640  
 GCGTGACAC TGTGATGACA CCCGAAATG TCTCAGGATG TTGAATGTG TCCTTGGGGG 2700  
 CAGAAGTGTC CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA 2760  
 TTTTGTGTTG ATCAAGTTC AAGGAAAAGG AACATCTCAG CCGGGCGTGG TGGTTCACGC 2820  
 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 CCCATCTCT ACAARAAAAA AAAAAGAAAG AAAGAAAATG AGAGATCCAG GTTTAAAAAT 2940  
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000  
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTTTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTCTTG GAAACATGAA AAAAAA

## A75 DNA SEQUENCE

Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor  
 Unigene number: Hs.227948  
 Probeset Accession #: AB035089  
 Nucleic Acid Accession #: AB035089  
 Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GGGCATGCGAC CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA 60  
 CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAAGAAGG 120  
 CCAAGAGGAA TAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTGGT 180  
 TTGGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG GCAGTGTGGC CAGATAGGA 240

	AGGAGGAAGG	GAGGCAAGAG	ATAATATCAT	TTTCTCTGTG	CTCCAAGTGT	ACTTACATAT	300
	GAGACTATTT	CCCTCTCTGC	TTTTCAAACC	TTACTGGAGT	TGTTTTCCCT	CATGAAAACC	360
	AAGAAAGGAA	AGCTAGTTAG	TCTTGTCTG	AGGTTGTTCA	ATGTATACAT	ATCTATATCT	420
	GTAGACAGAA	TCCTTGGGAA	TACAGTAATT	GACATATATT	CTGTTATTTG	ATGCTTGAAG	480
5	AATCTCTCTC	ACTAACCCAGT	TTCCCTATAG	ATTGCCACAA	GCACATAATA	AGAAACAATA	540
	AATAAAATGT	TCTCTTGACT	TTGTTACTTA	ACAATGCTGA	GAAAACCTTA	CAGCCTTCAT	600
	AAGGAAGTGA	GGTCCAGGAA	AATCTAGGAG	ATATTTCTTA	ACCAATCTAT	AAAGGCATTA	660
	GTAAATGACAG	GATATTTCTT	GAAAGTGTAA	TTTCCCAATT	AGGATTGTTT	TTTAATTTCT	720
10	GGATTCTCTG	AGCCAATGAA	GTTGGTGTAT	GTTTATGAAA	TATCAAGAGA	CATAAGTTGG	780
	CAAGTGTTC	TATGCAAAAA	CTTCTTGGA	TTTCTGAGTT	CTCTGTGGCA	ATATATGACA	840
	TCAGGATATG	TCCAGTCTCA	CACACCAGGA	TATGTCCTTT	CTAGCCTGTC	TATCAGATGC	900
	TAGGAGAACT	ATTTAGGAAC	AGAAAAAAT	GCCTGAAATG	ATTTCTCAT	TGAACATC	960
	CAAGCTTTCT	CTAAATTTAA	GCAAACTCCT	GGTCATTTTC	AGTTAGTACC	TTTCTTAAG	1020
15	TTCAACCTTC	AGGGCAAAACC	TCCGTGCCTC	AGACGTTTAG	CCATAGTCTG	AAATTCTCTT	1080
	CCATAGATTG	GTCCCTCTGA	ACCCCGTTTT	GTCTCAGCTT	GTTATCTCTG	TTTTTTCTTC	1140
	CCCTCCATTCC	CAGGATGAGC	TTGTTGCTTC	TGTCCTATGA	GACATTAGAT	TCCTTTTCTT	1200
	TGGTACCCGA	GTAAATCCAT	CCTACTCCAA	TAGAGGAAGG	TCCATTTTGT	TCTTATAGCG	1260
	CTGGATGCAG	ACTCAGCTGA	GAAGACCATT	ATTCATTTTT	GGAATTTCTT	ATCTCAGATA	1320
20	TTTCTCTCTT	TTTCTTTTTC	TTCTATCTTT	GGATTTTATG	TCCATCAACG	CCCCATTAGT	1380
	CTATTTCCCC	ACTTCAATCA	GGGAACCTAT	ACCTCTTAAA	CTCATTGAGA	GACTCAAAAC	1440
	ATATATATTG	ATACAGAGGA	CCTAAGAAGA	GCATGTCTTG	GGGGTTGAGG	AAACAGGCAG	1500
	GTGAGAAATT	TCCAGATTGG	AAACACAGCT	TCCTTTCTCC	CATCCAGCCC	CTACTTTCAG	1560
	CCTATGTGTT	TCTGGCACCT	TGTTGTAGAT	AAATCTCCCT	TGACTTTGTG	ATGTGCTGAG	1620
25	AAAACAAACT	CACGGCTGGT	GTTAAAAAGG	GCCCATGACA	ATACCAAGTG	TTGGGGAGAA	1680
	TGTGGAGAAA	TCAGAATCTT	ATTCACGGTC	GGTTGGAATG	CACACTTGTG	CAGAATTCTA	1740
	TGGAGAAGAG	TCTGGCATT	CCTCAAAATG	TAACTTGGGA	TTTACCATAT	GACCCAGCGA	1800
	TTTCAATTCAT	AGGTTTATAT	TCAAAAGAAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
	ATGAAAGGTC	ACAACATCAT	TATTCATAAT	AGTAAAAAGG	TGGAAACAAC	ACAAATGTCC	1920
	ATCAACTTAT	GATTAAGAAA	AATCTGGTCT	ATTCATAGAA	TGGAATATTA	TTCCAGCCACA	1980
30	AAAAGGAATG	ATGTACTGAT	CCATGCAATG	ATGTGGACAA	ACCATGAAAA	TAACACTAGA	2040
	TTAAAGAAAG	CAGTCACAAA	AGGACTTACT	GTATGATTCC	ATTTACCTGA	AATGTTTGGG	2100
	ATAGGCAAAAT	CCATAGAAAC	AGGAGGTAGA	TTCTGTGTTT	CCAGGGTCTC	CAGGAAGGGA	2160
	AGAATGAAGT	ACAGATTTTC	TTTTGGAGGT	AGTGAAATG	TTGTGGAATG	AGATCATGAT	2220
	GATGATAGCA	GACTTTTGTG	AATATAATAA	AATCATTTGA	TTGTACAGTT	GAATTTATGG	2280
35	TATATAAATT	ATATGTTAAT	AAAAAGGGGG	TCCACAAAAC	AAACAGCCCC	CCACTCTGGT	2340
	TGTGAGGAG	ATATTGGATT	AAATGGCCTT	GGACAACAAC	CCCTCTCCCT	GGCCACAGAC	2400
	ATTTCTCAGA	TTACAGAATA	TTCCAGGGGA	AACACTGGAA	TGAGTCTGAA	GCCAGGTGCT	2460
	AAACAGAAGG	ACCATTGAGA	AATGTTGTGA	TCCTGACAGG	TCAAGCAATT	TATTTTTCGG	2520
40	CTTCATTTTT	AAATGTAAAA	TTAGAAAGCT	GCCATTTAAA	ATGGCCCGTC	TGTTTCAATT	2580
	GCTCTTCTCA	GGTCTGAGCT	GTTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATACCT	GAGACTGGCA	AGAAAAAGAG	GTTTAAATGG	GCTTAGAGTT	CCACGTGATT	2700
	GGGGAGGCTC	CAGAAATCCA	GTAGGAGGCA	AAAGTTATTC	TTACATGGTG	GCTGCAAGAG	2760
	AAGATGAGGA	AGAAGCAAAA	GAAGAAACCC	CTGATAAACC	CATCGGATCT	CCTGAGGCTT	2820
45	ATTAACATCT	ATGAGAATAG	CACAAGAAAG	ACCGGCCCCC	ATGATTCAAT	TACCTCTACC	2880
	TGGGTCCCTC	CAATAACATG	TGGAAATTCT	GGTAGATACA	ATTCAGTTTG	AGATTTGGGT	2940
	GGGAACACAG	CCAAACCAT	TCACCTAGCA	AGGCAGATAA	CTTTCTCACT	GAGCCTATGC	3000
	AACAGAAAAC	CATCTGGGAT	GGTTGTAAGG	GGCACAGGAA	GTGACTGGTA	GGATCACTGC	3060
	CAAGCTGAG	CACCTCAGAG	AAGGCAATAG	AATCCTATT	TCCATAGTAT	GCTATAAGAT	3120
50	ACTGAAGTAC	ACTTCTTAC	TATCTCTTTG	GACTTAGAAT	TAGCACTACA	TTCTTGTGTA	3180
	TACAGAAAAA	TACTATAAGGA	AATTCATAGG	ATGACAAAAA	CTTTCAGAAC	TGAAAAACAG	3240
	GAAATGTAA	CTTTTATGTT	CTTTGGTATT	CGAAGTATGC	CTAAAAGACA	ATGCAAAATC	3300
	CAAGAAAAAG	ATGTTGGGTT	TTTTGTTTGT	TTGGTTTGT	TTTTGTTTGA	CAGCTGGAGT	3360
	AGAAATACAAA	GGGATGGAGT	TGAAACAAAT	GAGAGGAAAT	TGGAATTCTA	AACTTATCT	3420
55	CATTGGCATT	AGAAAGGCAC	CTACATGTAT	TTCACATGAG	CCGGTGACTG	CTGACTTGCA	3480
	TTCTTATTTT	TTCCCTATAG	ATTAAAAAGG	AGGTACAATG	GTAGAACTGT	AATCCTGTCC	3540
	TTTGTACATA	ATTTTCAATG	TCATAAAGGT	GAGTGTAGC	CCGCTTGTGA	AATCTGAAGT	3600
	TGAGTAACCT	CAATACTATA	CCACAGAGGG	AAAGGCAGCA	AGAGGAGAGG	CATAAATTTA	3660
	GGATCTCAC	CTTCAATCCA	CAGACACACA	CAGCCTCTCT	GCCCACCTCT	GCTTCTCTCA	3720
60	GGAAACACAG	TAAGAGCTTC	AAGCCTCTCC	AGCTTAATAA	CATGAATTAT	TTTTGAGAAT	3780
	AATAATGATA	CTGTGTTCTA	TATCATGCAT	CTCCTGCATT	CTGCTGATT	ATATTTTACT	3840
	TATTTCTGCC	GAGCAAAAT	AAAAATCCTA	TTTCATCTGA	TTTGTCCCTT	ATCTAAATG	3900
	CTTAGTTCCA	AGTAACCAA	GGCACTTTTA	GGAACACAGA	GGGAGAGTGC	CTTGACAGCA	3960
	GAGAGTCTTG	AAGGAGATGT	CAGGGACGCA	TCTTAACAGC	TGGTTGGATG	TGATCCACAG	4020
65	AGGTCTCCTG	TTAGCATTCA	TTGTAAAGCC	ATCCTACCTA	GCTCTAGTGT	AACCAGCAAT	4080
	GAAAGAAAGA	TAAAGAGGGT	CGATTACTTA	TTTACAATAG	TCTTTAAAAA	CGTAGTTTGT	4140
	TAAGCCTTCT	AATTAGGACA	TTAATATATT	TAATATATGC	ACATTGTAGA	AAGATTGAAG	4200
	CGTTAAAAAT	AAGAGAAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCATTTT	4260
	TTTAAGAAAA	TTGTACTACA	AAATACCAAT	CCATTTTATTA	AAGTCATTCT	GACAGGAATC	4320
70	TGATGCTTTT	CCAGGAGTTT	CAGATCACAT	CGAGTTCACT	ATGAATTCAC	TCAGTGAAGC	4380
	CAACACCAAG	TTTATGTTTG	ATCTGTTTCA	ACAGTTTACA	AAATCAAAAG	AGAACAACAT	4440
	CTTCTATTCC	CTTATCAGCA	TCACATCAGC	ATTAGGATG	GTCCCTCTAG	GAGCCAAAGA	4500
	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCTGTTGCAG	4560
	TTTTTCTCTG	GTTCCGTCGG	CTAGCACGCA	GATGGTAATA	GATGTGGTGG	TCTGATGGGT	4620
75	AGCACAGGGG	GCTGCTGAGG	AATTTCCATA	ACTGTGAGAC	CACCTGACTTA	AACAGATCTT	4680
	TTGAGTAAAG	TTTTCTTGTC	CCGCTTCATG	TCTCTTCCAG	GTCTTCACT	TTGATCAAGT	4740
	CACAGAGAAG	ACCACAGAAA	AAGCTGCAAC	ATATCATGTG	AGTCACAGAG	CACCTCTGAT	4800
	CAGCTTTAGA	TCCCTGAACA	GGTCATAGTT	TAAACCTGGA	ACTTCACAAA	AACTAAGAAA	4860
	AGGCCAGTTT	TAGGGAATAT	CTTGACACAA	AAGATTGAGA	CATACAGAGT	GGGTTGGCAT	4920
80	TTTCATGTC	ATAATTTATTA	TTCTCATTTT	CTGCGTTACT	AAAAGACAGT	CAGCACTGTA	4980
	CCTCAGAGCA	TAGGCTCTGA	TCAGGATAGG	CTGGGTTTCA	ACTCCAGCTT	TGCTCTTCA	5040
	AAATGATGAA	TAAAGACAGG	ACACAACCTG	TCGGAGTCCC	AGTGACCTCA	TCCCAGAAAA	5100
	CTAAGGGTAA	GAAAAAATCT	GACTCAATAC	ATGCAAAATG	ATGCAAAATG	TTACAACAGT	5160
	GCCTTGCCCA	TAAAGTGCAT	AATAAATGTT	ATTATTATTA	TAAAGTAGCT	ATAATTTATC	5220
	TAATCATAAAT	AATGTGAAAA	TAATTTAATT	TTCATTGAGT	CATTAAATGAG	ATTCAGAGGA	5280



	ATAAGCACAA	GTCCAAGTAT	ATTTTGAAAA	ATGATTGCTA	TGGAATATAT	TGGTTTAGAG	5340
	CCTTAATAGT	GC AAAATGCT	TTGCTGGAAG	GTAGAAAAGT	CTAGATTTAA	ACAGGCTTAG	5400
	GTTCAAAACT	TGGCACTTCT	AATTTATGTC	TCTATAAACA	GGGTTTTTTT	CCCCATTCTC	5460
5	TGAGCTTTCT	TGTGTTTCAT	TGAATTGAAC	TAAAGACTTA	GAGTTACCCA	TGTAAGTCC	5520
	TTAGCCATGG	ACCTGGCATA	CACCTCTCTT	ACGTGCAGAG	AATGACCATC	ATGAGGAAAG	5580
	AGCCACAGAT	CAGTCAATGT	GTCCTACAAG	ATAATAGCAC	CAACAGGTAT	AACAGGGCTT	5640
	CCTGGCATAA	TCTATTAAAA	ATATCCAACC	TTCAACATAC	TCGTATCCTT	GATGACTGTT	5700
	AGAAGTGAAA	TATGGTCCCT	GCCATAAAGG	AGCTGAGAGT	TTAACTGGGA	AGCTAAACCT	5760
10	AACCCCTTAA	ACCAACAAGG	AGAAAATCTA	CTGGTAGACA	CGCTGCATC	TTAGTTTCAG	5820
	AAGAGAAAAA	ATTGCAGTAC	GTTAGAGCAA	GAAGAAATTT	CTGGAAGAAG	TCAAATATAA	5880
	GGTGGATTTT	GAAGGGTATT	TGAGGTGAAA	TACACCAATT	ATCAGGGAAT	AACATCAAAAG	5940
	GTCTCTCAAT	AGACTACCAG	CATTTAGGGA	CTGATCTAAC	AGACTTAGCA	TGGGTTTAGT	6000
	ATTTACATTG	ATACAGCAAT	TGAATGATCT	CCTTTTTTGA	TGTTTGAAGG	TTGATAGGTC	6060
	AGGAAATGTT	CATCACCAGT	TTCAAAAGCT	TCTGACTGAA	TTCAACAAAT	CCACTGATGC	6120
15	ATATGAGCTG	AAGATCGCCA	ACAAGCTCTT	CGGAGAAAAG	ACGTATCAAT	TTTTACAGGT	6180
	AAATTTACCT	GGCTTACCCT	CATTTCAATT	GCATCCTGAT	GTCTGTGTCT	CTGAGTGGCC	6240
	AAATGGAAGA	AAGCAAGGCA	GATGAGCCTG	GCCGACCCAG	GTGGAGAGCA	TTTACTCAGA	6300
	GTGCATTAGC	TCCATTTCCA	CAACTCTCCC	CCACTGGAGT	GTCCCAGACC	CCAACGATAC	6360
20	ATCACTGAAG	TGTGGATTTA	GGGATAATCT	TGTGATAAAA	GAGGAGGTTG	TGTAATAGAG	6420
	TGAGTAAGAG	TAATAAGTAA	TAAGATACCA	TCGATAAACT	GGCACTGACT	CAGTACACATA	6480
	CGATACATCT	TGTTGGGAAA	TGTATGACTA	ATGGGATATT	ATTGGAATGG	GCAGGCTTGG	6540
	GTGAGTTCCT	GAGAATAGTT	GAGGAAGTAC	CAGGAATAT	TGAATGCACA	GGATGAAAGA	6600
	CAAAAAA	GATCAGAAAC	ATCATGGTTA	AAATTACTGG	AGAGAAGTCT	GAGAAGCAAT	6660
25	GAATCTCCTT	CAGGGAAGCC	TGCTCTGCAG	TTTGCAAAACC	ACAGCCTCTT	CTGCTTCTGC	6720
	CTTTTGCCAA	GATGATATTG	ACCTTCAGTG	ACCTCTTTCT	TGTGCCAGCC	CACATTCCCC	6780
	TTTTGCATTG	CCTACATGAC	ACCTGTATAA	AAATATCCAT	GGACAGGAGA	TACTGCATCT	6840
	ATTCAGGGTC	TGAGTTGAGC	TTACTGTTGT	TACAAATAAG	TAAGTTTGGT	AATATATAGT	6900
	TACATAAATT	ACTCCTAATT	CCTACTCTCT	CCTTCATATC	TCAAAGGAAT	ATTTAGATGC	6960
30	CATCAAGAAA	TTTTACAGGA	CCAGTGTGGA	ATCTACTGAT	TTTGCAAAATG	CTCCAGAAGA	7020
	AAGTCGAAAG	AAGATTAAC	CCTGGGTGGA	AAGTCAAAACG	AATGGTAGGA	GAGCCACCCA	7080
	TTATAGAAAC	ACCTTTGAGA	AACTATGCCC	AGTGAGCCTT	GTGCTTGACA	CTGCATGGGG	7140
	GAACAGGTGT	GGGAGTTGAG	ATGGGTTTGC	AGGGAGGGCT	GAAGAGGGCA	CTCCAGATGA	7200
	AGGATTTGTC	CAATAGTATA	TGAAGAGAGC	CTAGGGGAGC	CAAGGAGGAA	ATCACAGGAA	7260
35	GCCRAATTAGA	TGGAACAACA	CTGGAGAAT	TATTTGCTTA	TGGCCCTGCA	TGCAATAGC	7320
	TTTGTGGATC	CCCTGTCTCC	GCTCAGACCT	ATTTTGAGAT	CATATCCTTT	ACTTTAAATC	7380
	AGACTCAAA	TTTTATGATG	AATATTTAAT	AGAAAACATT	AGAAAGCGTC	TCTCGTCTCC	7440
	TTTACTAATT	GGGAAACAAG	CAGCTCTCTG	GTAAATCACC	CTTTTGTCTC	TGAGCTGGAG	7500
	CTGCCTGGAT	CACATCTGTA	GCCAAATGCT	TCTGCAGGGA	TTATCAGAGC	TCTCTTCCCC	7560
40	ATCAAGGGCA	AAGAGCTTGA	CAAAGTCTCC	ATTCTACAGA	CATCTTTCTT	ACCTCCCACC	7620
	TCTCATTACA	GGCCAAACTC	ACAGCAACTC	AACATGAGAG	TGAATAGGAA	GATACCCCCG	7680
	GAAGTAGTGT	CTGACAGCAG	AGGACATGCG	TTTCATATTA	CAGAGCTCAA	GTCACTCATC	7740
	CTAAATGCA	ATCAGGGCCT	CCTTCTCTG	AATGGGGACC	CCGTAGTTAA	AAAAAATAA	7800
	AAGTAGGAAG	AGGAGGGAGG	GAGAAAGGAA	AGACACATGT	TGGAAGAGTA	GACAAATCA	7860
45	GTTTATCAGT	ATTCCTAATC	AGATGATTGG	AGACATTCAT	ACACAGAGAA	CGTGAACCTC	7920
	TTCTCTATCA	CAAGAAGTGA	TGTCTCCATC	AAGGGTAACT	TTATACGACT	GGAGCCTTGA	7980
	AGAAAGCTGC	ATCTGGTGAA	CCACTGGTCA	GTGAGTCTAA	CAATTCAAAG	ATCAAAGTCA	8040
	GTGAGTCTCA	AGCAGGGATT	TGGGTCAATA	ATTAACGATC	AGTCACGAAC	ATTTGCAAAG	8100
	CATCTTCCAG	ACAAGCCATT	TGTAGCTTGT	GTAAAAGACT	CTTTTATTCT	TTCCCTTGCA	8160
50	GAAAAAATTA	AAAACTTATT	TCCTGATGGG	ACTATTGGCA	ATGATACGAC	ACTGGTTCTT	8220
	GTGAACGCAA	TCTATTTCAA	AGGGCAGTGG	GAGAATAAAT	TTAAAAAGA	AAACACTAAA	8280
	GAGGAAAAAT	TTTGGCCAAA	CAAGGTATTG	TCTATATTTT	ATTTATATAG	TGTAATATGT	8340
	TAATACATGG	AATGTTAAAC	ATTTCTGATG	GAATGTAAAC	TGATAAGTAA	AAAAATAAAA	8400
	TTGTTCAATG	CTGTTATTTT	GTTGTTTTAC	TCTTATAACT	TTATTAGTTT	AGGAATACCT	8460
55	GAAAAACTAT	TGTTTCTAAC	TCATGGAATT	CCTGGGTTAT	TTCTTAGAAG	AAGAAGGATG	8520
	TGTTGCTATC	TCAATAATAT	TATCTTTTTT	GTCTTGTGTT	TCACGTGTTA	TTTGTGGAC	8580
	ACATTGATTT	ATGTCAGAA	ACATACAAAT	CTGTACAGAT	GATGAGGCAA	TACAATTCCT	8640
	TTAATTTTGC	CTTGCTGAGG	GATGTACAGG	CCAAGGTCTT	GGAAATACCA	TACAAAGGCA	8700
	AAGATCTAAG	CATGATTGTG	CTGCTGCCAA	ATGAAATCGA	TGCTCTGCAG	AAGGTAAGAA	8760
60	CTTGATCTCA	CAACTCTTCC	TTCTACTGCC	GGACATTTT	CCAAAGATAC	CAAGTTTAAA	8820
	CAAGGTAATA	GCTTATGACC	GAGTTGCCCT	AAAATGATGA	AAAATCTTAA	ATGAGGAATG	8880
	ATGACTCACC	TTCAATTTAC	AAATATTTGA	GCATAGGGCC	TGACACAAAC	TGAAAGCTTA	8940
	GTTTTTGTGT	GTTTGTGTTG	TTTTATTATT	ATTATTATAA	TACTTTAAGC	TTTAGGGTAC	9000
	ATGTGCACAA	TGTGAGGTTT	AGTTACATAT	GTATACATGT	GCCATGCTGG	TGTGCTGCAC	9060
65	CCATTAACTC	ATCATTTAGC	GTTAGGTATA	TCTCCTAATG	CTATCCCTCC	CCCCCTCCCC	9120
	CACCCCAACA	CAGTCTCTAG	AGTGTGATGT	TACCTTCCTG	TGTCCAAGTG	TTCTCATTTG	9180
	TCAATTCCTA	TCTATGATTT	AATTCATCT	ATGGCTTAGT	TAATGATTAA	TTTATTAGAG	9240
	TTACATGCAT	TGGATATCAA	TTTGATGATA	TTATTATGCA	GCAATTTAAA	CTTGACTGGG	9300
	AGAAATATAT	ACCAATGTGA	GGAAAGTTTA	CAAATAGGCC	GAGTAGAAAA	GGGAATACAA	9360
70	ATTTAGGAAT	TTAGGGAATT	ACAATTTAAT	AATTGCAATG	TGTACTAAAT	AATGTATACA	9420
	GAAAAATATG	ATGAGCCTAT	TAAAAATGTA	CACATGTAGT	AGGCTGTTGG	CACAAGAAAT	9480
	AGTGATACAT	ACAGTTTCAAT	GTGTACAAAA	TAATGTAATC	ATATTTTACA	TGTGTATCAT	9540
	ACAGTTGTAT	ACATACATAT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600
	ACATACATGT	ATATACATAT	ACACATATAA	CCCAATGTAT	TTATATATTC	AGGACTCATA	9660
75	TTTTACCTAT	TAGAATAATA	ATGCTATTA	AAGTGAACCT	TCTGTATTTC	ACATTTATTG	9720
	CCAAAATAAC	GAATCTCCAC	ATAGTCAATT	CATTGTAAAG	GTGTATTAGA	GATCGACAGT	9780
	TAGTCATATC	AGTTTCTTTT	TTCCATTTGT	ATAGCTTGAA	GAGAACTCA	CTGCTGAGAA	9840
	ATTTAGTGA	TGGACAGATT	TGCAGAATAT	GAGAGAGACA	TGTGTCGATT	TACACTTACC	9900
	TCGGTTCAA	ATGGAAGAGA	GCTATGACCT	CAAGGACACG	TTGAGAACCA	TGGGAATGGT	9960
80	GAATATCTTC	AATGGGGGAT	CAGACCTCTC	AGGCATGACC	TGGAGCCACG	GTCTCTCAGT	10020
	ATCTAAAGTC	CTACACAAGG	CCTTTGTGGA	GGTCACTGAG	GAGGGAGTGG	AAGCTGCAGC	10080
	TGCCACCGCT	GTAGTAGTAG	TCGAATTATC	ATCTCCTTCA	ACTAATGAAG	AGTTCTGTGT	10140
	TAAATCACCCT	TTCTTATTCT	TCATAAGGCA	AAATAAGACC	AACAGCATCC	TCTTCTATGG	10200
	CAGATTCTCA	TCCCATAGA	TGCAATTAGT	CTGTCACTCC	ATTTAGAAAA	TGTTTCACTA	10260
	GAGGTGTTCT	GGTAACTGA	TTGCTGGCAA	CAACAGATTG	TCTTGGCTCA	TATTTCTTTT	10320

CTATCTCATC TTGATGATGA TAGTCATCAT CAAGAATTTA ATGATTAAAA TAGCATGCCT 10380  
 TTCTCTCTTT CTCTTAATAA GCCACATAT AATGTACTT TTCCTTCCAG AAAAATTTCC 10440  
 CTTGAGGAAA AATGTCCAAG ATAAGATGAA TCATTTAATA CCGTGTCTTC TAAATTTGAA 10500  
 ATATAATTCT GTTCTTGACC TGTTTTAAAT GAACCAAAACC AAATCATACT TTCTCTTCAA 10560  
 ATTTAGCAAC CTAGAAACAC ACATTTCTTT GAATTTAGGT GATACCTAAA TCCTTCTTAT 10620  
 GTTCTTAAAT TTTGTGATTC TATAAAACAC ATCATCAATA AAATAATGAC ATAAAAATCAT 10680  
 TTTTGCCTTA CCTGTTTTCT CTCTGGAAAG GGCAAGTGT CAGTTACACA TAGGAAAGAT 10740  
 AATTTAGAGA TATATTAATC ATATATAAAG GAAAATTAAA AACAGAGTAG TTCATGATGA 10800  
 GCCTGGAGTA GAAGGCATAT CCCAGAACAG GAGGAGCCTT GTAAACCACA TAGGAACTTC 10860  
 CTATTTTATG CTAAGGGGAT AAGAACTCA TTACAGGCTT TGATGTTGT TTGTCAAAGA 10920  
 GGGGCATAAA ATTATCATAT CCACATCTAG AAAATACATC TCTGGCTACG CTGATATCAA 10980  
 TGGATGCGAG GAAAGAACAG TGTGGTTACC ATATATAAAT TAGGAAATCA TTAGAGTATT 11040  
 GGGAGTGGAA ATGGAGAGAA AGAAAGAGCC TGGGGGAATT ATTTAGGAAA TAATAGTTAC 11100  
 AGAAGACAT CTAAGTTGCT GACCTATCTG ACTGGATGGA TGAAGAATA TCTTGTTCCT 11160  
 GAGAGAAAAA AAGACTTTGG GTTTAAATTT GTACTTGATG AATTAAGGTA CTTTAAATAT 11220  
 TCAAATGGAT TTGCTCGGCA GGCACCTGAA GATATTAGTC TAAATCTCAG AAACAGAATA 11280  
 TGATCTGAAG CTCTAAATTT GTGATATTC AATATAATAC TTTAGAGTCA TTGGGATAAA 11340  
 TATGGTAGTT GTGCTAAAAA GCAAAATAA GATACTAGGG AGAAAGGATA AAGTTAGAAG 11400  
 AAAGAAGAAT CTAGAATTGA CCTTGAAGTA TATCAGCATG TGTAAAGATC AGGAATTGAT 11460  
 CATTTTATT TTCCAGAAAG TAGCTTTTCT TAGGGTTCCA TATTTACTCC CATAGATTCT 11520  
 TCCC

**A76 Protein sequence:**

Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor  
 Unigene number: Hs.227948  
 Probeset Accession #: AB035089  
 Protein Accession #: BAB21525  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Serine Proteinase Inhibitor domain: 13-390  
 Cellular Localization: secreted

1 11 21 31 41 51  
 | | | | |  
 MNSLSEANTK FMFDLFQQFR KSKENNIFYS PISITSALGM VLLGAKDNTA QQISKVLHFD 60  
 QVTENTTEKA ATYHVDNRSGN VHHQFQKLLT EFNKSTDAYE LKIANKLFE KTYQFLQEYL 120  
 DAIKKFYQTS VESDFANAP BESRKKINSW VESQINEKIK NLFDPGTIGN DTTLVLVNAI 180  
 YFKGWENKF KKENTKEEFK WPNKNTYKSV QMMRQYNSFN FALLEDVQAK VLEIPYKGD 240  
 LSMIVLLPNE IDGLQKLEEK LTAELKMEWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300  
 TMGMVNIENG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAAATAVV VVELSSPSTN 360  
 EEFCCNHFFL PFIRQNKTNIS ILFYGRFSSP

**A77 DNA SEQUENCE**

Gene name: hypothetical protein FLJ13459  
 Unigene number: none found  
 Probeset Accession #: XM\_047266  
 Nucleic Acid Accession #: XM\_047266  
 Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CTGACCTCAA GTGATCCACC CACCTCTGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC 60  
 CACCATGCCA GGCCCTCTTA ACCTCTTCAA GTCTGTTTTC TCATCTGCAA AACAGAGGTA 120  
 ATAAGATCAG TATCTTCTTA ATGGAAGCAC CTGGACTACA TTTTCTTCAT TCATTGTTAT 180  
 CATAAATGAG GACTAACCTG TCTCCCGTTG GGAGTTTGA ACCTAGACCT CATGTCTTCA 240  
 TGACGTCACT ACTGCCCCAG GCCCAGCTGT GTCCCTACAC CAGCCCCAGC TGACGCATCT 300  
 TCTTTTCTCT CCGTAGAGTA TGGTTACAAT GCCTGCGGTG ATGCATTCTG GCCTTCGCAG 360  
 ATCCTGGCGG GGCTGTGCCA ACGCTGTGGC CTCCCTGCCC CTGAATACCG AGCCGGTGCT 420  
 GTCAAGGTGG GCAGCAAAGT CTTCTGACA CCACCGAGA CCCTGCCCC AGGGATCTCT 480  
 TCACATGTGG ATTGACATCT TTCCTCAAGA TGTGCTGCT CCACCCCAAG TTGACATCAA 540  
 GCCTCGGCAG CCAATCAGCT ATGAGCTCAG AGTTGTATC TGGAAACACGG AGGATGTGGT 600  
 TCTGGATGAC GAGAAATCCAC TCACCGAGA GATGTCGAGT GACATCTATG TGAAGAGCTG 660  
 GGTGAAGGGG TTGGAGCATG ACAAGCAGGA GACAGACGTT CACTTCAACT CCTGACTGG 720  
 GGAGGGGAAC TTCAATTGGC GCTTTGTGT CCGCTTTGAC TACCTGCCA CGGAGCGGGA 780  
 GGTGAGCGCT TGGCGCAGGT CTGGACCTTT TGCCCTGGAG GAGGCGGAGT TCCGGCAGCC 840  
 TGCAGTGTCT TCCTCTCAGG TCTGGGACTA TGACCGCATC TCTGCCAATG ACTTCTTTGG 900  
 ATCCCTGGAG TTGCAGCTAC CAGACATGGT GCGTGGGGCC CGGGGCCCC AGCTCTGCTC 960  
 TGTGCAGCTG GCCCGCAATG GGGCCGGGCC GAGGTGCAAT CTGTTTCGCT GCCGCCGCT 1020  
 GAGGGGCTGG TGGCCGGTAG TGAAGCTGAA GGAGGCAGAG GACCTGGAGC GGGAGGCGCA 1080  
 GGAGGCTCAG GCTGGCAAGA AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GGCCAGAAGA 1140  
 CCTGGAGTTC ACAGACATGG GTGGCAATGT GTACATCCTC ACGGGCAAGG TGGAGGCAGA 1200  
 GTTTGAGCTG CTGACTGTGG AGGAGGCCGA GAAACGGCCA GTGGGGAAGG GCGGGAAGCA 1260  
 GCCAGAGCCT CTGGGAGAAC CCAGCCGCCC CAAAACCTCC TTCAACTGTT TTGTGAACCC 1320  
 GCTGAAGACG TTTGTCTTCT TCATCTGCGC CCGTACTGCG GCACCTCTGG TGCTGCTGCT 1380  
 ACTGGTGCTG CTCACCGTCT TCCTCTCTCT GGTCTTCTAC ACCATCCCTG GCCAGATCAG 1440  
 CCAGGTCACT TTCGGTCCCC TCCCAAGTGT ACTCTGCTG ACCTTGGACA CTCACCCAGG 1500  
 GTGCCAACCC TTCAATGCCT GCTCCTGGAA GTCTTTCTTA CCCATGTGAG CTACCCCAAGA 1560  
 GTCTAGTGCT TCCTCTGAAT AAACCTATCA CAGCCACTG

**A78 Protein sequence:**

Gene name: hypothetical protein FLJ13459

Unigene number: none found  
 Probeset Accession #: XM\_047266  
 Protein Accession #: XP\_047266  
 Signal sequence: none found  
 Transmembrane domains: 291-313  
 C2 domain: 27-86  
 Cellular Localization: plasma membrane / ER

1 11 21 31 41 51  
 | | | | | |  
 MWIDIFPQDV PAPPFVDIKP RQPISEYELRV VIWNTEDVVL DDENPLTGEM SSDIYVKSUV 60  
 KGLEHDKQET DVHFNLSLTGE GNFNWRFFVR FDYLPTEREV SVWRRSGPFA LEEAEFRQPA 120  
 VLVLVQVWDYD RISANDFLGS LELQLPDMVR GARGPELCSV QLARNAGAGPR CNLFRCCRRLR 180  
 GWWPVVKLKE AEDVEREAQE AQAGKKRKQ RRRKGRPEDL EFTDMGGNVY ILTGKVEAEF 240  
 ELLTVBEAEK RPVGKGRKQP EPLEKPSRPK TSFNWFVNPL KTFVFFIWR RYWRTLVLLLL 300  
 VLLTVFLLLV FYTIPGQISQ VIFRPLHK

# A79 DNA SEQUENCE

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)  
 Unigene number: Hs.161031  
 Probeset Accession #: AL137708  
 Nucleic Acid Accession #: AL137708  
 Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | | |  
 GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60  
 GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCCTTTCTGT CTGTCTCCTT GCTCTGCCCC 120  
 AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180  
 ATGGCCTGGG CTGGGCCCTT GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAGG 240  
 CTCCTGTGGG CAAAGCAGGG GAGCGCCCAA TGTGGAGGAA CAGAGTCTCC TGGTGGCTG 300  
 CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCCTG 360  
 GGGTCACCGT AGGCCCATGT TAGCACCTTG GTTCCCCTGC CTGTAGGTGA CAGGAGCCAG 420  
 CCCAGCCAGG TGTGCTCCCT CCCAGGGCCC TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480  
 CGCCCGCCCC ACCTTCCTTC CCACCCACAT GCCGAAGGGT GGCCAGGCAG GCAGGTGGAC 540  
 GAGTCCAGGC AGCGGGCTGAG TCAGTGTGTG TGGAAATGTT TGGCCGCCTC CAGCTGCACC 600  
 CTGCCCCTAC CTGCCACAC CTAACCTTCA TCCTCAGGCG CTGCGGCCCT GAGCCCCCTG 660  
 CAGGAATGCA CCTTTAGCCC AGGCCTGCTC AGTGAGCTCC GCCGACAGCC AGCCCTGCTC 720  
 CTCGCCCAT GACCTGCGAG ACCCTCTGG GCTTCCAAGT TCCTGGGGGC TGCAGTGAAC 780  
 ATGCTCCACC TGCATGGCTG GCAAACCATG GTGGGCCCCA GCTGTGGTGC GTGCTGGGGT 840  
 AGAGGCAAGG AAGTGATGGG ACCGCAGAGA TGAGACCCCC AGGGATGAGA TGGGACCCCC 900  
 AGGACGGGCC CAGGGTCCAG GGCCAGGAG AGAGAAGCAG GGAGGGAGAG AGCTTCCTGG 960  
 TGGAGGACGC ATCCTACAGT GGGGGCAAGG GTGCTCTGAG GTCCGGTGAA GGCAGGGACT 1020  
 AGGCTGCCCA GGCCTGCCTT GCTTGGCTGG GGCTGGGGGG TGCTGGGAGG TGGCTGGGAG 1080  
 GCTGGGCTGA GGCAGCTAAG CTGGAGCTTT GGCCAGGGTC CAGAGCCTCC CTCCCTTCAG 1140  
 CTCTCTGCTG CACAGAACCC TCGCCCTTGG CCACCCCTGT CTGCCTCCTT GCCCTGGCAG 1200  
 ACCCAGCACT GGCTGCTGCT AGTCAGATGG GGTAGCGGGC AGGGGCCGGA GGGGCCACCC 1260  
 TCCCAGCTGA CCCAGCCTCC TGGGCGGCTT CTTCCAAACC AGCAGGGTAG AAAGATGGGG 1320  
 CACCCACAGG TCTCTCCAGC TGCCCGCGCC CCAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380  
 ATTCCAGACC TTGTGCGCGG GACCCCTGTG GAGTTGTGGG ATTCCCAAGA GGGGTGTGGG 1440  
 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC 1500  
 CCAGGGCCCC GCTGGGCTCT CATTGCCGGC GCCCTTGCCG CGGGCGTCTC CTCTGCTCTC 1560  
 TGCTCTCTCT GTGCTGCTGC CTGCTGCTGC CGCCGCCACA GGAAGAAGCC CAGGACCAAG 1620  
 GAGTCCGTGA GTCTGGGAGC TGCCCGCGGC ACCACCACCA CCCACCTGGT GAGGAGCGGC 1680  
 TCCTTGCTCA CTCAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740  
 GGCAGATTCA GCCCCAGGGA TGGTTTAACC CCCACAGAGG CAGGGCGTGG AGGACCTTCC 1800  
 TGGCAGGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCCAT 1860  
 GGGCCCCAGG GAGCCACAGC GGGTTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT 1920  
 TTTGGGTGGG TTTGGCCGGT CTCACAGAGC GAAGCCGACG ATTTGTGCCT GTTGGGTGGC 1980  
 CTGGCCTGGA GGCGGGGGTT CTTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCCAGGG 2040  
 CTCTGATGAG GCATGATGTC AGCACCACTT GCCCCTTGTC CCAACTCACT CCAGGTGCAA 2100  
 CCTGATGTGG ATGGCCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCCTGCAG 2160  
 CTCTCCCTGG AGTTTCACTT TGGAAAGCCAG GAGGTGAAGG GCCCGCTGC GCAGGACCAG 2220  
 CGGTTCTGCG AGTTTCCGGA AAGGGTGACG GGGGAAGGGC AGACCCCATG CCCTGGGTGG 2280  
 TGGGGAGCTG ACAGGGCAGG GGCCCTTGGC TGAGCCCAAC CGCTGGCTC CCAGATCAGG 2340  
 GTGGGCTTGA GGCAGCAGC CGACCTGAGG CCTGGGGGCA CCGTGGACCC CTATGCCCGG 2400  
 GTCAGCGTCT CACCCAGGCG CGGACACAGA CATGAGACAA AAGTGCACCG AGGCACGCTC 2460  
 TGCCCGTGT TTAGCAGAGC CTGCTGCTTC CACGTGAGTC AGGGATGGTC GGCTGGGTGG 2520  
 GCCTGGACGG CTGGATGGGC CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGCCTGGGCA 2580  
 GCTGGGTGGG CTGAGCTAG GGCAGCAGGG CCTGGCTCAC GCCGTGCTC CAGATCCCCG 2640  
 AGGCGGAGCT GCCAGGGGCC ACCCTGCAGG TGCAGCTTTT CAACTTCAAG CGCTTCTCGG 2700  
 GGCATGAGCC CTGGGTGAG CTCCGTCTGC CACTGGGCAC CGTGGATCTG CAGCATGTTC 2760  
 TGGAGCACTG GTACCTGCTG GGCCCGCCGG CTGCCACTCA GGTGAGGTGC TGGTCACCAG 2820  
 GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CCTGCCCTAT GGGCCATCGG AAAGACAGGC 2880  
 CTGATGGGCA GCATTTTCGG GGGTCTGAGC CCCAACTCGG CCAGAATCAC CCTCCCGGGC 2940  
 TGAAGCCCTT CTGTCTGCC ACAGCCGAG CAGGTGCGGG AGCTGTGCTT CTCTCTCCGG 3000  
 TACGTGCCCA GCTCAGGCCG GTGACCGTGT GTGGTGTCTG AGGCTCGAGG CTGCGTCCA 3060  
 GGACTTGCAG AGCCCTTACG GAAGGTCCAG CTCATGCTGA ACCAGAGGAA GTGGAAAGAG 3120  
 AGAAAGACAG CCACCAAAAA GGGCACGGCG GCCCCTACT TCAATGAGGC CTTCACCTTC 3180  
 CTGGTGCCTT TCAGCCAGGT CCAGAATGTG GACCTGGTGC TGGCTGTCTG GGACCGCAGC 3240  
 CTGCCGCTCC GAACTGAGCC CGTAGGCAAG GTGCACCTGG GTGCCCGGGC CTCGGGGCAG 3300

CCCCTGAGC ACTGGGCAGA CATGCTGGCC CACGCCCGGC GGCCCATTCG CCAGCGGCAC 3360  
 CCCCCTGCGG CAGCCAGGGA GGTGGACCGC ATGCTGGCCC TGCAGCCCCG CCTTCGCCCTG 3420  
 CGCCTGCCCT TGCCCCACTC CTGAATGCAC CACATGCCCT TGTCTCCCCG CTGAGCCCAG 3480  
 GCACTTGCCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC

**A80 Protein sequence:**

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)  
 Unigene number: Hs.161031  
 Probeset Accession #: AL137708  
 Protein Accession #: CAB70885  
 Signal sequence: none found  
 Transmembrane domains: 69-85  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MGHPVPSPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAKWGL QLSTDALSLA 60  
 STFGPRWALI AGALAAGVLL VSCLLCAACC CCRHRHKRKP DKESVGLGSA RGTTTTHLVR 120  
 SGSLLTQSRE GLKSRLQSPG QRGEFSRDRG LTPTEAGR

**A81 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51  
 | | | | |  
 GCGGAACACC GCGCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60  
 TCCTCTGTGG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGCGCCG 120  
 CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180  
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240  
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300  
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360  
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420  
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480  
 ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540  
 AGACAGGCTG GTTGTGTTGG AATAAGCCAC TGGACCCGGA GGAGATTGCC AAGTATGAGC 600  
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA 660  
 TCATCGTGAG CGACCAAGT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720  
 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780  
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840  
 AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900  
 CCAGTGGGCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960  
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020  
 ACAATGCTCC CATGTTTGAC CCCAGAAAGT ACGAGGCCCA TGTGCTGAG AATGCAAGTGG 1080  
 GCCATGAGGT CCAGAGGGTG ACGGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC 1140  
 GTGCCACCTA CTTATCATG GCGCGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200  
 CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGA GCGCAAAACC 1260  
 AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCCCTT TGTGCTGAAG CTCCCAACCT 1320  
 CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCCAC 1380  
 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440  
 CTGCAGAAAG CCCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500  
 CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTAC AGCTGTGGGC ACCCTCGACC 1560  
 GTGAGGATGA GCACTTTTGT AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 ATGGAAGCGT TCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680  
 ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAGC CCTGTGCCCC 1740  
 ACGTGCTGAA CATCAGGAC AAGGACCTGT CTCCCCACAC CTCCCCCTTC CAGGCCGAGC 1800  
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG 1920  
 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
 ATGTCGAAAC CTGCCCTGGA CCCTGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGGCTG 2040  
 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100  
 TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160  
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280  
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340  
 AGGCGGCTAA CACAGACCCC ACAGCCCCGC CTAACGACAC CCTCTTGGTG TTCGACTATG 2400  
 AGGGCAGCGG TCCCGACGCC GGTCCCTGA GCTCCCTCAC CTCCTCGGCC TCCGACCAAG 2460  
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520  
 ACGGTGGCGG GGAGGACGAC TAGGCGGCCCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC 2580  
 CACAGAGCAT CTCGAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTC 2640  
 GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700  
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760  
 CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCCAGAA GCCTCTTACC TGCCGTAAAA 2820  
 TGCTCAACCC TGTGTCCTGG GCCTGGGCCCT GCTGTGACTG ACCTACAGTG GACTTCTCT 2880  
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTNTTTT AATGCTATCT 2940  
 TCAAAACGTT AGAGAAAGTT CTTCAAAGT GCAGCCGAGA GCTGCTGGGC CCACTGGCCG 3000  
 TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060  
 ATACTGAGTT TGCCTAGGTT GCCCTTATTT TTTTATTTT CCGTGTGCGT TGCTATAGAT 3120  
 GAAGGTGTAG GACAACTGCT TATATGTACT AGAATTTTT TATTAAAGAA A

A82 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675 (second underlined sequence)

Cellular localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
KGPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREBIAK 180
YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGLVP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TDMGDGSGST TAVAVVEILD ANDNAPMFDP QKYEAHVPEV AVGHEVQRLT VTDLDAPNSP 360
AWRATYLMG GDDGDHFTIT THPESNQGIL TTRKGLDPEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDDPKE NQKISYRILR 480
DPAGWLAMPD DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLLD 540
VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPHSTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDK HGHVETCPGP WKGGFILPVL 660
GAVLALLFL LLLLLLVK RKIKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720
GLEARPEVVL RNDVAPTII PPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
DYEAGSGSDA SLSSLTSSAS DQDQDYDYLW EWGSRFKKLA DMYGGGEDD

```

A83 DNA SEQUENCE

Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Probeset Accession #: F07953  
 Nucleic Acid Accession #: NM\_016334  
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCAGCGTG CTGTGGCCTC 60
GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA 120
CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTTTGA TTTGGGTGGC TTTTCTTCAT 180
GCGCCAATTG TTTAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCTTCTCCGT 240
GACGTTTGCA TTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
GAATAGCAGC TCCCGTTATT TTTCACTGGAA AATGAACCTG TGCCTAATTC TGCTGATCCT 360
GGTTTTCATG GTGCTTTTTC ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA 420
TAAACAACGA CTGCTTTTTT CCTGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
ACTAGGAGAT CCGTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTCTTTCTCT GATTGTGGTG 600
TGTCACATGC CCATACACTT ACATGTCTTA CTCTCTCAGG AATGTGACTG ACACAGATAT 660
TCTAGCCCTG GAACGGCGAC TGCTGCAAAAC CATGGATATG ATCATAAGCA AAAAGAAAAG 720
GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG 780
TTTTCTGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAG ATCTTACTCT 840
TATTCAACAG GAAGTGGATG CTTTGAAGA ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAATATTTT 960
TAAATTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020
CAATATTGTT TTTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080
TGTGAATTAT CTGGGAATCC AATTGTATGT GAAGTTTGTG TCCCAACACA TTTCTTTCAT 1140
TCTTGTGGGA ATAATCATCG TCACATCCAT CAGAGGATG CTGATCACTC TTACCAAGTT 1200
CTTTTATGCC ATCTCTAGCA CTAAGTCTCT CAATGTCATT GTCCTGCTAT TAGCACAGAT 1260
AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTGAATA 1320
CCGCACCATA ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACCGTTGGTT 1380
TGATGTGATC TTCCTGGTCA GCGCTCTCTC TAGCATACTC TTCCTCTATT TGGCTCACA 1440
ACAGGCACCA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTAGAGGC 1500
CAGTGGTTTC AAAATTTAGA TATAAGAGGG GGGAAAAATG GAACCAGGGC CTGACATTTT 1560
ATAAACAAC AAAATGCTAT GGTAGCATTT TTCACCTTCA TAGCATACTC CTTCCCCCTC 1620
AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAAGTCAAG 1680
ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG 1740
CCAAGAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGGTAGC 1800
TGAGCCAAC ACGTAGGATT TCCGTTTAA GGTTCACATG GAAAAGGTTA TAGCTTTGCC 1860
TTGAGATTGA CTCATTAAAA TCAGAGACTG T

```

A84 Protein sequence

Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Protein Accession #: NP\_057418.1  
 Signal sequence: none found  
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51

```

	MSFLIDSSIM	ITSQILFFGF	GWLFFMRQLF	KDYEIRQYVV	QVIFSVTFAF	SCTMFELIIF	60
	EILGLNSSS	RYFHWKMNLC	VILLILVFMV	PFIYGYFIVS	NIRLLHKQRL	LFSCLLWLT	120
	MYFFWKLGDP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTYMSYFLRN	180
5	VTDTDILALE	RRLQLQMDMI	ISKKKRMAMA	RRTMFQKGEV	HNKPSGFWGM	IKSVTTSASG	240
	SENLTLIQGE	VDALBELSRQ	LFLETADLYA	TKERIEYSKT	FKGKYFNFLG	YFFSIYCVWK	300
	IFMATINIVF	DRVGKTDPVT	RGIEITVNYL	GIQFDVKFWS	QHSIFILVGI	IIVTSIRGLL	360
	ITLTKFYFAT	SSSKSSNVIV	LLLAQIMGMV	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
10	FYHRWFDVIF	LVSALSILF	LYLAHQAPE	KQMAP			

A85 DNA SEQUENCE:

Gene name: TTK protein kinase

Unigene number: Hs.169840

Probeset Accession #: M86699

Nucleic Acid Accession #: NM\_003318

Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
20	GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACTC	TTGTTGGCCA	GGCTGGAGTG	60
	CAATGGCACA	ATCTCAGCTT	ACTGCAACCT	CCGCCTCCCG	GGTTCAAGCG	ATTCTCCTGC	120
	CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACCTAATT	180
25	CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCTG	240
	ACCTCAGGTG	ATCCACTTGC	CTTGGCCTCC	CAAAGTGCTA	GGATTACAGC	CGTGAAACTG	300
	TGCTTGGCTG	ATTCTTTTTT	TGTTGTTGGA	TTTTTGAAAC	AGGCTCTCCC	TTGGTCGCCC	360
	AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACTATAACC	TCCACCTCCT	GGTTTCAAGT	420
	GATCCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	GCCTGCACCA	CCACACCCGG	480
30	CTAATTTTTG	TATTTTTATT	AGAGACAGGG	TTTCACCATG	TTGGCCAGGC	TGTTCTCAAA	540
	CTCCTGGACT	CAAGGGATCC	GCCTGCCTCC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
	AGTCACCATG	CCTGACCTTA	TAATTCCTAA	GTCAATTTTT	CTGGTCCATT	TCTTCCTTAG	660
	GGTCCTCACA	ACAAATCTGC	ATTAGGCGGT	ACAATAATCC	TTAACTTCAT	GATTCACAAA	720
	AGGAAGATGA	AGTGATTATC	GATTAGAAAA	GGGGAAGTAG	TAAGCCCACT	GCACACTCCT	780
35	GGATGATGAT	CTTAATCCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
	TTTGGTTTAA	ATTAATTATC	TAAATATCTA	AAAACATTTT	TGGATACATT	GTTGATGTGA	900
	ATGTAAGACT	GTACAGACTT	CCTAGAAAAA	AGTTTGGGTT	CCATCTTTTC	ATTTCCCCAG	960
	TGCAAGTTTC	TGTAGAAATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGATT	1020
	CCATAATGAA	CAAAGTGAGA	GACATTAAAA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
40	AACTAAGCTT	GAATAAAATT	TCTGCTGATA	CTACAGATAA	CTCGGGAAC	GTTAACCAAA	1140
	TTATGATGAT	GGCAAAACAAC	CCAGAGGACT	GGTTGAGTTT	GTTGCTCAAA	CTAGAGAAAA	1200
	ACAGTGTTC	GCTAAGTGAT	GCTCTTTTAA	ATAAATTGAT	TGGTCGTAC	AGTCAAGCAA	1260
	TTGAAGCGCT	TCCCCAGAT	AAATATGGCC	AAAATGAGAG	TTTTGCTAGA	ATTCAAGTGA	1320
	GATTTGCTGA	ATTAAGAGCT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAAAATG	1380
45	CCAGAGCAAA	CTGCAAGAAA	TTTGCTTTTG	TTCATATATC	TTTTGCACAA	TTTGAACTGT	1440
	CACAAAGTAA	TGTCAAAAAA	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CGTGGAGCAG	1500
	TACCACTAGA	AATGCTGGAA	ATTGCCCTGC	GGAATTTAAA	CCTCCAAAAA	AAGCAGCTGC	1560
	TTTCAGAGGA	GAAAAAGAAG	AATTTATCAG	CATCTACGGT	ATTAACCTGC	CAAGAATCAT	1620
	TTTTCCGGTT	ACTGGGTCAT	TTACAGAATA	GGAACAACAG	TTGTGATTCC	AGAGGACAGA	1680
50	CTACTAAAGC	CAGGTTTTTA	TATGGAGAGA	ACATGCCACC	ACAAGATGCA	GAAATAGGTT	1740
	ACCCGAATTC	ATTGAGACAA	ACTAACAAAA	CTAAACAGTC	ATGCCCATTT	GGAAGAGTCC	1800
	CAGTTAACTT	TCTAATATAG	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTTGTACCTT	1860
	GTTTTATGAA	AAGACAAACC	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
	AACCAAGTGG	AAATGATTCC	TGTGAATTAA	GAAATTTAAA	GTCTGTTCAA	AATAGTCATT	1980
55	TCAAGGAACC	TCTGGTGCA	GATGAAAAA	GTTCTGAAC	TATTATTACT	GATTCAATAA	2040
	CCCTGAAGAA	TAAACGGA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
	AAGAACCAGA	GGTTCCAGAG	AGTAACCAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
	GTATTAAACA	GAATCCTGCT	GCATCTTCAA	ATCACTGGCA	GATTCGGGAG	TTAGCCCGAA	2220
	AAGTTAATAC	AGAGCAGACT	CATACCCTTT	TTGAGCAACC	TGCTCTTTCA	GTTCCTCAAA	2280
60	AGTCACCACC	AATATCAACA	TCTAATGGT	TTGACCCAAA	ATCTATTTGT	AAGACACCAG	2340
	GCAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTGTAGAA	TCCAGTTGTA	AAGATGACT	2400
	TTCCACCTGC	TTGTCAGTTG	TCAACACCTT	ATGGCCAACC	TGCTGTGTTA	CAGCAGCAAC	2460
	AGCATCAAA	ACTTGCCACT	CCACTTCAAA	ATTTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
	ATGAATGCAT	TTGGTTTAA	GGAAGAATT	ATTCATATT	AAAGCAGATA	GGAAGTGGAG	2580
65	GTTCAAGCAA	GGTATTTTCA	GTGTTAAATG	AAAAGAAACA	GATATATGCT	ATAAAATATG	2640
	TGAACCTAGA	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	CCGGAACGAA	ATAGCTTATT	2700
	TGAATAAACT	ACAAACAAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAAATCACGG	2760
	ACCAGTACAT	CTACATGGTA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAAA	2820
	AGAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTACTG	GAAAAATATG	TTAGAGGCAG	2880
70	TTCACACAAT	CCATCAACAT	GGCATTGTTT	ACAGTGATCT	TAAACCAGCT	AACTTTCTGA	2940
	TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATTGC	AAACCAAAATG	CAACCAGATA	3000
	CAACAAGTGT	TGTTAAAGAT	TCTCAGTTG	GCACAGTTAA	TTATATGCCA	CCAGAAGCAA	3060
	TCAAGATAT	GTCTTCTTCC	AGAGAGAATG	GGAATCTTAA	GTCAAAGATA	AGCCCCAAAA	3120
	GTGATGTTTG	GTCTTAGGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCATTTC	3180
75	AGCAGATAAT	TAATCAGATT	TCTAAATTAC	ATGCCATAAT	TGACTCTAAT	CATGAAATTG	3240
	AATTTCCCGA	TATTCAGAG	AAAGATCTTC	AAGATGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
	ACCCAAAAAC	GAGGATATCC	ATTCTGAGC	TCCTGGCTCA	TCCATATGTT	CAAATTCAAA	3360
	CTCATCCAGT	TAACCAAAATG	GCCAAGGGAA	CCACTGAAGA	AATGAAATAT	GTTCTGGGCC	3420
	AACCTGTTGG	TCTGAAATCT	CCTAACTCCA	TTTTGAAAGC	TGCTAAAAC	TTATATGAAC	3480
	ACTATAGTGG	TGGTGAAAGT	CATAATTCTT	CATCCTCCAA	GACTTTTGAA	AAAAAAAGGG	3540
80	GAAAAAAATG	ATTTCAGATT	ATTCGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGAGT	3600
	GTTTACTCTT	TGAATCCCTG	TGGAAATCTA	CATTTGAAGA	CAACATCACT	CTGAAGTGT	3660
	ATCAGCAAAA	AAAAATTCAGT	GAGATTATCT	TTAAAAAGAA	ACTGTAAAAA	TAGCAACCCAC	3720
	TTATGGCACT	GTATATATTG	TAGACTTGT	TTCTCTGTTT	TATGCTCTTG	TGTAATCTAC	3780
	TTGACATCAT	TTTACTCTTG	GAATAGTGGG	TGGATAGCAA	GTATATTTCTA	AAAAACTTTG	3840

TAAATAAAGT TTTGTGGCTA AATAGA

A86 Protein sequence:

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Protein Accession #: NP\_003309  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

1	11	21	31	41	51	
MNKVRDIKKN	FKNEDLTDEL	SLNKISADTT	DNSGTVNQIM	MMANNPEDWL	SLLLKLEKNS	60
VPLSDALLNK	LIGRYSQLAE	ALPPDKYQON	ESFARIQVRF	AELKAIQEPD	DARDYFQMAR	120
ANCKKFAFVH	ISFAQFELSQ	GNVKKSKQLL	OKAVERGAVP	LEMLEIALRN	LNLOKKQLLS	180
EEKKQLNSAS	TVLTAQESFS	GSLGHLQNRN	NSCDSRGQTT	KARFLYGENM	PPQDAEIGYR	240
NSLRQTNKTK	QSCPFGRVPV	NLLNSPDCDV	KTDDSVVPCF	MKRQTSRSEC	RDLVVPGSKP	300
SGNDSCELRN	LKSVQNSHFK	EPLVSDEKSS	ELIITDSITL	KNKTESLLA	KLEETKEYQE	360
PEVPESNQKQ	WQAKRKSECI	NQNPAASSNH	WQIPELARKV	NTEQKHTTPE	QPVFSVSKQS	420
PPISTSKWFD	PKSICKTPSS	NTLDDYMSCF	RTPVVKNDFP	PACQLSTPYG	QPACFQQQHQ	480
QILATPLQNL	QVLASSSANE	CISVKGRIYS	ILKQIGSGGS	SKVFPVLNEK	KQIYAIKIVN	540
LEADNQTLID	SYRNEIAYLN	KLQQHSDEKI	RLYDYEITDQ	YIYMVMCEGN	IDLNSWLKKK	600
KSIDPWERKS	YWNMLAEVH	TIHQHGIVHS	DLKPANFLIV	DGMLKLIDFG	IANQMOPDIT	660
SUVKDSQVET	VNYMPEATK	DMSSRENGK	SKSKISPKSD	VWSLGCILY	MTYKGTPEFQ	720
IINQISKLHA	IIDPNHEIEF	PDIPEKDLQD	VLKCCCLKRDP	KQRISIPPELL	AHPYVQIQTH	780
PVNQMAKGT	EEMKYVLGQL	VGLNSPNSIL	KAAKTLYEHY	SGGESHNSSS	SKTFEKKRGR	840

A87 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719  
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
GGGCGCAGCG	GGGCCCCGTCT	GCAGCAAGTG	ACCGACGGCC	GGGACGGCCG	CCTGCCCCCT	60
CTGCCACCTG	GGGCGGTGCG	GGCCCGGAGC	CCGGAGCCCG	GGTAGCGCGT	AGAGCCGCGC	120
CGATGCACGT	CGCCTCACTG	CGAGCTGCGG	CGCCGCACAG	CTTCGTGGCG	CTCTGGGCAC	180
CCCTGTTCCT	GCTGCGCTCC	GCCCTGGCCG	ACTTCAGCCT	GGACAACGAG	GTGCACCTCGA	240
GCTTCATCCA	CCGGCGCCTC	CGCAGCCAGG	AGCGGCGGGA	GATGCAGCGC	GAGATCCTCT	300
CCATTTTGGG	CTTGCCCCAC	CGCCCGCGCC	CGCACCTCCA	GGGCAAGCAC	AACTCGGCAC	360
CCATGTTTAT	CTTGGACTCG	TACAACGCCA	TGGCGGTGGA	GGAGGGCGGC	GGGCCCCGCG	420
GCCAGGGCTT	CTCCTACCCC	TACAAGGCCG	TCTTCAGTAC	CCAGGGCCCC	CCTCTGGCCA	480
GCCTGCAAGA	TAGCCATTTC	CTCACCGACG	CCGACATGGT	CATGAGCTTC	GTCAACCTCG	540
TGGAACATGA	CAAGGAATTC	TTCCACCCAC	GCTACCACCA	TCGAGAGTTC	CGGTTTGATC	600
TTTCCAAGAT	CCCAGAAGGG	GAACTGTCA	CGGCAGCCGA	ATTCCGGATC	TACAAGGACT	660
ACATCCGGGA	ACGCTTCGAC	AATGAGACGT	TCCGGATCAG	CGTTTATCAG	GTGCTCCAGG	720
AGCACTTGGG	CAGGGAATCG	GATCTCTTCC	TGCTCGACAG	CCGTACCCTC	TGGGCCTCGG	780
AGGAGGGCTG	GCTGGTGTTC	GACATCACAG	CCACCAGCAA	CCACTGGGTG	GTCAATCCGC	840
GGCACAACTT	GCGCTCGACG	CTCTCGGTGG	AGACGTGGA	TGGGCAGAGC	ATCAACCCCA	900
AGTTGGCGGG	CCTGATTGGG	CGGCACGGGC	CCCAGAACAA	GCAGCCCTTC	ATGGTGGCTT	960
TCTTCAAGCG	CACGGAGGTC	CACTTCCGCA	GCATCCGGTC	CACGGGGAGC	AAACAGCGCA	1020
GCCAGAAACC	CTCCAAGACG	CCCAAGAACC	AGGAAGCCCT	CGCGATGGCC	AACGTGGCAG	1080
AGAACAGCAG	CAGCGACCCG	AGGCAGGCCT	GTAAGAAGCA	CGAGCTGTAT	GTCAAGCTTC	1140
GAGACCTGGG	CTGGCAGGAC	TGGATCATCG	CGCCTGAAGG	CTACGCCGCC	TACTACTGTG	1200
AGGGGGAGTG	TGCCTTCCTT	CTGAACCTCT	ACATGAACGC	CACCAACCAC	GCCATCGTGC	1260
AGACGCTGGT	CCACTTCATC	AACCCGGAAG	CGGTGCCCAA	GCCCTGTGTG	GCGCCACGCG	1320
AGCTCAATGC	CATCTCCGTC	CTCTACTTCG	ATGACAGCTC	CAACGTATAT	CTGAAGAAAT	1380
ACAGAAACAT	GGTGGTCCGG	GCCTGTGGCT	GCCACTAGCT	CCTCCGAGAA	TTCAGACCCT	1440
TGCGGGCCAA	GTTTCTCTGG	ATCCTCCATT	GCTCGCCTTG	GCCAGGAACC	AGCAGACCAA	1500
CTGCCTTTTG	TGAGACCTTC	CCCTCCCTAT	CCCCAACTTT	AAAGGTGTGA	GAGTATTAGG	1560
AAACATGAGC	AGCATATGGC	TTTTGATCAG	TTTTTCAGTG	GCAGCATCCA	ATGAACAAGA	1620
TCCTACAAGC	TGTGACGGCA	AAACCTAGCA	GGAAAAAA	ACAACGCATA	AAGAAAAATG	1680
GCCGGGCCAG	GTCATTGGCT	GGGAAGTCTC	AGCCATGCAC	GGACTCGTTT	CCAGAGGTAA	1740
TTATGAGCGC	CTACCAGCCA	GGCCACCCAG	CCGTGGGAGG	AAGGGGGCGT	GGCAGGGGGT	1800
GGGCACATGG	GTGTCTGTGC	GAAAGGAAAA	TTGACCCGGA	AGTTCTCTGA	ATAATGTGTA	1860

A88 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Protein Accession #: NP\_001710.1  
 Signal sequence: 1-30  
 Pfam domains: TGFb\_propeptide [37-281]  
 Transmembrane domains: none found  
 Cellular Localization: secreted

1 11 21 31 41 51  
| | | | | |  
5 MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRRLRSQE RREMQREILS 60  
ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120  
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHREFRFDL SKIPEGEAVT AAEFRIYKDY 180  
IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVEFDITA TSNHWVVPNR 240  
HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300  
10 QNRSKTPKNQ EALRMANVAE NSSSDQROAC KKHLYVSFR DLGWQDWIIA PEGYAAYCE 360  
GECAFLPNSY MNATNHAIVQ TLVHFINFET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420  
RNMVVRACGC H

**A89 DNA SEQUENCE:**

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)  
Unigene number: Hs.27373  
15 Probeset Accession #: F13036  
Nucleic Acid Accession #: AC012478  
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
| | | | | |  
25 ATGCGCGCCG TCGCGCTGCC CGCCCCGCTC CTGCGCGCTG TGCTGCTCGC GCTCCTGGCC 60  
GCTCCCGCCG CCGCGCCGAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120  
CGCGAGTCGC GGCACCCGCC CGGCCCGGGG CCGGGGAACA CCACCCGGTT TGGGTCTGGG 180  
CGCGCGGGCG GCAGCGGCAG CTCCAGCTCC AACAGCAGTG GCGACGCCTT GGTGACCCGC 240  
ATTTCATATC TCCTCCGCGA CCTACCCACC CTCAAGGCAG CCGTGATCGT GGCCTTCGCC 300  
TTTACCACCC TCCTCATCGC CTGCCTGCTG CTGCGCGTCT TCAGGTTCGGG AAAGAGGTTA 360  
AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGCGCCA 420  
30 CTAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480  
TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT 540  
GTGCCCCCAG CCTTCATCCT CGACATTGAC CTTCAGCAA GATGCACTGG AAGGCCTGAT 600  
GGTGGATCAA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAAGTTGG 660  
TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGCGT CGGAGGTGTT 720  
35 GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTC AGGCATCTGC 780  
TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCAACCAA TGGAGTTGCT TCTGCCACCC 840  
TTTGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAAATGCGA 900  
CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGTCCATCT 960  
GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGTG CTGAAAGTGA CCTTCCAAAT 1020  
40 CCTTGGTGGC CATTCAGCGC CACAGGCTCT CCAATAAAAA CCTTTACAC ACAAACCATG 1080  
AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGGCCAGC GGGGCACCTT TGTGTAAGAC 1140  
AGAGCAGTGA CTAAGGTTCT CCAGGTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200  
GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260  
ACCCATCTGT TCAAGTTGGC TCGTTTCAGT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320  
45 AGGGTGTTCG GCGTCCGCGC GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380  
TGCTTTTGGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTCTACAAA 1440  
ATCTGTCTCC CCTGCTGTGC CGTGGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500  
GTCTTTGCGT CATTTGAGCA GAGCCACAAA AAGGCAGCTG CTGCCCACGG GGAGCCTGTC 1560  
50 AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620  
GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCACGTGA GGATGTCACT 1680  
CACCTGGAG GAGACTTGA TGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740  
GATGGCAGAT GCCAGAAGT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800  
TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTTCTCTT 1860  
TCCCCCGGAC AGCCCTGTT TCTGTCCAGG CCCTGA

**A90 Protein sequence:**

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)  
Unigene number: Hs.27373  
60 Probeset Accession #: F13036  
Protein Accession #: FGENESH predicted  
Signal sequence: 1-27  
Transmembrane domains: 94-115, 448-469  
Cellular Localization: not determined

1 11 21 31 41 51  
| | | | | |  
70 MRAVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTRFGSG 60  
AAGSGSSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FTTLLIACLL LRVFRSGKRL 120  
KKTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGCTLLTVP 180  
VPPPFILDI LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSVGGV 240  
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPP FGHFPKVPPT STPHGFRQLQ 300  
LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAAESDLFN PWWHFSATGS PIKTLYTQTM 360  
75 STLGLDVFCG AQQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESFPPHLL RLLRECPPLS 420  
THPVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480  
ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHAHGEVP KRGPSSQLTR HTCPCGWGITH 540  
ANLQTTIPDTQ GQEGEPREDVT HPGGDLGVA NFYLEEEGFQ DGRQCQKMLVM SEEGPPSLTG 600  
CERLTGSHHF SSHSKWSWFL SPRQLFLSR P

**EWING****A91 DNA SEQUENCE**

Gene name: G protein-coupled receptor 64  
Unigene number: Hs.184942



Probeset Accession #: AA435577  
 Nucleic Acid Accession #: NM\_005756  
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

1      11      21      31      41      51
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60
CTCGCGGTCA GGATGGTTTT CTCTGTCAAG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
GTTTTACTGA CGTTCAAGAT ATTCCCTGTG ATCATTGTGC TTCATGTCGT TCTGGTAACA 180
TCCCTGGAAG AAGATACTGA TAATCCAGT TTGTCAACC CACCTGCTAA ATTATCTGTT 240
GTCAGTTTTG CCCCTCCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAATCA CTATAGTAAA AACCTTCAAT 360
GCTTCAGGCG TCAAACCCCA GAGAAATATC TGCAATTGTG CATCTATTTG CAATGACTCA 420
GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAA 480
CAACATATAA CGAATGGCAC CTAACTGGA GTCCTGTCTC TAAGTGAATT AAAACGCTCA 540
GAGCTCAACA AAACCTTCCA AACCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
GAGGCCAAAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA 660
TGCTGTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTTCGAC CAATGGAACA CTGCTGTCTG 720
TCTGTCAAGA TACCCTGCCC TTCTCCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATTTTC TTCCAGCCAA 840
TCCATCCCAG TGGTGCCTCG GGCCACTGTG CTTTCCCAGG TCCCCAAAGC TACCTCTTTT 900
GCTGAGCCTC CAGATTATTC ACCTGTGACC CACAATGTTT CCTCTCCAAT AGGGGAGATT 960
CAACCCCTTT CACCCCAAGC TTCAGCTCCC ATAGCTTCCA GCCCTGCCAT TGACATGCCC 1020
CCACAGTCTG AAACGATCTC TTCCCTATG CCCCACAAAC ATGTCTCCGG CACCCCACT 1080
CCTGTGAAAG CCTCATTTTC CTCTCCACCC GTGTCTGCCC CTGCGAATGT CAACACTACC 1140
AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTTCTGA TCTTGAGAAC 1200
CAAGTGTGTC AGATGGAGAA GGCTCTGTCC TTGGGCAGCC TGGAGCCTAA CCTCGCAGGA 1260
GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCGCCGC CTGACATGCT GGGCCCTCTG 1320
GCTCAAGATG TGCTGAAAGT AGTGGATGAC ATTGGCCTAC AGCTGAACCT TTCAAACACG 1380
ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
TTCAACACAA CTACCTTTGT GGCCCAAGAC CCTGCAATC TTCAGGTTTC TCTGGAAC 1500
CAAGTCTCTG AGAACGATG TGGCACAATT ACTCTTCTT CATCGCTGAT GAATAAATTA 1560
CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTCTTGA AACACCTGCT 1620
TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTATC ATCATCGAGT 1680
GTTGCAAACC TGACCGTCAG GAACCTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
AAACCGAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAATAGT 1800
GGCAGAGGAG GCTGTGTCAG CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAAACC 1860
ATCTGTACCT GTAGCCATCT AACAAGCTTC GGCGTTCTGC TGGACCTATC TAGGACATCT 1920
GTGCTGCCTG CTCAAATGAT GGCTCTGACG TCCATTACAT ATATTGGTTG TGGGCTTTCA 1980
TCAATTTTTC TGTGAGTGAC TCTGTAAACC TACATAGCTT TTGAAAGAT CCGGAGGGAT 2040
TACCCCTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CTGTGCTTCT 2100
CTCCTGGACT CGTGGATTGC TCTGTATAAG ATGCAAGGCC TCTGCATCTC AGTGGCTGTA 2160
TTTCTTCATT ATTTTCTCTT GGTCTCATTC ACATGGATGG GCCTAGAAGC ATTCATATG 2220
TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATCTCTG 2280
ATTGTGCGTT GGGGGGTACC AGCTGTGGTT GTGACCATCA TCCTGACTAT ATCCCCAGAT 2340
AACTATGGGC TTGGATCCTA TGGGAAATTC CCCAATGGTT CACCGGATGA CTTCTGCTGG 2400
ATCAACAACA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTTG 2460
CTGAACGTCA GCATGTTTAT TGTGGTCTCT GTTCAGCTCT GTCGAATTA AAAGAGAAG 2520
CAACTGGGAG CCCAGCGAAA AACCAGTATT CAAGACCTCA GGAGTATCGC TGGCCTTACA 2580
TTTTTACTGG GAATAACTTG GGGCTTTGCC TTCTTTGCCT GGGGACCAGT TAACGTGACC 2640
TTCATGTATC TGTTTGCCAT CTTTAATACC TTACAAGGAT TTTTCATATT CATCTTTTAC 2700
TGTGTGGCCA AAGAAAATGT CAGGAAGCAA TGGAGGCGGT ATCTTTGTTG TGGAAAGTTA 2760
CGGCTGGCTG AAAATTTCTG CTGGAGTAAA ACTGCTACTA ATGGTTTAAA GAAGCAGACT 2820
GTAACCAAGG GAGTGTCCAG CTCTTCAAAT TCCTTACAGT CAAGCAGTAA CTCCACTAAC 2880
TCCACCACAC TGCTATGTGA TAATGATTGC TCAGTACACG CAAGCGGGA TGGAAATGCT 2940
TCTACAGAGA GGAATGGGGT CTCTTTTAGT GTTCAGAATG GAGATGTGTG CCTTCACGAT 3000
TTCACTGGAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCCGT 3060
ATGGCTCTCA GAAGGACTTC AAAGCGGGA AGCTTACACT TTATTGAGCA AATGTGATTC 3120
CTTTCTTCTA AATCAAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA 3180
CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT 3240
AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300
TTTAGACATT TCTGATTTGG TTTCTTATCT TTCAATTTAT AAGAAGGTTG GTTTTAAACA 3360
ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420
TTTAAAGAGG CTAAGTTATC TTTGATAACA TCATATAAAG CAACTGTTGA CTTACAGCTG 3480
TTGGTGAGTT TAGTTGTGCA TGCCTTTGTG GTATATAAGC TAAATTCTAG TGACCCATGT 3540
GTCAAAAATC TTACTTCTAC ATTTTGTGTG ATTTATTTTC TACTGTGTA ATGTATTCTT 3600
TTGTAGAAATC ATGGTTGTTT TGTCTCACGT GATAATTCTG AAAATCCTTG CTCGTTCCGC 3660
AAATCCTAAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA 3720
TCAAGAAATG ATGATCCCAG CCAGACTGAG AAAATGTAAAG CAGACAGTGC CACAGTTAGC 3780
TCATACAGTG CCTTTGAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840
TGGGTCAATGG TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900
GTGCACGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCCATCCC CTGACCCGAT 3960
CCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020
AGAGGGATGA ACTGTCATCC AGACCATGTG TCAGGAAAT TGTGAACGTA GATGAGGTAC 4080
ATACACTGCC GCTTCTCAAA TCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC 4140
CTTCTCTTAA AAAGGTACAT ATATATGGAA AAAAATCATA TTGCCGTTCT TTAAGAGGCA 4200
ACTGCATGGT ACATGTTGTA TTGTTATGAC TGGTACACTC TGGCCAGGCC AGAGCTATAA 4260
TTGTTTTTTA AATGTTGCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320
GGGAAGTCTC CTACACTGCT ATTGTGCTA CATGTATCGA GCCTTGATTG CTCCTAGTTA 4380
TATACAGGAT CATCTTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCCTC AAGTACATCC 4440
TATTAGGAA CATTCTTAA CCCCCTTTAG TAAGTCTTTC ACTAAGGTTT TCTTGCATAT 4500
ATTTCAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560
CTGACTTGTC TTTGCAATAT TTCTTTCTG ATTTATTTAA TTTTCTGTA TTTATATGTT 4620

```

AAAATCAAAA ATGTTAAAAAT CAATGAAATA AATTTGCAGT TAAGA

#### A92 Protein sequence

Gene name: G protein-coupled receptor 64  
 Unigene number: Hs.184942  
 Protein Accession #: NP\_005747.1  
 Signal sequence: 1-38  
 GPS domain: 564-615  
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
15  MVFSVRQCGH VGRTEEVLIT FKIFLVIICL HVVLVTSLEE DTDNSSLSP PAKLSVVSFA 60
    PSSNEVETTS LNDVTLSELL SNETEKTKIT IVKTFNASGV KQQRNICNLS SICNDSAFFR 120
    GEIMFYDKLE STVPQNHIT NGTLTGVLSL SELKRSELNK TLQTLSETYF IMCATAEAQS 180
    TLNCTFTIKL NNTMNAACAI AALERVKIRP MEHCCCSVRI PCPSSPEELG KLQCDLQDPI 240
    VCLADHPRGP PFSSSQSIPV VPRATVLSQV PKATSFAPPP DYSPVTHNVP SPIGEIQPLS 300
    PQPSAPIASS PAIDMPFQSE TISSPMPQTH VSGTPPPVKA SFSSPTVSAP ANVNNTSAPP 360
    VQTDIVNTSS ISDLENQVLQ MEKALSLGSL EPNLAGEMIN QVSRLHSPS DMLAPLAQRL 420
    LKVVDDIGLQ LNFSTNTISL TSPSLALAVI RVNASSFNIT TFVAQDPANL QVSLETQAPE 480
    NSIGTTITLPS SLMNNLPAHD MELASRVQFN FFETPALFQD PSLENLSLIS YVISSSVANL 540
    TVRNLTRNVT VTLKHINPSQ DELTVRCVFW DLGRNNGRRGG WSDNGCSVKD RRLNETICTC 600
    SHLTSFGVLL DLSRTSVLPA QMMALTFITY IGCGLSSIFL SVTLVITYIAF EKIRRDYPSK 660
25  ILIQLCAALL LNLNVLFLDS WIALYKMQGL CISVAVFLHY FLLVVSFTWMG LEAFHMYLAL 720
    VKVENTYIRK YILKFCIVGW GVPVAVVTII LTISPDPNYGL GSYGKFPNGS PDDFCWINNN 780
    AVFYITVVG YFCVIFLLNVS MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLIG 840
    ITWGAFFAW GPVNVTFMYL FAIFNTLQGF FIFIFYCVAK ENVRKQWRRY LCCGKLRLAE 900
30  NSDWSKTATN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SNGNMASTER 960
    NGVSFSVQNG DVCLHDFTGK QHMFNEKEDS CNGKGRMALR RTSKRGSLSHF IEQM
  
```

#### Fibrosis

#### A93 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Nucleic Acid Accession #: NM\_015507  
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

```

40  1      11      21      31      41      51
    |      |      |      |      |      |
    CCGCAGAGGA GCCTCGGCCA GGCTAGCCAG GCGCGCCCCA GCCCTCCCCC AGGCCGCGAG 60
    CGCCCTTGCC GCGGTGCTCT GCCTCCCTCT CCAGACTGCA GGGACAGCAC CCGGTAACATG 120
    CGAGTGGAGC GAGGAGACCC AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
45  GGGTCCGGCC GCGCCCTTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCGAGA 240
    ATGCTCTGCG CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
    GGGAACGCGG CCACTGCAAG GCATCAGCGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC 360
    TGTCACTATG GAACATAACT GGCTGCTGCT TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
    TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
50  AGATGCTTTT CAGGATACAC CGGGAAGAAC TGCACTCAAG ATGTGAATGA GTGTGAATG 540
    AAACCCCGGC CAGTCAACAC CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
    CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATC 660
    ATAAACTGTC ATACAGCATG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
    TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCT 780
55  GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGGAAG CTACTACTGC 840
    AAATGTACCA TTGTTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
    AATGAATGTA CTATGGAATG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
    GGGTCCCTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTCTCTGCT 1020
    ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACCTG GTACCATCAA AGACAGAATC 1080
60  AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAAATTAA AAATGTTACC 1140
    CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
    ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAATGAAA 1260
    GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
    AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCTGATT 1380
65  CTGCTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT 1440
    GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
    TGGAAATCCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGSCA 1560
    GGTCAACAAG AAGACATTGG CCGATTGAAA CTCTCTCTAC CTGACCTGCA ACCCCAAGC 1620
    AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCCCGAGACA AAGTCGGGAA ACTTCGAGTG 1680
70  TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
    TGGAAGACAG GGAATTTCA GTTGATATCA GGAACATGAT CTACCAAAAG CATCATTTT 1800
    GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTGCTTGT 1860
    TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
    TTGACTTTGT ATGTGAGTTC CTTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
75  TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
    TCTTGATATA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
    TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT TCCCCCTCCT 2160
    CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220
    TAGAAAAAAA AGCACAAGAA AATGTTTAA TGTTTGACTC TTATGATACT TCTTGAAAAA 2280
80  TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340
    TGTATATTTA AATTCTTTGT AATAATAATA TCCAATCAT CAAAAAATAA AAAAAAAA
  
```

A94 Protein sequence:

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Protein Accession #: NP\_056322.2  
 Signal sequence: 1-21  
 Transmembrane domains: none found  
 MAM domain: 402-546  
 EGF domain: 80-259  
 Cellular Localization: secreted

1	11	21	31	41	51	
MPLPWSLALP	LLLSWVAGGF	GNAASARHHG	LLASARQPGV	CHYGTKLACC	YGWRRNSKGV	60
CEATCEPGCK	FGECVGNPKC	RCFPGYTGKT	CSQDVNECGM	KPRPCQHRVC	NTHGSYKFC	120
LSGHMLMPDA	TCVNSRTCAM	INCQYSCEDT	EEGPQCLCPS	SGLRLAPNGR	DCLDIDECAS	180
GKVICPYNRR	CVNTFGSYYC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SHHANCFTNQ	240
GSFKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KKLLAHKNSM	KKKAKIKNVT	300
PEPTRTPTFK	VNLQPFNYEE	IVSRGGNSHG	GKKGNEEKMK	EGLEDEKREE	KALKNDIEER	360
SLRGDVFFPK	VNEAGEFGLI	LVQRKALTSK	LEHKDLNISV	DCSFNHGICD	WKQDREDDFD	420
WNPADRDNAI	GFYMAVPALA	GHKKDIGRLK	LLLPDLQFQS	NFCLLFYDYL	AGDKVGLLRV	480
FVKNSNNALA	WEKTTSEDEK	WKTGKIQLYQ	GTDATKSIIF	EAERKGKGTG	EIAVDGVLLV	540
SGLCPDSSL	VDD					

GLIOBLASTOMAA95 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1	11	21	31	41	51	
AGCAACGACG	CCGGGCGACG	GGAGCGGCGG	CCGCGCCATG	TGGCTGCTGG	GGCCGCTGTG	60
CCTGCTGCTG	AGCAGCGCCG	CGGAGAGCCA	GCTGCTCCCC	GGGAACAACT	TCACCAATGA	120
GTGCAACATA	CCAGGCAACT	TCATGTGCAG	CAATGGACGG	TGCATCCCGG	GCGCCTGGCA	180
GTGTGACGGG	CTGCTGACT	GCTTCGACAA	GAGTGATGAG	AAGGAGTGCC	CCAAGGCTAA	240
GTGGAATGT	GGCCCAACCT	TCCTCCCTG	TGCCAGCGGC	ATCCATTGCA	TCATTGGTCG	300
CTTCCGGTGC	AATGGGTTTG	AGGACTGTCC	CGATGGCAGC	GATGAAGAGA	ACTGCACAGC	360
AAACCCCTCT	CTTTGCTCCA	CCGCCCGCTA	CCACTGCAAG	AACGGCTCT	GTATTGACAA	420
GAGCTTCATC	TGCGATGGAC	AGAATAACTG	TCAAGACAAC	AGTGATGAGG	AAAGCTGTGA	480
AAGTTCTCAA	GAACCCCGCG	GTGGGCAGGT	GTTTGTGACT	TCAGAGAACC	AACTTGTGTA	540
TTACCCGAGC	ATCACCTATG	CCATCATCGG	CAGCTCCGTC	ATTTTTGTGC	TGGTGGTGCC	600
CCTGCTGGCA	CTGGTCTTGC	ACCACCAGCG	GAAGCGGAAC	AACCTCATGA	CGTGCCCGT	660
GCACCGGCTG	CAGCACCTCG	TGCTGCTGTC	CCGCCTGGTG	GTCCTGGACC	ACCCCCACCA	720
CTGCAACGTC	ACCTACACG	TCAATAATGG	CATCCAGTAT	GTGGCCAGCC	AGGCGGAGCA	780
GAATGCGTGC	GAAGTAGGCT	CCCCACCTCT	CTACTCCGAG	GCCTTGCTGG	ACCAGAGGCC	840
TGCGTGGTAT	GACCTTCTCT	CACCGCCCTA	CTCTTCTGAC	ACGGAATCTC	TGAACCAAGC	900
CGACCTGCCC	CCCTACCGCT	CCCGTCCGG	GAGTGCCAAC	AGTGCCAGCT	CCCAGGCAGC	960
CAGCAGCCTC	CTGAGCGTGG	AAGACACCAG	CCACAGCCCG	GGGCAGCCTG	GCCCCCAGGA	1020
GGGCACCTGT	GAGCCAGGGG	ACTCTGAGCC	CAGCCAGGGC	ACTGAAGAAG	TATAAGTCCC	1080
AGTTATTCCA	AAGTCCATAT	GGGTTAATCT	GCTCTGACTT	GTGCCCATT	TAAACAATTG	1140
TGCTCATGGG	AAGCTCTTTA	AGCACCTGTA	AGGATGTCTC	AAGTTACAGT	TTGGGATATT	1200
AACTATCTCT	GCATTCCCTT	CCTCCCCCAG	ACTTCAGAGA	TGTTTTCTGT	CGGTCTCAGT	1260
TGACATGATC	TGTTGTGCGT	CTTTTCTGTC	AGGTCACTCT	TCCCTTGGGA	CCCAGATCA	1320
CACCTCATTT	TTTACATTA	TTCTGTTTCT	GTTGGAGAGA	CAGCATATAA	AACAGTATTG	1380
AAATAGGCTG	GGAGAGAGCA	ATGTTTCTGT	GCTATATTGG	ATGCTCAGAA	GTGCAGGAGA	1440
CGCTGGACCC	AATTCTCTCT	GCTGGGTAGT	TACCTTATAG	CATTGGGGA	TTTGGGTTAG	1500
ATGATCTAAC	CAGGAGGCCA	TCACTGGATG	GTCAACCCCC	CAAAAAAATT	CCATTTGAGC	1560
ATCAAAACCT	GCTTTGCACA	ATCCTATTGG	ATGCCCCAG	TTCAGCAGAG	TCAGTGGCCA	1620
AAGAAAACCT	TGGACGTGAG	TAACACCTTT	CAGCAGTCGC	AACGTTATTT	TGGTTTTGTG	1680
AAGGACTCTG	AAACCATCTA	CCCTGTATAA	ATTCTGGCTT	TAGAAATTGG	CCCAAGAATG	1740
CTCATCTGGA	GAGCTTTCTT	CAGCAGCATA	TATCATCAGC	CTCATCTTAA	AATAGGCAGG	1800
GAGCCCTCTC	CATGAGTTTA	TCCAAGTTCT	CAGCTCCTAA	AATGCAGGCT	GCCAAGACCC	1860
TACACCTGCC	CTGGCTCTAC	AGCCACTTAC	CTGGTTTCTG	GACTGTCAAC	CTCCACGCTG	1920
ACCTGCCCGT	AGCCAAGGAA	TGAGGACCTA	ACTTGAGTTG	GCCCAAGCTC	TGACCTGGCT	1980
GTATGTCCCT	GTGGCCACAC	CCCAGCCTGT	CTTGCTCATT	CATGCAGCCT	CAACACTGGC	2040
CTCCAAAGTT	CCCTTAACAC	TTGCAAGTCT	CTTTTACCT	GTGCATTTGG	ACTTGAGGAC	2100
ACTGGTTTCT	ATCACAGTGT	AGAGCCATGT	TCAATACCTC	CAGCAAGCTC	TCCTGGCTCC	2160
CTGCACTGTG	CACGCTCCTC	TTCCCAAGGT	CCCAATACCA	GCACCTCTAG	TTAGAGTTAG	2220
GGTCAGGGTC	AGGCCTCTCC	CAACATCCCA	GTAAGTTTCT	CTCTGAGACA	CATGGGCAAG	2280
AGACAATTGG	GAGTCAAGAT	TTTCCATTGG	GATCTATTTT	AAATCTTTTA	GAAATGCATT	2340
TGAAACAGTG	TGTTTGTTTT	TTCCCTTCTA	GTTAAGGGAC	TATTTATATG	TGTATAGGAA	2400
AGCTGTCTCT	TTTTTGTGTT	TTCTTTTAAC	AAGGTCCAAA	GAAAGATGCA	AAAGGAGATC	2460
ACACCCCTTG	CCCGCTGAGC	CCCGTGATAA	CAAGTCACTC	CAGACTAACC	TGTGTGCCAG	2520
ACATTGTGTC	ATTGTTGCAC	TTTGAGGTTA	TTATTATATCA	AGTTCTTGAA	GGAAGCAGAA	2580
AGAGGGACTC	CTCTCTCCCT	CCGTGTATAG	TCTCTATGTT	TGTGCTAGTT	TTTCTTTTTT	2640
TTCTCTGTGT	CCAGTCAAGC	ACAGGGCCCG	CCTCCCTGCA	GGAATAAGGG	GTAACACGTT	2700
AGGTGTTGTT	TGGCAAGAAA	CCACACTGAC	TGATGAGGGG	TAAATGGGAA	CCAGGTAGAG	2760
ACCTCCGGG	CAGCTGTCAA	CCATTGAGAA	CTTCTTCCG	CAGCTGAAGA	AATGTTCACT	2820
AACCTGTTTG	ACGCTAATTA	AAACAGAGCC	TGCAGGAAGT	GGGGCTAAAG	TGGCATTTCAG	2880

TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTTACAGAA 2940  
 AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA 3000  
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060  
 CTGAGTAATC CAATAAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120  
 CATTTTCATCT CTTGTGAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTTCTTC 3180  
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAA TGGTTTTAGT 3300  
 AGATAAGGGA TGCCCTACTAA TGCTTTTTTA AAACAAACAG GGACATTTT ATTATAGATT 3360  
 TGATTTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420  
 TTTTGGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG 3540  
 AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT 3600  
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660  
 TTTTAAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTIA ATGTAAACTG 3720  
 GAAAGGTTGT GTGTCTGTGC TTTTGTGTTT TGGTTAGGC TGGTTTGTG TTTTAAATTG 3780  
 TTATACTTTC TAATAAATTT GCAGTTTCAT TCTTTCTGTT TGTGCAAANG GWMCTAMARM 3840  
 AAMMAAAAA AWYWTGGGG GGGCTTGGGC CTCGGAAGAA GTTTTAAACA CCACTTCGGG 3900  
 TGGGGCGGCG GGGCCACACT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAAG 3960  
 GAAACCCTGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAAA ACGCCCGGG 4020  
 GGAACCGCA GAGTGTGCG TAAACCACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

## A96 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MWLLGLPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCSNG RCIPGAWQCD GLPDCFDKSD 60  
 EKECPKAKSK CGPTFFPCAS GIHCLIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 KNGLCIDKSF ICDGNQNCQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180  
 VIFVLVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240  
 YVASQAEQNA SEVGSPPSYS EALLDQRPAP YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEEV

## LUNG

## A97 DNA SEQUENCE

Gene name: putative GPCR, Weakly similar to dJ365012.1  
 Unigene number: Hs.256897  
 Probeset Accession #: BE001836  
 Nucleic Acid Accession #: BE001836  
 Coding sequence: 1-2955 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGGCCGTC AATCTTTTTC CTTCACACT GGGAAATGATG GGCTAGACCC AGACCCAATC 60  
 ATGTTAAGTA TGATAGGGAT CAGTGGCCCA GCTGGTGTGG AAGACAAGTG GGTCACTACTG 120  
 GGTTTAGGCC CACATAGCAC TAAAGGTCTT CAACATGCAA TTAGAAGCTC AAATGTTGAC 180  
 GGGAAATATG TTCACCTCTAA AAAAGATGTT TCTATTAGAA TTTACTTACT CTTTCATGAA 240  
 AACATAGATG CTTCCTCTTT CTTGATTAGT GATGGCCATC AGTTAAACCA AGTGCACCTCA 300  
 GAGAAGTCAA ATTCTGACAC AATCCAGCAA GTAACATATAA AAACGTATGG CCCAGTCGAA 360  
 GAATATCAGC TGCTGCTTCA GGTGACCTAT AGAGATTCCA AGGAGAAAAG AGATTGAGA 420  
 AATTTTCTGA AGCTCTTGAA GCCTCCATTA TTATGGTCAC ATGGGCTAAT TAGAATTATC 480  
 AGAGCAAAGG CTACCACAGA CTGCAACAGC CTGAATGGAG TCCTGCAGTG TACCTGTGAA 540  
 GACAGCTACA CTTGGTTTCC TCCCTCATGC CTTGATCCCC AGAAGTCTA CTTTCACACG 600  
 GCTGGAGCAC TCCCAAGCTG TGAATGTCAT CTCAACAACC TCAGCCAGAG TGTCAATTTT 660  
 TGTGAGAGAA CAAAGATTGG GGGCACTTTC AAAATTAATG AAAGGTTTAC AAATGACCTT 720  
 TTGAATTCAT CTTCTGCTAT ATACTCCAAA TATGCAATG GAATTGAAAT TCAACTTAAA 780  
 AAAGCATATG AAAGAATTCA AGGTTTGTAG TCGGTTTCAG TCACCCAATT TCGAAATGGA 840  
 AGCATCGTTG CTGGGTATGA AGTTGTTGGC TCCAGCAGTG CATCTGAAC TCTGTGAGCC 900  
 ATTGAACATG TTGCCGAGAA GGCTAAGACA GCCCTTCACA AGCTGTTTCC ATTAGAAGAC 960  
 GGCTCTTTCA GAGTGTTCGG AAAAGCCCAG TGTAATGACA TTGTCTTTGG ATTTGGGTCC 1020  
 AAGGATGATG AATAATACCT GCCCTGCAGC AGTGGCTACA GGGGAACAT CACAGCCAAG 1080  
 TGTGAGTCCT CTGGGTGGCA GGTTCATCAGG GAGACTTGTG TGCTCTCTCT GCTTGAAGAA 1140  
 CTGAACAAGA ATTTTCAGTAT GATTGTAGGC AATGCCACTG AGGCAGCTGT GTCATCCTTC 1200  
 GTGCAAAATC TTTCTGTCAT CATTGCGCAA AACCCATCAA CCACAGTGGG GAATCTGGCT 1260  
 TCGGTGGTGT CGATTCTGAG CAATATTTCA TCTCTGTAC TGGCCAGCCA TTTTCAGGTG 1320  
 TCCAATTCAA CAATGGAGGA TGTTCATCAGT ATAGCTGACA ATATCCTTAA TTCAGCCTCA 1380  
 GTAACCAACT GGACAGTCTT ACTGCGGGAA GAAAAGTATG CCAGCTCACG GTTACTAGAG 1440  
 ACATTAGAAA ACATCAGCAC TCTGGTGCC TCCGACAGCTC TTCTCTGAA TTTTCTCGG 1500  
 AAATTCATG ACTGGAAGAG GATTCCAGTG AACAAAAGCC AACTCAAAG GGGTTACAG 1560  
 TATCAGATTA AAATGTGTCC CCAAAATACA TCTATTCCCA TCAGAGGCCG TGTGTTAATT 1620  
 GGGTCAGACC AATTCAGAG ATCCCTTCCA GAAACTATTA TCAGCATGGC CTCGTGTACT 1680  
 CTGGGGAACA TTCTACCCGT TTCCAAAAT GGAATGCTC AGGTCAATGG ACCTGTGATA 1740

5 TCCACGGTTA TTCAAACCTA TTCCATAAAT GAAGTTTTC TATTTTTTTC CAAGATAGAG 1800  
 TCAAACCTGA GCCAGCCTCA TTGTGTGTTT TGGGATTTC GTCAATTGCA GTGGAACGAT 1860  
 GCAGGCTGCC ACCTAGTGAA TGAAACITCAA GACATCGTGA CGTGCCAATG TACTCACTTG 1920  
 10 ACCTCCTTCT CCATATTGAT GTCACTTTT GTCCCCCTTA CAATCTTCCC CGTTGTAAAA 1980  
 TGGATCACCT ATGTGGGACT GGGTATCTCC ATTGGAAGTC TCATTTTATG CCTGATCATC 2040  
 GAGGCTTGT TTTGGAAGCA GATTAAAAAA AGCCAAACCT CTCACACACG TCGTATTATG 2100  
 ATGGTGAACA TAGCCCTGTC CCTCTTGATT GCTGATGTCT GGTTTATTGT TGGTGCCACA 2160  
 GTGGACACCA CGGTGAACCC TTCTGGAGTC TGCACAGYTG CTGTGTTCTT TACACACTTC 2220  
 TTCTACCTCT CTTTGTCTCT CTGGATGCTC ATGCTTGGCA TCCTGCTGGC TTACCGGATC 2280  
 ATCCTCGTGT TCCATCACAT GGCCAGCAT TTGATGATGG CTGTTGGATT TTGCCTGGGT 2340  
 TATGGGTGCC CTCTCATAT ATCTGTCAAT ACCATTGCTG TCACGCAACC TAGCAATACC 2400  
 TACAAAAGGA AAGATGTGTG TTGGCTTAAC TGGTCCAATG GAAGCAAACC ACTCCTGGCT 2460  
 TTTGTTGTCC CTGCACTGGC TATTGTGGCT GTGAACCTCG TTGTGGTGCT GCTAGTTCTC 2520  
 15 ACAAAGCTCT GGAAGGCCAG TGTGTTGGGAA AGACTGAGTC GGGATGACAA GGCCACCATC 2580  
 ATCCGCTGGG GGAAGAGCCT CCTCATCTG ACCCCTCTGC TAGGGCTCAC CTGGGGCTTT 2640  
 GGAATAGGAA CAATAGTGGA CAGCCAGAAT CTGGCTTGGC ATGTTATTTT TGCTTTACTC 2700  
 AATGCATTCC AGGGAATTTT TATCTTATGC TTTGGAATAC TCTTGACAG TAAGCTGCGA 2760  
 CAACTTCTGT TCAACAAGTT GTCTGCCTTA AGTTCTTGGG AGCAAAACAGA AAAGCAAAA 2820  
 20 TCATCAGATT TATCTGCCAA ACCCAAATTC TCAAAGCCTT TCAACCCACT GCAAAACAAA 2880  
 GGCATTATG CATTTTCTCA TACTGGAGAT TCCTCCGACA ACATCATGCT AACTCAGTTT 2940  
 GTCTCAATG AATAA

**A98 PROTEIN SEQUENCE**

25 Gene name: putative GPCR, Weakly similar to dJ365012.1  
 Unigene number: Hs.256897  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Pfam domain: 7tm\_2 [561-820]  
 30 Transmembrane domains: 545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789  
 Cellular Localization: plasma membrane

35 1 | 11 | 21 | 31 | 41 | 51 |  
 MHALLLCFSV | LNASGLSL | QSPVEEYQLL | LQVTYRDSKE | KRDLRNFLKL | LKPPLLWSHG 60  
 LRRIIRAKAT | TDCNSLNGVL | QCTCEDSYTW | FPPSCLDPQN | CYLHTAGALP | SCECHLNLS 120  
 QSVNFCERTK | IWGTFKINER | FTNDLLNSSS | AIYSKYANGI | EIQLKKAYER | IQGFESVQVT 180  
 40 QFRNGSIVAG | YEUVGSSSSA | ELLSAIEHVA | EKAKTALHKL | FPLEDGSFRV | FGKAQCNDIV 240  
 FGFGSKDDEY | TLPCSSGYRG | NITAKCESSG | WQVIRETCVL | SLLEELNKNF | SMIVGNATEA 300  
 AVSSFVQNL | VIIRQNPSTT | VGNLASVSVI | LSNISLSLSA | SHFRVSNSTM | EDVISIADNI 360  
 LNSASVTNWT | VLLREBKYS | SRLLTLENI | STLVPPTALP | LNFSRKFIDW | KGIPVNKSQL 420  
 KRGSYQIKM | CPQNTSIPIR | GRVLIGSDQF | QRSLPETIIS | MASLTILNLI | PVSKNAGNV 480  
 NGPVIQSTV | NYSINBVFLE | FSKIESNLSQ | PHCVWFDFSH | LQWNDAGCHL | VNETQDIVTC 540  
 45 QCTHLTSFSL | LMSPPFVPSI | FPVVKWITYV | GLGISIGSLI | LCLIIIEALFW | KQIKKSQTS 600  
 TRRICMVNIA | LSLLIADVWF | IVGATVDTTV | NPSGVCTAAV | FTFHFYLSL | FFWMLMLGIL 660  
 LAYRIILVPH | HMAQHLMMAV | GFCLGYGCPL | IISVITIAVT | QPSNTYKRKD | VCWLNWSNGS 720  
 KPLLAFVPPA | LAIVAVNFV | VLLVLTKLWR | PTVGERLSRD | DKATIIRVGK | SLLILTPLLG 780  
 LTWGFIGITI | VDSQNLAWHV | IFALLNAFQV | RTVTITYCIV | K

**A99 DNA SEQUENCE**

55 Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Probeset Accession #: F07953  
 Nucleic Acid Accession #: NM\_016334  
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

60 1 | 11 | 21 | 31 | 41 | 51 |  
 AGCACCTGGG | AAAAGGCAGA | CGGTGTGAGG | GGGCCTGTGG | CCCAGCGTGG | CTGTGGCCTC 60  
 GGGAGTGGG | AAGTGGAGGC | AGGAGCCTTC | CTTACACTTC | GCCATGAGTT | TCCTGATCGA 120  
 CTCCAGCATC | ATGATTACCT | CCCAAATACT | ATTTTTTGA | TTTGGGTGGC | TTTTCTTCAT 180  
 65 GCGCAATTG | TTTAAAGACT | ATGAGATACG | TCAGTATGTT | GTACAGGTGA | TCTTCTCCGT 240  
 GACGTTTGA | TTTTCTTGCA | CCATGTTTGA | GCTCATCATC | TTTGAAATCT | TAGGAGTATT 300  
 GAATAGCAGC | TCCCGTTATT | TTCCTGGGAA | AATGAACCTG | TGCCTAATTC | TGCTGATCCT 360  
 GGTTTTCATG | GTGCCCTTTT | ACATTGGCTA | TTTTATTGTG | AGCAATATCC | GACTACTGCA 420  
 TAAACAACGA | CTGCTTTTTC | CCTGTCTCTT | ATGGCTGACC | TTTATGTATT | TCTTCTGGAA 480  
 70 ACTAGGAGAT | CCCTTTCCCA | TTCTCAGCCC | AAAACATGGG | ATCTTATCCA | TAGAACAGCT 540  
 CATCAGCCGG | GTTGGTGTGA | TTGGAGTGAC | TCTCATGGCT | CTTCTTTCTG | GATTTGGTGC 600  
 TGTCAACTGC | CCATACACTT | ACATGCTTTA | CTTCTCAGG | AATGTGACTG | ACACAGATAT 660  
 TCTAGCCCTG | GAACGCGCAC | TGCTGCAAAAC | CATGATATG | ATCATAAGCA | AAAAGAAAAG 720  
 GATGGCAATG | GCACGAGAAA | CAATGTTCCA | GAAGGGGGAA | GTGCATAACA | AACCATCAGG 780  
 75 TTTCTGGGGA | ATGATAAAAA | GTGTTACCAC | TTCAGCATCA | GGAAGTGAAA | ATCTTACTCT 840  
 TATTCAACAG | GAAGTGGATG | CTTTGAAGA | ATTAAGCAGG | CAGCTTTTTC | TGGAAACAGC 900  
 TGATCTATAT | GCTACCAAGG | AGAGAATAGA | ATACTCCAAA | ACCTTCAAGG | GGAAATATTT 960  
 TAATTTCTT | GGTACTTTT | TCTCTATTTA | CTGTGTTTGG | AAAATTTTCA | TGGCTACCAT 1020  
 CAATATTGTT | TTTGATCGAG | TTGGGAAAAC | GGATCCTGTC | ACAAGAGGCA | TTGAGATCAC 1080  
 80 TGTGAATTAT | CTGGGAATCC | AATTTGATGT | GAAGTTTGGG | TCCCAACACA | TTTCTTTCAT 1140  
 CTTTGTGGA | ATAATCATCG | TCACATCCAT | CAGAGGATG | CTGATCACTC | TTACCAAGTT 1200  
 CTTTATGCC | ATCTCTAGCA | GTAAGTCCTC | CAATGTCAAT | GTCCTGCTAT | TAGCACAGAT 1260  
 AATGGGCATG | TACTTTGTCT | CCTCTGTGCT | GCTGATCCGA | ATGAGTATGC | CTTTAGAATA 1320  
 CCGCACATA | ATCACTGAAG | TCCTTGGAGA | ACTGCAGTTC | AACTTCTATC | ACCGTTGGTT 1380  
 TGATGTGATC | TTCTTGGTCA | GCGCTCTCTC | TAGCATACTC | TTCCTTATT | TGGCTACAA 1440

ACAGGCACCA GAGAAGCAAA TGGCACCTTG AACTTAAGCC TACTACAGAC TGTTAGAGGC 1500  
 CAGTGGTTTC AAAATTTAGA TATAAGAGGG GGGAAAAATG GAACCAGGC CTGACATTT 1560  
 ATAAACAAAC AAAATGCTAT GGTAGCATTT TTCACCTTCA TAGCATACTC CTTCCCCCTC 1620  
 AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAACCTCAAG 1680  
 ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG 1740  
 CCAAGAAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGGTAGC 1800  
 TGAGCCAAAC ACGTAGGATT TCCGTTTAA GGTTCACATG GAAAAGGTTA TAGCTTTGCC 1860  
 TTGAGATTGA CTCATTAAAA TCAGAGACTG T

# A100 Protein sequence

Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Protein Accession #: NP\_057418.1  
 Signal sequence: none found  
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MSFLIDSSIM ITSQILFFGF GWLFFMRQLF KDYEIRQYV VQVIFSVTFAF SCTMFELIIF 60  
 EILGVLNSSL RYFHWKMLNC VILLILVFMV PFYIGYFIVS NIRLLHKQRL LFSCLLWLTF 120  
 MYFFWKLGDG PFILSPKHGI LSIEQLISRV GVIGVTLMAL LSGFGAVNCP YTYMSYFLRN 180  
 VDTDILALE RRLQTMMDI ISKKRMAA RRTMFQKGEV HNKPSGFWMG IKSVTTSASG 240  
 SENLTLIQE VDALELSRQ LPLETADLYA TKERIEYSKT FKGKYFNFLG YFFSIYCVWK 300  
 IFMATINIVF DRVGKTDPTV RGIETVNYL GIQFDVKFWS QHISFILVGI IIVTSIRGLL 360  
 ITLTFFFYAI SSSKSSNVIV LLLAQIMGY FVSVLLIRM SMPLEYRTII TEVLGELQFN 420  
 FYHRWFVDF LVLSALSSILF LYLAHKQAPE KQMAP

# A101 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60  
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120  
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180  
 CTGGGCCAGC GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240  
 CGGCTACTCG CCAAGGTACA AGAGGTGGCC CGGTGCTGCG GGGAGCTGCT GGCTGCAGCC 300  
 TGTGCCAGCG GGGCCCTGCC CCGCTCCTCC TCCGGGCCCC CCTGCGCTGC CCTGACGTCC 360  
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420  
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG 480  
 GCGCTCATTA AGCAGCTGTT TGAGGCCCCG GCCCTGAGCC AGCAGGACCG GGGACCTCTG 540  
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CTGGCACTC 600  
 AGCCCTTCGA GGGTGGGCGC CCCATCGCAC CCACCTCTC TGGCTGGAGA CCCCCGCGAG 660  
 GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CCTGCGCCCC TTGCCAGATG GGCTCCCCAG 720  
 GCCTGCCCCC GCGTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGYTG 780  
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGAG CTAATACTGG CCGCTGTCTG 840  
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCGG TTCCAGCGG TGCCGCGCTG 900  
 GGTCCCATCT TCAGGGAAAG GCACTGCCCA CGCCAGGCTG CACTTCCAAC AACGGGCGAGC 960  
 AGAGGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020  
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080  
 GTAAGCGGGG GGTGCTTGGC TGGCTGGGGA GCCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140  
 CTGGCCAAGG CTGAGGGACC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200  
 GGCCTGCATG TGCCTCCCAC AGACCTTGGG GTGATGGCCT TCCCCCTCTT GGCCGGGACG 1260  
 TTGCCCCACG TTGATGCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA 1320  
 GACAGCTCCC AGGCACGTCA TAGGCAAGC CTGTTTCCCC CGACTCAGGA TTCCAAGGC 1380  
 CTGGGGTCTC GCTCACCCCC CTTGTCTCTC ACGCCAGGCC TGTCCCCAGG TTTCACTGCTG 1440  
 GAGAGGCCAC CTCCCTCAGC CAAGGAAAAA GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500  
 GGCAGGTCCC CTTGGGTGTC ACTCCCTCAG CCCCTGCCCA GGCCCACTCC CGCTGGTGCT 1560  
 GGAGTACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTACCA 1620  
 GAACCAGGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680  
 TCAGTGTGTG TGGGCGCGAG GGCCTCCGAT GCGGGGTGAG TGCCTGGGGG GCGCAGGGCC 1740  
 CCCGATGCGG GGTACGTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACTTTGGT 1800  
 ACACTGTCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC 1860  
 CCTTCCGGAG CCCAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920  
 TGCTGCACCT GGTCTGCAGG GGTGTCCCAG GACAGGCCCA AGTCAGGCCA GCATGCAGCT 1980  
 GCGCTCTTAC CTTGAAGATG GGAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCCTGG 2040  
 ACCTCTCTGG CAGGAAAGGG TGCAGTCTCT GAGGGCCTGT GCCCCACAGC CCCAGCACCC 2100  
 AGGTGGACTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCCGTGAGC 2160  
 GGCTGGGGTC TGCCACCCAG GGCCTCCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCC 2220  
 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280  
 GGTGACTTCA TCAGAGAGCC GCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340  
 GAGACAGGCT GGCACCTCCG GAAAACTGC CTTTCAGCCT TGGTGTTCGG TGCAAGGTGA 2400  
 AAAGAAATAG GTCTCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAC 2460  
 CACGAGGGGA GAATTTAAAG GCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520  
 GCAGACCCCT CTTGAGCTCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580  
 GAGCAGCGTC CTTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACACGT 2640  
 GCGTGACAC TGTGATGACA CCCGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700  
 CAGAAGTGTG CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGG 2760  
 TTTTGTGTTC ATCAGTTTCC AAGGAAAGG AACATCTCAG CCGGGCGTGG TGGTTACGC 2820

CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 CCCCATCTCT ACAAAAAA AAAAGAAAAG AAAGAAAATG AGAGATCCAG GTTTAAAAAT 2940  
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000  
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTTCCTG GAAACATGAA AAAAAA

A102 DNA SEQUENCE

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTATGCCCC GTGTGAGCCA 60  
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACTGTGGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180  
 AGAGGTCCTG AAAATAGTAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAAAAT GTCCTGTGTC ACCAGATGCA 300  
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCAATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACGCAATGTT TGCTGTGCCC CACTGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAACCTCA GAGTGAAGTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT TCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTGC GCCACGTGGT TACCTTGACG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900  
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGAATTGTAC CTCCTCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGAGACAA TCCAGCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140  
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACCTTCCC 1200  
 GATGAAAAAG TGTCTGAGC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCTGTCC TGAACACGCG GGCCGTCCCT TTGATTCCA ACAAGATCTG CAACCACAGG 1320  
 GACGTGTACG GTGGCATCAT CTCCTCTGCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380  
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACGAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCCGTG TCACTCTCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA 1620  
 TCCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCTTGG GAGCTCTGAG 1680  
 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCTTCCA TCTGATTCCA GCACAACCTT 1740  
 CAAGCTGCTT TTTGTTTTT GTTTTTTTGA GGTGAGTCT CGCTCTGTTG CCCAGGCTGG 1800  
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860  
 TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCACACC CAACTAATTT 1920  
 TTGATTTTTT AGTAGAGACA GGGTTTCACT ATGTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAATGTA TGTGCTGCT TCAGCCTCCC ACAGTGCTGG GATTACAGGC ATGGGCCACC 2040  
 ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 AGGGGCGGCT TTCCCACTGT TTTCTCTCCA GGGGCTTGTG AAAATTCCTG 2160  
 ACGAGATAAG CAGTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCAGTTC TTTCTCTCTA GGGACCAAG 2280  
 CCAAACCCAC CCTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCCAT TTTATGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400  
 TTGTCTTTG ATTCCAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAA

A103 Protein sequence:

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPC domain: 216-444  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MGENDPFAVE APFSFRSLFG LDDLKISVPA PDADAVAAQI LSLLPLKFFP IIVIGIIALI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLQVF 120  
 TAASWKTMCs DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180  
 VTALHHSVIV REGCASGHVY TLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQFQGYH 240  
 LCGGSVITPL WIITAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGA GDASPVNLHA 360  
 AVPLISNKIC NHRDVGYGII SPSMLCAGYL TGGVDSCQGD SGGPLVCQER RLWKLVGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIEHQMEL DLKT

A104 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)  
 Unigene number: Hs.208229  
 Probeset Accession #: AI819198  
 Nucleic Acid Accession #: NM\_032551.1  
 Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
10  ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCTCTGGG GGGCACCCGGC CAACGCCTCC 60
    GGCTGCCCCG GCTGTGGCGC CAACGCCTCG GACGGCCCCAG TCCCTTCGCC GCGGGCCGTG 120
    GACGCCTGGC TCGTGCCGCT CTCTCTCGCG GCGCTGATGC TGCTGGGCCT GGTGGGGAAC 180
    TCGCTGGTCA TCTACGTCA CTGCCGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240
15  ATCCCAACC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGCGTCCC CTTCACGGCC 300
    CTGCTGTACC CGCTGCCCCG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT CGTCAACTAC 360
    ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420
    TGGTACGTGA CGGTGTTCCC GTTGCGCGCC CTGCACCGCC GCACGCCCCG CCTGGCGCTG 480
    GCTGTACGCC TCAGCATCTG GGTAGGCTCT GCGGCGGTGT CTGCGCCGGT GCTCGCCCTG 540
    CACCGCCTGT CACCGGGGCC GCGCGCCTAC TGCAGTGAGG CCTTCCCCAG CCGCGCCCTG 600
20  GAGCGCGCCT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCCGCT GCTCGCCACC 660
    TCGCCTGTCT ATGCGGCCAT GCTGCGCCAC CTGGGCGCGG TCGCCGTGCG CCCCGCGCCC 720
    GCCGATAGCG CCCTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGGCCCAAG 780
    GTCTCGCGCG TGGTGGCGCG CGTGGTCTCT CTCTTCGCGG CTGCTGGGG CCCCATCCAG 840
    CTGTTCTCTG TGCTCAGGCG GCTGGGCCCC GCGGGCTCCT GGCACCCAG CAGTACGCC 900
25  GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCTTACA GCAACTCCGC GCTGAACCCG 960
    CTGCTCTACG CCTTCTCTGG CTGCACTTTC CGACAGGCCT TCCGCGCGGT CTGCCCCTGC 1020
    GCGCGCGCGC GCCCGCGCGG CCCCCGCGCG CCGGACCCCT CGGACCCCGC AGCCCCACAC 1080
    GCGGAGCTGC ACCGCTGGG GTCCACCCG GCGCGCGCAA GGGCGCAGAA GCCAGGGAGC 1140
30  AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA
  
```

A105 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA  
 Unigene number: Hs.208229  
 Protein Accession #: AI819198  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [59-323]  
 Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
45  MHTVATSGPN ASWGAPANAS GCPGCGANAS DGPVPSRAV DAWLVPLFFA ALMLLGLVGN 60
    SLVIYVICRH KPMRTVTNFI IANLAATDVT FLCCVCPFTA LLYPLPGWVL GDFMCKFVNY 120
    IQQVSQVATC ATLTAHSVDR WYVTVFPLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180
    HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240
    ADSALQQGVL AERAGAVRAK VSRLVAAVVL LFAACWGPQI LFLVLQALGP AGSWHPRSVA 300
50  AYALKTWAHC MSYNSNALNP LLYAFLGSHF RQAFRRVCPA APRRRRRPRR PGPSDPAAPH 360
    AELHRLGSHP APARAQKPGS SGLAARGLCV LGEDNAPL
  
```

A106 DNA SEQUENCE

Gene name: integrin, beta 8  
 Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Nucleic Acid Accession #: NM\_002214  
 Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
60  CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCTTGCC AGCCAGGACG 60
    CTGCCGACTT GTCTTTGCCG GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
    GTTGGCCTCC CTGCCACCTT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT 180
65  TCCCTTCGAC CTCGCCGGCG TACCCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
    TAGGGTGGTT TCCCCCCCAG CTTGCGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300
    CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAG CTCTTTTCTT 360
    TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCG GCCGGGCCCT 420
    TGGCCGTGCA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCGTGCC GAGCCGGGAG 480
    GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGGCC GCTTACCTGC ACCGCTTGCT 540
70  CCGAGCCGCG GGGTCCGCTT GCTAGGCTCG CGAATAACGT CCTAGCGACA CTCGCCCGCG 600
    GGCCCCGAGG TCGCCCCGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGGCG 660
    GGGCGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTTTTACC GCTGCATTGT 720
    TCTGCCTGCA AAACGACCGG CGAGGTCCCG CCTGTTTCTT CTGGGCGAGC TGGGTGTTTT 780
    CACTTGTCTT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGATCTTCA AATGCAGCAT 840
75  CCTGTGCCAG GTGCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTC 900
    TTTCAAGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTTAATA AGCAAAGGCT 960
    GCTCAGTTGA TTCAATAGAA TACCATCTG TGATGTTAT AATACCCACT GAAAATGAAA 1020
    TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT CCGTCCAGGA GCCGAAGCTA 1080
80  ATTTTATGCT GAAAGTTTCA CCTCTGAAGA AATATCTGT GGTCTTTTAT TATCTTGTGT 1140
    ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAT TTCCGTGGA AACGATTAT 1200
    CTAGAAAAAT GGCATTTTTC TCCGTGACT TTCTGCTTGG ATTTGGCTCA TACGTTGATA 1260
    AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAATGACT 1320
    ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA 1380
    TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440
  
```



5 AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500  
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCATCATCTC GCTCTTGATA 1560  
 GCAAAATTGGC AGGCATAGTG GTGCCCCAATG ACGGAAACTG TCATCTGAAA AACAACTGCT 1620  
 ACGTCAAATC GACCAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680  
 ACAACAACAT TAAATGTCATC TTTGCAGTTC AAGGAAAACA ATTTTCATGG TATAAGGATC 1740  
 TTCTACCCCT CTTGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACTCA 1800  
 ATAATTTGGT AGTGAAGGCC TATCAGAAGC TCATTTTCTG AGTGAAAGTT CAGGTGGAAA 1860  
 ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920  
 CAGGCATGGA AGGATGACGA AACGTGACGA GCAATGATGA AGTTCCTTTC AATGTAACAG 1980  
 10 TTACAATGAA AAAATGTGAT GTCACAGGAG GAAAAAATA TGCAATAATC AAACCTATTG 2040  
 GTTTTAAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTCTG TGTGAGGACA 2100  
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTTCCAG TGTTCAGT 2160  
 GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220  
 15 ACAAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280  
 ACAAATTAAT GCTTGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTG 2340  
 CATATCACC TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400  
 GCTTCAGTGG CTGGAAGGTG GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460  
 TCAATTCAAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520  
 20 GCACCGATCC CAGGAGCATC GGCCTGCTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580  
 GCAAGGAAAA CTGGAATGTG ATGCAATGCC TTCACCCCTCA CAATTTGTCT CAGGCTATAC 2640  
 TTGATCAGTG CAAACCTCA TGTGCTCTCA TGGAAACACA GCATTATGTC GACCAAACTT 2700  
 CAGAATGTTT CTCAGCCCA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760  
 TCTTGATTGG GTTGCTTAAA GTCCTGATCA TTAGACAGGT GATACTACAA TGGAAATAGTA 2820  
 25 ATAAATTAAT GTCTCTCATCA GATTACAGAG TGTGAGCTC AAAAAAGGAT AAGTTGATTC 2880  
 TGCAAAAGTGT TTGACACAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940  
 TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAACCTCTAA AAAAAGATT 3000  
 TTAAACACTT AATGGGAAAC TGGAAATTGT AATAATTGCT CCTAAAGATT ATAATTTTAA 3060  
 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTGTG ACCTCGAAC 3120  
 30 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180  
 AAAATGTGTC TTACTACTGT TTGAGACTAG TGTGCTGTGA GCACCTTACT GTAATATATA 3240  
 ACTTATTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300  
 TACCTGTTAT CCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT 3360  
 CACTACAAGG GTACAGTAAT CCCTGCACCTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420  
 35 TATATCTTAA GGTTCCTAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480  
 ATGAATAAAT GATTCGTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540  
 AAAGATTATT GCTTTTAAAA GTGTGTAGTT TTATGCAATG GTGTTTATGG TTTGCTTATT 3600  
 TTTGCAAGAT GGATACATA TCCAGCATTC TCTCCTCTTT GCCTTTATGT TTTGTTTCT 3660  
 TTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720  
 40 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT 3780  
 GAATGTAA

#### A107 Protein sequence:

45 Gene name: Integrin, beta 8  
 Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Protein Accession #: NP\_002205.1  
 Signal sequence: 1-39  
 50 Transmembrane domains: 682-704  
 EGF domain: 552-584  
 INB domain: 54-469  
 Cellular Localization: plasma membrane

55  
 1 11 21 31 41 51  
 | | | | |  
 MCGSALAFET AAFVCLQND RGPASFLWAA WVFSVLVLGL QGEDNRCASS NAASCARCLA 60  
 60 LGPECGWCVCQ EDFISGGGRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120  
 GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSRKMAFF 180  
 SRDFRLGFGS YVDKIVSPYI SIHPERIHQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA 240  
 VHRQKISGNI DTPEGGFDAM LQAAVCESHI GWRKEAKRL LVMTDQTSHL ALDSKLAGIV 300  
 VPNDGNCHLK NNVYVKSTM BHPSLGQLSE KLIDNNINVI FAVQKQPHW YKDLLPLLF 360  
 65 TIAGEIESKA ANLNNLVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420  
 NVTSDNDEL V NVTVMKKCD VTGGKNYAI KPIGFNETAK IHIHRNCSQ CEDNRGPKGK 480  
 CVDETFLDSK CFQCDENKCH FDEDQFSSES CKSHKQDPVC SGRGVCVCGK CSCHKIKLGK 540  
 VYGKYCEKDD FSCPYYHGNL CAGHGECEAG RCQCFSGWEG DRCQCPASAA QHCVNSKGQV 600  
 CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNL QALDQCKTS 660  
 70 CALMBQQHYV DQTECFSSP SYLRIFFIIF IVTFLIGLLK VLIIRQVILQ WNSNKKSSS 720  
 DYRVASAKKD KLILQSVCTR AVTYRREKPE EIKMIDSKLN AHETFRCNF

#### A108 DNA sequence

75 Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 | | | | |  
 ATGCTGTCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCAGA 60  
 GGAAGAGAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCGAGG GCGAGGCAGC 120  
 GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240

	CCGCGGCCGC	CGCCAGCTGG	GCAGGCTCCC	GGGACTGCGG	CTGGGGGCGC	GCAGGACCCT	300
	CGCTCGCTC	CTGGACGTTT	CCGGGGGAGG	GTCCGGTTGC	CAGTGAAACC	TCCAGAGGCT	360
	TCCGGACGAC	AGCCCCGGGG	GCCTTCTGAC	TGCATCCCGA	GATTTCATC	AGCGAGTGCA	420
5	ACTCATAAGG	CAGTCCCTAA	GGGGACCGGG	CCACCGGCTG	AGGACGGGGA	TGGCTTAGGA	480
	GCTCCTGGAC	CTAGGGCCCG	GCCTCGTCGC	CTCCTGGGCG	TGCGGCGAGA	GGGGAGTGGC	540
	CCGCGCGGAA	AGCGCCGCGG	GACAGTCAGT	GACGAGGCCC	GGGGGTGCGC	GGGGCCAAGA	600
	CTTCTCGGAG	ACCGTCTCTG	GCTCTCTGGA	GACGCGCTGT	CCGCGCCGAG	GGTGGTGCCA	660
	TGTGGGGCGC	TCGCCGCTCG	TCCGTCTCCT	CATCCTGGAA	CGCCGCTTCG	CTCCTGCAGC	720
	TGCTGCTGGC	TGCGCTGCTG	GCGGCGGGGG	CGAGGGCCCA	GCGGCGAGTA	CTGCCACGGC	780
10	TGGCTGGACG	CGCAGGCGGT	CTGGCGCATC	GGCTTCCAGT	GTCCCCGAGC	CTTCGACGGC	840
	GGCGACGCCA	CCATCTGCTG	CGGCAGCTGC	GCCTTGGCGT	ACTGCTGCTC	CAGCGCCGAG	900
	GCGCGCCTGG	ACCAGGGCGG	CTGCGACAAT	GACCGCCAGC	AGGCGGCTGG	CGAGCCTGGC	960
	CGGGCGGACA	AAGACGGGCC	CCGACGGCTC	GGCAGGGCTT	CATGTCTTAG	GGGTACCCAA	1020
	GGAGACGGCG	AGGGTGGCGC	CCCACCCGTG	AGGGCCTGGC	AGCGGTGCTC	CCCTGAAGGC	1080
15	TCCCCGAAAG	GAAGGCAGCT	CCTCAGGGCT	TTCCCCGGGC	TGCTGCCCCG	TGCCAGACGC	1140
	CGGGGATTCC	CATCTTCTCC	ACGCGGCGGC	CCCTCTCCCC	TGCAGCGGCC	CGCCTTGCCC	1200
	ATCTACGTGC	CGTTCTCTAT	TGTTGGCTCC	GTGTTTGTCT	CCTTTATCAT	CTTGGGGTCC	1260
	CTGGTGGCAG	CCTGTTGCTG	CAGATGTCTC	CGGCCTAAGC	AGGATCCCCA	GCAGAGCCGA	1320
20	GCCCCAGGGG	GTAACCGCTT	GATGGAGACC	ATCCCCATGA	TCCCCAGTGC	CAGCACTTCC	1380
	CGGGGGTTCG	CCTCACGCCA	GTCCAGCACA	GCTGCCAGTT	CCAGCTCCAG	CGCCAACTCC	1440
	GGGGCCCGGG	CGCCCCCAAC	AAGGTCACAG	ACCAACTGTT	GCTTGCCGGA	AGGGACCATG	1500
	AACAACGTGT	ATGTCAACAT	GCCACCGAAT	TTCTCTGTGC	TGAACGTGCA	GCAGGCCACC	1560
	CAGATTGTGC	CACATCAAGG	GCAGTATCTG	CATCCCCCAT	ACGTGGGGTA	CACGGTGCAG	1620
25	CAGACTCTG	TGCCCATGAC	AGCTGTGCCA	CCTTTCATGG	ACGGCTTGCA	GCCTGGCTAC	1680
	AGGCAGATTC	AGTCCCCCTT	CCCTCACACC	AACAGTGAAC	AGAAGATGTA	CCCAGCGGTG	1740
	ACTGTATAAC	CGAGAGTCAC	TGGTGGGTTT	CTTTACTGAA	GGGAGACGAA	GGCAGGGGTG	1800
	GATTCTCGAG	GTGGAAGTCC	GCACATGTCT	GTGGTATTTA	TGGCACGATT	CCTTTGGATG	1860
	GCTTCATTTG	CCCCCAGACT	GTATGAAAAC	ATCTCCGAAT	TAGCATTTCT	GGATATGTTT	1920
30	CATCCAGGGT	ATCATTGATT	TATGATGGAA	AACCGGCTCT	AGCTGGAGAT	GACTGTGATG	1980
	TTGCTGATGG	GTGTATAACA	AATGCTTGAG	TCCGAAGTGC	CCTTGAGATA	TGGTTGACGA	2040
	AAGAATTTTA	TAAACTGATA	AATTAAGGAT	TTTTATTATG	TTGTTATTAT	TATTTCTTTT	2100
	TTGTTGTTGA	TCGCACAGGA	TCAAAATGCC	TGTTATCTCC	CTTTTACTGG	GACTTTTTTT	2160
	TTTTTTTTTT	TTTTTTTTTAA	TCAGACAGGG	TCTTGCTCTG	TTGCCCAGGC	TGGAGTGCAG	2220
35	TGGTGCATC	TCGGCTCACT	GCAACTTCAG	CCTCCTGGAT	TCAGGCAACA	CTCCTGCCTC	2280
	AGCTCCCCAC	GTGGCTGGGA	TTACAGGTGC	CTGCCCCCAT	GGCTAATTTT	TTGTATTTTT	2340
	TGTAGAGATG	GGGTTTCACC	ATGTTGGCTG	GGCTGGTCTC	ACTCTCCTGA	CCTCAAGCAA	2400
	TCTGCTGTGC	TCAGCCTCCC	AAAGTGCTGG	GATTACAGGC	GTGAGCCACC	GCCCCAGGCC	2460
	TGAGCCTTTT	TTTTTTTCTA	ATGCATCCAA	GGTTAAGGGG	AAGACGCAAA	TAACAGGACT	2520
40	ATTCATAAAG	GAAACCTGTT	TGAACCTCTG	GAGATCAGTC	ATCAGTCTCA	GTATTCACA	2580
	GGCACACCTT	AATTTCAATT	TAAAAAGATA	TATATATTTT	GTCTATTTTT	GTGCTTTTGG	2640
	GGGCCTATTT	TGTGCTTTTT	TACCTTATGT	AGAGATCTTA	TTACAAAGTG	ATTTTCTACA	2700
	TTAAAAAAGG	ACTGAAATAA	ATTGTATAGT	TACTTAACTA	ATGAAGACAT	TTCAGAACTC	2760
	TGGGATGATT	TTAATCTTGA	AGTAGTAGGT	GGTATAGTCA	TAAAACCATT	CATCCCCTTC	2820
45	TTGATTGTAT	CTTAATTTTC	TGGCTTTAAG	GTGACATCTG	AGAGGTAATG	CATTCTTTTT	2880
	TATATTGAAG	TCATAAAACT	TCACCCGCTG	CTTCTCTGAG	TTACTTTTAA	TTTTGCCTTG	2940
	TGGTTATGGT	TTGGCGTTTC	CTTCTGTTTG	GTTTTCAGAG	CCCATGTCTC	ATATAGTCCT	3000
	GAGTGCAAGT	AATTACTATA	CTTGTAATG	AAGATCAGTA	TTTCTGCCTA	GATCTGATAA	3060
	AAAAATTTTC	TTGCTTGTAG	TATAAAAATT	CAAAGAAATG	TGTTACAAAG	ATACTTAGTA	3120
50	TAGCTCCTCA	GCCATAACCT	GAGACTTGGG	ATGAAATTTA	AACCAGATAC	GATTTACTTT	3180
	GCAGATCATA	AGGCTTTTAA	TACTCTTGTG	ATCAAAATGG	CTTATTTTTC	AGGCACTAAG	3240
	GATTGTTAAG	AGAAAAGCTT	TTCAACGAAG	GATTGCCTTT	CTTCTCCAC	ACTGTTCTTG	3300
	ATTTCTCTCT	TCTTTCAGGC	CTCAACAGGC	ACTGTATTCA	TTGCCAATGT	TCCAAATTAT	3360
	CAAAATCAAG	TGAATTTATT	TGTGTGTTCT	TTACTTATAT	AAAAAAGAT	AACTTTAAGG	3420
55	ATGTGCAAGT	ACATTTCCAA	CTGCTAGCAC	AACCAGTATT	TTGTAATTAA	ACAAATCGCT	3480
	GTATGGTATG	GCTTCTTACA	CATTTATGTC	TATAGATATC	TATGATCAT	CTTCTATTCT	3540
	TGTTTCATGA	CTGAATAATG	TAAAACCACT	GTTGGCAATT	GGTATCATCA	ATGATACTCA	3600
	TTTTTTAATA	ACCAAAGGCA	GGGGAAAAATC	ATTTTACTTA	TTAATAAATA	TTTTATGATG	3660
60	TGAAAAAATA	AAAAAATAAT	AAAAAATAAT				

**A109 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

70	1	11	21	31	41	51	
	MLSGFLMSPS	TQHRAQYTFG	GKKLPWEASI	GAHTSRGRGS	DRERESRPEA	AGLLWDRAAA	60
	GAEKGNRGE	PPAWIRAQQQ	PRPPFAGQAP	GTAAGGAQDP	RLRPGRSRGR	VRLPVKPEPA	120
75	SGRQPRGPSD	CIPRFPSASA	THKAVPKGTG	PPAEDGDGLG	APGPRARRRR	LLGVAAEGSG	180
	PRGKRRGTVS	DEARGSPGPR	LLGDRPALSG	DALSAPRVVP	CGALAARPS	HPGTPLRSCS	240
	CCWLRCWRRG	RGPSGEYCHG	WLDAGGVWRI	GFQCPERFDG	GDATICCGSC	ALRYCCSSAE	300
	ARLDQGGCDN	DRQQGAGEFG	RADKDGPRRL	GRASCLRGTQ	GDGEGAPPV	RAWQRCSPG	360
	SPKGRQLLRA	FPGLPRARR	RGFPSPPRG	PSPLQRPALP	IYVPFLIVGS	VVFVAFILGS	420
80	LVAACCCCL	RPKQDPQQR	APGNNRLMET	IPMIPSASTS	RGSSSRQSST	AASSSSSANS	480
	GARAPPTRSQ	TNCCLEPGTM	MNVVNMPTN	FSVLNCOQAT	QIVPHQGYL	HPPIVGYTVQ	540
	HDSVEMTAVP	PFMDGLQPGY	RQIQSPFPHT	NSEQKMYPAV	TV		

**A110 DNA SEQUENCE:**

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]

Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

5

```

1      11      21      31      41      51
|      |      |      |      |      |
10 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTCTGAGAG AGTCTCTAGA AGACATGATG 60
   CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTCGTCACAG TTTCTTCCAA CCTTGCCATT 120
   GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
   ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
   ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGCCC 300
   CAAATGAAG  AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
   GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
   GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
   TATGAGCCTC GGGATTATAC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
   CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTCA 600
   GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
   TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
   TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

```

25 A11 Protein sequence:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

30

```

35 1      11      21      31      41      51
   |      |      |      |      |      |
   MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
   PLMVIHLED  CQYSQALKKV FAQNEEQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM 120
   FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

```

40

A112 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

45

```

50 1      11      21      31      41      51
   |      |      |      |      |      |
   ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
   AAACCCCGTA TCCCACATGA GACCTTCAGA AAGGTGGGGA TCCCACATCAT CATAGCACTA 120
   CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC 180
   TACTTCTCT  GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
   CTGGACTGTC CTTGGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
   GCAGTGGCAG TCCGCCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
   GGGAACTGGT TCTCTGCCTG TTTCGACAA TCCACAGAAG CTCTCGCTGA GACAGCCTGT 420
   AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
   GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGATGCG GAACTCAAGT 540
   GGGCCCTGTC TCTCAGGCTC CTGTGCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG 600
   AAGACCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
   AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCCTGGGTC 720
   CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
   GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
   TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
   ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
   GCCACCCAC TCTGGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020
   GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
   GCGTACCAGG GGGAAAGTCAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
   GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
   GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
   AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

```

75 A113 Protein sequence:  
 Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 LDLa domain: 54-94  
 Tryp\_SpC domain: 204-429  
 Cellular Localization: plasma membrane/ER

80

1	11	21	31	41	51	
MLQDPDSDQP	LNSLDVKKPLR	KPRIPMETFR	KVGIPIIIAL	LSLASIIIVV	VLIKVILDKY	60
YFLCGQPLHF	IPRKQLCDGE	LDCPLGEDEE	HCVKSFPEGP	AVAVRLSKDR	STLQVLDSAT	120
GNWFSACFDN	FTEALAEATC	RQMGYSKPT	FRAVEIGPDQ	DLDVVEITEN	SQELRMRNSS	180
GPCLSGSLVS	LHCLACGKSL	KTPRVVGEE	ASVDSWPQVQ	SIQYDKQHVC	GGSLDPHWV	240
LTAACHCRKH	TDVFNWKVRA	GSDKLGSFPS	LAVAKIIIE	FNPMPKDND	IALMKLQFPL	300
TFSGTVRPIC	LPFFDEELTP	ATPLWIIIGW	FTKQNGGKMS	DILLQASVQV	IDSTRCNADD	360
AYQGEVTEKM	MCAGIPEGGV	DTCQGDGSGP	LMYQSDQWHV	VGIVSWGYGC	GGPSTPGVYT	420
KVSAYLNWIY	NVWKAEL					

A114 DNA SEQUENCE:

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Nucleic Acid Accession #: NM\_003318  
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
GGAAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACTC	TTGTTGGCCA	GGCTGGAGTG	60
CAATGGCACA	ATCTCAGCTT	ACTGCAACCT	CCGCCTCCCG	GGTTCAAGCG	ATTCTCCTGC	120
CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACATAATTT	180
CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACTCCTG	240
ACCTCAGGTG	ATCCACTTGC	CTTGGCCTCC	CAAAGTGCTA	GGATTACAGC	CGTGAAACTG	300
TGCTTGGCTG	ATTCTTTTTT	TGTTGTTTGA	TTTTTGAAAC	AGGGTCTCCC	TTGGTCGCCC	360
AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACATAAACC	TCCACCTCCT	GGTTTCAAGT	420
GATCCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	CGGTGCACCA	CCACACCCGG	480
CTAATTTTTT	TATTTTTTAT	AGAGACAGGG	TTTCAACATG	TTGGCCAGGC	TGTTCTCAAA	540
CTCCTGGACT	CAAGGGATCC	GCCTGCCCTC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
AGTCACCATG	CCTGACCTTA	TAATTTCTAA	GTCAATTTTT	CTGGTCCATT	TCTTCCCTAG	660
GGTCTCCACA	ACAAATCTGC	ATTAGGCGGT	ACAATAATCC	TAACTTTCAT	GATTCAACAA	720
AGGAAGATGA	AGTGATTTCAT	GATTAGAGAA	GGGGAAGTAG	TAAGCCCACT	GCACACTCCT	780
GGATGATGAT	CCTAAATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
TTTGGTTTAA	ATTAATTTAT	TAAATATCTA	AAAACATTTT	TGGATACATT	GTTGATGTGA	900
ATGTAAGACT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCCTCAG	960
TGCAGTTTTT	TGTAGAAATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGATT	1020
CCATAATGAA	CAAAGTGAGA	GACATTAAAA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
AACTAAGCTT	GAATAAAAT	TCTGCTGATA	CTACAGATAA	CTCGGGAAC	GTTAAACCAA	1140
TTATGATGAT	GGCAACAAC	CCAGAGGACT	GGTTGAGTTT	GTTGCTCAAA	CTAGAGAAAA	1200
ACAGTGTTC	GCTAAGTGAT	GCTCTTTTAA	ATAAATTGAT	TGGTCGTTC	AGTCAAGCAA	1260
TTGAAGCGCT	TCCCCAGAT	AAATATGGCC	AAAATGAGAG	TTTTGCTAGA	ATTCAAGTGA	1320
GATTTGCTGA	ATTAAGAGCT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAATGG	1380
CCAGAGCAAA	CTGCAAGAAA	TTTGCTTTTG	TTTATATATC	TTTTGCACAA	TTTGAAGTGT	1440
CACAAGGTAA	TGTCAAAAAA	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CGTGGAGCAG	1500
TACCACTAGA	AATGCTGGAA	ATTGCCCTGC	GGAATTTTAA	CCTCCAAAAA	AAGCAGCTGC	1560
TTTCAGAGGA	GGAAAAGAAG	AATTTATCAG	CATCTACGGT	ATTAAGTCCC	CAAGAATCAT	1620
TTTCCGGTTC	ACTTGGGCAT	TTACAGAATA	GGAAACAAC	TTGTGATTCC	AGAGGACAGA	1680
CTACTAAAGC	CAGTTTTCAT	TATGGAGAGA	ACATGCCACC	ACAAGATGCA	GAAATAGGTT	1740
ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAAACAGTC	ATGCCCAATT	GGAAGAGTCC	1800
CAGTTAAGCT	TCTAATATAG	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTTGTACCTT	1860
GTTTATGAAA	AAGACAACCT	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
AACCAAGTGG	AAATGATTCC	TGTGAATTAA	GAAATTTTAA	GTCTGTTCAA	AATAGTCATT	1980
TCAAGGAACC	TCTGGTGTC	GATGAAAAGA	GTTCTGAAC	TATTATTACT	GATTCAATAA	2040
CCCTGAAGAA	TAAACCGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
AAGAACCAGA	GGTTCCAGAG	AGTAACCAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
GTATTAAACA	GAATCCTGCT	GCATCTTCAA	ATCACTGGCA	GATTCCGGAG	TAGCCCGGAA	2220
AAGTTAATAC	AGAGCAGAAA	CATACCACCT	TTGAGCAACC	TGCTTTTCAA	GTTTCAAAAC	2280
AGTCACCACC	AATATCAACA	TCTAATGGT	TTGACCCAAA	ATCTATTTGT	AAGACACCAA	2340
GCAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTGTAGAA	TCCAGTTGTA	AAGAATGACT	2400
TTCCACCTGC	TGTGAGTTG	TCAACACCTT	ATGGCCAACC	TGCTGTTTTC	CAGCAGCAAC	2460
AGCATCAAT	ACTTGCCACT	CCACTTCAAA	ATTTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
ATGAATGCAT	TTGGGTTTAA	GGAAGAATTT	ATTCCATATT	AAAGCAGATA	GGAAGTGGAG	2580
GTTCAAGCAA	GGTATTTTCA	GTGTTAAATG	AAAAGAAACA	GATATATGCT	ATAAAATATG	2640
TGAACCTTAG	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	CCGGAACGAA	ATAGCTTATT	2700
TGAATAAACT	ACAACAACAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAAATCACGG	2760
ACCACTACAT	CTACATGGTA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAAA	2820
AGAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAAAAATATG	TTAGAGGCGA	2880
TTACACAAT	CCATCAACAT	GGCATTTGTC	ACAGTGATCT	TAAACCACT	AACCTTCTGA	2940
TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATTGC	AAACCAATG	CAACCAAGATA	3000
CAACAAGTGT	TGTTAAAGAT	TCTCAGGTTG	GCACAGTTAA	TTATATGCCA	CCAGAAGCAA	3060
TCAAAGATAT	GTCTTCTCTC	AGAGAGAATG	GGAAATCTAA	GTCAAAGATA	AGCCCCAAAA	3120
GTGATGTTTG	GTCTTATAGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCATTTG	3180
AGCAGATAAT	TAATCAATTAC	TCTAAATTAC	ATGCCATAAT	TGATCTTAAT	CATGAAATGC	3240
AATTTCCCGA	TATCCAGAG	AAAGATCTTC	AAGATGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
ACCCAAAAAC	GAGGATATCC	ATTCCTGAGC	TCCTGGCTCA	TCCATATGTT	CAAAATTCAAA	3360
CTCATCCAGT	TAACCAAAATG	GCCAAAGGAA	CCACTGAAGA	AATGAAATAT	GTTCTGGGCC	3420
AACCTGTTGG	TCTGAATTC	CCTAACTCCA	TTTTGAAAGC	TGCTAAAACT	TTATATGAAC	3480
ACTATAGTGG	TGGTGAAGT	CATAATCTCT	CATCCTCCAA	GACTTTTGAA	AAAAAAGGG	3540
GAAAAAATG	ATTTGCGATT	ATTCGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGACT	3600
GTTTACTCT	TGAATCCCTG	TGGAATCTA	CATTGAAGA	CAACATCACT	CTGAAGTGT	3660
ATCAGCAAAA	AAATTCAGT	GAGATTATCT	TTAAAGAAA	ACTGTAAAAA	TAGCAACAC	3720

TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC 3780  
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAAGTTTG 3840  
 TAAATAAAGT TTTGTGGCTA AAATGA

A115 Protein sequence:

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Protein Accession #: NP\_003309  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

1	11	21	31	41	51	
MNKVRDIKKN	FKNEDLTDEL	SLNKISADTT	DNSGTVNQIM	MMANNPEDWL	LLLLKLEKNS	60
VPLSDALINK	LIGRYSQAIE	ALPPDKYQON	ESFARIQVRF	AELKAIQEPD	DARDYFQMAR	120
ANCKKFAFVH	ISFAQFELSQ	GNVKKSKQLL	QKAVERGAVP	LEMLEIALRN	LNLQKKQLLS	180
EEKKNLAS	TVLTAQESFS	GSLGHLQNRN	NSCDSRGQTT	KARFLYGENM	PPQDAEIGYR	240
NSLRQTNKTK	QSCPFGRVPV	NLLNSPDCDV	KTDDSVVPCF	MKRQTSRSEC	RDLVVPGSKP	300
SGNDSCELRN	LKSVQNSHFH	EPLVSDEKSS	ELIITDSITL	KNKTESSLLA	KLEETKEYQE	360
PEVPESNQKQ	WQAKRKSECI	NQNPAASSNH	WQIPELARKV	NTEQKHTTFF	QPVFSVSKQS	420
PIISTSKWFD	PKSICKTPSS	NTLDDYMSCF	RTPVVKNDFF	PACQLSTPYG	QPACFQQQOH	480
QILATPLQNL	QVLASSSANE	CISVKGRIYS	ILKQIGSGGS	SKVFQVLNEK	KQIYAIVYVN	540
LEEADNQTLN	SYRNEIAYLN	KLQHQHSDKII	RLYDYEITDQ	YIYVMVECGN	IDLNSWLKKK	600
KSIDPWKRK	YWKNMLEAVH	TIHQHGVHVS	DLKPANFLIV	DGMLKLIDFG	IANQMOPDIT	660
SVVKDSQVGT	VNYMPEAIK	DMSSSRENGK	SKSKISPKSD	VWSLGCILYY	MTYKGTFFQQ	720
IINQISKLHA	IIDPNHEIEF	PDIEPKDLQD	VLKCKLKRDP	KQRISIPELL	AHPVYVQIQT	780
PVNQMAKGT	BEKMYVLGQL	VGLNSPNSIL	KAAKTLYEHY	SGGESHNSSS	SKTFEKKRKG	840
K						

OVARIANA116 DNA SEQUENCE

Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Nucleic Acid Accession #: NM\_001508  
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
ATGGCTTCAC	CCAGCCTCCC	GGGCAGTGAC	TGCTCCCAA	TCATTGATCA	CAGTCATGTC	60
CCCAGATTG	AGGTGGCCAC	CTGGATCAAA	ATCACCCCTTA	TTCTGGTGTA	CCTGATCATC	120
TTCTGTATGG	GCCTTCTGGG	GAACAGCGCC	ACCATTTCGGG	TCACCCAGGT	GCTGCAGAAG	180
AAAGGATACT	TGCAGAAGGA	GGTGACAGAC	CACATGGTGA	GTTTGGCTTG	CTCGGACATC	240
TTGGTGTTCC	TCATCGGCAT	GCCCATGGAG	TTCTACAGCA	TCATCTGGAA	TCCCCTGACC	300
ACGTCCAGCT	ACACCCGTGC	CTGCAAGCTG	CACACTTTCC	TCTTCGAGGC	CTGCAGCTAC	360
GCTACGCTGC	TGCACGTGCT	GACACTCAGC	TTTGAGCGCT	ACATCGCCAT	CTGTACCCCC	420
TTCAGGTACA	AGGCTGTGTC	GGGACCTTGC	CAGGTGAAGC	TGCTGATTGG	CTTCGTCTGG	480
GTCACTCCCG	CCCTGGTGGC	ACTGCCCTTG	CTGTTTGCCA	TGGGTACTGA	GTACCCCTTG	540
GTGAACGTGC	CCAGCCACCG	GGGTCTCACT	TGCAACCGCT	CCAGCACCCG	CCACCACGAG	600
CAGCCCGAGA	CCTCCAATAT	GTCCATCTGT	ACCAACCTCT	CCAGCCGCTG	GACCGTGTTT	660
CAGTCCAGCA	TCTTCGGCGC	CTTCGTGGTC	TACCTCGTGG	TCCTGCTCTC	CGTAGCCTTC	720
ATGTGCTGGA	ACATGATGCA	GGTGCTCATG	AAAAGCCAGA	AGGGCTCGCT	GGCCGGGGGG	780
ACGCGGCCTC	CGCAGCTGAG	GAAGTCCGAG	AGCGAAGAGA	GCAGGACCGC	CAGGAGGCAG	840
ACCATCATCT	TCCTGAGGCT	GATTGTTGTG	ACATTGGCCG	TATGCTGGAT	GCCCAACCAG	900
ATTCGAGGGA	TCATGGCTGC	GGCCAAACCC	AAGCACGACT	GGACGAGGTC	CTACTTCCGG	960
GCGTACATGA	TCCTCCTCCC	CTTCTCGGAG	ACGTTTTTCT	ACCTCAGCTC	GGTCATCAAC	1020
CCGCTCCTGT	ACACGGTGTC	CTCGCAGCAG	TTTCGGCGGG	TGTTCTGTGA	GGTGTGTGTC	1080
TGCCGCTGTG	CGCTGCAGCA	CGCCAACCAC	GAGAAGCGCC	TGCGCGTACA	TGCGCACTCC	1140
ACCACCGACA	GCGCCCGCTT	TGTGCAGCGC	CCGTGTCTCT	TCGCGTCCCG	GCGCCAGTCC	1200
TCTGCAAGGA	GAAGTGAAGG	GATTTCCTTA	AGCACTTTTC	AGAGCGAGGC	CGAGCCCCAG	1260
TCTAAGTCCC	AGTCATTGAG	TCTCGAGTCA	CTAGAGCCCA	ACTCAGGCGC	GAAACCAGCC	1320
AATTCTGCTG	CAGAGAAATG	TTTTTCAGGAG	CATGAAGTTT	<u>GA</u>		

A117 Protein sequence:

Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Protein Accession #: NM\_001508, NP\_001409  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [72-172, 224-344]  
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342  
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MASPSLPGSD	CSQIIDHSHV	PEFEVATWIK	ITLILVYLII	FVMGLLGNSA	TIRVTQVLQK	60

KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120  
 ATLLHVLTLF FERYIAIICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL 180  
 VNVPSHRGLT CNRSSTRHHE QPETSNSMIC TNLSSRWTFV QSSIFGAFVY YLVVLLSVAF 240  
 MCNMWQVLM KSQKGSLAGG TRPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCWMPNQ 300  
 IRRIMAAKPF KHDWTRSYFR AYMLLLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC 360  
 CRLSLQHANH EKRLRVHAHS TTD SARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPO 420  
 SKSQSLSLSE LEPNSGAKPA NSAAENGFOE HEV

**A118 DNA sequence**

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.87223  
 Probeset Accession #: AA250737  
 Nucleic Acid Accession #: NM\_001203  
 Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CGCGGGGCGC GGAGTCGCGC GGGCCTCGCG GGACGCGGCG AGTGGCGAGA CCGCGGCGCT 60  
 GAGGACGCGG GAGCCGGGAG CGCAGCGCGG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120  
 GTGAAAGGAA AGGAAGATCA TTTTCATGCT TGTGATATAA GGTTCAGACT TCTGCTGATT 180  
 CATAACCAAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240  
 TGCCATAAGT GAGAGCAAAA CTTCTTGAT AACATGCTTT TGCGAAGTGC AGGAAAATTA 300  
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC 360  
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420  
 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480  
 GGTTCGCTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG ACACCTCCAT TCCTCATCAA 540  
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCCTACA 600  
 CTGCTCTCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660  
 ATATCTGTGA CTGCTCTGTAG TTTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCCGG 720  
 TATAAAGAGC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC 780  
 ATTCCTCTG GAGAACTCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840  
 TCAGGCTTCC CTCTGCTGGT CCAAGGACT ATAGCTAAGC AGATTGAGAT GGTGAAACAG 900  
 ATTGGAAGAG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GGCCTGGCGA AAAGGTAGCT 960  
 GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAT 1020  
 ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATATG CTGCAGATAT CAAAGGGACA 1080  
 GGGTCCTTGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140  
 TATCTGAAGT CCACCACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200  
 AGTGGCTTAT GTCATTTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260  
 CATCGAGATC TGAAAGTAA AAACATTCTG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320  
 GACCTGGGCC TGGCTGTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380  
 ACTCGAGTTG GCACCAACAG CTATATGCCT CCAGAAAGTGT TGGACGAGAG CTTGAACAGA 1440  
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCTCAT CTCTTGGGAG 1500  
 GTTGTAGGTA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560  
 CTAGTGCCCA GTGACCCCTT TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAAGTTA 1620  
 CGCCCTCAT TCCCAAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAAACCT 1680  
 ATGACAGAAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740  
 ACACCTGCCA AAATGTCAGA GTCCAGGAC ATTAACTCT GATAGGAGAG GAAAGTAAG 1800  
 CATCTCTGCA GAAAGCCAAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA 1860  
 TAAGCATCCA CAGTACCAAGC CTGGAACATC GTCCTGCTTC CCAGTGGGTT CAGACCTCAG 1920  
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980  
 TCTGTTTGTG GCGGAGAAAA CCGTTGGGTA ACTTGTTCAT GATATGATGC AT

**A119 Protein sequence**

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.72472 / Hs.87223  
 Probeset Accession #: AA250737 / U89326  
 Protein Accession #: NP\_001194  
 Signal sequence: 1-13  
 Transmembrane domains: 128-144  
 PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFTMIEED 60  
 DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120  
 GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPARY IGLEQDETYI PPGESLRDLI 180  
 EQSQSSSGSGS GLPLLVRTI AKQIQMVKQI GKGRYGEVWM GKWRGEKVAV KVFFTTTEAS 240  
 WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
 MLKLAYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNLLV KNGTCCCIAD LGLAVKFISD 360  
 TNEVDLPPNT RVGTRKRYMP EVLDESLNRN HFQSYIMADM YSFGILILEV ARRCVSGGIV 420  
 EBYQLPYHDL VSPDSPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHPAS 480  
 RLTAIRVKKKT LAKMESQDI KL

**A120 DNA SEQUENCE**

Gene name: L1V-1 protein, estrogen regulated  
 Unigene number: Hs.79136  
 Probeset Accession #: U41060  
 Nucleic Acid Accession #: NM\_012319.2  
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	CTCGTGCCGA	ATTCCGGCACG	AGACCGCGTG	TTCCGCGCCTG	GTAGAGATTT	CTCGAAGACA	60
	CCAGTGGGCC	CGGTGTGGAA	CAAACCTGCG	CGCGTGGCCG	GGCCGTGGGA	CAACGAGGCC	120
	GCGGAGACGA	AGCGGCAATG	GCGAGGAAGT	TATCTGTAAT	CTTGATCCTG	ACCTTTGCCC	180
5	TCTCTGTAC	AAATCCCTTT	CATGAACATA	AAGCAGCTGC	TTTCCCCAG	ACCAGTGAGA	240
	AAATTAGTCC	GAATTGGGAA	TCTGGCATT	ATGTTGACTT	GGCAATTTCC	ACACGGCAAT	300
	ATCATCTACA	ACAGCTTTTC	TACCGCTATG	GAGAAAATAA	TTCTTTGTCA	GTGGAAGGGT	360
	TCAGAAAATT	ACTTCAAAT	ATAGGCATAG	ATAAGATTAA	AAGAATCCAT	ATACACCATG	420
10	ACCACGACCA	TCACTCAGAC	CACGAGCATC	ACTCAGACCA	TGAGCGTCAC	TCAGACCATG	480
	AGCATCACTC	AGACCACGAG	CATCACTCTG	ACCATGATCA	TCACTCTCAC	CATAATCATG	540
	CTGCTTCTGG	TAAAAATAAG	CGAAAAGCTC	TTTCCCCAGA	CCATGACTCA	GATAGTTCAG	600
	GTAAGATCC	TAGAAACAGC	CAGGGGAAAG	GAGCTCACCG	ACCAGAACAT	GCCAGTGGTA	660
	GAAGGAATGT	CAAGGACAGT	GTTAGTGCTA	GTGAAGTGAC	CTCAACTGTG	TACAACACTG	720
15	TCTCTGAAGG	AACTCACTTT	CTAGAGACAA	TAGAGACTCC	AAGACCTGGA	AAACTCTTCC	780
	CCAAAGATGT	AAGCAGCTCC	ACTCCACCCA	GTGTCACTAT	AAAGAGCCGG	GTGAGCCGGC	840
	TGGCTGGTAG	GAAACAAAT	GAATCTGTGA	GTGAGCCCGG	AAAGGCTTTT	ATGTATTCCA	900
	GAAACACAAA	TGAAAATCCT	CAGGAGTGTT	TCAATGCATC	AAAGCTACTG	ACATCTCATG	960
	GCATGGGCAT	CCAGGTTCCG	CTGAATGCAA	CAGAGTTCAA	CTATCTCTGT	CCAGCCATCA	1020
20	TCAACCAAAT	TGATGCTAGA	TCTTGTCTGA	TTCATACAAG	TGAAAAGAAG	GCTGAAATCC	1080
	CTCCAAAGAC	CTATTCATTA	CAAAATAGCT	GGGTGTGGTG	TTTTATAGCC	ATTTCCATCA	1140
	TCAGTTTCCT	GTCTCTGCTG	GGGGTTATCT	TAGTGCCTCT	CATGAATCGG	GTGTTTTTCA	1200
	AAATTTCTCT	GAGTTTCTTT	GTGGCACTGG	CCGTTGGGAC	TTTGAGTGGT	GATGCTTTTT	1260
	TACACCTTCT	TCCACATCT	CATGCAAGTC	ACCACCATAG	TCAATGCTAT	GAAGAACCAG	1320
25	CAATGGAAT	GAAAGAGGGA	CCACTTTTCA	GTCTCTGTCT	TTCTCAAAAC	ATAGAAGAAA	1380
	GTGCCTATTT	TGATTCACG	TGGAAGGGTC	TAACAGCTCT	AGGAGGCTGT	TATTTTCATG	1440
	TTCTTGTGA	ACATGTCTCT	ACATTGATCA	AACAATTTAA	AGATAAGAAG	AAAAAGAATC	1500
	AGAAGAAAC	TGAAAATGAT	GATGATGTGG	AGATTAAAGAA	GCAGTTGTCT	AAGTATGAAT	1560
	CTCACTTTTC	AACAATGAGC	GAGAAAGTAG	ATACAGATGA	TCGAAGCTGAA	GGCTATTATC	1620
30	GAGCAGACTC	AACAGAGCCC	TCCCACTTTG	ATTCTCAGCA	GCCTGCAGTC	TTGGAAGAAG	1680
	AAGAGGTCAT	GATAGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GTACCCAGAG	1740
	GGTGCAAGAA	TAAATGCCAT	TCACATTTCC	ACGATACACT	CGGCCAGTCA	GACGATCTCA	1800
	TTCAACCAAA	TCATGACTAC	CATCATATTC	TCCATCATCA	CCACCACCAA	AACCACCATC	1860
	CTCAGAGTCA	CAGCCAGGCG	TACTCTCGGG	AGGAGCTGAA	AGATGCCGGC	GTGCCCATCT	1920
35	TGGCCTGGAT	GGTGATAATG	GGTGATGGCC	TGCACAATTT	CAGCGATGGC	CTAGCAATTG	1980
	GTGCTGCTTT	TACTGAAGGC	TTATCAAGTG	GTTTAAAGTAC	TTCTGTTGCT	GTGTTCTGTC	2040
	ATGAGTTGCC	TCATGAAATTA	GGTGACTTTG	CTGTTCTACT	AAAGGCTGGC	ATGACCGTTA	2100
	AGCAGGCTGT	CCTTTATAT	GCATTGTCTAG	CCATGCTGGC	GTATCTTGGA	ATGGCAACAG	2160
	GAATTTTCAT	TGCTCATTAT	GCTGAAAATG	TTTCTATGTG	GATATTTGCA	CTTACTGCTG	2220
40	GCCTATTTCAT	GTATGTTGCT	CTGGTTGATA	TGGTACCTGA	AATGCTGCAC	AATGATGCTA	2280
	GTGACCATGG	ATGTAGCCGC	TGGGGGTATT	TCTTTTACAA	GAATGCTGGG	ATGCTTTTGG	2340
	GTTTTGGAAT	TATGTTACTT	ATTTCCATAT	TGGAACATAA	AATCGTGTTC	CGTATAAATT	2400
	TCTAGTTAAG	GTTTAAATGC	TAGAGTAGCT	TAAAAGTTTG	TCATAGTTTC	AGTAGGTCAT	2460
	AGGGAGATGA	GTTTGTATGC	TGTACTATGC	AGCGTTTAAA	GTTAGTGGGT	TTTGTGATTT	2520
45	TTGTATTGAA	TATTGCTGTC	TGTTACAAAG	TCAGTTAAAG	GTACGTTTAA	ATATTTAAGT	2580
	TATTTCTATCT	TGGAGATAAA	ATCTGTATGT	GCAATTCACC	GGTATTACCA	GTTTATTATG	2640
	TAAACAGAG	ATTTGGCATG	ACATGTTCTG	TATGTTTCAG	GGAAAATGT	CTTTAATGCT	2700
	TTTTCAAGAA	CTAACACAGT	TATTCCTATA	CTGGATTTTA	GGTCTCTGAA	GAACTGCTGG	2760
	TGTTTAGGAA	TAAAGATGTG	CAATGAAGCCT	AAAATACCAA	GAAAGCTTAT	ACTGAATTTA	2820
50	AGCAAAAGAA	TAAAGGAGAA	AAGAGAAGAA	TCTGAGAATT	GGGGAGGCAT	AGATTCTTAT	2880
	AAAAATCACA	AAATTTGTTG	TAAATTAGAG	GGGAGAAATT	TAGAATTAAG	TATAAAAAGG	2940
	CAGAATTAGT	ATAGAGTACA	TTCAATTAAAC	ATTTTGTGCA	GGATTATTTT	CCGTAAAAAC	3000
	GTAGTGAGCA	CTCTCATATA	CTAATTAGTG	TACATTTAAC	TTGTGATAAT	ACAGAAATCT	3060
	AAATATATT	AATGAATTCA	AGCAATATAC	ACTTGACCAA	GAAATTTGAA	TTTCAAAATG	3120
55	TTCTGCGGG	TTATATACCA	GATGAGTACA	GTGAGTAGTT	TATGTATCAC	CAGACTGGGT	3180
	TATTTGCCAAG	TTATATATCA	CCAAAAGCTG	TATGACTGGA	TGTTCTGGTT	ACCTGGTTTA	3240
	CAAAATATATC	AGAGTAGTAA	AACCTTTGATA	TATATGAGGA	TATTAAAACT	ACACTAAGTA	3300
	TCATTTGATT	CGATTGAGAA	AGTACTTTGA	TATCTCTCAG	TGCTTCAGTG	CTATCATTGT	3360
	GAGCAATTGT	CTTTATATAC	GGTACTGTAG	CCATACTAGG	CTGTCTGTG	GCATTCTCTA	3420
60	GATGTTTCTT	TTTTACACAA	TAAATTCCTT	ATATCAGCTT	G		

**A121 PROTEIN SEQUENCE**

Gene name: LIIV-1 protein, estrogen regulated  
 Unigene number: Hs.79136  
 Protein Accession #: NP\_036451  
 Signal sequence: 1-21  
 Pfam domain: Zip[591-743]  
 Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745  
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
	MARKLSVILI	LTFALSVTNP	LHELKAAAFP	QTTEKISPNW	ESGINVDLAI	STRQYHLQQL	60
	FYRYGENNSL	SVGEFRKLLQ	NIGIDKIKRI	HIHHDHDS	DHEHSDHER	HSDHEHSDH	120
75	EHHSDDHDS	HNHNAAGSKN	KRKALCPDHD	SDSSGKDPNR	SQKGARHPE	HASGRNRVKD	180
	SVSASEVTST	VYNTVSEGTH	FLETIETPRP	GKLPFKDVSS	STPPSVTSKS	RVSRLAGRKT	240
	NESVSEPRKG	FMYSRNTNEN	PQECFNASKL	LTSHGMGIQV	PLNATEFNLY	CPAIIINQIDA	300
	RSCLHTSEK	KAETPPKTY	LQIAWVGFI	AISIISFLSL	LGVLVPLMN	RVFFKFLLSF	360
80	LVALVGLSL	GDAPFLHLLP	SHASHHSHS	HEEPAMEMKR	GPLFSLHSSQ	NIEESAYFDS	420
	TWKGLTALGG	LYFMFLVEHV	LTLIKQFKDK	KKKNQKKPEN	DDDFEIKKQL	SKYESQLSTN	480
	EKVDTDDRT	EGYLRADSQE	PSHFDSQPPA	VLEEEVEMIA	HAHPQEVYNE	YVPRGCKNKC	540
	HSHFHDTLGQ	SDDLIIHHHD	YHHILHHHH	QNHHPHSHSQ	RYSRREELKDA	GVATLAWMVI	600
	MGDLHNFSD	GLATGAAPTE	GLSSGLSTSV	AVFCHLPHE	LGDFAVLLKA	GMTVKQAVLY	660
	NALSAMLAYL	GMATGIFIGH	YAENVSMWIF	ALTAGLFMYV	ALVDMVPEML	HNDASDHGCS	720

RWGYFFLQNA GMLLGFGIML LISIFEHKIV FRINF

**A122 DNA SEQUENCE**

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Nucleic Acid Accession #: NM\_015507  
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
CCGCAGAGGA GCCTCGGCCA GGCTAGCCAG GCGCGCCCCA GCCCTCCCCC AGGCCGCGAG 60
CGCCCCCTGCC GCGGTGCCTG GCCTCCCTC CCAGACTGCA GGGACAGCAC CCGTAACTG 120
CGAGTGGAGC GGAGGACCCG AGCGCTGAG GAGAGAGGAG GCGCGCGCTT AGCTGCTACG 180
GGGTCCGCCG GCGCCCTCCG CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCAGAG 240
ATGCCTCTGC CTTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
GGGAACGCGG CCAGTGCAAG GCATCACGGG TTGTAGCAT CGGCACGTCA GCCTGGGGTC 360
TGTCACATATG GAACTAAACT GGCTGCTGCG TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
TGTAAGATCA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
AGATGCTTTC CAGGATACAC CGGAAAACCC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT 780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840
AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
GGGTCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020
ATCCCTGAAA ATCTCTGTGA GGAAGTCTCT AGAGCACCCTG GTACCATCAA AGACAGAATC 1080
AAGAAAGTTG TTTGCTACAA AAACAGCATG AAAAAGAAGG CAAAATTAA AAATGTTACC 1140
CCAGAACCCA CAGGACTCC TACCCCTAAG GTGAAGTTCG AGCCCTTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAAAGAAA 1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAAT CCGCCTGATT 1380
CTGGTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT 1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
TGGAATCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTC GGCCTTGGCA 1560
GGTCAACAAG AAGACATTGG CCGATTGAAA CTTCTCCTAC CTGACCTGCA ACCCCAAAGC 1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCCGAGACA AAGTCGGGAA ACTTCGAGTG 1680
TTTGTGAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
TGGAAGACAG GGAATAATCA GTTGATCAA GGAAGTATG CTACCCAAAG CATCATTTT 1800
GAAGCAGAAC GTGGCAAGGG CAAACCGGCG GAAATCGCAG TGGATGGCGT CTGCTTGTT 1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTGT ATGTCAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
TCTTGATATA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCCCTCCT 2160
CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTTAGAAAA 2220
TAGAAAAAAA AGCACAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC 2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340
TGATATTTTA AATTCCTTGT AATAATAATA TCCAAATCAT CAAAAAATA AAAAAAAA

```

**A123 Protein sequence:**

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Protein Accession #: NP\_056322.2  
 Signal sequence: 1-21  
 Transmembrane domains: none found  
 MAM domain: 402-546  
 EGF domain: 80-259  
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRSKGV 60
CEATCEPGCK FGECVGPNNK RCFPGYTGKT CSQDVNECGM KPRPCQHRV NTHGSYKFC 120
LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQCLCPS SGLRLAPNGR DCLDIDECAS 180
GKVICPYNRR CVNTFGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCNTQ 240
GSPFKCKQKG YKNGNLRCSA IPENSVKEVL RAPGTIKDRI KLLLAHKNSM KKKAKIKNVT 300
PEPTRPTPK VNLQPFNYEE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER 360
SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGICD WKQDREDDFD 420
WNPADRDNAI GFYMAVPALA GHKKIDIGRLK LLLPDLQFQS NFCLLFYDRL AGDKVGLKLV 480
FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERKGKGTG EIAVDGVLLV 540
SGLCPDSSL S VDD

```

**A124 DNA SEQUENCE**

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719



Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

```

5      1      11      21      31      41      51
|      |      |      |      |      |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCCGGTGC GGGCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTCGTGGCG CTCTGGGCAC 180
CCCTGTTCCT GCTGCGCTCC GGCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
10 GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGCGCGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
GCCAGGGCTT CTCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
GCCTGCAAGA TAGCCATTTC CTCACGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
15 TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
TTTCCAAGAT CCCAGAAGAG GAAGCTGTCA CGGCAGCCGA ATTCGGGATC TACAAGGACT 660
ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGTCTCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCTCTCG 780
AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC 840
GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGTGGA TGGGCGAGAG ATCAACCCCA 900
AGTTGGCGGG CTGATTGGG CGGCACGGGC CCCAGAACA CGAGCCCTTC ATGGTGGCTT 960
TCTTCAAGGC CACGGAGGTC CACTTCCGCA GCATCCGGTC CACGGGAGC AAACAGCGCA 1020
GCCAGAACCG CTCCAAGACG CCCAAGAACC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
AGAACAGCAG CAGCGACCG AGGCAGCCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
25 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG 1200
AGGGGGAGTG TGCCTTCCCT CTGAATCCTT ACATGAACGC CACCAACCAC GCCATCGTGC 1260
AGACGCTGGT CCACTTCATC AACCCGGAAC CGGTGCCCAA GCCCTGCTGT GCGCCACGC 1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
30 TTGGGGCCAA GTTTTTCTGG ATCTCTCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCCCTTTG TGAGACCTTC CCCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
TCTTACAAGC TGTGCAGGCA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
GCCGGGCCAG GTCATTGGCT GGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
35 TTATGAGCGC CTACCAGCCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
GGGCACATTG GTGCTGTGTC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAACCG AATGAATG

```

40 A125 Protein sequence:  
Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number: Hs.170195  
Probeset Accession #: BE616633  
Protein Accession #: NP\_001710.1  
Signal sequence: 1-30  
Pfam domains: TGFb\_propeptide [37-281]  
Transmembrane domains: none found  
Cellular Localization: secreted

```

50      1      11      21      31      41      51
|      |      |      |      |      |
MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRRLRSQE RREMQREILS 60
ILGLPHRRRP HLQKHNHNSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
55 LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRYKYD 180
IRERFDNETF RISVYQLVQE HLGRESLFL LDRSLWASE EGWLVDITA TSNHWVNVNR 240
HNLGLQLSVE TLDGLSINPK LAGLGRHGP QNKQPFMVA FKAETVHFRS IRSTGSKQRS 300
QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAYYCE 360
GECAFLNSY MNAITHAIVQ TLVHFIPET VPKPCCAPTQ LNAISVLYFD DSSNVILKXY 420
60 RNMVVRACGC H

```

#### A126 DNA SEQUENCE

Gene name: integrin, beta 8  
Unigene number: Hs.52620  
Probeset Accession #: AA479726  
Nucleic Acid Accession #: NM\_002214  
Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

```

70      1      11      21      31      41      51
|      |      |      |      |      |
CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGACG 60
CTGCCGACTT GTCTTTGCCG GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
GTTGGCCTCC CTGCCACCTT GTGGAAGCAA CTGCGCTGAT TGATCGGCA CAGACTTTTT 180
TCCCTTCGAC CTCGCGCGG TACCCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
75 TAGGGTGGTT TCCCCCCAG CTTCGGGCTT TGTGGGGT TGATTGTGTT TGGCTCTTCG 300
CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCCTTTCTT 360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT 420
TGGCCGTCGA AGGAGGTGCT TCTCGCGGAG ACCCGGGGAC CCGCGGTGCC GAGCCGGGAG 480
GGCCGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT 540
CGAGCCCGG GGGTCCGCTT GCTAGGCTTG CGGAAAACGT CCTAGCGACA CTCGCCCGCG 600
GGCCCCGAGG TCGCCCGGGA GGCCGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGCGCG 660
GGGGCGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTTTTACC GCTGCATTTC 720
80 TCTGCCTGCA AAACGACCGG CGAGGTCCCG CCTCGTTCTT CTGGGACGCC TGGGTGTTTT 780

```

	CACCTTGTCT	TGGACTGGGC	CAAGGTGAAG	ACAATAGATG	TGCATCTTCA	AATGCAGCAT	840
	CCTGTGCCAG	GTGCCCTTGGC	CTGGGTCCAG	AATGTGGATG	GTGTGTTCAA	GAGGATTTCA	900
	TTTCAGGTGG	ATCAAGAAGT	GAACGTTGTG	ATATTGTTTC	CAATTTAATA	AGCAAAGGCT	960
5	GCTCAGTTGA	TTCAATAGAA	TACCCATCTG	TGCATGTTAT	AATACCCACT	GAAAAAGGAA	1020
	TTAATACCCA	GGTGACACCA	GGAGAAGTGT	CTATCCAGCT	GCCTCCAGGA	GCCGAAGCTA	1080
	ATTTTATGCT	GAAAGTTCAT	CCTCTGAAGA	AATATCCTGT	GGATCTTTAT	TATCTTGTTG	1140
	ATGTCCTCAGC	ATCAATGCAC	AATAATATAG	AAAAATTAAA	TTCCGTTGGA	AACGATTTAT	1200
	CTAGAAAAAT	GGCATTTTTC	TCCCGTGACT	TTGTCCTTGG	ATTGGCTCA	TACGTTGATA	1260
10	AAACAGTTT	ACCATACATT	AGCATCCACC	CCGAAAGGAT	TCATAATCAA	TGCAGTGACT	1320
	ACAATTTAGA	CTGCATGCCT	CCCCATGGAT	ACATCCATGT	GCTGTCTTTG	ACAGAGAACA	1380
	TCACTGAGTT	TGAGAAAGCA	GTTTCATAGAC	AGAAGATCTC	TGGAAACATA	GATACACCAG	1440
	AAGGAGGTTT	TGACGCCATG	CTTCAGGCAG	CTGTCTGTGA	AAGTCATATC	GGATGGCGAA	1500
	AAGAGGCTAA	AAGATTGCTG	CTGGTGATGA	CAGATCAGAC	GTCTCATCTC	GCTCTTGATA	1560
	GCAAAATGGC	AGGCATAGTG	GTGCCCAATG	ACGGAACACTG	TCATCTGAAA	AACAACGTCT	1620
15	ACGTCAAATC	GACAACCATG	GAACACCCCT	CCTAGGCCA	ACTTTTCAGAG	AAATTAATAG	1680
	ACAACAACAT	TAATGTTCATC	TTTGCAGTTC	AAGGAAAAACA	ATTTCATTGG	TATAAGGATC	1740
	TTCTACCCCT	CTTGCCAGGC	ACCATTGCTG	GTGAAATAGA	ATCAAAGGCT	GCAAACTCTA	1800
	ATAATTTGGT	AGTGGGAAGC	TATCAGAAGC	TCATTTTCAGA	AGTGAAGTT	CAGGTGGAAA	1860
20	ACCAGGTACA	AGGCATCTAT	TTTAACATTA	CCGCCATCTG	TCCAGATGGG	TCCAGAAAGC	1920
	CAGGCATGGA	AGGATGACAGA	AACGTGACGA	GCAATGATGA	AGTTCTTTTC	AATGTAACAG	1980
	TTACAATGAA	AAAATGTGAT	GTACACAGAG	GAAAAAATA	TGCAATAATC	AAACCTATTG	2040
	GT'TTAAATGA	AACCGCTAAA	ATTTCATATC	ACAGAACTG	CAGCTGTCTG	TGTGAGGACA	2100
	ACAGAGGACC	TAAAGGAAAG	TGTGTAGATG	AACTTTTCT	AGATTCCAAG	TGTTTCCAGT	2160
25	GTGATGAGAA	TAAATGTCAT	TTTGTGAAAG	ATCAGTTTTT	TTCTGAGAGT	TGCAAGTCAC	2220
	ACAAGGATCA	GCCTGTTTGC	AGTGGTCGAG	GAGTTTGTGT	TTGTGGGAAA	TGTTCTAGTC	2280
	ACAAAATTAA	GCTTGGAAAA	GTGTATGGAA	AATACTGTGA	AAAGGATGAC	TTTCTTGTCT	2340
	CATATCACCA	TGAAATCTGT	TGTGCTGGGC	ATGGAGAGTG	TGAAGCAGGC	AGATGCCAAT	2400
	GCTTCAGTGG	CTGGGAAGGT	GATCGATGCC	AGTGGCCCTTC	AGCAGCAGCC	CAGCACTGTG	2460
30	TCAATTCAAA	GGGCCAAAGTG	TGCGATGGAA	GAGGCACGTG	TGTGTGTGGA	AGGTGTGAGT	2520
	GCACCGATCC	CAGGAGCATC	GGCCGCTTCT	GTGAACACTG	CCCCACCTGT	TATACAGCCT	2580
	GCAAGGAAAA	CTGGAATTGT	ATGCAATGCC	TTACCCCTCA	CAATTTGTCT	CAGGCTATAC	2640
	TTGATCAGTG	CAAAACCTCA	TGTGCTCTCA	TGGAACAACA	GCATTATGTC	GACCAAACTT	2700
	CAGAATGTTT	CTCCAGCCCA	AGCTACTTGA	GAATATTTT	CATCATTTTC	ATAGTTACAT	2760
35	TCTTGATTGG	GTTGCTTAAA	GTCCCTGATCA	TTAGACAGGT	GATACTACAA	TGGAATAGTA	2820
	ATAAAATTAA	GTCTCTATCA	GATTACAGAG	TGTGAGCCTC	AAAAAAGGAT	AAGTTGATTG	2880
	TGCAAAAGTG	TTGCACAAGA	GCAGTCACCT	ACCGACGTGA	GAAGCCTGAA	GAATAAAAAA	2940
	TGGATATCAG	CAAAATTAAAT	GCTCATGAAA	CTTTCAGGTG	CAACTTCTAA	AAAAAGATTT	3000
	TTAAACACTT	AATGGGAAAC	TGGAATTGTT	AATAATTGCT	CCTAAAGATT	ATAATTTTAA	3060
40	AAGTCACAGG	AGGAGACAAA	TTGCTCACGG	TCATGCCAGT	TGCTGGTTGT	ACACTCGAAC	3120
	GAAGACTGAC	AAGTATCCTC	ATCATGATGT	GACTCACATA	GCTGCTGACT	TTTTTCAGAGA	3180
	AAAATGTGTC	TTACTACTGT	TTGAGACTAG	TGTCGTTGTA	GCACCTTACT	GTAATATATA	3240
	ACTTATTTAG	ATCAGCATAG	AATGTAGATC	CTCTGAAGAG	CACGTATTAC	ACTTACAGG	3300
	TACCTGTTAT	CCCTACGCTT	CCCAGAGAGA	ACAATGCTGT	GAGAGAGTTT	AGCATTTGTT	3360
45	CACATCAAGG	GTACAGTAA	CCCTGCACTG	GACATGTGAG	GAAAAAATA	ATCTGGCAAG	3420
	TATATTTCAA	GGTTGCCAAA	CACCTCAACA	GTTGGTGGTT	GAATAGACAA	GAACAGCTAG	3480
	ATGAATAAAT	GATTCGTGTT	TCACCTTTTC	AAGAGGTGAA	CAGATACAAC	CTTAATCTTA	3540
	AAAGATTATT	GCTTTTAA	GTGTGTAGTT	TTATGCATGT	GTGTTTATGG	TTTGCTTATT	3600
	TTTGCAAGAT	GGATACTAAT	TCCAGCATTC	TCTCCTCTTT	GCCTTTATGT	TTTGTTTCT	3660
50	TTTTTACAGG	ATAAGTTTAT	GTATGTCACA	GATGACTGGA	TTAATTAAGT	GCTAAGTTAC	3720
	TACTGCCATA	AAAAACTAAT	AATACAATGT	CACTTTATCA	GAATACTAGT	TTTAAAGCT	3780
	GAATGTTAA						

**A127 Protein sequence:**

Gene name: Integrin, beta 8  
 Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Protein Accession #: NP\_002205.1  
 Signal sequence: 1-39  
 Transmembrane domains: 682-704  
 EGF domain: 552-584  
 INB domain: 54-469  
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
70	MCGSALAFFT	AAFVCLQNDR	RGFASFLWAA	WVFSVLVLGLG	QGEDNRCASS	NAASCARCLA	60
	LGPECGWCVC	EDFISGGSR	ERCDIVSNLI	SKGCSVDSIE	YPSVHVIIPT	ENEINTQVTP	120
	GEVSIQLRRP	AEANFMLKVH	PLKKYPVDLY	YLVVDVSASMH	NNIEKLNSVG	NDLSRKMAFF	180
	SRDFRLGFGS	YVDKTVSPYI	SIHPERIHNQ	CSVDYNLDCMP	PHGYIHVLSL	TENITEFEKA	240
	VHRQKISGNI	DTPEGGFDM	LQAAVCESHI	GWRKEAKRLL	LVMTDQTSHL	ALDSKLAGIV	300
75	VPDNGNCHLK	NNVYVKSTTM	EHPSLGQLSE	KLIDNNINVI	FAVGKQFHW	YKDLLPLLP	360
	TIAGEIESKA	ANLNNLVVEA	YQKLISEVKV	QVENQVQGIY	FNITAIKCPDG	SRKPGMEGCR	420
	NVTSNDEVLF	NVTVTMKKCD	VTGGKNYAI	KPIGFNETAK	IHIHRNCSCQ	CEDNRGPKGK	480
	CVDETFLDSK	CFQCENKCH	FDEDQFSSES	CKSHKDQPV	SGRGVCVCGK	CSCHKIKLKG	540
	VYGKYCEKDD	FSCPYHHGNL	CAGHGECEAG	RQCQPSGWE	DRCQCPSSAA	QHCVNSKGV	600
80	CSGRGTCVCG	RCECTDPSI	GRFCEHCPTC	YTACKENWNC	MQCLHPHNLS	QAILDQCKTS	660
	CALMEQQHYV	DQTSECFSSP	SVLRIFFIIF	IVTFLIGLLK	VLIIRQVILQ	WNSNKIKSSS	720
	DYRVASASKD	KLILQSVCTR	AVTYRREKPE	EIKMDISKLN	AHETFRCNF		

**A128 DNA SEQUENCE**

Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942  
 Probeset Accession #: AA435577  
 Nucleic Acid Accession #: NM\_005756  
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5

```

1      |      |      |      |      |      |
10     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
15     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
20     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
25     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
30     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
35     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
40     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
45     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
50     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
55     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
60     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
65     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
70     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
75     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
80     |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |
      |      |      |      |      |      |

```

CTGACTTGTC TTGCAATAT TTCTTTTCTG ATTTATTTAA TTTTCTTGTA TTTATATGTT 4620  
 AAAATCAAAA ATGTTAAAAA CAATGAAATA AATTGTCAGT TAAGA

# A129 Protein sequence

Gene name: G protein-coupled receptor 64  
 Unigene number: Hs.184942  
 Protein Accession #: NP\_005747.1  
 Signal sequence: 1-38  
 GPS domain: 564-615  
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880  
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MVFSVRQCGH	VGRTEEVLIT	FKIFLVIICL	HVVLVTSLEE	DTDNSLSLSP	PAKLSVVSFA	60
PSSNEVETTS	LNDVTLSLLP	SNETEKTKIT	IVKTFNASGV	KPQRNICNLS	SICNDSAFFR	120
GEIMFYQDKE	STVPQNOHIT	NGTLTGVLIS	SELKRSELNK	TLQTLSETYF	IMCATAEAQS	180
TLNCTFTIKL	NNTMNACAAI	AALERVKIRP	MEHCCCSVRI	PCPSSPEELG	KLQCDLQDPI	240
VCLADHPRGP	PFSSSQSIPV	VPRATVLSQV	PKATSFAEPP	DYSPVTHNVP	SPIGEIQPLS	300
PQPSAPIASS	PAIDMPQOSE	TISSPMPQTH	VSGTPPPVKA	SFSPTVSAP	ANVNTTSAPP	360
VQTDIVNTSS	ISDLENQVLQ	MEKALSLGSL	EPNLAGEMIN	QVSRLHSP	DMLAPLAQRL	420
LKVVDIDIGLQ	LNFSNTTISL	TSPSLALAVI	RVNASSFNIT	TFVAQDPANL	QVSLETQAPE	480
NSIGTTILPS	SLMNNLPAHD	MELASRVQFN	FFETPALFQD	PSLENLSLIS	YVISSSVANL	540
TVRNLTRNRV	VTILKHINPSQ	DELTIVRCVFW	DLGRNGGRGG	WSDNGCSVKD	RRLNETICTC	600
SHLTSGVLL	DLSTSVLPA	QMMALTFITY	IGCGLSSIFL	SVTLVTYIAF	EKIRRDYPSK	660
ILILQCAL	LLNLVFLDLS	WIALYKMQGL	CISVAVFLHY	FLLVSTWMG	LEAFHMYLAL	720
VKVFNTYIRK	YILKFCIVGW	GVPVAVVTII	LTISPNDNYGL	GSYGKFPNGS	PDDFCWINNN	780
AVFYITVVGW	FCVIFLLNVS	MFIVVLVQLC	RIKKKKQLGA	QRKTSIQDLR	SIAGLTFLLG	840
ITWGFADFV	GPVNVTFMYL	FAIFNTLQGF	FIFIFYCVAK	ENVRKQWRRY	LCCGKLRLAE	900
NSDWSKTATN	GLKKQTVNQG	VSSSSNSLQS	SSNSTNSTTL	LVNNDCSVHA	SGNGNASTER	960
NGVSFSVQNG	DVCLHDFTGK	QHMFNEKEDS	CNGKGRMALR	RTSKRGSLSHF	IEQM	

# A130 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 ProbeSet Accession #: AA460530  
 Nucleic Acid Accession #: NM\_003667  
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
GTGGCGGCAA	CCGGCACCTC	AGTCCCCGCC	GCGCTTCTCC	TCGCCGCCCA	CGCCGTGGGG	60
TCAGGAACGC	GGCGTCTGGC	GCTGCAGACG	CCCGCTGAGT	TGCAGAAGCC	CACGAGCGGG	120
CGCCCGGCGC	GCCACGGCCC	GTAGCAGTCC	GGTGCTGCTC	TCCGCCCGCG	TCCGGCTCGT	180
GGCCCCCTAC	TTGGGGCACC	ATGGACACCT	CCCGCTCGG	TGTGCTCTGT	TCCTTGCTGT	240
TGCTGCTGCA	GCTGGCGACC	GGGGGCGAGT	CTCCAGGTC	TGGTGTGTTG	CTGAGGGGCT	300
GCCCCACACA	CTGTCATTGC	GAGCCCGACG	GCAGGATGTT	GCTCAGGGTG	GACTGCTCCG	360
ACCTGGGGCT	CTCGGAGCTG	CCTTCCAACC	TCAGCGTCTT	CACCTCCTAC	CTAGACCTCA	420
GTATGAACAA	CATCAGTCAG	CTGCTCCCGA	ATCCCTGCC	CAGTCTCCGC	TTCTTGAGAG	480
AGTTACTGCT	TGCGGGAAC	GCTCTGACAT	ACATTCCCAA	GGGAGCATTC	ACTGGCCTTT	540
ACAGTCTTAA	AGTTCCTTATG	CTGCAGAATA	ATCAGCTAAG	ACACGTACCC	ACAGAAGCTC	600
TGCAGAAATT	GCGAAGCCTT	CAATCCCTGC	GTCTGGATGC	TAACCACATC	AGCTATGTGC	660
CCCCAAGCTG	TTTCAAGTGC	CTGCATTCCC	TGAGGCACCT	GTGGCTGGAT	GACAAATGCGT	720
TAACAGAAAT	CCCCGTCCAG	GCTTTTAGAA	GTTTATCGGC	ATTGCAAGCC	ATGACCTTGG	780
CCCTGAACAA	ATATACACCAC	ATACCAGACT	ATGCCTTTGG	AAACCTCTCC	AGCTTGGTAG	840
TTCTACATCT	CCATAACACT	AGAAATCCACT	CCCTGGGAAA	GAAATGCTTT	GATGGGCTCC	900
ACAGCCTAGA	GACTTTAGAT	TTAAATTACA	ATAACCTTGA	TGAATCCCC	ACTGCAATTA	960
GGACACTCTC	CAACTTTAAA	GAACCTAGGAT	TTCATAGCAA	CAATATCAGG	TCGATACCTG	1020
AGAAAGCATT	TGTAGGCAAC	CCTTCTCTTA	TTACAATACA	TTTCTATGAC	AATCCCATCC	1080
AATTGTGTGG	GAGATCTGCT	TTTCAACATT	TACCTGAAC	AAGAACACTG	ACTCTGAATG	1140
GTGCTCACCA	AATAACTGAA	TTTCTTGATT	TAACTGGAAC	TGCAAACTCG	GAGAGCTCTGA	1200
CTTTAACTGG	AGCACAGATC	TCATCTCTTC	CTCAAACCGT	CTGCAATCAG	TTACCTAATC	1260
TCCAAAGTCT	AGATCTGTCT	TACAACCTAT	TAGAAGATTT	ACCCAGTTTT	TCAGTCTGCC	1320
AAAAGCTTCA	GAAAATTGAC	CTAAGACATA	ATGAAATCTA	CGAAATTAAA	GTTGACACTT	1380
TCCAGCAGTT	GCTTAGCCTC	CGATCGCTGA	ATTGGGCTTG	GAACAAAATT	GCTATTATTC	1440
ACCCCAATGC	ATTTTCCACT	TTGCCATCCC	TAATAAAGCT	GGACCTATCG	TCCAACCTCC	1500
TGTGCTCTTT	TCCTATAACT	GGGTACATG	GTTTAACTCA	CTTAAATTA	ACAGGAAATC	1560
ATGCCTTACA	GAGCTTGATA	TCATCTGAAA	ACTTTCAGAA	ACTCAAGGTT	ATAGAAATGC	1620
CTTATGCTTA	CCAGTGCTGT	GCAATTTGGAG	TGTGTGAGAA	TGCCTATAAG	ATTCTAATC	1680
AATGGAATAA	AGGTGACAA	AGCAGTATGG	ACGACCTTCA	TAAGAAAGAT	GCTGGAATGT	1740
TTCAGGCTCA	AGATGAACGT	GACCTTGAAG	ATTTCCTGCT	TGACTTTGAG	GAAGACCTGA	1800
AAGCCCTTCA	TTCAGTGCAG	TGTTACACCT	CCCCAGGCC	CTTCAAACCC	TGTGAACACC	1860
TGCTTGATGG	CTGCTGATC	AGAATTGGAG	TGTGGACCAT	AGCAGTCTCG	GCACTTACTT	1920
GTAATGCTTT	GGTGACTTCA	ACAGTTTTCA	GATCCCTCT	GTACATTTCC	CCATTAAAC	1980
TGTTAATTGG	GGTCATCGCA	GCAGTGAACA	TGCTCACGGG	AGTCTCCAGT	GCCGTGCTGG	2040
CTGGTGTGGA	TGCGTTCAT	TTTGGCAGCT	TTGCACGACA	TGGTGCCTGG	TGGGAGAATG	2100
GGGTGTGGTG	CCATGTCATT	GTTTCTTGT	CCATTTTGC	TTCAGAAATCA	TCTGTTTCC	2160
TGCTTACTCT	GGCAGCCCTG	GAGCGTGGGT	TCTCTGTGAA	ATATTTCTGCA	AAATTTGAAA	2220
CGAAAGCTCC	ATTTCTAGC	CTGAAAGTAA	TCATTTTGCT	CTGTGCCCTG	CTGGCCTTGA	2280
CCATGGCCGC	AGTTCCCTCG	CTGGGTGGCA	GCAAGTATGG	CGCCTCCCTG	CTCTGCCCTG	2340
CTTTGCCCTT	TGGGAGGCC	AGCACCATGG	GCTACATGGT	CGCTCTCATC	TTGCTCAATT	2400
CCCTTGCTCT	CCTCATGATG	ACCATTGCTT	ACACCAAGCT	CTACTGCAAT	TTGGACAAGG	2460

5 GAGACCTGGA GAATATTTGG GACTGCTCTA TGGTAAAACA CATTGCCCTG TTGCTCTTCA 2520  
 CCAACTGCAT CCTAAACTGC CCTGTGGCTT TCTGTGCTT CTCTCTTTA ATAAACCTTA 2580  
 CATTATATCAG TCTTGAAGTA ATTAAGTTTA TCCTTCCTGGT GGTAGTCCCA CTTCCTGCAT 2640  
 GTCTCAATCC CTTTCTCTAC ATCTTGTTCA ATCCTCACTT TAAGGAGGAT CTGGTGAGCC 2700  
 TGAGAAAGCA AACCTACGTC TGGACAAGAT CAAAACACCC AAGCTTGATG TCAATTAACT 2760  
 CTGATGATGT CGAAAAACAG TCCTGTGACT CAACTCAAGC CTTGGTAACC TTTACCAGCT 2820  
 CCAGCATCAC TTATGACCTG CCTCCAGTT CCGTGCCATC ACCAGCTTAT CCAGTGACTG 2880  
 AGAGCTGCCA TCTTTCTCT GTGGCATTTG TCCCATGTCT CTAATTAATA TGTGAAGGAA 2940  
 10 AATGTTTTCA AAGGTTGAGA ACCTGAAAAT GTGAGATTGA GTATATCAGA GCAGTAATTA 3000  
 ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

A131 Protein sequence

15 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Protein Accession #: NP\_003658.1  
 Signal sequence: 1-22  
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825  
 20 Cellular Localization: plasma membrane

25 1 11 21 31 41 51  
 | | | | | |  
 MDTSRLGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVL 120  
 LQNNQLRHVP TEALQNLRLSL QSLRLDANHI SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLSALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLLETLD 240  
 30 LNNYNLDEFP TAIRTLNLSK ELGFHSNNIR SIPEKAFVGN PSPLITIHPYD NPIQFVGRSA 300  
 FQHLPELRRL TLNGASQITE FPDLTGTANL ESLTLTGAQI SSSLQTVCNQ LPNLQVLDDL 360  
 YNLEDLPSF SVQCKLQKID LRHNEIYEIK VDTFQQLSL RSLNLAWNKI AIHPNAFST 420  
 LPSLIKLDLS SNLLSFPFIT GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPYAYQCC 480  
 AFGVCENAYK ISQWNKGDN SSMDDLHKKD AGMFQAQDER DLEDFLDLFE EDLKALHSVQ 540  
 CSPSPGPFPK CEHLDDGLWI RIGVNTIAVL ALTCNALVTS TVFRSPLYIS PIKLLIGVIA 600  
 35 AVNMLTGVS AVLAGVDAFT FGSFARHGAW WENGVGCHVI GFLSIFASES SVFLTLAAL 660  
 ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGE 720  
 STMGYMVALI LLNSLCFLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LLFTNCILNC 780  
 FVAFSLFSSL INLTFISPEV IKFILLVVVP LPACLNPLLY ILFNPFPKED LVSLRKQTYV 840  
 40 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900  
 VAFVPCFL

A132 DNA SEQUENCE

45 Gene name: parathyroid hormone receptor 2  
 Unigene number: Hs.159499  
 Probeset Accession #: U25128  
 Nucleic Acid Accession #: NM\_005048  
 Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 | | | | | |  
 GGCCGGTGGC CCGGCCCGGA CCACCCAGC TCGCGTCTGT TACTGGCCAC AAGTTTGCTC 60  
 TGGGCCAGCC AAGTTGGCAA CTTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120  
 55 TCTTCTTACA GCCGTCCGG GCATGGCCGG GCTGGGGCG TCGCTCCACG TCTGGGGTTG 180  
 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCAGCTG GATTCTGATG GCACCATTA 240  
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300  
 AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTGTGTT 360  
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATG CCTCCTTATA TTTATGACTT 420  
 60 CAACCATAAA GGAATGTGCT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480  
 CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCCT CGCTTCTGCG AGCCAGATAT 540  
 CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600  
 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCAT TGGTTACTTCA GACGATTGCA 660  
 TTGCACTAGG AACTATATCC ACATGCACTT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720  
 65 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780  
 AATAATGCAG GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCACAATA 840  
 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG 900  
 GATCTCTGGT GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTTCT TTTCCGACAC 960  
 70 CAAATACCTG TGGGGCTTCA TCTGTATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC 1020  
 ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TCCGAGGTGC TGGGAACCTA GTGCTGGAGA 1080  
 CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140  
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200  
 CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCCTGGTCC TAGTCTTTGG 1260  
 AGTGCAATTAC ATCGTGTTCG TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320  
 75 CGCATGTCAT TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TCTTTGTGTT CTATCATCTA 1380  
 CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440  
 CTCCGTGAGC TGGAAAAGGA CACCGCCATG TGGCAGCCGC AGATGCGGCT CAGTGCTCAC 1500  
 CACCGTGACG CACAGCACCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGCT 1560  
 TATCTCTGCG AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC 1620  
 80 TGGCTATGTC TGGAGTAAC TCAAGCAGGA CTGCCTGCCA CAGCTTTTCC ACGAGGAGAC 1680  
 CAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740  
 GGAATCTAAC CAGACACTG AAGGATGCCA AGGAGAACT GAGGATGTTT TCTGAATGGA 1800  
 CATTTGTGGC TGACTTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860  
 ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT 1920  
 TTTTAGGCTC CATGAATTGG CTCTGTGAAA TACTAACGCAC ATGAAAATGC AAGTGTCAT 1980

5 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 2040  
 GCTCTGTGAT TGTTCATTTT TTCTGTCTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100  
 GCTGTAGCTT TCTCTCATAT ATATCACCCCT AAATATAATG AAGATCTTTT AGTGTGTATC 2160  
 ATTTTCCTTT TAGAACTAG TATTCTCTTA TTCTTACTT TAATGTACTT CTATCACTGC 2220  
 ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280  
 GATCTAAGAA CAAGTACTTG CTGGAAATTT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340  
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAAG AATATTTCAC 2400  
 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACCTCTTTC 2460  
 10 TTCTTTGTAA ACCATGTCAT GTGGAAAGAT TTCCTCAGTT AGTGAGCTTG TGTCTGCAAA 2520  
 TTGATTTTGT TTGTAAATGA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTCTTG 2580  
 TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAATAATTT GTTTTAAAAA 2640  
 T

**A133 PROTEIN SEQUENCE**

15 Gene name: parathyroid hormone receptor 2  
 Unigene number: Hs.159499  
 Protein Accession #: NP\_005039.1  
 Signal sequence: 1-25  
 Pfam domain: 7tm\_2 [141-420]  
 20 Transmembrane domains: 177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419  
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51  
 | | | | |  
 MAGLGASLHV WGLWMLGSCL LARAQLSDG TITIEEQIVL VLKAKVQCEL NITAOQLEGE 60  
 GNCFPENDGL ICFPRGTVGK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA 120  
 NYSDCLRFLQ PDISIGKQEF FERLYVMYTV GYSISFGLA VAILIIGYFR RLHCTRNYYH 180  
 30 MHLEFVSFMLR ATSIFFVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240  
 VMPFIYFLATN YYWILVEGLY LHNLIFFVAFF SDTKYLWGFI LIGWGFPAAF VAAWAVARAT 300  
 LADARCWELS AGDIKWYQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK 360  
 LAKSTLVVLV VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFVVS IICYCNGEV 420  
 QAEVKMKWSR WNLSDVDNKRTP PCGSRRCGS VLTVTHTSTS SQSQVAASR MVLISGKAAC 480  
 35 IASRQPDSDI TLPGYVWSNS EQDCLPHSFH BETKEDSGRQ GDDILMEKPS RPMESNPDE 540  
 GCQGETEDVL

**A134 DNA sequence**

40 Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 | | | | |  
 ATGCTGTCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCAGG 60  
 GGAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCAGAG GCGAGGCAGC 120  
 GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 50 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240  
 CCGCGGCGCG CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCTT 300  
 CGCTTGCCTC CTGACAGTTC CCGGGGAGG GTCCGGTTCG CAGTGAACCC TCCAGAGGCT 360  
 TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCATC AGCGAGTGCA 420  
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 55 GCTCCTGGAC CTAGGGCCCG GCGTCGTGCG CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC 540  
 CCGCGCGGAA AGCGCCGCGG GACAGTCAGT GACGAGGCCG GGGGGTTCGC GGGGCCACGA 600  
 CTTCTCGGAG ACCGTCCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660  
 TGTGGGGGCG TCGCCGCTCG TCCGCTCCTT CATCTGGAA CGCCGCTTCG CTCCTGCAGC 720  
 TGCTGCTGGC TGCGCTGCTG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780  
 TGGCTGGACG CGCAGGGGCT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840  
 60 GCGGACGCCA CCATCTGCTG CCGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900  
 GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960  
 CGGGCGGACA AAGACGGGGC CCGACGGGCT GGCAGGGGCT CATGTCTTAG GGGTACCCAA 1020  
 GGAGACGGCG AGGGTGCGCC CCCACCCGTG AGGGCCTGGC AGCGGTGCTC CCCTGAAGGC 1080  
 TCCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCGCCGGGC TGCTGCCCGG TGCCAGACGC 1140  
 65 CGCGGATTCC CATCTTCTCC ACGCGGCGGC CCCTCTCCCC TGACGCGGCC CGCCTTGCCC 1200  
 ATCTACGTGC CGTTCCTCAT TGTGGGCTCC GTGTTGTGCG CCTTTATCAT CTTGGGGTCC 1260  
 CTGGTGGCAG CCTGTGCTG CAGATGTCTC CGGCCAAGC AGGATCCCCA GCAGAGCCGA 1320  
 GCCCCAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCAGTGTC CAGCACCTCC 1380  
 70 CGGGGGTCTG CCTCAGCCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCACTTCC 1440  
 GGGGCCCCGG CGCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCCGGA AGGGACCATG 1500  
 AACAACTGTG ATGTCAACAT GCCACGAAT TTCTCTGTGC TGAACGTGTA GCAGGCCACC 1560  
 CAGATGTGTC CACATCAAGG GCAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGCAG 1620  
 CACGACTCTG TGCCCATAGC AGCTGTGCCA CCTTTCATGG ACGGCCTGCA GCCTGGCTAC 1680  
 75 AGGCAGATTG AGTCCCCCTT CCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740  
 ACTGTATAAC CGAGAGTCAC TGGTGGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTCGAG GTGGAGTCTC GCACATGTCG GTGGTATTTA TGGCACGATT CTTTGGATG 1860  
 GCTTCATTGG CCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920  
 CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCCTC AGCTGGAGAT GACTGTGATG 1980  
 80 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040  
 AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100  
 TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTFTT 2160  
 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCCAGGC TGGAGTGCAG 2220  
 TGGTGCATC TGGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCAACA CTCCTGCCTC 2280  
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTT 2340

TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400  
 TCTGCCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460  
 TGAGCCTTTT TTTTCTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520  
 ATTCTAAAAG GAAACCTGTT TGAACCTCTG GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580  
 GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640  
 GGGCCTATTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTCTTACA 2700  
 TTAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760  
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCATTT CATCCCCTTC 2820  
 TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCCTTTT 2880  
 TATATTGAAA TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940  
 TGGTTATGGT TTGGCGTTTC CTTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCTC 3000  
 GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060  
 AAAAAATTTT TTGCTCTAGT TATAAAATTT CAAAGAAATG TGTTACAAAG ATACTTAGTA 3120  
 TAGTCTCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTTT 3180  
 GCAGATCATA AGGCTTTTTT TACTCTTGTT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240  
 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCTTTT CTTCTCCAC ACTGTTCTTG 3300  
 ATTTCTCTC TCTTTCAGGC CTCACAGGC ACTGTATTCA TTGCCAATGT TCCAATTTAT 3360  
 CAAATTCAG TGAATTTATT TGTGTGTTCT TTAATTATAT AAAAAAGAT AACTTTAAGG 3420  
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAATCGCT 3480  
 GTATGGTATG GTCTTCTACA CATTATATGC TATAGATATC TATCGATCAT CTTTCTATTC 3540  
 TGTTTTATGA CTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600  
 TTTTAAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660  
 TGAAAAAATA AAAAAAATA AAAAAAATA

# A135 Protein sequence

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

1 11 21 31 41 51  
 MLSGFLMSPS TQHRAQYTPG GKKLPEWASI GAHTSRGRGS DRERESRPEA AGLLDWRAAA 60  
 GEAEKGNRGE PPAAWIRAQQ PRPPPAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPEA 120  
 SGRQPRGSD CIPRFPSASA THKAVPKGTG PPAEDGDGLG AFGPRARRRR LLGVAAEGSG 180  
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAFVRVP CGALAARPS HPGTPLRSCS 240  
 CCWLRCWRRG RGPSGEYCHG WLDAQGVWRI GFQCPERFDG GDAITCCGSC ALRYCCSSAE 300  
 ARLDQGGCND DRQQGAGEPG RADKDGPRRL GRASCLRGTD GDGEGAPPV RAWQRCSPG 360  
 SPKGRQLLRA PFGLLFRARR RGFPSSPRGG PSPLQRPALP IYVPLIVGS VFVAFIILGS 420  
 LVAACCCRLC RKQDPQQR APGGRNLMET IPMIPASST RGSSSRQSSS AASSSSSANS 480  
 GARAPPTRSQ TNCCLEPEGTM NNVVYVNMPTN FSVLNCQQAT QIVPHQGGYL HPPYVGYTVQ 540  
 HDSVPMATAVP PFMDGLQPGY RQIQSPFPH T NSEQMYPAPV TV

# A136 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTA AGAGAGTGA 60  
 GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120  
 CAGCAAAGGT ACACACACCT GGTGCAATT CAAACCAAAG AAGAGATTGA GTACCTAAAC 180  
 TCCATATTGA GCTATTACAC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACATGTG 240  
 TGGGTCTGGG TAGGAAACCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300  
 GAACCAACA ATAGGCCAAA AGATGAGGAC TGGCTGGAGA TCTACATCA GAGAGAAAA 360  
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420  
 GCTGCTGTGA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480  
 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAAT TGTGAAGTGT 540  
 ACAGCCCTGG AATCCCTCTG GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAACTTTC 600  
 AGCTACAATT CTTCCCTGCT TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660  
 ACCATGCAGT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720  
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTTGGA 780  
 AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTGTA ACTAATGGGA 840  
 GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900  
 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960  
 CCTGCTGGAG AGTTCACTCT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020  
 TTGAGGGAG CAGCCAGGT TGAATGCACC ACTCAAGGCG AGTGGACACA GCAAAATCCA 1080  
 GTTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAAACCCG AGCGAGGCTA CATGAATTGT 1140  
 CTTCTAGTGT CTTCTGGCAG TTTCCGTAT GGGTCCAGCT GTGAGTCTC CTGTGAGCAG 1200  
 GGTTTTGTGT TGAAGGGATC CAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260  
 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320  
 GTGAGGTGTG CTCATTCCCC TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCCCTTCAG 1380  
 TGTGAGGAGG GATTGGAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440  
 TGGACAGAAG AGGTTCCTTC CTGCCAAGTG GTAAATGTT CAAGCCTGGC AGTTCGGGA 1500  
 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGCA CTGTGTGCAA GTTCGCTGT 1560  
 CCTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTCGACAT GTGGAGCCAC AGGACACTGG 1620  
 TCTGGCCTGC TACTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680  
 CTTTCTGCTG CTGGACTCTC CCTCTGACA TAGCACCAT TTCTCTCTG GCTTCGGAAA 1740

TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800  
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

# A137 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)  
Unigene number: Hs.89546  
Probeset Accession #: M24736  
Protein Accession #: NP\_000441  
Signal sequence: 1-22  
Transmembrane domains: 555-573  
C-lectin domain: 23-139  
Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QORYTHLVAI QNKKEIEYLN 60
SILSYSPSYW WIGIRKVN NV WVVVGTKQKL TEEAKNWAPG EFNNRQKDED CVEIYIKREK 120
DVGWMWDERC SKKKLALCYT AACTNTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
ECDAVTNPAN GFVECFQNP G SFPWNTTCTF DCEEGFELMG AQSLQCTSSG NWDNEKPTCK 300
AVTCRAVRQP QNGSVRC SHS PAGEFTFKSS CNFTCEE GFM LQGPAQVECT TQGQWTQQIP 360
VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GFVLKGSKRL QCGPTGEWDN 420
EKPTCEAVRC DAVHQPPKGL VRCAHSPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
WTEEVPSQCV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHV 540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLLWLRL CLRKAKKFVP ASSCQSLESD 600
GSYQKPSYIL

```

# A138 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
Nucleic Acid Accession #: AA487468  
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTTGGGTCT CTGCTCTCTTA CTCGTCACAG TTTCTTCCAA CCTTGCCATT 120
GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
ATGGTTATTC ATCACTGGA G GATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGTC 300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
GACCCCTTCT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
TATGAGCCTC GGGATTTACC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTCA 600
GAAGAAAAAC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAAT 660
T TACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

```

# A139 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
Protein Accession #: none found  
Signal sequence: 1-23  
Transmembrane domains: none found  
Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTL SRGWGD DITWVQTYEE GLFYAQKSKK 60
PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFI MLNL MHETTDKNLS PDGQYVPRIM 120
FVDP SLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

```

# A140 DNA SEQUENCE

Gene name: TMPRSS3a  
Unigene number: Hs.298241  
Probeset Accession #: AI538613  
Nucleic Acid Accession #: AB038157  
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTCA TGCCC GTGTGAGCCA 60
GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACTGTGGC CTACTATCTC TTCCGTGGTG 120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCCGATGTC 180
AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240

```



TCATTCCGAT CGCTTTTGG CCTGTGATGAT TTGAAAATAA GTCCTGTTGC ACCAGATGCA 300  
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 5 TCAGGGAAGT ACAGATGTCT CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAGA CCATGTGCTC CGATGACTGG 600  
 AAGGTCACCT ACGCAATGT TGCCTGTGCC CAACTGGGT TCCCAAGCTA TGTGAGTTCA 660  
 10 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTG GCCACCTGGT TACCTTGCA GGCACAGCCT GTGGTCATAG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900  
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCCT GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTA TGACTTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 15 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTGG TGGAGAAGAT TGTCTACCAC 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140  
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC 1200  
 GATGGAAGA TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260  
 TCCCTGTCT TGAACACGCG GGCCGTCCCT TTGATTCCA ACAAGATCTG CAACCAACAG 1320  
 20 GACGTGTACG GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380  
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG GAGCGACCA CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500  
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560  
 ACCTGAAGAG GAAGGCCACC AGTAGCCACC TGAGTTCTTG AGGTGATGAA GACAGCCCGA 1620  
 25 TCCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCTTG GAGCTCTGAG 1680  
 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCCTCCA TCTGATCCA GCACAACCTT 1740  
 CRAAGTGCCT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800  
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860  
 TTTCCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACACACC CAACTAATT 1920  
 30 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980  
 CCTCAAATGA TGTGCTGCT TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGGCCACC 2040  
 ACGCCCTAGC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100  
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160  
 ACGAGATAAG CAGTTATGTG ACCTCAGCTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220  
 35 GCACCAAGCC AGAAGTGACG AACTGCAGTC ACTGCAGTT TTCTCTCTA GGGACCAGAA 2280  
 CCAACCAACC CCTTCTACT TCCAAGACTT ATTTTCACAT GTGGGAGGT TAATCTAGGA 2340  
 ATGACTCGTT TAAGGCCTAT TTTCTGATG TCTTGTAGC ATTTGTGCT TGACGTATTA 2400  
 TTGTCCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAAAA

#### A141 Protein sequence:

Gene name: TMPRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 45 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPc domain: 216-444  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLEPLKFFP IIVIGIIALI 60  
 55 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVIVQV 120  
 TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180  
 VTALHHSYVY REGCASGHV VTLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240  
 LCGGSVITPL WIITAACVYI DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGA GDASPVNLHA 360  
 60 AVPLISNKIC NHRDVGGLII SPSMLCAGYL TGGVDSQCQD SGGPLVCQER RLWKLVGATS 420  
 FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT

#### A142 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 65 Probeset Accession #: AA314779  
 Nucleic Acid Accession #: none found  
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CCAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60  
 75 CTGAGATCCT TGCCTAGACT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120  
 CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180  
 AGACCCAGCT GTGCTCTGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTAATCTCAGG 240  
 AAGCTGAGGA ACTGGTCTGA TGCCGAGCTC GAGTGTCACT CTACGGAAA CGGAGCCAC 300  
 CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360  
 80 CAGAGAAGCC AGCCGATAG GATTGGCCTG CACGACCCAC AGAAGAGGCA GCAGTGGCAG 420  
 TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480  
 AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTTAA CTTGGAGCAG CAACGAATGC 540  
 AACAAAGGCC AACACTTCCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600  
 AACTCTCGCA CAGCAGCCGT CCTCTTCCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660  
 TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GCCTTTTTTA 720

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

GGCTTAGAGA CAGAAACTTT AGCATTGGGC CCAGTAGTGG CTCTAGCTC TAAATGTTTG 780
CCCCGCCATC CCTTTCACCA GTATCCTTCT TCCCTCCTCC CCTGTCTCTG GCTGTCTCGA 840
GCAGTCTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900
AAAGATTGTA AGACAGAAGG AAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
ACACCCCTCT GCCCTCTCTC CATTGCCTGC ACCCCACCCC AGCCACTCAA CTCCTGCTTG 1020
TTTTTCCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTG ATGTGGGCCA 1080
TACATTCTTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA
  
```

#### A143 Protein sequence:

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Protein Accession #: none found  
 Signal sequence: 1-22  
 Transmembrane domains: none found  
 C-type lectin domain: 47-156  
 Cellular Localization: secreted

```

1      11      21      31      41      51
MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWFYHKS N CYGYFRKLRN WSDAELECCS 60
YNGNAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG 120
KSMGKNKHCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP
  
```

#### A144 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

```

1      11      21      31      41      51
GCGGAACACC GCGCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
TCCTCGTGCG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGC CGCG 120
CCTCCGAGCC GTCCCGGGCG GTCTTCAGGG AGGCTGAAAGT GACCTTGGAG CGCGGAGGCG 180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
AAAGAAGGCT ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAA GGCAAGGGTC 420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
ACAGCATCAC GGGGCCGGGG SCAGACAGCC CCCCTGAGGG TGCTTTCGCT GTAGAGAAGG 540
AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA 660
TCATCGTGAC CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
AGGACCCACA CGACCTCATG TTCACAATT CACCGAGCAC AGGCACCATC AGCGTCATCT 900
CCAGTGGCCT GGCACGGGAA AAGTCCCTTG AGTACACACT GACCATCCAG GCCACAGACA 960
TGGATGGGGA CGGTCTCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
ACAATGCTCC CATGTTTGAC CCCCAGAAGT ACGAGGCCCA TGTGCCTGAG AATGCAGTGG 1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC 1140
GTGCCACCTA CCTTCTACTG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
AGCACACCCT GTACGTTGAA GTGACCAACG AGGCCCCCTT TGTGCTGAAG CTCCCAACCT 1320
CCACAGCCAC CATAGTGTGC CACGTGGAGG ATGTGAATGA GGCACTGTG TTTGTCCAC 1380
CCTCCAAAGT CGTTGAGTGC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
CTGCAGAAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500
CAGGTTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTAC AGCTGTGGGC ACCCTCGACC 1560
GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGAGA 1620
ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAGC CCTGTGCGCC 1740
ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCCCTTC CAGGCCAGC 1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG 1920
ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
ATGTGGAAC CTGCCCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTT GGTGAGAAAG AAGCGGAAGA 2100
TCAAGGAGCC CCTCCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160
AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
AGGCCAGGCG GGAGGTGTTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
AGGCGGTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTGGTG TTCGACTATG 2400
AGGCGAGCGG CTCGACGCC GCGTCCCTGA GCTCCCTCAC CTCCCTCGCC TCCGACCAAG 2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGCTT CAAGAAGCTG GCAGACATGT 2520
ACGGTGGCGG GGAGGACGAC TAGGCGGCCCT GCCTGCAGGG CTGGGGACCA AACGTCAGG 2580
CACAGAGCAT CTCCAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTC 2640
GGAAGTGGCC GTAGCAACTT GCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760
CACCTGGGCC AGGGTTCCTC CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820
TGCTCAACCC TGTGTCTTGG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTCTCT 2880
CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940
  
```

TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAGA GCTGCTGGGC CCACTGGCCG 3000  
 TCCTGCATT CTGGTTTCCA GACCCCAATG CCTCCCATTG GGATGGATCT CTGCGTTTTT 3060  
 ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CCTGTGCGT TGCTATAGAT 3120  
 GAAGGGTGAG GACATCGTG TATATGTACT AGAAGTTTTT TATTAAAGAA A

**A145 Protein sequence:**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675

Cellular localization: plasma membrane

1 11 21 31 41 51  
 MGLPRGPLAS LLLQLVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIPPSKR ILRRHKRDWV VAPISVPENG 120  
 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK 180  
 YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGLVP GTSVMQVTAT 240  
 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAVHPEN AVGHEVQRLT VTDLDAPNSP 360  
 AWRATYILMG GDDGDHFTTT THPESNQGL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPSPKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLTLTLID 540  
 VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPHSTSPFQ AQLTDDSDIY WTAEVNNEEGD 600  
 TVVLSLKKFL KDPTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660  
 GAVLALLFL LLLLLLVRKK RKIKEPLLLP EDDTRDNVfy YGEEGGGEED QDYDITQLHR 720  
 GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIIIE NLKAANTDPT APPYDITLLVF 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

**A146 DNA SEQUENCE:**

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Nucleic Acid Accession #: NM\_003318  
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GGAATTCCTT TTTTCTTTT TTTGAGATGG AGTTTCACTC TTGTTGGCCA GGCTGGAGTG 60  
 CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCCTCCCG GGTTCAGCG ATTCTCCTGC 120  
 CTGAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT 180  
 CTTTCTTCTT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240  
 ACCTCAGGTG ATCCACTTGC CTTGGCCTCC CAAAGTGCTA GGATTACAGC CGTGAAACTG 300  
 TGCTCGGCTG ATTCTTTTTT TGTGTTGGA TTTTGAAGC AGGGTCTCCC TTGGTCGCCC 360  
 AGGCTGGAGT GCAGTGGTGC GATCTTGGCT CACTATAACC TCCACCTCCT GGTTCAGAGT 420  
 GATCCTCCCA CTTTAGCCTC CTGAGTAGCT GTGATTACAG GCGTGACCCA CCACACCCGG 480  
 CTAATTTTGT TATTTTCTT AGAGACAGGG TTTCAACATG TTGGCCAGGC TGTCTCTCAA 540  
 CTCCTGGACT CAAGGGATCC GCCTGCCTCC ACTTCCCAAA GTCCCGAGAT TACAGGTGTG 600  
 AGTCACCATG CCGTACCTTA TAATTTCTAA GTCAATTTTT CTGGTCCATT TCTTCCTTAG 660  
 GGTCTCACA AACTATCTGC ATTAGGCGGT ACAATAATCC TTAACCTCAT GATTACAAAA 720  
 AGGAAGATGA AGTGATTCAT GATTAGAAA GGGGAAGTAG TAAGCCCACT GCACACTCCT 780  
 GGATGATGAT CCTAAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAAA 840  
 TTTGGTTTAA ATTAATTATC TAAATATCTA AAAACATTTT TGGATACATT GTTGATGTGA 900  
 ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCCAG 960  
 TGCAGTTTTC TGTAAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACAATTGATT 1020  
 CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG 1080  
 AACTAAGCTT GAATAAAATT TCTGCTGATA CTACAGATAA CTCGGGAAGT GTTAACCAAA 1140  
 TTATGATGAT GGCAACAAC CCAGAGGACT GGTGAGTTT GTTGCTCAAA CTAGAGAAAA 1200  
 ACAGTGTTC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTCGTAC AGTCAAGCAA 1260  
 TTGAAGCGCT TCCCCAGAT AAATATGCC AAAATGAGAG TTTTGCTAGA ATTCAAGTGA 1320  
 GATTTGCTGA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAAATGG 1380  
 CCAGAGCAAA CTGCAAGAAA TTTGCTTTTG TTCTATATATC TTTTGACAAA TTTGAACTGT 1440  
 CACAAGGTAA TGTCAAAAAA AGTAAACAAC TTCTTCAAAA AGCTGTAGAA CGTGGAGCAG 1500  
 TACCACTAGA AATGCTGGA ATTGCCCTGC GGAATTTTAA CCTCCAAAAA AAGCAGCTGC 1560  
 TTTCAGAGGA GGAAGAAGAG AATTATCAG CATCTACGGT ATTAACCTGCC CAAGAATCAT 1620  
 TTTCCGGTTC ACTTGGGCAT TTACAGAATA GGAACAACAG TTGTGATTCC AGAGGACAGA 1680  
 CTACTAAAGC CAGGTTTTTA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT 1740  
 ACCGGAATTC ATTAGACAAA ACTAACAAA CTAAACAGTC ATGCCCATTT GGAAGAGTCC 1800  
 CAGTTAAGCT TCTAAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGATACCT 1860  
 GTTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGGTTGTG CCTGGATCTA 1920  
 AACCAGTGG AAATGATTCC TGTGAATTAA GAAATTTTAA GTCTGTTCAA AATAGTCATT 1980  
 TCAAGGAACC TCTGGTGTCA GATGAAAAGA GTTCTGAAC TATTATTACT GATTCAATAA 2040  
 CCCTGAAGAA TAAACCGGAA TCAAGTCTTC TAGCTAAATT AGAAGAAACT AAAGAGTATC 2100  
 AAGAACCAGA GGTTCAGAG AGTAACCAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT 2160  
 GTATTAAACA GAATCCTGCT GCATCTTCAA ATCACTGGCA GATTCGGGAG TTAGCCCGAA 2220  
 AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTTCA GTTTCAAAAC 2280  
 AGTCAACACC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTGTG AAGACACCAA 2340

GCAGCAATAC CTTGGATGAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGAATGACT 2400  
 TTCCACCTGC TTGTTCAGTTG TCAACACCTT ATGGCCAACC TGCCTGTTTC CAGCAGCAAC 2460  
 AGCATCAAAT ACTTGGCCACT CCACTTCAAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA 2520  
 ATGAATGCAT TTCGGTTAAA GGAAGAATTT ATTCATATT AAAGCAGATA GGAAGTGGAG 2580  
 GTTCAAGCAA GGTATTTTCAG GTGTTAAATG AAAAGAAACA GATATATGCT ATAAAAATATG 2640  
 TGAACCTAGA AGAAGCAGAT AACCAACTC TTGATAGTTA CCGGAACGAA ATAGCTTATT 2700  
 TGAATAAACT ACAACAACAC AGTGATAAGA TCAATCCGACT TTATGATTAT GAAATCACGG 2760  
 ACCAGTACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAAA 2820  
 AGAAAAAATC CATGTATCCA TGGGAACGCA AGAGTTACTG GAAAAATATG TTAGAGGCAG 2880  
 TTCACACAAT CCATCAACAT GGCATTGTTT ACAGTGATCT TAAACCAGCT AACTTTCTGA 2940  
 TAGTTGATGG AATGCTAAAG CTAATTGATT TTGGGATGTC AAACCAATG CAACCAGATA 3000  
 CAACAAGTGT TGTAAAGAT TCTCAGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3060  
 TCAAAAGATAT GTCTTCCCTC AGAGAGAATG GGAATCTAA GTCAAGATA AGCCCCAAAA 3120  
 GTGATGTTTG GTCTCTAGGA TGTATTTTGT ACTATATGAC TTACGGGAAA ACACCATTTT 3180  
 AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAATTG 3240  
 AATTTCCCGA TATTCCAGAG AAAGATCTTC AAGATGTGTT AAAGTGTGTT TTA AAAAGGG 3300  
 ACCCAAAACA GAGGATATCC ATTCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA 3360  
 CTCATCCAGT TAACCAATG GCCAAGGGA CCACTGAAGA AATGAATAT GTTCTGGGCC 3420  
 AACTTGTTGG TCTGAATTCT CCTAATCCCA TTTGAAAGC TGCTAAACT TTATATGAAC 3480  
 ACTATAGTGG TGGTGAAGT CATAATTCTT CATCTCCAA GACTTTTGAA AAAAAAGGG 3540  
 GAAAAAATG ATTTGCAATT ATTCTGAATG TCAGATAGGA GGTATAAAAT ATATTGGACT 3600  
 GTTATACTCT TGAATCCCTG TGGAAATCTA CATTTGAAGA CAACATCACT CTGAAGTGTT 3660  
 ATCAGCAAAA AAAATCTAGT GAGATTATCT TTAAAGAAA ACTGTAAAA TAGCAACCAC 3720  
 TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAACTAC 3780  
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATCTA AAAAACTTG 3840  
 TAAATAAAGT TTTGTGGCTA AAATGA

**A147 Protein sequence:**

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Protein Accession #: NP\_003309  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51  
 MNKVRDIKNN FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLLKLEKNS 60  
 VPLSDALLNK LIGRYSAIE ALPPDKYQGN ESFARIQVRF AELKATQEPD DARDYFQMAR 120  
 ANCKKFAFVH ISFAQFELSQ GNVKKSQQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180  
 EEEKKNLSAS TVLTAQESFS GSLGHLQNRN NSCDNRGQTT KARFLYGENM PPQDAEIGYR 240  
 NSLRQTNKTK QSCPFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPGSKP 300  
 SGNDSCBLRN LKSVQNSHFH EPLVSDKSS ELIITDSITL KNKTESLLA KLEETKEYQE 360  
 PEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHTTFE QPVFVSQKQS 420  
 PPISTSKWFD PKSICKTPSS NTLDDVMSCF RTPVVKNDFF PACQLSTPYG QPACFQQQOH 480  
 QILATPLQNL QVLASSANE CISVKGRIS ILKQIGSGGS SKVFQVINEK KQIYAIKYVN 540  
 LEEADNQLD SYRNEIAYLN KLQHQSDKII RLYDYBITDQ YIYVMMECGN IDLNSWLKKK 600  
 KSIDPWERKS YWKNMLEAVH TIHQHGIVHS DLKPANFLIV DGMLKLIDFG IANQMOPDIT 660  
 SVVKDSQVGT VNYMPPEAIK DMSSSRENGK SKSKISPKSD VWSLGCILYV MTYGKTPFQ 720  
 IINQISKLHA IIDPNHEIEF PDIPEKDLQD VLKCCCLKRDP KQRISIPELL AHPYVQIQTH 780  
 PVNQMAKGT EEMKYVLGQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRGK 840  
 K

**A148 DNA SEQUENCE**

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
 Unigene number: Hs.258583  
 Probeset Accession #: NM\_012152  
 Nucleic Acid Accession #: NM\_012152  
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CTTCTTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60  
 GACAAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTCTGA TGAAGTGACA 120  
 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTT TCTGCCTGTT TATTTTCTTT 180  
 TCTAATTCTC TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCAATT CCCCTTCTAC 240  
 TACCTGTTGG CTAATTTTAC TGCTGCCGAT TTCTTCGCTG GAATGCGCTA TGTATTCTCTG 300  
 ATGTTTAAACA CAGGCCCACT TTCAAAACT TTGACTGTCA ACCCGTGGTT TCTCCGTCAG 360  
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT GCGCGTGAG 420  
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480  
 CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTATATG GGGCGGTCCT CACACTGGGC 540  
 TGGAAATTGCC TCTGCAACAT CTCTGCCCTG TCTTCCCTGG CCCCATTATA CAGCAGGAGT 600  
 TACCTTGTTT TCTGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGTGATC 660  
 CTGCGGATCT ACGGTGACGT CAAGAGGAAA ACCAACGTCT TGTCTCCGCA TACAAGTGGG 720  
 TCCATCAGCC GCCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780  
 GCGTTTGTGG TATGCTGGAC CCCGGGCTCG GTGGTCTGTC TCCTCGACGG CCTGAAGTGC 840  
 AGGCAGTGTG GCGTGCAGCA TGTGAAAGG TGGTTCCTGC TGCTGGCGCT GCTCAACTCC 900  
 GTCGTGAACC CCATCATCTA CTCCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960  
 ATGATCTGCT GCTTCTCTCA GGAGAACCAC GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020  
 GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080

GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGGCCACCCA GGTGATGACT 1140  
GTCTTAGG

5

A149 Protein sequence:

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
Unigene number: Hs.258583  
Probeset Accession #: NM\_012152  
Protein Accession #: NP\_036284  
Signal sequence: none found  
Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295  
Cellular Localization: plasma membrane

10

15

1	11	21	31	41	51	
MNECHYDKHM	DFFYNRSNTD	TVDDWTGTKL	VIVLCVGTFF	CLFIFFSNLS	VIAAVIKNRK	60
PHFPFYLLA	NLAAADFFAG	IAYVFLMFNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
LVIAVERHMS	IMRMVRHNSL	TKKRVTLIL	LVWAIAIFMG	AVPTLGWNCL	CNISACSSLA	180
PIYSRSYLVE	WTVSNLMAFL	IMVVVYLRIY	VYVKRKINVL	SPHTSGSISR	RRTPMKLMKT	240
VMTVLGAFVV	CWTPGLVLL	LDGLNCRQCG	VQHVKRWFLL	LALLNSVVP	IIYSYKDEDM	300
YGTMKMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK	STS	

20

25

ProstateA150 DNA SEQUENCE

Gene name: ESTs  
Unigene number: Hs.293616  
Probeset Accession #: AW043782  
Nucleic Acid Accession #: none found  
Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

30

35

1	11	21	31	41	51	
AGCAACGACG	CGGGGACGCG	GGAGCGGCGG	CGCGGCCATG	TGGCTGCTGG	GGCCGCTGTG	60
CCTGCTGCTG	AGCAGCGCCG	CGGAGAGCCA	GCTGCTCCCC	GGGAACAACT	TCACCAATGA	120
GTGCAACATA	CCAGGCAACT	TCATGTGCAG	CAATGGACGG	TGCATCCCGG	GCGCCTGGCA	180
GTGTGACGGG	CTGCCTGACT	GCTTCGACAA	GAGTGATGAG	AAGGAGTGCC	CCAAGGCTAA	240
GTGGAATATG	GGCCCAACCT	TCTTCCCTGT	TGCCAGCGCG	ATCCATTGCA	TCATTGGTGC	300
CTTCCGGTGC	AATGGGTTTG	AGGACTGTCC	CGATGGCAGC	GATGAAGAGA	ACTGCACAGC	360
AAACCCCTCT	CTTTGCTCCA	CGCCCCGCTA	CCACTGCAAG	AACGGCCTCT	GTATTGACAA	420
GAGCTTCATC	TGCGATGGAC	AGAATAACTG	TCAAGACAAC	AGTGATGAGG	AAAGCTGTGA	480
AAGTTCTCAA	GAACCCGGCA	GTGGGCGAGT	GTTTGTGACT	TCAGAGAACC	AACTTGTGTA	540
TTACCCGAGC	ATCACCTATG	CCATCATCGG	CAGCTCCGTC	ATTTTTGTGC	TGGTGGTGGC	600
CCTGTGCGCA	CTGGTCTTGC	ACCACCAGCG	GAAGCGGAAC	AACCTCATGA	CGCTGCCCCG	660
GCACCGGCTG	CAGCACCCCT	TGCTGCTGTC	CGCCTGGTGC	GTCTTGGAAC	ACCCCAACCA	720
CTGCAACGTC	ACCTACAACG	TCAATAATGG	CATCCAGTAT	GTGGCCAGCC	AGGCGGAGCA	780
GAATGCGTCG	GAAGTAGGCT	CCCCACCCCT	CTACTCCGAG	GCCTTGCTGG	ACCAGAGGCC	840
TGCGTGGTAT	GACCTTCCTC	CACCCGCCCTA	CTCTTCTGAC	ACGGAATCTC	TGAACCAAGC	900
CGACCTGCCC	CCCTACCGCT	CCCGTCCCGG	GAGTGCCAAC	AGTGCCAGCT	CCCAGGCAGC	960
CAGCAGCCTC	CTGAGCGTGG	AAGACACCAG	CCACAGCCCG	GGGACGCTCG	GCCCCCAGGA	1020
GGGCACTGCT	GAGCCCAGGG	ACTCTGAGCC	CAGCCAGGGC	ACTGAAGAAG	TATAAGTCCC	1080
AGTTATTCCA	AGTCCATAT	GGGTTAATCT	GCTCTGACTT	GTGCAATTC	TAACATTTG	1140
TGCTCATGGG	AAGCTCTTTA	AGCACTGTGA	AGGATGTCTC	AAGTTACAGT	TTGGGATATT	1200
AACTATCTCT	GCATTCCTCT	CCTCCCCCAG	ACTTCAGAGA	TGTTTTCTGT	GCGTCTCAGT	1260
TGACATGATC	TGTTGTGCGT	CTTTTCTGTC	AGGTCACTCT	TCCCTTGGGA	CCCGAGATCA	1320
CACCCCTATT	TTTCACATTA	TTCTGTTTCT	GTGGGAGAGA	CAGCATATAA	AACAGTATTG	1380
AAATAGGCTG	GGAGAGAGCA	ATGTTTCTGT	GCTATATTGG	ATGCTCAGAA	GTGCAGGAGA	1440
CGCTGGACCC	AATTCTCTCT	GCTGGGTAGT	TACCTTATAG	CATTTGGGGA	TTGGGTTAG	1500
ATGATCTAAC	CAGGAGGCCA	TCACTGGATG	GTCAACCCCG	CAAAAAAATT	CCATTTGAGC	1560
ATCAAAACCT	GCTTTGCACA	ATCCTATTGG	ATGCCCCCG	TTCAAGAGAG	TCAGTGGCCA	1620
AAGAAAACCT	TGGACGTGAG	TAACACCCCT	CAGCAGTCGC	AACGTTATT	TGGTTTGTG	1680
AAGGACTCTG	AAACCATCTA	CCCTGTATAA	ATTCTGGCTT	TAGAAATTTG	CCCAAGAAATG	1740
CTCATCTCTG	GAGCTTTCCT	CAGCAGCATA	TATCATCAGC	CTCATCTTAA	AATAGGCAGG	1800
GAGCCCCCTC	CATGAGTTTA	TCCAAGTTCT	CAGCTCCTAA	AATGCAGGCT	GCCCAAGACC	1860
TACACCTGCC	CTGGCTCTAC	AGCCACTTAC	CTGGTTTCTG	GACTGTCAAC	CTCCAGCTG	1920
ACCTGCCCGT	AGCCAAGGAA	TGAGGACCTA	ACTTGAGTTG	GCCCAAGTCT	TGACCTGGCT	1980
GTATGTCCCT	GTGGCCACCA	CCCAGCCTGT	CTTGCTCATT	CATGCAGCCT	CAACACTGGC	2040
CTCCAAAGTT	CCCTTAAAC	TTGCAAGATC	CTTTTACCT	GTGCAATTGG	ACTTGAGGAC	2100
ACTGGTTTCT	ATCACAGGTG	AGAGCCATGT	TCAATACCTC	CAGCAAGCTC	TCCTGGCTCC	2160
CTGCACTGTG	CAGCTCTCTC	TTCCCAAGGT	CCCAATACCA	GCACCTCTAG	TTAGAGTTAG	2220
GGTCAGGGTC	AGGCCTCTCC	CAACATCCCA	GTAGTTTCTC	CTCTGAGACA	CATGGGCAAG	2280
AGACAATTGG	GAGTCAAGAT	TTTCCATTGG	GATCTATTTT	AAATCTTTTA	GAAATGCATT	2340
TGAACAGAGT	TGTTTGTGTT	TTCCCTTCTA	GTTAAGGGAC	TATTTATATG	TGTATAGGAA	2400
AGCTGTCTCT	TTTTTTGTGTT	TTCTTTTAAC	AAGGTCACAA	GAAAGATGCA	AAAGGAGATC	2460
ACACCCCTGC	CCGCTGAGC	CCCGTGATAA	CAAGTCACTC	CAGACTAACC	TGTGTGCCAG	2520
ACATTTGTGC	ATTGTTGAC	TTTGAGGTTA	TTATTTATCA	AGTTCTTGAA	GGAAGCAGAA	2580
AGAGGGACTC	CTCTCTCCCT	CCGTGTATAG	TCTCTATGTT	TGTGCTAGTT	TTTCTTTTTT	2640
TTCTCTGTGT	CCAGTCAGCC	ACAGGGCCCG	CCTCCCTGCA	GGAATAAGGG	GTAACACGTT	2700
AGGTGTTTGT	TGGCAAGAAA	CCACACTGAC	TGATGAGGGG	TAAAAAGGAA	CCAGGTAGAG	2760
CCACTCCGGG	CAGCTGTAC	CCATTGAGAA	CTTCTTTCCG	CAGCTGAAGA	AATGTTTCAGT	2820

75

80

AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTTCAG 2880  
 TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAAACCA ATCCAAAGGA TGTTACAGAA 2940  
 AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA 3000  
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060  
 CTGAGTAATC CAATAAAGAA CTTTTGATGA CAGCCAGAAAT GTGTTAGAAC TCTGGCTGAA 3120  
 CATTTTCATCT CTGTGAGTGC AGAAGGGCTT TATTTCTCCC TTGATGGGG CCCCTTCTTC 3180  
 TTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATCTA ATTTTAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTGTAGT 3300  
 AGATAAGGGA TGCTACTATA TGCTTTTATA AAACAAACAG GGACATTTT ATTATAGATT 3360  
 TGATTTTATTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420  
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG 3540  
 AAAATAGTCT CATCTCTTTT TTCTCAAAAT GAGATCCGTG TTTTATTTA GCATTAAAT 3600  
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660  
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720  
 GAAAGGTTGT GTGTCGTGTC TTTTGTGTT TTGGTTAGGC TTGGTTTGT TTTTAAATTT 3780  
 TTATACTTTC TAATAAATTT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GWMCTAMARM 3840  
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCACTTCGGG 3900  
 TGGGGCGGCG GGGCCACGT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAAG 3960  
 GAAACCTG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCGCCGGG 4020  
 GGAAACCGCA GAGTGTGCG TAAACACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

# A151 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MWLLGPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFDKSD 60  
 EKECPKAKSK CGPTFFPCAS GIHCCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120  
 KNLGLCIDKSF ICDQNNCQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180  
 VIFVLVALL ALVLHHQRKR NNLMTLPVHR LQHPVLRL VLDLHPHHCN VTYNVNNGIQ 240  
 YVASQAQNA SEVSGSPSYS EALLDQRPFW YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300  
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEV

# A152 DNA SEQUENCE

Gene name: Transmembrane protease, serine 2 (TMPRSS2)  
 Unigene number: Hs.105807  
 Probeset Accession #: T48536  
 Nucleic Acid Accession #: NM\_005656.1  
 Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 GTCATATGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTGATAAC AGCAAGATGG 60  
 CTTTGAATC AGGTACACCA CCAGCTATTG GACCTACTA TGAAAACCAT GGATACCAAC 120  
 CGGAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG 180  
 CTCAGTACTA CCCGTCCCCC GTGCCCCAGT ACGCCCCGAG GGTCTGACG CAGGCTTCCA 240  
 ACCCCGTCGT CTGCACGCAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAAGACTA 300  
 AGAAAGCACT GTGCATCAC TTAGCCCTGG GGACCTTCTT CGTGGGAGCT GCGCTGGCCG 360  
 CTGGCCTACT CTGGAAGTTC ATGGGCAGCA AGTGCTCCAA CTCTGGGATA GAGTGCAGT 420  
 CCTCAGGTAC CTGCATCAAC CCCTCTAACT GGTGTGATGG CGTGTACAC TGCCCCGGCG 480  
 GGGAGGACGA GAATCGGTGT GTTCGCCTCT ACGGACCAAA CTTCATCCTT CAGATGTACT 540  
 CATCTCAGAG GAAGTCTTGG CACCCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600  
 GGGCGGCTG CAGGACATG GGCTATAAGA ATAATTTTCT CTCTAGCCAA GGAATAGTGG 660  
 ATGACAGCGG ATCCACCAGC TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT 720  
 ATAAAAAAT GTACCACAGT GATGCCCTGT CTTCAAAGC AGTGGTTTCT TTACGCTGTT 780  
 TAGCCTGCGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG 840  
 CGTCCCGGG GGCCTGGCCC TGGCAGGTCA GCCTGCACGT CCAGAACGTC CACGTGTGCG 900  
 GAGGCTCCAT CATCACCCCC GAGTGATCG TGACAGCCGC CCACTGCGTG GAAAAACCTC 960  
 TTAACAATCC ATGGCATTGG ACGGCATTG CGGGGATTTT GAGACAATCT TTCAATGTCT 1020  
 ATGGAGCCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA 1080  
 AGAACAAATGA CATTCGCTG ATGAAGCTGC AGAAGCCTCT GACTTCAAC GACCTAGTGA 1140  
 AACCACTGTG TCTGCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGTGGGATT 1200  
 CCGGGTGGGG GGCCACCGAG GAGAAAGGGA AGACCTCAGA AGTGTGAAC GGTGCCAAG 1260  
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAAC CTGATCACAC 1320  
 CAGCATGAT CTGTGCCGCG TTCTGCGAGG GGAACGTCGA TTCTTGCCAG GGTGACAGT 1380  
 GAGGGCTCT GGTCACTTCG AACACAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440  
 GTTCTGGCTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTTCAGG 1500  
 ACTGGATTTA TCGACAATG AAGGCAACG GCTAATCCAC ATGGTCTTCG TCCTTGACGT 1560  
 CGTTTACAA GAAACAATG GGGCTGGTTT TGCTTCCCG TGATGATTT ACTCTTAGAG 1620  
 ATGATTGAGA GGTCACTTCA TTTTATTAA ACAGTGAAC TGTCTGGCTT TGGCACTCTC 1680  
 TGCCATACTG TGCAGGCTGC AGTGGCTCCC CTGCCAGGCC TGCTCTCCT AACCCCTTGT 1740

CCGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGGAAGAGG 1800  
 GTTGGAGGCT GCCCCATTG AGATCTTCCT GCTGAGTCCT TTCCAGGGGC CAATTTTGA 1860  
 TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920  
 GGAAGAGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTTGGTAGTG 1980  
 TCCCAGCCT ACTTACAAAG GGGATTTTGC TGATGGGTTC TTAGAGCCTT AGCAGCCCTG 2040  
 GATGGTGGCC AGAAATAAAG GGACAGCCCT TTCATGGGTG GTGACGTGGT AGTCACTTGT 2100  
 AAGGGGAACA GAAACATTTT TGTTCTTATG GGGTGAGAAAT ATAGACAGTG CCCTTGGTGC 2160  
 GAGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220  
 CATTGGGTGG GGCTCCTGGG AGGGAGACTC AGCCTTCCTC CTCATCCTCC CTGACCCTGC 2280  
 TCCTAGCACC CTGAGAGTG AATGCCCTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340  
 ATGTCGGCCT CTTAGGCCT GATAGTCATT GGAATTGAG GTCCATGGGG GAAATCAAGG 2400  
 ATGCTCAGTT TAAGGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460  
 CTGAGTTCAA AGCCATCTT

A153 Protein sequence:

Gene name: Transmembrane protease, serine 2 (TMPRSS2)  
 Unigene number: Hs.105807  
 Probeset Accession #: T48536  
 Protein Accession #: NP\_005647.1  
 Signal sequence: none found  
 Transmembrane domains: 85-107  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYFSPVP QYAPRVLTQA 60  
 SNPVVCTQPK SPSTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120  
 DSSGTCINPS NWCDGVSHCP GGEDENRCVR LYGPNFILQM YSSQRKSWHP VCQDDWNENY 180  
 GRAACRDMGY KNMFYSSQGI VDDSGTSFM KLNTSAGNVD IYKLYHSDA CSSKAVVSLR 240  
 CLACGVNLNS SRQSRIVGGE SALPGAWPWQ VSLHVQNVHV CGGSIITPEW IVTAAHCVKEK 300  
 PLNNPWHWTA FAGILRQSFY FYGAGYQVQK VISHPNYDSK TKNNIDIALMK LQKPLTFNDL 360  
 VKPVCPLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLETQRC NSRYVYDNL 420  
 TPAMICAGFL QGNVDSQCGD SGGPLVTSNN NIWWLIGDTS WSGGCAKAYR PGVYGNVMVF 480  
 TDWIYRQMK NG

A154 DNA SEQUENCE

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039  
 Unigene number: Hs.129179  
 Probeset Accession #: A1694767  
 Nucleic Acid Accession #: A1694767  
 Coding sequence: 130-1086 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CAGAGAGGCT GTATTTTCACT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60  
 GGGGTACAC ATTCCTTCCA TACGGTTGAG CCTCTACCTG CTTGGTGTCTG GTCACAGTTC 120  
 AGCTTCTTCA TGATGGTGGG TCCCAATGGC AATGAATCCA GTGCTACATA CTTTCATCCTA 180  
 ATAGGCTCC CTGGTTTAGA AGAGGCTCAG TTCTGGTTGG CCTTCCCAT GTGCTCCCTC 240  
 TACCTTATTG CTGTGCTAGG TAACTTGACA ATCATCTACA TTGTGCGGAC TGAGCAGAGC 300  
 CTGCATGAGC CCATGTATAT ATTTCTTTGC ATGCTTTTCA GCATTGACAT CCTCATCTCC 360  
 ACCCTATCCA TGCCCAAAAT GCTGGCCATC TTCTGGTTCA ATTCCACTAC CATCCAGTTT 420  
 GATGCTTGTC TGCTACAGAT GTTTGCCATC CACTCCTTAT CTGGCATGGA ATCCACAGTG 480  
 CTGCTGGCCA TGCTTTTGA CCGCTATGTG GCCATCTGTC ACCCACTGCG CCATGCCACA 540  
 GTACTTACGT TGCTCTGTGT CACCAAAATT GGTGTGGCTG CTGTGTGCGG GGGGGCTGCA 600  
 CTGATGGCAC CCCTTCTGTG CTTTCATCAAG CAGCTGCCCT TCTGCCGCTC CAATATCCTT 660  
 TCCCATTCCT ATGCTCTACA CCAAGATGTC ATGAAGCTGG CCTGTGATGA TATCCGGGTC 720  
 AATGTCGTCT ATGGCCTTAT CGTCATCATC TCCGCCATTG GCCTGGACTC ACTTCTCATC 780  
 TCCTTCTCAT ATCTGCTTAT TCTTAAGACT GTGTGGGCT TGACACGTGA AGCCAGGCC 840  
 AAGGCATTG GCACCTTGGT CTCTCATGTG TGTGCTGTGT TCATATTCTA TGTACCTTTC 900  
 ATTGGATTGT CCATGGTGCA TCGCTTAGC AAGCGGCGTG ACTCTCCACT GCCCGTCATC 960  
 TTGGCCAATA TCTATCTGCT GGTTCCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020  
 ACAAGGAGA TTGCACAGCG CATCCTTCGA CTTTTCATG TGGCCACACA CGCTTCAGAG 1080  
 CCCTAGGTGT CAGTGATCAA ACTTCTTTTC CATTACAGAT CCTCTGATTG AGATTTTAAT 1140  
 GTTAACATTT TGGAGAGCAG TATTCAGAAA AAAAATTTCC TTAATAAAAA TACAATCAG 1200  
 ATCCTTCAAA TATGAACTG GTTGGGGAAT CTCCATTTT TCAATATTAT TTTCTTCTTT 1260  
 GTTTCTTGC TACATATAAT TATTAATACC CTGACTAGGT TGTGGTTGGA GGGTTATTAC 1320  
 TTTTCATTTT ACCATGCACT CCAATCTTAA ACTGCTTCTA CTGATGGTTT ACAGCATTTCT 1380  
 GAGATAAGAA TGGTACATCT AGAGAACATT TGCCAAAGGC CTAAGCAGAG CAAAGGAAAA 1440  
 TAAACACAGA ATATAATAAA ATGAGATAAT CTAGCTTAAA ACTATAACTT CCTCTTCA 1500  
 ACTCCCAACC ACATTGGATC TCAGAAAAAT ACTGTCTTCA AAATGACTTC TACAGAGAAG 1560  
 AAATAATTTT TCCCTTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620  
 AGAGTACATT TACCTACGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT 1680  
 ATGGACCTCT TTTTCTCTAT TTAATTTTCT TATCAACCTT TTAATTAGGC AAAGATATTA 1740  
 TTAGTACCTG CATGTAGCC ATGGGAAAA TGTGTTTCTG TGGGGATCAG TGAATTAAT 1800  
 GGGGTCATAC AAGTATAAAA ATTAATAAAA AAAGACTTCA TGCCCAATCT CATATGATGT 1860  
 GGAAGAACTG TTAAGAGAC CAACAGGGTA GTGGGTAGA GATTTCAGA GTCTTACATT 1920  
 TTCTARAGGA GGTATTTAAT TTCTTCTCAC TCATCCAGTG TTGTATTAG GAATTTCTCTG 1980  
 GCAACAGAAC TCAATGGCTT AATCCCACTA GCTATTGCTT ATTGTCTCTG TCCAATTGCC 2040  
 AATTACCTGT GTCCTGGAAG AAGTGATTTA TAGGTTTACC ATTATGGAAG ATTCTTATTC 2100  
 AGAAAGTCTG CATAGGGCTT ATAGCAAGTT ATTTATTTT AAAAGTTCCA TAGGTGTTTC 2160  
 TGATAGGCAG TGAGGTTAGG GAGCCACCAG TTATGATGGG AAGTATGGAA TGGCAGGTGT 2220  
 TGAAGATAAC ATTGCCCTTT TGAGTGTGAC TCGTAGCTGG AAAGTGAGGG AATCTTCAGG 2280

ACCATGCTTT ATTTGGGGCT TTGTGCAGTA TGGAACAGGG ACTTTGAGAC CGGGAAAGCA 2340  
 ATCTGACTTA GGCATGGGAA TCAGGCATT TTGCTTCTGA GGGGCTATTA CCAAGGGTTA 2400  
 ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAAACTC AAATACATA 2460  
 TACTAAAACA TGTGATCATA TATGTGGTAA GTTTCATTTT CTTTTTCAAT CCTCAGGTTT 2520  
 CCTGATATGG ATTCCTATNA CATGCTTTCA TCCCTTTTG TAATGGATAT CATATTTGGA 2580  
 AATGCTTATT TAATACTTGT ATTTGCTGCT GGACTGTAAG CCCATGAGGG CACTGTTTAT 2640  
 TATTGAATGT CATCTCTGTT CATCATTTGAC TGCTCTTTGC TCATCATTGA ATCCCCAGC 2700  
 AAAGTGCCTA GAACATAATA GTGCTTATGC TTGACACCGG TTATTTTTC TCAAACCTGA 2760  
 TTCCTTCTGT GCTGAACACA TAGCCAGGCA ATTTTCCAGC CTTCTTTGAG TTGGGTATTA 2820  
 TTAAATTTTA GCCATTACTT CCAATGTGAG TGGAAAGTAC ATGTGCAATT TTTATACCTG 2880  
 GCTCATAAAA CCCTCCCATG TGCAGCCTTT CATGTTGACA TTAATGTGA CTTGGGAAGC 2940  
 TATGTGTTAC ACAGAGTTAA TTAACNGAA AGGCCTGGNA ATTTTGTGNN AANNAACTG 3000  
 TGGCCNNGAG GCCCNCAACC CTTTTNNNA ATTTGGCAAN NTCCCACTT GTANTTTGGT 3060  
 AAGGAGGCCA GTTGGATAAG TGAAAAATAA AGTACTATTG TGTC

**A155 PROTEIN SEQUENCE**

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039  
 Unigene number: Hs.129179  
 Protein Accession #: not available  
 Signal sequence: none found  
 Pfam domain: 7tm\_1 [43-293]  
 Transmembrane domains: 29-51, 57-79, 82-104, 203-225, 239-261, 273-295  
 Cellular Localization: not determined

1 11 21 31 41 51  
 | | | | |  
 MVDPNNGNESS ATYFILIGLP GLEEAQFWLA FPLCSLYLIA VLGNLTIIYI VRTEHSLHEP 60  
 MYIFLCMLSG IDILISTSSM PKMLAIFWFN STTIQFDACL LQMFHLSLS GMESTVLLAM 120  
 AFDRYVAICH PLRHATVLTL PRVTKIGVAA VVRGAALMAP LPVFIKQLPF CRSNILSHSY 180  
 CLHQDVMKLA CDDIRNVVY GLIVIIISAIG LDSLLISFSY LLILKTVLGL TREAQAKAFG 240  
 TCVSHVCAVF IFYVPIGLS MVHRFSKRRD SPLPVILANI YLLVPPVLNP IVYGVKTKEI 300  
 RQRILRLPHV ATHASEP

**A156 DNA SEQUENCE**

Gene name: vasoactive intestinal peptide receptor 1  
 Unigene number: Hs.198726  
 Probeset Accession #: X77777  
 Nucleic Acid Accession #: NM\_004624.1  
 Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)

TCGGAGCCTG CGGAGGGTGG TGGTGGTGGT GGTGGTGGCC CTCGCCCGCC TCACTCATGC 60  
 CTCCTCCTCC TCTGCTCTCG CTCAGGCGCC TCGGTGGCGG TTGGTGGCGG GTTACGCGGC 120  
 TGGTGGTCCG GCGCGCGCGG GCTCGCTCTC GGGGAGGCCG GGGCGGATCT CCGCGCGCAG 180  
 GCGGCGGCGG CCGAGGTGGG GTGCGCGCGG GGAGGCGGCT CGAGCTTCGT GCTGCGCGCT 240  
 CGCTCTTGGG CTCTCGCTG CAGGAGGAGT GTGACTATGT GCAGATGATC GAGGTGCAGC 300  
 ACAAGCAGTG CCTGGAGGAG GCCCAGCTGG AGAATGAGAC AATAGGCTGC AGCAAGATGT 360  
 GGGACAACCT CACTCTGCTG CCAGCCACCC CTCGGGGCCA GGTAGTTGTC TTGGCTGTGC 420  
 CCCTCATCTT CAAGCTCTTC TCCTCCATTC AAGGCCGCAA TGTAGCCGC AGCTGCACCG 480  
 AGCAAGGCTG GACGCACCTG GAGCCTGGCC CGTACCCCAT TGCCTGTGGT TTGGATGACA 540  
 AGGCAGCGAG TTTGGATGAG CAGCAGACCA TGTCTACCG TTCTGTGAAG ACCGGCTACA 600  
 CCATTGGCTA CGGCTCTGTC CTCGCCACCC TTCTGGTCTG CACAGCTATC CTGAGCCTGT 660  
 TCAGGAAGCT CCACTGCACG CGGAACATCA TCACATGCA CCTCTTCATA TCCTTCATCC 720  
 TGAGGGCTGC CGCTGTCTTC ATCAAAGACT TGGCCCTCTT CGACAGCGGG GAGTCGGACC 780  
 AGTGCTCCGA GGGCTCGGTG GGCTGTAAGG CAGCCATGGT CTTTTTCCAA TATTGTGTCA 840  
 TGGCTAACTT CTCTGGCTG CTGGTGGAGG GCCTCTACCT GTACACCCCTG CTTGCCGTCT 900  
 CCTTCTTCTC TGAGCGGAAG TACTTCTGGG GGTACATACT CATCGGCTGG GGGGTACCCA 960  
 GCACATTCAC CATGGTGTGG ACCATCGCCA GGATCCATT TGAAGATTAT GGTCTGTCTCA 1020  
 GGTGCTGGGA CACCATCAAC TCCTCACTGT GGTGGATCAT AAAGGGCCCC ATCCTCACTT 1080  
 CCATCTTGGT AAACCTTCATC CTGTTTATTT GCATCATCCG AATCCTGCTT CAGAACTGC 1140  
 GGCCCCCAGA TATCAGGAAG AGTGACAGCA GTCCATACTC AAGGCTAGCC AGGTCCACAC 1200  
 TCCTGCTGAT CCCCCTGTTT GGAGTACACT ACATCATGTT CGCCTTCTTT CCGGACAATT 1260  
 TTAAGCCTGA AGTGAAGATG GTCTTTGAGC TCGTCTGGGG GTCTTTCCAG GGTTTTGTGG 1320  
 TGGCTATCCT CTACTGCTTC CTCATAGGTG AGGTGCAGGC GGAGCTGAGG CGGAAGTGGC 1380  
 GCGGCTGGCA CCTGCAGGGC GTCTCTGGGT GGAACCCCAA ATACCGGCAC CCGTCGGGAG 1440  
 GCAGCAACGG CGCCACGTGC AGCACGCAGG TTTCCATGCT GACCCGCGTC AGCCAGGTG 1500  
 CCGCGCGCTC CTCAGCTTC CAAGCCGAAG TCTCCCTGGT CTGACCACCA GGATCCCAGC 1560  
 CCAAGCGGCC CCTCCCGCCC CTTCCCACTC GCAGCAGACG CCGGGGACAG AGGCCTGCCC 1620  
 GGGCGCGCCA GCCCGGCCCC TGGGCTCGGA GGCTGCCCCC GGCCCCCTGG TCTCTGGTCC 1680  
 GGACACTCCT AGAGAACGCA GCCCTAGAGC CTGCCTGGAG CGTTTCTAGC AAGTGAGAGA 1740  
 GATGGGAGCT CCTCTCTGG AGGATGCAGG TGGAACTCAG TCATTAGACT CCTCTCCAA 1800  
 AGGCCCCCTA CGCCAATCAA GGGCAAAAAG TCTACATACT TTACCTCTGA CTCTGCCCCC 1860  
 TGCTGGCTCT TCTGCCCAAT TGGAGGAAG CAACCGGTGG ATCCTCAAAC AACACTGGTG 1920  
 TGACCTGAGG GCAGAAAGGT TCTGCCCGGG AAGGTCAACA GCACCAACAC CACGGTAGTG 1980  
 CCTGAAATTT CACCATTGCT GTCAAGTTCC TTTGGGTAA GCATTACCAC TCAGGCATT 2040  
 GACTGAAGAT GCAGCTCACT ACCCTATTCT CTCTTTACGC TTAGTTATCA GCTTTTAAA 2100  
 GTGGGTTATT CTGGAGTTT TGTTTGGAGA GCACACCTAT CTTAGTGGTT CCCCACCGAA 2160  
 GTGGACTGGC CCCTGGGTCA GTCTGGTGGG AGGACGGTGC AACCACAGGA CTGAGGGACT 2220  
 CTGAAGCCTC TGGGAAATGA GAAGGCAGCC ACCAGCAAT GCTAGGTCTC GGACTAAGCC 2280  
 TACCTGCTCT CCAAGCTCA GTGGCTTCAT CTGTCAAGTG GGAATCAAGA GACTGCCCTC CTTGTCCACC 2340  
 TTCTTATCTC TCTGTGCTGT GGAAGCAACA GGAATCAAGA GACTGCCCTC CTTGTCCACC 2400  
 CACCTATGTG CCAACTGTTG TAACTAGGCT CAGAGATGTG CACCCATGGG CTCTGCACGA 2460



AAGCAGATCC TCACCCCTGCT ACACATACAG GATTTGAAGT CAGATCTGTC TGATAGGAAT 2520  
 GTGAAAGCAC GGACTCTTAC TGCTAACTTT TGTGTATCGT AACCAGCCAG ATCCTCTTGG 2580  
 TTATTTGTTT ACCACTTGTA TTATTAATGC CATTATCCCT GAATTCCTCTG TCCACCCCA 2640  
 CCCTCCCTGG AGTGTGGCTG AGGAGGCTC CATCTCATGT ATCATCTGGA TAGGAGCTG 2700  
 CTGGTCACAG CCTCCTGTGT CTGCCCTTCA CCCCAGTGGC CACTCAGCTT CCTACCCACA 2760  
 CCTCTGCCAG AAGATCCCTT CAGGACTGCA ACAGGCTTGT GCAACAATAA ATGTTGGCTT 2820  
 GGAAAAA AAAA

**A157 Protein sequence:**

Gene name: vasoactive intestinal peptide receptor 1  
 Unigene number: Hs.198726  
 Probeset Accession #: X77777  
 Protein Accession #: JC2195  
 Signal sequence: none found  
 Transmembrane domains: 181-202, 214-236, 255-277, 290-311, 332-354, 377-399, 408-430  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MPPPPLLSLR RLGGGWSAVT RLVVAAAGAR SRGGGRGSRG AGGGGRGGVA RRRRLRLRAA 60  
 RSLLGSSSLQE ECDYVQMIEV QHKQCLEEAQ LENETIGCSK MWDNLTCPWA TPRGQVVVLA 120  
 CPLIFKLFSS IQGRNVSRSR TDEGWHLEP GPYPYIACGLD DKAASLDEQQ TMFYGSVKTG 180  
 YTIYGLSLA TLLVATAILS LFRKLHCTRN YIHMHLFISF ILRAAAVFIK DLALFDSGES 240  
 DQCEGSGVGC KAAMVFFQYC VMANFFWLLV EGLYLYTLA VSFFSERKYF WGYILIGWGV 300  
 PSTFTMVWTI ARIHFEDYGL LRCWDITNSS LWWIIGPIL TSILVNFIIF ICIIRILLQK 360  
 LRPPDIRKSD SSPYSRLARS TLLLIPLFGV HYIMFAFFPD NFKPEVKMVF ELVVGVSFQGF 420  
 VVAILYCFLN GEVQABLRRK WRRWHLQGV L GWNPKYRHPS GGSNGATCST QVSMLTRVSP 480  
 GARRSSSFQA EVSLV

**A158 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Nucleic Acid Accession #: AL133619  
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGAGCGGTG CGGGGGTGGC GGTCTGGGACG CGGCCCCCCA GCTCGCCGAC CCCGGGCTCT 60  
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCTT TGAGGCGGCA GAGCCCGCAG 120  
 CTGAGGAGCA GCGACCCGCA GAAACCGAAG CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180  
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240  
 GAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCCTCCCA GGCACACTCA 300  
 AACTGCGCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA 360  
 GGGGGAACAC AGGACGGGGA GCCCTCCAG ACTGTCTTGG CCCACCTGGC TGCACTGGCC 420  
 CCTGTATGCC AATCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGTACCTCT 480  
 AGCCGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCAGC TGCTGCTCTC GGAAGAGCCA 540  
 GGGCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGGT GCTCCCGAGA CCTCCCTCCT 600  
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG 660  
 CCTCAGATTG CTGCTGTGGC CAGGCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720  
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTCTG TTCTTGCCA CTGTGTCGAAG 840  
 GCATCTCCCC ATCTGTACAG CGGCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900  
 GCTCACTTCC CATATCTTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGGA 960  
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCTTA GGGCTCTCCC TTCCAGGGA 1020  
 GACATGGAGA AGGGGGTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080  
 CTGTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCTGCAGTGC TGGGGAAGCT 1140  
 GACAGGACAC GGAAGAGGC CATGCTTTCC CTGCGGACCT GCTGTTCCAT GTGTCCCAAG 1200  
 CCCTCCTGCT TTCCAGATGG CCCCTCAGGA AACCACTTT CCAGGGCTC TGCTCCCTTG 1260  
 GGCCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320  
 AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGG 1380  
 GGCAGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440  
 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGG 1500  
 TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCAGCA AGGCGGACCT GGAAGAGGAG 1560  
 CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTGGGG TACAAGGGCA GGCAGAAAG 1620  
 GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAGGGC 1680  
 AGGCAGATGG GGGCGGGGGC ACACCCCAAT ATGATCCTGC CCCTTCCCTT GCGAAAGCCC 1740  
 ACCACACTTA GGCAGTGCAG AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCCTGCAG 1800  
 ACCCAAGAGC TGGCGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860  
 CCGGAGGAAG CTAGCTTTCC CAGGAGCCAA GAAGCCACGC ATTTCCCAAA GGTCTCCACC 1920  
 AAGAGCCTCT CCAAGAAATG CTTGAGCCCA CTTGTGGCGG AGCGTGCCAT CTGCCCCGCA 1980  
 CTGAAGCAGA CCCCAAGAA CAACCTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040  
 AAACGGCGCC TGCATCGCTC AGTGCTTTGA

**A159 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Protein Accession #: T43457  
 Signal sequence: none found  
 Transmembrane domains: 303-322  
 Cellular Localization: not determined

5	1	11	21	31	41	51	
	MSGAGVAAGT	RPPSSPTPGS	RRRRQRPSVG	VQSLRPQSPQ	LRQSDPQKRN	LDLEKSLQFL	60
	QQQHSEMLAK	LHEEIEHLKR	ENKGEFARGP	RPALPPQAH	TLPLPQHRNT	AINSSTRLGS	120
	GGTQDGEPLQ	TVLAHLAALA	PVCQPSGYRF	WGTWTDAA	SRGWTMLCSQ	AQHVLLSGSP	180
	GPEVIAGRQV	ATGCSPLDLP	PSRAEMGRNP	WDSFPCPARSL	PQIAAVARPR	ISSPMALSPH	240
10	MLGAQGIWTH	SIQGSPLAIW	AATMGTKGGS	RVLFPCHLSK	ALPHPDSSGPH	PAQDPGLWSQ	300
	AHFPLSLGLG	LTSGGHLTGG	WSQPGNIAAG	AVPRALPSQ	DMEKGVGGP	FPSRCGNSSE	360
	LFWAKCGFSR	QPQPCSGADA	DRTREEMLS	LGTCCSMCPK	PSCFPDGPFG	NHLSRASAPL	420
	GARWVCINGV	WVEPGGSPSA	RLKEGSSRTH	RPGGKRGRLA	GGSDTVRSP	ADSLSMSSFO	480
	SVKSISNSAN	SQKARQPG	SFNKQDSKAD	VSQKADLEEE	PLHNSKLDK	VPGVQQQARK	540
15	EKAASNAGA	ACMGNQHQG	RQMGAGAHPP	MILPLPLRKP	TTLRQCEVLI	RELWNTNLLQ	600
	TQELRHLKSL	LEGSQRQAAA	PEEASFPRDQ	EATHFPKVST	KSLSKKCLSP	PVAERAILPA	660
	LKQTPKNFA	ERQKRLQAMQ	KRRLHRSVL				

## A160 DNA SEQUENCE

Gene name: LIV-1 protein, estrogen regulated

Unigene number: Hs.79136

Probeset Accession #: U41060

Nucleic Acid Accession #: NM\_012319.2

Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

30	1	11	21	31	41	51	
	CTCGTGCCGA	ATTTCGGCAG	AGACCGCGTG	TTCGCGCCTG	GTAGAGATTT	CTCGAAGACA	60
	CCAGTGGGCC	CGTGTGGAAC	CAAACTCTGC	CGCGTGGCCG	GGCCGTGGGA	CAACGAGGCC	120
	GCGGAGACGA	AGGCGCAATG	GCGAGGAAGT	TATCTGTAA	CTTGATCTTG	ACCTTTGCC	180
	TCTCTGTAC	AAATCCCCTT	CATGAACATA	AAGCAGCTGC	TTTCCCCCAG	ACCACTGAGA	240
	AAATTAGTCC	GAATTGGGAA	TCTGGCATT	ATGTTGACTT	GGCAATTTCC	ACACGGCAAT	300
	ATCATCTACA	ACAGCTTTTC	TACCGCTATG	GAGAAAATAA	TTCTTTGTCA	GTTGAAGGGT	360
35	TCAGAAAATT	ACTTCAAAAT	ATAGGCATAG	ATAAGATTAA	AAGAATCCAT	ATACACCATG	420
	ACCACGACCA	TCATCTCAGC	CACGAGCATC	ACTCAGACCA	TGAGCGTCAC	TCGACCATG	480
	AGCATCACTC	AGACCACGAG	CATCACTCTG	ACCATGATCA	TCATCTCTAC	CATAATCATG	540
	CTGCTTCTGG	TAAAATAAAG	CGAAAAGCTC	TTTGCCCGAGA	CCATGACTCA	GATAGTTCAG	600
40	GTAAGATTC	TAGAAACAGC	CAGGGGAAAG	GAGCTCACCG	ACCAGAACAT	GCCAGTGGTA	660
	GAAGGAATGT	CAAGGACAGT	GTTAGTGCTA	GTGAAGTGAC	CTCAACTGTG	TACAACACTG	720
	TCTCTGAAGG	AACTCACTTT	CTAGAGACAA	TAGAGACTCC	AAGACCTGGA	AAACTCTTCC	780
	CCAAAGATGT	AAGCAGCTCC	ACTCCACCCA	GTGTACATC	AAAGAGCCGG	GTGAGCCGGC	840
	TGGCTGGTAG	GAAAACAAAT	GAATCTGTGA	GTGAGCCCGG	AAAAGGCTTT	ATGTATTCCA	900
45	GAAACACAAA	TGAAAATCCT	CAGGAGTGTT	TCAATGCATC	AAAGCTACTG	ACATCTCATG	960
	GCATGGGCAT	CCAGGTTCCG	CTGAATGCAA	CAGAGTTCAA	CTATCTCTGT	CCAGCCATCA	1020
	TCAACCAAT	TGATGCTAGA	TCTTGTCTGA	TTCATACAAG	TGAAAAGAAG	GCTGAAATCC	1080
	CTCCAAAGAC	TATTTCATTA	CAAAATAGCCT	GGGTTGGTGG	TTTTATAGCC	ATTTCCATCA	1140
	TCAGTTTCTC	GTCTCTGCTG	GGGGTTATCT	TAGTGCCTCT	CATGAATCGG	GTGTTTTTCA	1200
50	AAATTCTCCT	GAGTTTCTCT	GTGGCACTGG	CCGTTGGGAC	TTTGAGTGGT	GATGCTTTTT	1260
	TACACCTTCT	TCCACATCTT	CATGCAAGTC	ACCACCATAG	TCATAGCCAT	GAAGAACCAG	1320
	CAATGGAAT	GAAAAGAGGA	CCACTTTTCA	GTCTCTGTGC	TTCTCAAAAC	ATAGAAGAAA	1380
	GTGCTTATTT	TGATTCCACG	TGGAAGGGTC	TAACAGCTCT	AGGAGGCTCG	TATTTTCATG	1440
	TTCTTGTTGA	ACATGTCCTC	ACATTGATCA	AACAATTTAA	AGATAAGAAG	AAAAAGAATC	1500
55	AGAAGAAACC	TGAAAATGAT	GATGATGTGG	AGATTAAAGAA	GCAGTTGTCC	AGGTATGAAT	1560
	CTCAACTTTT	AACAAATGAG	GAGAAAGTAG	ATACAGATGA	TCGAACTGAA	GGCTATTTAC	1620
	GAGCAGACTC	ACAAGAGCCC	TCCCACCTTG	ATTCTCAGCA	GCCTGCAGTC	TTGGAAGAAG	1680
	AAGAGGTCAT	GATAGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GTACCCAGAG	1740
	GGTGCAAGAA	TAAATGCTAT	TCACATTTCC	ACGATACACT	CGGCCAGTCA	GACGATCTCA	1800
60	TTACACACCA	TCATGACTAC	CATCATATTC	TCCATCATCA	CCACACACAA	AACCAACATC	1860
	CTCAGAGTCA	CAGCCAGCGC	TACTCTCGGG	AGGAGCTGAA	AGATGCCCGC	GTCCGCACTT	1920
	TGGCTTGGAT	GGTGATAATG	GGTGATGGCC	TGCACAAATT	CAGCGATGGC	CTAGCAATTG	1980
	GTGCTGCTTT	TACTGAAGGC	TTATCAAGTG	GTTTAAGTAC	TTCTGTTGCT	GTGTTCTGTC	2040
	ATGAGTTGCC	TCATGAATTA	GGTGACTTTG	CTGTTCTACT	AAAGGCTGGC	ATGACCGTTA	2100
	AGCAGGCTGT	CCTTTATAAT	GCATTGTCTG	CCATGCTGGC	GTATCTTGGA	ATGGCAACAG	2160
65	GAATTTTCT	TGGTCTTAT	GCTGAAAATG	TTTCTATGTG	GATATTGCA	TTTACTGCTG	2220
	GCTTATTCAT	GTATGTTGCT	CTGGTTGATA	TGGTACCTGA	AATGCTGCAC	AATGATGCTA	2280
	GTGACCATGG	ATGTAGCCGC	TGGGGGTATT	TCTTTTATCA	GAATGCTGGG	ATGCTTTTGG	2340
	GTTTGGGAAT	TATGTTACTT	ATTTCCATAT	TTGAACATAA	AATCGTGTTC	CGTATAAAT	2400
70	TCATGTTAAG	GTTTAAATGC	TAGAGTAGCT	TAAAAAGTTG	TCATAGTTTC	AGTAGGTCAT	2460
	AGGGAGATGA	GTTTGTATGC	TGTACTATGC	AGCGTTTAAA	GTTAGTGGGT	TTTGTGATTT	2520
	TTGTATTGAA	TATTGCTGTC	TGTTACAAAG	TCAGTTAAAG	GTACGTTTTC	ATATTTAAGT	2580
	TATTTCTATG	TGGAGATAAA	ATCTGTATGT	GCAATTCACC	GGTATTACCA	GTTTATTATG	2640
	TAAACAAGAG	ATTTGGCATG	ACATGTTCTG	TATGTTTCAG	GGAAAATGT	CTTTAATGCT	2700
75	TTTTCAAGAA	CTAACACAGT	TATTCCTATA	CTGGATTTTA	GGTCTCTGAA	GAAGTCTGG	2760
	TGTTTAGGAA	TAAAGATGTG	CATGAAGCCT	AAAATACCAA	GAAAGCTTAT	ACTGAATTTA	2820
	AGCAAGAGAA	TAAAGAGAGAA	AAGAGAGAGAA	TCTGAGAATT	GGGAGGCGAT	AGATTCTTAT	2880
	AAAAATCACA	AAATTTGTTG	TAAATTAGAG	GGGAGAAATT	TAGAATTAA	TATAAAAGG	2940
	CAGAATTAGT	ATAGAGTACA	TTCATTAAAC	ATTTTGTGCA	GGATTATTTT	CCGTAATAAC	3000
80	GTAGTGAGCA	CTCTCATATA	CTAATTAGTG	TACATTAAAC	TTTGATATAAT	ACAGAAATCT	3060
	AAATATATTT	AATGAATTCA	AGCAATATAC	ACTTGACCAA	GAAATTTGAA	TTTCAAAATG	3120
	TTCTGTCGGG	TTATATACCA	GATGAGTACA	GTGAGTAGTT	TATGTATCAC	CAGACTGGGT	3180
	TATTGCAAG	TTATATATCA	CCAAAAGCTG	TATGACTGGA	TGTTCTGGTT	ACCTGGTTTA	3240
	CAAAATTATC	AGAGTAGTAA	AACTTTGATA	TATATGAGGA	TATTTAAACT	ACACTAAGTA	3300
	TCATTTGATT	CGATTTCAGAA	AGTACTTTGA	TATCTCTCAG	TGCTTCAGTG	CTATCATTTG	3360

GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420  
GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

# A161 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated  
Unigene number: Hs.79136  
Protein Accession #: NP\_036451  
Signal sequence: 1-21  
Pfam domain: Zip[591-743]  
Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745  
Cellular Localization: plasma membrane

1	11	21	31	41	51	
MARKLSVILI	LTFALSVTNP	LHELKAAAPP	QTTEKISPNN	ESGINVDLAI	STRQYHLQQL	60
FYRYGENNSL	SVEGFRKLLQ	NIGIDKIKRI	HIHHDHDDHS	DHEHSDHER	HSDHEHSDH	120
EHHSDDHDS	HNHNAASGKN	KRKALCPDHD	SDSSGKDPNN	SQKGGAHRPE	HASGRNRVKD	180
SVSASEVTST	VYNTVSEGTH	FLETIETPRP	GKLFPPKDVSS	STPPSVTSKS	RVSRLAGRKT	240
NESVSEPRKG	FMYSRNTNEN	PQECFNASKL	LTSHGMGIQV	PLNATEFNYL	CPAIINQIDA	300
RSCLIHSTSEK	KAEIPPKTYS	LQIAWVGFI	AISIISFLSL	LGVILVPLMN	RVFFKFLLSF	360
LVALAVGTLG	GDAFLHLLPH	SHASHHSHS	HEEPAMEMKR	GPLFSLSSQ	NIEESAYFDS	420
TWKGLTALGG	LYPMFLVEHV	LTLIKQFKDK	KKKNQKKPEN	DDDVEIKKQL	SKYESQLSTN	480
EEKVDTDDRT	EGYLRADSQE	PSHFDSSQPA	VLEEEVEMIA	HAHPQEVYNE	YVPRGCKNKC	540
HSHFHDTLGG	SDDLIIHHND	YHHILHHHHH	QNHHPHSHSQ	RYSRREELKDA	GVATLAWMVI	600
MGDGLHNFSD	GLAIGAAFTG	GLSSGLSTSV	AVFCHPELPE	LGDFAVLLKA	GMTVKQAVLY	660
NALSAMLAYL	GMATGIFIGH	YAENVSMWIF	ALTAGLFMYV	ALVDMVPEML	HNDASDHGCS	720
RWGYFFLQNA	GMLLGFGIML	LISIFEHKIV	PRINF			

# A162 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.87223  
Probeset Accession #: AA250737  
Nucleic Acid Accession #: NM\_001203  
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
CGCGGGGCGC	GGAGTCGGCG	GGGCGCTCGC	GGACGCGGGC	AGTGCGGAGA	CCGCGGCGCT	60
GAGGACGCGG	GAGCGGGGAG	CGCAGCGCGC	GGGTGGAGTT	CAGCCTACTC	TTTCTTAGAT	120
GTGAAAGGAA	AGGAAGATCA	TTTCATGCCT	TGTTGATAAA	GGTTCAGACT	TCTGCTGATT	180
CATAACCAT	TGGCTCTGAG	CTATGACAAG	AGAGGAAACA	AAAAGTTAAA	CTTACAAGCC	240
TGCCATAAGT	GAGAAGCAAA	CTTCCTTGAT	AACATGCTTT	TGCGAAGTGC	AGGAAAATTA	300
AATGTGGGCA	CCAAAGAAAG	GGATGGTGAG	AGTACAGCCC	CCACCCCGCC	TCCAAAGGTC	360
TTGCGTTGTA	AATGCCACCA	CCATTGTCCA	GAAGACTCAG	TCAACAATAT	TTGCGACACA	420
GACGATATAT	GTTTCACGAT	GATAGAAGAG	GATGACTCTG	GGTTGCTGT	GGTCACTTCT	480
GGTTGCTTAG	GACTAGAAGG	CTCAGATTTT	CAGTGTCTGG	ACACTCCCAT	TCCTCATCAA	540
AGAAGATCAA	TTGAATGCTG	CACAGAAAGG	AACGAATGTA	ATAAAGACCT	ACACCCTACA	600
CTGCCTCCAT	TGAAAAACAG	AGATTTTGT	GATGGACCTA	TACACCACAG	GGCTTTACTT	660
ATATCTGTGA	CTGTCTGTAG	TTTGCTCTTG	GTCCTTATCA	TATTTATTTG	TTACTTCCGG	720
TATAAAGAC	AAGAACCAG	ACCTCGATAC	AGCATTGGGT	TAGAACAGGA	TGAAACTTAC	780
ATTCCTCCTG	GAGAATCCCT	GAGAGACTTA	ATTGAGCAGT	CTCAGAGCTC	AGGAAGTGGA	840
TCAGGCCCTC	CTCTGCTGGT	CCAAGGACT	ATAGCTAAGC	AGATTCAGAT	GGTGAAACAG	900
ATTGGAAGAG	GTCGCTATGG	GGAAGTTTGG	ATGGGAAAGT	GGCGTGCGCA	AAAGGTAGCT	960
GTGAAAGTGT	TCTTCACCAC	AGAGGAAGCC	AGCTGGTTCA	GAGAGACAGA	AATATATCAG	1020
ACAGTGTGTA	TGAGGCATGA	AAACATTTTG	GGTTTCATTG	CTGCAGATAT	CAAAGGGACA	1080
GGGTCTGTGA	CCAGTTGTGA	CCTAATCACA	GACTATCATG	AAAATGGTTC	CCTTTATGAT	1140
TATCTGAAGT	CCACCACCT	AGACGCTAAA	TCAATGCTGA	AGTTAGCCTA	CTCTTCTGTC	1200
AGTGGCTTAT	GTCATTTACA	CACAGAAATC	TTTAGTACTC	AAGGCAAACC	AGCAATTGCC	1260
CATCGAGATC	TGAAAAGTAA	AAACATTCTG	GTGAAGAAAA	ATGGAACCTG	CTGTATTGCT	1320
GACCTGGGCC	TGGCTGTTAA	ATTTATTAGT	GATACAAATG	AAGTTGACAT	ACCACCTAAC	1380
ACTCGAGTTG	GCACCAAAAG	CTATATGCCT	CCAGAAGTGT	TGGACGAGAG	CTTGAACAGA	1440
AATCACTTCC	AGTCTTACAT	CATGGCTGAC	ATGTATAGTT	TTGGCCTCAT	CCTTTGGGAG	1500
GTGTCTAGGA	GATGTGTATC	AGGAGGTATA	GTGGAAGAA	ACCAGCTTCC	TTATCATGAC	1560
CTAGTGCCCA	GTGACCCCTC	TTATGAGGAC	ATGAGGGAGA	TTGTGTGCAT	CAAGAAAGTTA	1620
CGCCCTCAT	TCCCAAAACG	GTGGAGCAGT	GATGAGTGTC	TAAGGCAGAT	GGGAAAACCT	1680
ATGACAGAAT	GCTGGGCTCA	CAATCCTGCA	TCAAGGCTGA	CAGCCCTGCG	GGTTAAGAAA	1740
ACACTTGCCA	AAATGTCAGA	GTCCAGGAC	ATTAACTCT	GATAGGAGAG	GAAAAGTAAG	1800
CATCTCTGCA	GAAAGCCAAC	AGGTACTCTT	CTGTTTGTGG	GCAGAGCAAA	AGACATCAAA	1860
TAAGCATCA	CAGTACAAGC	CTTGAACATC	GTCCTGCTTC	CCAGTGGGTT	CAGACCTCAC	1920
CTTTGAGGGA	GCGACCTGGG	CAAAGACAGA	GAAGCTCCCA	GAAGGAGAGA	TTGATCCGTG	1980
TCTGTTTGTA	GGCGGAGAAA	CCGTTGGGTA	ACTTGTTC	GATATGATGC	AT	

# A163 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.72472 / Hs.87223  
Probeset Accession #: AA250737 / U89326  
Protein Accession #: NP\_001194  
Signal sequence: 1-13  
Transmembrane domains: 128-144  
PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
Cellular Localization: plasma membrane

	1	11	21	31	41	51			
5	MLLR	SAGKLN	VGTKKEDGES	TAPT	PRPKVL	RCKCHHHCPE	DSVNNICSTD	GYCFTMIEED	60
	DSGL	PVVTSG	CLGLESDDFQ	CRDT	PIPHQR	RSIECCTERN	ECNKDLHPTL	PPLKNRDFVD	120
	GPIH	RALLI	SVTVCSLLLV	LIIL	FCYFRY	KRQETRPYS	IGLEQDETYI	PPGESLRDLI	180
	EQSQ	SSGSGS	GLPLLVRTI	AKQI	QMVKQI	GKGRYGEVWM	GKWRGEKVAV	KVFFTTEEAS	240
	WFRE	TEIYQT	VLMRHNILG	FIAAD	IKGTG	SWTQLYLITD	YHENGSLYDY	LKSTTLDAKS	300
10	MLKL	AYSSVS	GLCHLHTEIF	STQK	PAIAH	RDLKSKNILV	KKNGTCCCIAD	LGLAVKFISD	360
	TNEVD	IPPNP	RVGTRKYMPP	EVLD	ESLNRN	HFQSYIMADM	YSFGLILWEV	ARRCVSGGIV	420
	EEYQL	PHYHDL	VPBDPSYEDM	REIV	CIKKLR	PSFPNRWSSD	ECLRQMGKLM	TECWAHPAS	480
	RLTAL	RVKKT	LAKMSESDI	KL					

## A164 DNA sequence

15 Gene name: ESTs  
 Unigene number: Hs.157601  
 ProbeSet Accession #: W07459  
 Nucleic Acid Accession #: AC005383  
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51		
25	GACAGT	GTTC	GCGGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGCGTAGAAG	TGAAGTACTT	60
	TTTTAT	TATGTC	AGACCTGGGG	CGATGCCGCT	TTAAAAAAGC	CGAGGGGGCTC	TATGCACCTC	120
	CCTGGC	GGTA	GTTCCCTCCG	CCTCAGCCGG	GTCGGGTCGT	GCCGCCCTCT	CCCAGGAGAG	180
	ACAAAC	AGGT	GTCCCACTGT	GCAGCCGCGC	CCCGGGCGCC	CCTCCTGTGA	TCCCGTAGCG	240
	CCCCCT	GGCC	CGAGCCGCGC	CCGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG	300
30	TCCGCG	CTCT	CCTCCGTTA	TATCAACATG	CCCCCTTCC	TGTTGCTGGA	GGCCGTCTGT	360
	GTTTTCT	CGT	TTTCCAGAGT	GCCCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAGCAA	420
	GAAACCAT	CG	GGAGATTTC	AGCTGCCAGC	AAAATGATGT	GGTGCTCGGC	TGCAGTGGAC	480
	ATCATGTT	TC	TAGATGG	GTCTAACAGC	GTCGGGAAAG	GGAGCTTGA	AAGGTCCAAG	540
	CACTTTGCCA	TCACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600	
	GCATTCCAGT	TCAGTTCCAC	TCCTCATCTG	GAATTCCTCT	TGGATTCTT	TTCAACCCAA	660	
35	CAGGAAGTGA	AGGCAAGAAT	CAAGAGGATG	GTTTTCAAAG	GAGGGCGCAC	GGAGACGGAA	720	
	CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCTCTGAG	GCAGAAATGC	TTCTGTGCCC	780	
	CAGATCCTCA	TCATCGTCA	TGATGGGAAG	TCCCAGGGGG	ATGTGGCACT	GCCATCCAAG	840	
	CAGCTGAAGG	AAAGGGGTGT	CACGTGTGTT	GCTGTGGGGG	TCAGGTTTCC	CAGGTGGGAG	900	
40	GAGCTGCATG	CACCTGGCCAG	CGAGCCTAGA	GGGCAGCACG	TGCTGTGTCG	TGAGCAGGTG	960	
	GAGGATGCCA	CCAACGGCCT	CTTCAGACCC	CTCAGCAGCT	CGGCCATCTG	CTCCAGCGCC	1020	
	ACGCCAGACT	GCAGGGTCTG	GGCTCACCCC	TGTGAGCACA	GGACGCTGGA	GATGGTCCGG	1080	
	GAGTTCTGCTG	GCAATGCCCC	ATGCTGGAGA	GGATCGCGGC	GGACCTTTCG	GGTGCTGGCT	1140	
	GCACACTGTC	CCTTCTACAG	CTGGAAGAGA	GTGTTCCTAA	CCCACCTGTC	CACCTGCTAC	1200	
45	AGGACCACCT	GCCCAGGGCC	CTGTGACTCG	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT	1260	
	CCAGAAGGAC	TGGACGGCTA	CCAGTGCCCTC	TGCCCGCTGG	CCTTGGAGG	GGAGGCTAAC	1320	
	TGTGCCCTGA	AGCTGAGCCT	GGAAATGCAGG	GTCGACCTCC	TCTTCCTGCT	GGACAGCTCT	1380	
	GCGGGCACCA	CTCTGGACGG	CTTCCTGCGG	GCCAAAGTCT	TCGTGAAGCG	GTTTGTGCGG	1440	
	GCCGTGCTGA	GCGAGGACTC	TGCGGCCCGA	GTGGGTGTGG	CCACATACAG	CAGGGAGCTG	1500	
50	CTGGTGGCGG	TGCCTGTGGG	GGAGTACCAG	GATGTGCCCTG	ACCTGGTCTG	GAGCCTCGAT	1560	
	GGCATTCCTT	TCCGTGGTGG	CCCCACCTTG	ACGGGCAGTG	CCTTGCAGCA	GCGGCAGAG	1620	
	CGTGGCTTCG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAGT	GGTGGTTTTG	1680	
	CTCACTGAGT	CACACTCCGA	GGATGAGGTT	GCGGGCCAG	CGCGTACAGC	AAGGGCGCGA	1740	
	GAGCTGTCTC	TGCTGGGTGT	AGGCAGTGAG	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA	1800	
	GGCAGCCCAA	AGCATGTGAT	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT	1860	
55	GAGCTGCAGG	GGAAAGCTGTG	CAGCCGGCAG	CGGCCAGGGT	GCCCGACACA	AGCCCTGGAC	1920	
	CTCGTCTTCA	TGTTGGACAC	CTCTGCCTCA	GTAGGGCCCG	AGAATTTTGC	TCAGATGCAG	1980	
	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGACGTGAC	ACAGGTCCGC	2040	
	CTGGTGGTGT	ATGGCAGCCA	GGTGCAACT	GCCTTCGGGC	TGGACACCAA	ACCCACCCGG	2100	
60	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	2160	
	ACCGCCCTGC	TGCACATCTA	TGACAAAGTG	ATGACCGTCC	AGAGGGGTGC	CCGGCCTGGT	2220	
	GTCCCCAAG	CTGTGGTGGT	GCTCACAGGC	GGGAGAGGCG	CAGAGGATGC	AGCCGTTTCT	2280	
	GCCCCAGAAG	TGAGGAACAA	TGGCATCTCT	GTCTTGGTCT	TGGGCGTGGG	GCCTGTCTTA	2340	
	AGTGAGGGTC	TGCGGAGGCT	TGCAGGTCCC	CGGGATTCCC	TGATCCACGT	GGCAGCTTAC	2400	
65	GCCGACCTGC	GGTACCACCA	GGACGTGCTC	ATTGAGTGGC	TGTGTGGAGA	AGCCAAGCAG	2460	
	CCAGTCAACC	TCTGCAAAAC	CAGCCCGTGC	ATGAATGAGG	GCAGCTGCGT	CCTGCAGAAT	2520	
	GGGAGCTACC	GCTGCAAGTG	TGGGATGGC	TGGGAGGGCC	CCCACTGCGA	GAACCGTGAG	2580	
	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	GGATGGATT	TTGAGACGCC	CCTGAGGCAC	2640	
	ATGGCTCCCG	TGCAGGAGGG	CAGCAGCCGT	ACCCCTCCCA	GCAACTACAG	AGAAGGCCTG	2700	
70	GGCACTGAAA	TGGTGCTTAC	CTTCTGGAAT	GTCTGTGCC	CAGGTCCCTTA	GAATGTCTGC	2760	
	TTCCCGCCGT	GGCCAGGACC	ACTATTCTCA	CTGAGGGAGG	AGGATGTCCC	AACTGCAGCC	2820	
	ATGCTGCTTA	GAGACAAGAA	AGCAGCTGAT	GTCAACCCACA	AACGATGTTG	TTGAAAAGTT	2880	
	TTGATGTGTA	AGTAAATACC	CACCTTCTGT	ACCTGCTGTG	CCTTGTGTAG	GCTATGTCAT	2940	
	CTGCCACCTT	TCCCTTGAGG	ATAAACAAAG	GGTCTGAAG	ACTTAAATTT	AGCGGCCTGA	3000	
75	CGTTCCCTTG	CACACAATCA	ATGCTCGCCA	GAATGTGTT	GACACAGTAA	TGCCAGCAG	3060	
	AGGCCCTTAC	TAGAGCATCC	TTTGACGGC	GAAGGCCACG	GCCTTCAAG	ATGGAAGCA	3120	
	GCAGCTTTTC	CACCTTCCCA	GAGACATTCT	GGATGCATTT	GCATTGAGTC	TGAAAGGGGG	3180	
	CTTGAGGGAC	GTTTGTGACT	TCTTGGCGAC	TGCCCTTTGT	GTGTGGAAGA	GACTTGGAAA	3240	
	GGTCTCAGAC	TGAATGTGAC	CAATTAACCA	GCTTGGTTGA	TGATGGGGGA	GGGGCTGAGT	3300	
80	TGTGCATGGG	CCCAGTCTG	GAGGGCCACG	TAAATCGTT	CTGAGTCGTG	AGCAGTGTCC	3360	
	ACCTTGAAGG	TCTTC						

A165 Protein sequence

Gene name:  
 Unigene number:  
 Protein Accession #:  
 Signal sequence:  
 Transmembrane domains:  
 VGM domains:  
 EGF domains:  
 Cellular Localization:

ESTs  
 Hs.157601  
 none found  
 1-17  
 none found  
 49-223; 341-518; 529-706  
 298-333; 715-748  
 secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
MPFFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
MVFKGGRRET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
FAVGVRFRPW EELHALASEP RQGHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVFKRFV RAVLSBDSRA RVGVATYSRE LLVAVPVGEY QDVFDLVWSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSATRT GQDRPRRVV LLTESHSEDE VAGPARHARA RELLLLGVS 480
EAVRAELEEI TGSPPKHMVY SDPQDLFNQI PELQGKLCR QRPQCRTQAL DLVFMLD TSA 540
SVGPENFAQM QSFVRSCALQ FEVNPDVTV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLGGVGSA GTALLHIYDK VMTVQRGAR GVPKAVVLT GGRGAEDAAV PAQKLRRNGI 660
SVLVVGVGPV LSEGLRRLAD PRDSLHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP 720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCS QGWILETPLR HMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP

```

A166 DNA sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR  
 Unigene number: Hs.37744  
 Probeset Accession #: AA011176  
 Nucleic Acid Accession #: AF272890  
 Coding Sequence: 87-1520 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
TGCTACCCGC GCCCGGGCTT CTGGGGTGTG CCCCACCCAC GCGCCAGCCC TGCCACACCC 60
CCCCCCCCCG GCCTCCGCGC CTGCGCATGG GCGCGGGGGT GCTCGTCTCG GCGCGCTCCG 120
AGCCCGGTAA CCTGTGCTCG GCGGCACCGC TCCCGGACGG GCGCGCCACC GCGCGCGGGC 180
TGCTGGTGCC CGCGTCGCGC CCGGCCTCGT TGCTGCCTCC GCGCAGCGAA AGCCCCGAGC 240
CGCTGTCTCA GCAGTGGACA GCGGGCATGG GTCTGCTGAT GCGGCTCATC GTGCTGCTCA 300
TCGTGGCGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCCGCGG CTGCAGACGC 360
TCACCAACCT CTTTCATCAT TCCCTGGCCA GCGCCGACCT GGTTCATGGG CTGCTGCTGG 420
TGCCGTTTCG GCGGCACCAT GTGGTGTGGG GCGGCTGGGA GTACGGCTCC TTCTTCTGCG 480
AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540
TTGCCCTGGA CCGCTACCTC GCCATCACCT CGCCCTTCCG CTACCCAGAG CTGCTGACGC 600
GCGCGCGGGC GCGGGGCTCT GTGTGCACCG TGTGGGCCAT CTCGGCCCTG GTGTCTCTCC 660
TGCCCATCCT CATGCACCTG TGGCGGGCGG AGAGCGACGA GCGCGCGCGC TGCTACAAAC 720
ACCCCAAGTG CTGCGACTTC GTCACCAACC GGGCCTACGC CATCGCCTCG TCCGTAGTCT 780
CCTTCTACGT GCCCTGTGTC ATCATGGCCT TCGTGTACCT GCGGGTGTTC CGCGAGGCCC 840
AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCCGTTT CCTCGCGCGC CCAGCGCGGC 900
CGCCCTCGCC CTCGCCCTCG CCGTCCCGCG GCGCGCGCGC GCGCGCGCGA CCGCGCGCGC 960
CGCGCGCGCG CGCGCCACCG GCCCGCTGG CCAACGGGCG TGCGGGTAAG CGCGCGCCCT 1020
CGCGCCTCGT GGCCTACGCG GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG 1080
TCTTACGCTT GTCTGCTGCT CCCTTCTTCC TGGCCAACGT GGTGAAGGCC TTCCACCGCG 1140
AGCTGGTGCC CGACCGCTCT TTCGTCTTCT TCAACTGGCT GGGCTACGCC AACTCGGCCT 1200
TCAACCCCAT CATCTACTCG CGCAGCCCG ACTTCCGCAA GGCCTTCCAG GGACTGCTCT 1260
GCTGCGCGCG CAGGGCTGCC CGCGCGCGCC ACGCGACCCA CGGAGACCGG CCGCGCGCCT 1320
CGGGCTGTCT GGCCCGGGCC GAGCCCGCGC CATCGCCCGG GCGCGCCTCG GACGACGACG 1380
ACGACGATGT CGTCGGGGCC ACGCCGCGCG CGCGCCTGCT GGAGCCCTGG GCGCGCTGCA 1440
ACGCGCGGGC GCGCGCGGAC AGCGACTCGA GCCTGGACGA GCGGTGCCGC CCGCGCTTCG 1500
CCTCGGAATC CAAGGTGTAG GCGCCGCGCG GGGCGCGCGA CTCGGGCGAC GGCTTCCCAG 1560
GGGAACGAGG AGATCTGTGT TTACTTAAGA CCGATAGCAG GTGAACCTGA AGCCACAAT 1620
CCTCGTCTGA ATCATCCGAG GCAAAGAGAA AAGCCACGGA CCGTGCACA AAAAGGAAAG 1680
TTTGGGAAGG GATGGGAGAG TGGCTTGTG ATGTTCCTTG TTG

```

A167 Protein sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR  
 Unigene number: Hs.37744  
 Protein Accession #: AA011176  
 Signal sequence: none found  
 Transmembrane domains: 62-84, 95-117, 135-157, 177-198, 226-248  
 Pfam domain: 7tm\_1 [75-377]  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MGAGVLVLGA SEPGNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQWTAG 60
MGLMLALIVL LIVAGNVLVI VAIKTPRLQ TLTNLFIMSL ASADLVMGLL VVPFGATIVV 120

```

WGRWEYGSFF CELWTSVDVL CVTASIELTC VIALDRYLAI TSPFRYQSLI TRARARGLVC 180  
 TWVAISALVS FLPILMHWR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM 240  
 AFVYLRVFRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPF RPAATAATAP 300  
 LANGRAGKRR PSRLVALREQ KALKTLGIIM GVFTLCWLPF FLANVVKAFH RELVDPRLFV 360  
 FFWNLGYANS AFNPPIYCRS PDRKAFQGL LCCARRAARR RHATHGDRPR ASGCLARPGP 420  
 PPSPGAASDD DDDDVVGATP PARLLEPWAG CNGGAAADSD SSLDEPCRPG FASESKV

**Al68 DNA sequence**

Gene name: CEGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Nucleic Acid Accession #: AJ400877  
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 GCGCTCCGCG CACACCTCCC CGCGCCGCGC CCGCCACCGC CCGCACTCCG CCGCCTCTGC 60  
 CCGCAACCGC TGAGCCATCC ATGGGGGTCG CCGGCCGCAA CCGTCCCGGG GCGGCCTGGG 120  
 CGGTGCTGCT GCTGCTGCTG CTGCTGCGCG CACTGCTGCT GCTGGCGGGG GCGCTCCCGC 180  
 CCGGTCCGGG CCGTGCCTCG GGGCCGCAAG AGGATGTAGA TGAGTGTGCC CAAGGGCTAG 240  
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCTTACAAG TGCTCTTGCA 300  
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAAATGAGC 360  
 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGTT 420  
 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG 480  
 AGAACAAATG CCGCTGCCAG CATACCTGTG TCAACGTCAT GGGGAGCTAT GAGTGTGCTG 540  
 GCAGGAGGGG GTTTTTCTCT AGTGACAATC AGCACACCTG CATTCACCGC TCGGAAGAGG 600  
 GCCTGAGCTG CATGAATAAG GATCAGGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660  
 GCAGGCTCGC CTGTGAGTGC AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720  
 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780  
 GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840  
 AGCGAGAGGA CACTGTCTGT GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900  
 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAA TGGAGCTGTG 960  
 ACCGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGCTCTGTT GGATTCACCT 1020  
 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT 1080  
 GTGATCATT TCGCAAAAAC ATCGTGGGCA GTTTTGACTG CCGCTGCAAG AAAGGATTTA 1140  
 AATTATTAA CAGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT 1200  
 GTGACCAAG CTGCATCAAC CACCCTGGCA CATTTGCTTG TGCTTGCAAC CGAGGGTACA 1260  
 CCCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320  
 GTGAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CCTGGGTACA 1380  
 AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCCGCCC ACAAGTGTGT 1440  
 CACCCCGTGT GTCCCTGCAC TGGCGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT 1500  
 GTCACTCTGG CATTCACCTC TCTTCAGATG TCACCACCAT CAGGACAAGT GTAACCTTTA 1560  
 AGCTAAATGA AGGCAAGTGT AGTTTGAAAA ATGCTGAGCT GTTTCGCGAG GGTCTGCGAC 1620  
 CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT 1680  
 GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCACCCCT AAGGAAATGT 1740  
 TTATCACTGT TGAGTTTGAG CTTGAAACTA ACCAAAAGGA GGTGACAGCT TCTTGTGACC 1800  
 TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACCTCAGAA 1860  
 AGGCGGTCCA TTTCACTTCC AGCTCTCAGG CATGAACCTC CAGTGGGCTA 1920  
 AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCTTG TGGAGTGGGC CAGGGTCATG 1980  
 CAGAAAACCA ATGTGTGAGT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAAGCT 2040  
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT 2100  
 GCCCAAGACC AGGAAATTCT GGGGCCCTGA AGACCCGAGA AGCTTGAAT ATGTCTGAAT 2160  
 GTGGAGGTCT GTGTCAACCT GGTGAATATT CTGCAGATGG CTTTGCACCT TGCCAGCTCT 2220  
 GTGCCCTGGG CAGTAAAGCT CCGTGAAGCTG GTCGAACTTC CTGCTTCCCC TGTGGAGGAG 2280  
 GCCTTGCCAC CAACATCAGG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT 2340  
 GTTCACTGG ACATTTCTAC AACACCACCA CTCACCGATG TATTCGTTGC CCAGTGGGAA 2400  
 CATACCAGCC TGAATTTGGA AAAAATAATT GTGTTTCTTG CCCAGGAAAT ACTACGACTG 2460  
 ACTTTGATGG CTCCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520  
 GAGATTTTAC TGGGTACATT GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACACCG 2580  
 AGTGTACGTG GACCATCAAC CCACCCCCCA AGCGCCGCTG CCTGATCGTG GTCCCTGAGA 2640  
 TCTTCCCTGC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTTCTCAT 2700  
 CCAATTCTGT GACAACATAT GAAACCTGCC AGACCTACGA ACGCCCCATC GCCTTCACCT 2760  
 CCAGGTCAAA GAAGCTGTGG ATTCAATTCA AGTCCAATGA AGGGAACAGC GCTAGAGGGT 2820  
 TCCAGGTCCC ATACGTGACA TATGATGAGG ACTACCGAGA ACTCATTGAA GACATAGTTC 2880  
 GAGATGGCAG GCTCTATGCA TCTGAGAACC ATCAGGAAAT ACTTAAGGAT AAGAACTTA 2940  
 TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAAGTAC ACAGCCCAGG 3000  
 AGTCCCGAGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT 3060  
 TTTTGAGACC TTACAAATGA CTCAGCCCACT GTGCCACTCA ATACAAATGT TCTGCTATAG 3120  
 GGTTGGTGGG ACAGAGCTGT CTTCTTCTG CATGTCAGCA CAGTCGGGTA TTGCTGCCTC 3180  
 CCGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGGTAAATT 3240  
 GAACCTTGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300  
 CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CCGGCTGGCT GAGCTGAGCT 3360  
 TTGCTGAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTACTCTTCC TCAAGGAGTC 3420  
 TGTAGTGGAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTTCAGC TTCCTCTAGC 3480  
 CCGGCCCTCT CTAAGGGAGC CCTCTGCAC CTGTGCGAGG CTTCTGACAG GCAGAACAGG 3540  
 CAAGAGGGGA GGGAGGGAGA CCCCTGCAGG CTCCTCCAC CCACCTTGAG ACCTGGGAGG 3600  
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACCTG 3660  
 AGTTCTAAGC AGTGCTCGTG AAAAAAAGAA GCAGAAAGAA TTAGAAATAA ATAAAACTA 3720  
 AGCACTTCTG GAGACAT

**Al69 Protein sequence**

Gene name: CEGP1  
 Unigene number: Hs.222399

Probeset Accession #: AA256485  
 Protein Accession #: CAB92285  
 Signal sequence: 1-31  
 Transmembrane domains: none  
 PFAM domains: EGF-like\_domains [49-84,132-167,177-213,286-321,407-442] CUB\_domain [809-918]  
 Cellular Localization: may be secreted

10 1 11 21 31 41 51  
 | | | | | |  
 MGVAGRNRPQ AANAVLLLLL LPLPLLLLAG AVPPGRGRRA GPQEDVDECA QGLDDCHADA 60  
 LCQNTPTSYK CSCKPGYQGE GRQCEDIDEC GNEINNGGCVH DCLNIPGNYS CTCFDGFMFLA 120  
 HDGHNCLDND ECLNNGGCGQ HTCVNVMGSY ECCCKEGFFL SDNQHTCIHR SEEGLSGMNK 180  
 15 DHGCSHICKE APRGSVACEC RPFELAKNQ RDCILTCNHG NGGCQHSCHD TADGPECSCH 240  
 PQYKMHDTGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCRTCKDT 300  
 STGVHSCSPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFLLTDEK 360  
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCQVQCVN 420  
 TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480  
 20 SSVDTTIRTS VTFKLNEGKC SLKNAELFPE GLRPALEPKH SSVKESFRYV NLTCSSGKQV 540  
 PGAPGRPSTP KEMFITVEFE LETNQKEVIA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600  
 FHLQLSGMNL DVAKKPPRTS ERQAESCQVG QGHAEQCQVS CRAGTYDGA RERCILCPNG 660  
 TFQNEEQGMT CEPCPRPONS GALKTPAWN MSECGGLCQP GEYSADGFAP CQLCALGTFFQ 720  
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHFY NTTTHRCIRC PVGTYPQPEFG 780  
 25 KNNCVSCPGN TTTDFDGSIN ITQCKNRRCG GELGDFGTGI ESPNYPGNYP ANTECTWTIN 840  
 PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSNSNVTTY ETCQTYERPI AFTSRSKKLW 900  
 IQPKSNEGNS ARGFQVPYVT YDEYQELIE DIVRDGLRYA SENHQEILKD KKLKALFDV 960  
 LAHPQNYFKY TAQESREMPF RSFIRLLRSK VSRFLRPYK

#### A170 DNA sequence

Gene name: DEME-6 protein (KIAA0452)  
 Unigene number: Hs.125783  
 Probeset Accession #: AL039402  
 Nucleic Acid Accession #: AF007170  
 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

35 1 11 21 31 41 51  
 | | | | | |  
 AAGGAGGCGG CCTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60  
 CTGGACCACT CAGTACACGC CCTGGACCTC TTCCTCACCA ACCAGTTCTC AGAAGCACTC 120  
 40 AGCTACCTCA AGCCACAGAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180  
 CTGGAGATGC AGGCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCAACATG 240  
 ATGAAGGAGG CACAGATGCT GTGTGAGAG CACCGGAGGA AGTCTTCTGT AACAGATTCC 300  
 TTCAGCAGCC TGGTGAACCG CCCACGCTG GGCCAATTCA CTGAAGAAGA AATCCACGCT 360  
 GAGGTCTGCT ATGCAGATG CCTGCTGCAG CGAGCAGCCC TGACCTTCCT GCAGGACGAG 420  
 45 AACATGCTGA GCTTCATCAA AGGCGGCATC AAAGTTCGAA ACAGCTACCA GACCTACAAG 480  
 GAGCTGGACA GCCTTGTGTA GTCCCTCAAA TACTGCAAGG GTGAGAACCA CCGCACTTT 540  
 GAAGGAGGAG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCTCTAT 600  
 AGGATCCTGA GGCTGTTGGA GTTTGTGGGG TTTTCAGGAA ACAAGGACTA TGGGCTGCTG 660  
 CAGCTGGAGG AGGAGCGCTC AGGGCACAGC TTCGCTCTG TGCTCTGTGT CATGCTCCTG 720  
 50 CTGTGCTACC ACACCTTCTC CACTTTCGTG CTCGCTACTG GGAACGTCAC CATCGAGGAG 780  
 GCCGAGAAGC TCTTGAAGCC CTACCTGAAC CGGTACCTTA AGGGTGCCAT CTTCTCTGTT 840  
 TTTGCAAGGA GGATTAAGT CATTAAAGGC AACATTGATG CAGCCATCCG GCGTTTCGAG 900  
 GAGTGCTGTG AGGCCACGCA GCACTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960  
 55 ATGTGGTGCT TCACCTACAA GGGCCAGTGG AAGATGTCTT ACTTCTACGC CGACCTGTCT 1020  
 AGCAAGGAGA ACTGCTGTGT CAAGGCCACC TACATTTACA TGAAGGCCGC CTACCTCAGC 1080  
 ATGTTTGGGA AGGAGGACCA CAAGCCGCTC GGGGACGACG AAGTGAATTT ATTTGAGACT 1140  
 GTGCCAGGCC TGAAGCTCAA GATTGCTGGG AAATCTCTAC CCACAGAGAA GTTTGCCATC 1200  
 CGGAAGTCCC GGCCTACTT CTCTTCCAA CCTATCTGCG TGCCAGTGCC TGCTCTGGAA 1260  
 60 ATGATGTACA TCTGGAACCG CTACGCCGTG ATTGGGAAGC AGCCGAAACT CACGATGGG 1320  
 ATACTTGAGA TTATCACTAA GGCTGAAGAG ATGCTGGAGA AAGGCCCAGA GAACGAGTAC 1380  
 TCAGTGGATG ACGAGTGCTT GGTGAAATTT TTGAAAGGCC TGTGTCTGAA ATACCTGGGC 1440  
 CGTGTCCAGG AGGCCGAGGA GAATTTTAGG AGCATCTCTG CCAATGAAAA GAAGATTAAA 1500  
 TATGACCACT ACTTGATCCC AAACGCCCTG CTGGAGCTGG CCCTGCTGCT TATGGAGCAA 1560  
 65 GACAGAAACG AAGAGGCCAT CAAACTTTTG GAATCTGCCA AGCAAAACTA CAAGAATTAC 1620  
 TCCATGGAGT CAAGGACACA CTTTGAATC CAGGCAGCCA CACTCCAAGC CAAGTCTTCC 1680  
 CTAGAGAACA GCAGCAGATC CATGGTCTCA TCAGTGTCTT TGTAGCTTTG TGCAGCAGTT 1740  
 CCGGGCTGGA AGACAGAGAC AGCTGGACAG AGCTCCTGAA AACATTTCAA AATACCCCTT 1800  
 CCCCCTGCCC TGCCCTGCCT TTGGGGTCCA CCGGCACTCC AGTTGGATGG CACAACATAG 1860  
 70 TGTATCCGTG CAGAAGCCGA GCTGGCATT TCAACAGTGT AGCCAAGGGC CTTTGCCCAAG 1920  
 GGCAGAGCAG GTGGAGCCCT CTGCCTGCCC TATCACACAT ACGGGTACTT GCTTTTCACT 1980  
 GTGATGTTTA AGAGAATGTA TGAACAGTTT ACATTTTCCT TAGAAATACA TTGATGGGAT 2040  
 CACAGTTGGC TTTAAAAACC AACAAATC AACCACCTGT AAGTCTTTGT CTTACCTTAT 2100  
 TATCATCTGG AGGTAAATCT CTTTATATGA TGTATGCCAA GGGCAAATGT CTTTCAAAT 2160  
 75 TCAGCAAGTT CTCAGCTTGT GTGACGGAAG GTCCTTCAGA GGACCTGAGG AATGCCTGGG 2220  
 AGAGGCTAAG CCTCAGGCTT CAATGCTTCT GGGGTGAGG ATGAGGATGT ACACAGACAC 2280  
 CCACTACCTT ACTACTCACA CTCCTTTTGT AAATTTTCAA TTTAAAAATC 2340  
 AAGCAGCTCT TTTTGTAGT ATAAATCTG AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400  
 AGTAGAAAAAT GCCAGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460  
 80 AAATTTGGGG GGCAGGAGGA GGTTCCTAGA ATCCAGCTG TATCTTTGCT GTATGCCAAA 2520  
 CTGAAACCACT TGGGAATAAT TTATGAAACA TAAAAATCTT CTGTACTTCA CTCCAAGGTA 2580  
 CATTTGCTTA CTGACAGCAT TTTTGTTAAA ACTGTTATTC TTGAAAAAAA AAAAAAAA 2640  
 AA

#### A171 Protein sequence

Gene name: DEME-6 protein (KIAA0452)  
 Unigene number: Hs.125783  
 Probeset Accession #: AL039402  
 Protein Accession #: AAC39582  
 Signal sequence: none  
 Transmembrane domains: 210-226  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MTALDLFLTN QFSEALSYLEK PRTKESMYHS LTYATILEMQ AMMTFDPQDI LLAGNMMKEA 60  
 QMLCQRHRRK SSVTDSFSSL VNRPTLGQFT EEEIHAEVCY AECLLQRAAL TFLQDENMVS 120  
 FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHFEGGV KLGVGAFNLT LSMLPTRLIR 180  
 LLEFVGFSGN KDYGLLQLEE GASGHSFRSV LCVMLLLCYH TFLTFLVLTG NVNIEEAEKL 240  
 LKPYLNRYPK GAIFLFFAGR IEVIKGNIDA AIRRFEECCE AQQHWKQFHH MCYWELMWCF 300  
 TYKGQWKMSY FYADLLSKEN CWSKATYIYM KAAVLSMFGK EDHKPFQDDE VELFRAVPGL 360  
 KKKIAGKSLP TEKFAIRKSR RYFSSNPISL PVPALMMYI WNGYAVIGKQ PKLTDGILEI 420  
 ITKAEEMLEK GPENEYVDD ECLVKLLKGL CLKYLGRVQE AEENFRSISA NEKKIKYDHY 480  
 LIPNALLELA LLLMEQDRNE EAIKLLLESAK QNYKNYSMES RTHFRIQAAT LQAKSSLENS 540  
 SRSMVSSVSL

# A172 DNA sequence

Gene name: EST  
 Unigene number: Hs.200102  
 Probeset Accession #: AL117406  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-4044 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGACTAGGA AGAGGACATA CTGGGTGCC AACTCTTCTG GTGGCCTCGT GAATCGTGCC 60  
 ATCGACATAG GCGATGACAT GGTTCAGGA CTTATTTATA AAACCTATAC TCTCCAAGAT 120  
 GGCCCTCGGA GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCACCG 180  
 TGGGGGAAGT ATGATGCTGC CTTGAGAACC ATGATTCCCT TCCGTCCCAA GCCGAGGTTT 240  
 CCTGCCCCCC AGCCCTCGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC 300  
 ACCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCTCCACTG 360  
 TCAGTCCATG ATGCCTCAGA CAAAATGTC CAAAGGCTTC ACCGCCTTG GGAAGAAGAA 420  
 GTCTCAAGGC GAGGGATTGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA 480  
 ACAAGGTTGA TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATTGCCAG TGTACTCGGG 540  
 CCAATATTGA TTATACCAA GATCTCGGAA TATTCAGAA AGCAGTTGGG GAATGTTGTC 600  
 CATGGAGTGG GACTCTGTCT TGCCCTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTT 660  
 TCCTCCAGTT GGATCATCAA CCAACGCACA GCCATCAGGT TCCGAGCAGC TGTTTCTCTC 720  
 TTTGCTTTG AGAAGCTCAT CCAATTTAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC 780  
 ATCAGCTTCT TCCACGGTGA TGTAAGTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA 840  
 GTACTGATCA CCTGCGCATC GCTGGTCATC TGCAGCATTT CTCTCTACTT CATATTGGA 900  
 TACTGTGAT TATTGTCCAT CTTATGCTAT CTCTGGTTT TCCCACTGGC GGTATTATG 960  
 ACAAGAATGG CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGCGACCA GCGCATCCGT 1020  
 GTGACCACTG AAGTTCTCAC TTGCATTAA CTGATTAAAG TGTACACATG GGAGAAACCA 1080  
 TTTGCAAAAA TCATTGAAGT TATGGAAGT CTGACTTTCT GCTCCAAAC TGGTGATGGC 1140  
 ATGGCCTTCA GCATGTGGC CTCTTGAAT CTCCTTCGGC TGTGAGTTT CTTTGTGCTT 1200  
 ATTGCAGTCA AAGGTCTCAC GAATTCGAAG TCTGCAGTGA TGAGGTTCAA GAAGTTTTTC 1260  
 CTCAGGAGA GCGCTGTTTT CTATGTCCAG ACATACCAAG ACCCCAGCAA AGCTCTGGT 1320  
 TTTGAGGAG CCACCTTGTG ATGGCAACAG ACCTGTCCCG GGATCGTCAA TGGGGCACTG 1380  
 GAGCTGGAGA GGAACGGGCA TGCTTCTGAG GGGATGACCA GGCTTAGAGA TGCCCTCGGG 1440  
 CCAGAGGAAG AAGGGAACAG CCTGGGCCA GAGTTGCACA AGATCAACCT GGTGGTGTCC 1500  
 AAGGGGATGA TGTTAGGGGT CTGCGGCAAC ACGGGGAGTG GTAAGAGCAG CCTGTTGTCA 1560  
 GCCATCTGG AGGAGATGCA CTTGCTCGAG GGCTCGGTGG GGGTGCAGGG AAGCCTGGCC 1620  
 TATGTCCCCC AGCAGCCCTG GATCGTCAGC GGAACATCA GGGAGAACAT CCTCATGGGA 1680  
 GGCATATG ACAAGGCCG ATACCTCCAG GTGCTCCACT GCTGCTCCCT GAATCGGGAC 1740  
 CTGGAACCTC TGCCCTTTGG AGACATGACA GAGATTGGAG AGCGGGGCTT CAACCTCTCT 1800  
 GGGGGGAGAGA AACAGAGGAT CAGCCTGGCC CGCGCCGTCT ATTCCGACCG TCAGATCTAC 1860  
 CTGCTGGAGC ACCCCTGTG TGCTGTGGAC GCCACGTGG GGAAGCACAT TTTTGAGGAG 1920  
 TGCATTAAGA AGACACTCAG GGGGAAGACG GTCGTCTGG TGACCCACCA GCTGCAGTAC 1980  
 TTAGAATTTT GTGGCCAGAT CATTTTGTTG GAAATGGGA AAATCTGTGA AAATGGAAC 2040  
 CACAGTGAGT TAATGCAGAA AAAGGGGAAA TATGCCCAAC TTATCCAGAA GATGCACAA 2100  
 GAAGCCACTT CGGACATGTT GCAGGACACA GCAAAGATAG CAGAGAAGCC AAAGGTAGAA 2160  
 AGTCAGGCTC TGGCCACCTC CTGGAAGAG TCTCTCAACG GAAATGCTGT GCCCGAGCAT 2220  
 CAGCTCACAG AGGAGGAGGA GATGGAAGAA GGCTCCTTGA GTTGGAGGGT CTACCCACC 2280  
 TACATCCAGG CAGCTGGAGG TTACATGGTC TCTTGATATA TTTTCTCTT CGTGGTGCTG 2340  
 ATCGTCTTCT TAACGATCTT CAGCTTCTGG TGGCTGAGCT ACTGTTTGA GCAGGGCTCG 2400  
 GGGACCAATA GCAGCCGAGA GAGCAATGGA ACCATGGCAG ACCTGGGCAA CATTGCAGAG 2460  
 AATCTCTAAC TGTCCTTCTA CCAGCTGGTG TACGGGCTCA ACGCCCTGCT CCTCATCTGT 2520  
 GTGGGGGTCT GCTCCTCAGG GATTTTCACC AAAGTCACGA GGAAGGCATC CACGGCCCTG 2580  
 CACAAACAAG TCTTCAACAA GGTTTTCCGC TGCCCCATGA GTTTCTTTGA CACCATCCCA 2640  
 ATAGGCCGGC TTTTGAACAG CTTGCGAGGG GACTTGAAC AGCTGGACCA GCTCTTGCCC 2700  
 ATCTTTTCTG AGCAGTCTCT GGTCTGTGCT TTAATGGTGA TCGCCGTCTT GTTGATTGTC 2760  
 AGTGTGCTGT CTCCATATAT CCGTGTAAAG GGAGCCATAA TCATGGTTAT TTGCTTCATT 2820  
 TATTATATAT TGTTCAGAA GGCCATCGGT GTGTTCAAGA GACTGGAGAA CTATAGCCGG 2880  
 TCTCTTTAT TCTCCACAT CCTCAATTCT CTGCAAGGCC TGAGCTCCAT CCATGCTCTAT 2940  
 GGAATAAAGT AAGACTTCTC CAGCCAGTTT AAGAGGCTGA CTGATGCGCA GAATAACTAC 3000  
 CTGCTGTTGT TTCTATCTTC CACACGATGG ATGGCATTGA GGCTGGAGAT CATGACCAAC 3060  
 CTTGTGACCT TGGCTGTGTC CCTGTTCGTG GCTTTTGGCA TTTCCTCCAC CCCCTACTCC 3120



TTTAAAGTCA TGGCTGTCAA CATCGTGTCTG CAGCTGGCGT CCAGCTTCCA GGCCACTGCC 3180  
 CGGATTGGCT TGGAGACAGA GGCACAGTTC ACGGCTGTAG AGAGGATACT GCAGTACATG 3240  
 AAGATGTGTG TCTCGGAAGC TCCTTTACAC ATGGAAGGCA CAAAGTGTCC CCAGGGGTGG 3300  
 CCACAGCATG GGGAAATCAT ATTTCCAGGAT TATCACATGA AATACAGAGA CAACACACCC 3360  
 ACCGTGCTTC ACGGCATCAA CCTGACCATC CGCGGCCACG AAGTGGTGGG CATCGTGGGA 3420  
 AGGACGGGCT CTGGGAAGTC CTCTTGGGC ATGGCTCTCT TCCGCCTGGT GGAGCCCATG 3480  
 GCAGCCCGGA TTCTCATTTA CGGCGTGGAC ATTTGCAGCA TCGGCTTGA GGAAGTGGCG 3540  
 TCCAAGCTCT CAGTGATCCC TCAAGATCCA GTGCTGCTCT CAGGAACCAT CAGATTCAAC 3600  
 CTAGATCCCT TTGACCGTCA CACTGACCAG CAGATCTGGG ATGCTTGA GAGGACATTC 3660  
 CTGACCAAGG CCATCTCAAA GTTCCCAAAA AAGCTGCATA CAGATGTGGT GGAAAACGGT 3720  
 GGAAACTTCT CTGTGGGGGA GAGGCAGCTG CTCTGCATTG CCAGGGCTGT GCTTCGCAAC 3780  
 TCCAAGATCA TCCTTATCGA TGAAGCCACA GCCTCCATTG ACATGGAGAC AGACACCCCTG 3840  
 ATCCAGCGCA CAATPCGTGA AGCCTTCAG GGCTGCACCG TGCTCGTCAT TGCCACCCGT 3900  
 GTCACCATG TGCTGAAGT TGACCATATC CTGGTTATGG GCAATGGGAA GGTGGTAGAA 3960  
 TTTGATCGGC CGGAGGTACT GCGGAAGAAG CCTGGGTCAT TGTTCGAGC CCTCATGGCC 4020  
 ACAGCCACTT CTCTACTGAG ATAAGGAGAT GTGGAGACTT CATGGAGGCT GGCAGCTGAG 4080  
 CTCAGAGGTT CACACAGGTG CAGCTTCGAG GCCCAGATC TGCGACCTTC TTGTTTGGAG 4140  
 ATGAGAACTT CTCCTGGAAG CAGGGGTAAA TGTAGGGGGG GTGGGGATTG CTGGATGGAA 4200  
 ACCCTGGAAT AGGCTACTTG ATGGCTCTCA AGACCTTAGA ACCCCAGAAC CATCTAAGAC 4260  
 ATGGGATTCA GTGATCATGT GTTCTCTCTT TTAACCTTACA TGCTGAATAA TTTTATAATA 4320  
 AGGTAAAAGC TTATAGTTT CTGATCTGTG TTAGAAGTGY TGCAATGCT GTACTGACTT 4380  
 TGTAAATAT AAAACTAAGG AAAACTCAAA AAAAAA AAAAAA

**A173 Protein sequence**

Gene name: EST  
 Unigene number: Hs.200102  
 Probeset Accession #: AL117406  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 169-185, 199-215, 275-291, 304-320, 387-403, 770-786, 829-845, 907-923, 927-943, 1018-1034  
 PFAM domains: ABC\_transporter [502-673], ABC\_membrane\_region [163-432, 771-1060]  
 ATP-binding\_domains [508-516, 1139-1147]  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | | |  
 MTRKRTYVWP NSSGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQERNP EAPGRAAVPP 60  
 WGKYDAALRT MIPFRPKPRF PAPQPLDNAG LFSYLTVSWL TPLMIQSLRS RLDENTIPPL 120  
 SVHDASDKNV QRLHRLWEEE VSRRGIEKAS VLLVMLRFQR TRLIFDALLG ICFCIASVLG 180  
 PILIIPKILE YSEBQLGNV HGVGLCFALF LSECVKLSLF SSSWIINQRT AIRFRAAVSS 240  
 FAPEKLIQFK SVIHITSGEA ISFTTGDVNY LFEGVCYGPL VLITCASLVI CSISSYFIIG 300  
 YTAFAIALCY LLVFLAVFM TRMAVKAQHH TSEVSDQIRI VTSEVLTCIK LIKMYTWEKP 360  
 FAKIIEGMES LTFCKPGDG MAFSMLASLN LLLSVFFVP IAVKGLTNSK SAVMRFKKFF 420  
 LQESPVFYVQ TLQDPSKALV FEEATLSWQQ TCGIVNGAL ELERNHASE GMTRPRDALG 480  
 PEEEGNSLGP ELHKINLVVS KGMMLGVCGN TSGSKSSLLS AILEEMHLE GSVGVQGSLS 540  
 YVPQQAIVS GNIRENLMG GAYDKARYLQ VHHCCSLNRD LELLFPDGT EIGERGLNLS 600  
 GGQQRISLA RAVYSDRIY LLDDPLSAVD AHVGKHIFEE CIKKTLRGKT VVLVTHQLQY 660  
 LEFCGQIILL ENKICENG T HSELMQKKGK YAQLIQMHK EATSDMLQDT AKIAEKPKVE 720  
 SQALATSLEE SLNNAVPEH QLTQEEEMEE GSLSWRVYHH YIQAGGYMV SCIFFFVVL 780  
 IVFLTIFSFV WLSXWLEQGS GTNSSRESNG TMADLGNLAD NPQLSFYQLV YGLNALLLIC 840  
 VGVCSGIFT KVTRKASTAL HNKLFNKVFR CPMSFFDTIP IGRLLNCFAG DLEQLDQLP 900  
 IFSEQFLVLS LMVIAVLIV SVLSPIYLLM GAIIMVICFI YMMFKKAIK VFKRLNYSR 960  
 SPLFSHILNS LQGLSSIHVY GKTEDFISQF KRLTDAQNNY LLLFLSSTRW MALRLEIMTN 1020  
 LVTLAVALFV LQGISSTPYS FKVMVNIIVL QLASSFQATA RIGLETEAQF TAVERILQYM 1080  
 KMCVSEAPLH MEGTSCPGW PQHGEIIFQD YHMKYRDNTF TVLHGINLTI RGEHVVGIVG 1140  
 RTSGKSSLS MALFRLVEPM AGRILIDGVD ICSIGLEDLR SKLSVIPQDP VLLSGTIRFN 1200  
 LDPPDRHTDQ LTKAISFPK KLHTDVVENG GNFSVGERQL LCIAARAVLRN 1260  
 SKIILIDEAT ASIDMETDTL IQRTIREAFQ GCTVLVIAHR VTTVLNCDHI LVMGNKGKVE 1320  
 FDRPEVLRRK PGSFAALMA TATSSLR

**A174 DNA sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | | |  
 ATGCTGTCTG GCTTCTTGAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60  
 GGAAGAAAC TCCGTGGGA GGCTTCCATC GGTGCACACA CCTCCGAGG GCGAGGCGAGC 120  
 GACCGGGAGA GGGAGAGCCG GCCGGAGGCT GCCGGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCTC GGATCCGCGC CCAGCAGCAGT 240  
 CCGCGGCCGC CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCTC 300  
 CGCCTGCGTC CTGGACGTTT CCGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360  
 TCCGACGACG AGCCCGGGG GCCTTCTGAC TGCATCCCGA GATTTCATC AGCAGTGCA 420  
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 GCTCTCTGAC CTAGGCCCCG CGTCTGTCGC CTCCTGGGCG TCGCGGCAGA GGGGAGTGGC 540  
 CCGCGGGGAA AGCGCGCCGC GACAGTCAGT GACGAGGCCG GGGGGTCCG GGGGCCACGA 600  
 CTTCTCGGAG ACCGTCCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660  
 TGTGGGGCGC TCGCGCTCGT TCCGTCTCCT CATCTGGGAA CGCGGCTCG CTCCTGCAGC 720  
 TGCTGCTGCG TCGCTGCTG GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780

5 TGGCTGGACG CGCAGGGCGT CTGGCGCATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840  
 GGCGACGCCA CCATCTGCTG CGGCGAGTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900  
 GCGCGCCTGG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960  
 CGGGCGGACA AAGACGGGCC CGGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020  
 GGAGACGGCG AGGGTGCGCC CCCACCGTG AGGGCTGGC AGCGGTGCTC CCTGGAAGGC 1080  
 TCCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCCG TGCCAGACGC 1140  
 CGCGGATTCC CATCTTCTCC ACGCGGCGGC CCTCTCCCC TGCAGCGGCC CGCCTTGCCC 1200  
 ATCTACGTGC CGTTCCTCAT TGTGGCTCC GTGTTGTGCG CCTTTATCAT CTGCGGTGCC 1260  
 10 CTGGTGGCAG CTGTGTGCTG CAGATGTCTC CGGCCAAGC AGGATCCCCA GCAGAGCCGA 1320  
 GCCCCAGGGG GTAACCGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACCTCC 1380  
 CGGGGGTTCG CTTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440  
 GGGGCCCGGG CGCCCCAAC AAGGTACAG ACCAAGTGT GCTTGCCGGA AGGGACCATG 1500  
 AACAACTGTG ATGTCAACAT GCCACGAAT TTCTCTGTGC TGAAGTGTCA GCAGGCCACC 1560  
 CAGATTGTGC CACATCAAGG CAGATATCTG CATCCCCCAT ACGTGGGGTA CACGGTGCAG 1620  
 15 CAGCACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCCTGGCTAC 1680  
 AGGCAGATTG AGTCCCCCTT CCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740  
 ACTGTATAAC CGAGAGTCAC TGGTGGGTTC CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTCGAG GTGGAAGTCC GCACATGTGC GTGGTATTTA TGGCAGGAT CCTTTGGATG 1860  
 20 GCTTCATTTG CCCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920  
 CATCCAGGGT ATCATTTGAT TATGATGGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040  
 AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100  
 TTGTTGTTGA CTCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160  
 25 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTGTCTCTG TTGCCAGGC TGGAGTGCAG 2220  
 TGGTGGCATC TCGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCAACA CTCTGCCCTC 2280  
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTTT 2340  
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGTGCTCTC ACTCTCCTGA CCTCAAGCAA 2400  
 TCTGCCTGTC TCAGCCTCCC AAGTGTCTGG GATTACAGGC GTGAGCCACC GCCCCAGGCC 2460  
 30 TGAGCCTTTT TTTTTTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520  
 ATTCTAAAGG GAAACCTGTT TGAAGTCTGT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580  
 GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG 2640  
 GGCCTATTTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTCAAAGTG ATTTTCTACA 2700  
 TAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760  
 35 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCCCTTC 2820  
 TTGATTGTAT CTTAATTTTC TGGCTTAAAG GTGACATCTG AGAGGTAATG CATCTTTTTT 2880  
 TATATTGAAA TCATAAACTA TCACCCGCTG CTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940  
 TGGTTATGGT TTGGCGTTTC CTCTGTTTG GTTTTCAGAG CCCCATGTCT ATATAGTCCT 3000  
 GAGTGCAAGT AATTACTATA CTTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060  
 40 AAAAAATTTT TTGCTTATG TATAAAATC CAAAGAAATG TGTTACAAAG ATACTTAGTA 3120  
 TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACAGATAC GATTTACTTT 3180  
 GCAGATCATA AGGCTTTTTA TACTCTTGTT ATCAAATGG CTTATTTTTT AGGCACCTAAG 3240  
 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCCTTT CTCTCTCCAC ACTGTTCTTG 3300  
 ATTTCTCTCT TCTTTCAGGC CTCACAGGC ACTGTATTCA TTGCCAATGT TCCAAATAT 3360  
 45 CAAATTCAG TGAATTTATT TGTGTGTCT TTACTTATAT AAAAAAAGAT AACTTTAAGG 3420  
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAAGTATT TTGTAATTAA ACAAATCGCT 3480  
 GTATGGTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATTC 3540  
 TGTTCATGTA CTGAATAATG TAAACCAAGT GTTGGCAATT GTTATCATCA ATGATACTCA 3600  
 50 TTTTTTAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660  
 TGAATAAATA AAAAAAATA AAAAAAATA

A175 Protein sequence

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

60 1 11 21 31 41 51  
 | | | | |  
 MLSGFLMSPS TQHRAYQYTPG GKKLPEWASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60  
 65 GEAEGKNGRGE PPAWIRAQQQ PRPPFAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPPPEA 120  
 SGRQPRGPSD CIPRFPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG 180  
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAAPRVVP CGALAARPS PPGTPLRSCS 240  
 CCWLRCWRRG RGPSGEYCHG WLDAGQVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300  
 ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTQ GDGEGAPPPV RAWQRCSPG 360  
 70 SPKGRQLLRA PFGLLRARR RGFPSSPRGG PSFLQRPALP IYVPFLIVGS VFVAFIILGS 420  
 LVAACCCRCL RPKQDPQQSR APGGRNLMET IPMIPSASTS RGSSSRQSST AASSSSSANS 480  
 GARAPPTRSQ TNCCLPEGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGGYL HPPVVGTVQ 540  
 HDSVPMTAVP PFMDLQPGY RQIQSPFPHT NSEQKMPAV TV

A176 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 | | | | |  
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60

5	CTGAAGAAAA	AGGAGCTGGA	GCAGGAGAAG	GAGGTGCTGC	TGCAGGGTTT	GGAGATGATG	120
	GCGCGGGGCC	GCGACTGGTA	CCAGCAGCAG	CTGCAACGAG	TGCAGGAGCG	CCAGCGCCGC	180
	CTGGGCGCAG	GCAGAGCCAG	CGCCGACTTT	GGGGCTGCG	GGAGCCCCCG	CCCACTGGGG	240
	CGGCTACTGC	CCAAGGTACA	AGAGGTGGCC	CGGTGCCTGG	GGGAGCTGCT	GGCTGCAGCC	300
	TGTGCCAGCC	GGGCCCTGCC	CCCGTCTCC	TCCGGGCCCC	CCTGCCCTGC	CCTGACGTCC	360
	ACCTCACCCC	CGGTCTGGCA	GCAGCAGACC	ATCCTCATGC	TGAAGGAGCA	GAACCGACTC	420
	CTCACCCAGG	AGGTGACCGA	GAAGAGTGAG	CGCATCACGC	AGCTGGAGCA	GGAGAAGTCG	480
	GCGCTCATT	AGCAGCTGTT	TGAGGCCCCG	GCCCTGAGCC	AGCAGGACGG	GGGACCTCTG	540
10	GATTCCACCT	TGATCTAGTC	CTTGTGGGCC	GCGTGGGCCC	CCAGGGCCAG	CCTGGCACTC	600
	AGCCCTTCGA	GGGTGGGCGC	CCCATCGCAC	CCACCCTCTC	TGGCTGGAGA	CCCCCGCAG	660
	GCCCGGCGAC	AGTCCCGGAG	TGGGCGCCTT	CCTGCCGCCC	TTGCCAGATG	GGCTCCCCAG	720
	GCCTGCCCCC	GGCTGTCC	CGCACCAGGC	GCTTGACTCC	GTTTGGGCTC	CTGGTTGYTG	780
	ACATGGGCTG	GGGGCTCTCT	TGAGTCCGCA	TAGTCCGCG	CTACTACTGG	CCGCTGTGAG	840
	TGGACAGTGG	TGTACCCCTC	CATGAGTTAG	CGTCCCCCGG	TTTCCAGCGG	TGCCCGCCCTG	900
15	GGTCCCACCT	TGAGGGAAAG	GCACCTGCCA	CGCCAGGCTG	CACCTTCCAAC	AACGGGCAGC	960
	AGAGGGCGCG	GGCGGGCTCC	GACGCGGGTC	CAAGGGCAGC	TTCCCGCTCA	ACCAGGGCAC	1020
	CAGGACGAGG	TGGCTGTAGC	TGGGACGGAC	GGGAGTAGAT	GGAGGGGGTG	GGGACGGCCT	1080
	GTAAGCGGGG	GGTGCCTGCC	TGGCTGGGGA	GCCCCAGGGA	TAGCGGTGCG	ACTTCAGGTT	1140
	CTGGCCAAAG	CTGAGGGACC	CTGGCTGCG	CGGATCGGCA	CGCCGGGTGG	GCGAGAGCTT	1200
20	GGCTGTGATG	TGCTTCCAC	AGACCTGGG	GTGATGGCTT	TCCCCCTCTT	GGCCGGGACG	1260
	TTGCCCCACG	TTGAGTCCCA	CACAACATCC	TGTGAGCCTG	GCTCCCCAGG	AGGGCCCCCA	1320
	GACAGCTCCC	AGGCACGTCA	TAGGCAAAAG	CTGTTTCCCC	CGACTCAGGA	TTTCCAAGGC	1380
	CTGGGGTCTT	GCTCACCCCT	CTTGTCTCTC	ACGCCAGCG	TGTCCCCAGG	TTTCACTGCG	1440
	GAGAGGCCAC	CTCCCTCAGC	CAAGGAAAG	GAGAACCCTC	AGGGTACAGG	AGGAGGCTGG	1500
25	GGCAGGTCCC	CTTGGGTGTC	ACTCCCTCAG	CCCCTGCCCA	GGCCCACTCC	CGCTGGTGCT	1560
	GGAGTACGCA	CTGGTGGGGG	GGCCCTGCTC	AGCCCCAACC	GGAGGGTCCC	AGTGTACCCA	1620
	GAACCAAGGG	CACGGCAACA	GCATCGATGG	GTTCTGCAGC	CCAGGGCCCC	CGATGCGGGG	1680
	TCAGTGTGTG	TGGGGCGCAG	GGCCTCCGAT	GCGGGGTGAG	TGCGTGGGGG	GCGCAGGGCC	1740
30	CCCGATGCGG	GGTCAGTGGC	TGGGGGGCGC	AGGGCCCCCT	CGTGTCCAGG	GCACCTTGGT	1800
	ACACTGTCCC	ACAAGGCACC	TGCTCTCAGG	GAGGGGGCCT	GGCAGGCAGC	GTGGCAACTC	1860
	CCTTCCGGAG	CCAGCTTCCA	TGCTAAACCTG	CCACAGCAAA	CCCCACAGAG	CCACATTTCC	1920
	TGCTGCACCT	GGTCTGCAGG	GGTGTCCAG	GACAGGCCCA	AGTCAGCCCA	GCATGCAGCT	1980
	GCCCTCCTAC	CCTGAAGATG	GGAGTGGGCT	TTCCAGGGGA	CATAAGGATG	CCAGGCCTGG	2040
35	ACCTCTTGGG	CAGGAAAGGG	TGCAGGTCTT	GAGGGCTGCT	CCCCCACAGC	CCAGCACCCC	2100
	AGGTGGAAGT	CAGCGCAGTG	GGTGGGCCAG	TGGCAGCCAG	GGAGAAGCCC	CCCGTCAGCA	2160
	GGCTGGGGTC	TGCCCCACAG	GGCCTCCCCA	CGTCTGCCTT	TGAGGGTGGC	TGCCATGCC	2220
	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
	GGTGACTTCA	TGAGGAGACC	GCCCACATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
40	GAGACAGGCT	GGCACCTCCG	GAAAACTGCT	CTTTCAGCCT	TGGTGTTCCT	TGCAAGGTGA	2400
	AAAGAAATAG	GTCTCTCCAG	TTTACAGCTT	GAAATCAGGC	TAGTGAGTGG	CCCTGGAGAC	2460
	CACGAGGGGA	GAATTTAAAG	GCCCCGGCTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCTCG	CCTGGAGCCT	GCCCTAGGAC	CGTGGGGCGG	TCAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CTTGGGCTCT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAGGT	ACATACACCT	2640
45	GCGTGCACAC	GGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
	CAGAAGTGTG	CCCAGTTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTTGTGTTG	ATCAAGTTTC	AAGGAAAGGG	AACATCTCAG	CCGGGCGTGG	TGGTTACAGC	2820
	CTGGAATCCC	AGCACTTGAG	GCCAGGAGTT	CCAGAGCAGC	CTGGGCAACG	CAGTGAGAGA	2880
	CCCCATCTCT	ACAARAAAAA	AAAAGAAAG	AAAGAAATG	AGAGATCCAG	GTTTAAAAAT	2940
50	TCATAAACAC	CACAAGGAAA	CAATACACTA	TGAGACCCAG	CAGAAGCAAC	AGATTGACTC	3000
	TAGACCCAGA	TACTAGAATT	ATCAGAGAGA	ATATAAAGTA	ACAGTGTTTT	ATATATCTAA	3060
	AGAAATAAAA	GAGATTTCTG	GAAACATGAA	AAAAAA			

## A177 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

60	1	11	21	31	41	51	
	GCGGAACACC	GGCCCGCCGT	CGCGGCAGCT	GCTTCACCCC	TCTCTCTGCA	GCCATGGGGC	60
	TCCCTCGTGG	ACCTCTCGCG	TCTCTCCTCC	TTCTCCAGGT	TTGCTGGCTG	CAGTGC CGG	120
	CCTCCGAGCC	GTGCCGGGCG	GTCCTCAGGG	AGGCTGAAGT	GACCTTGAGG	GCGGGAGGCG	180
65	CGGAGCAGGA	GCCC GGCCAG	GCGCTGGGGA	AAGTATT CAT	GGGCTGCCCT	GGGCAAGAGC	240
	CAGCTCTGTT	TAGCACTGAT	AATGATGACT	TCAGTGTGCG	GAATGGCGAG	ACAGTCCAGG	300
	AAAGAAGGTC	ACTGAAGGAA	AGGAATCCAT	TGAAGATCTT	CCCATCCAAA	CGTATCTTAC	360
	GAAGACACAA	GAGAGATTGG	GTGGTTGCTC	CAATATCTGT	CCCTGAAAAT	GGCAAGGGTC	420
	CCTTCCCCCA	GAGACTGAAT	CAGCTCAAGT	CTAATAAAGA	TAGAGACACC	AAGATTTTCT	480
70	ACAGCATCAC	GGGGCCGGGG	GCAGACAGCC	CCCCTGAGGG	TGTCTTCGCT	GTAGAGAAGG	540
	AGACAGGCTG	GTGTTGTGTT	AATAAGCCAC	TGGACCCGGA	GGAGATTGCG	AAGTATGAGC	600
	TCTTTGGCCA	CGCTGTGTCA	GAGAAATGGT	CCTCAGTGGA	GGACCCCATC	AACATCTCCA	660
	TCATCGTGAC	CGACCAAGAT	GACCACAAGC	CCAAGTTTAC	CCAGGACACC	TTCCGAGGGA	720
	GTGTCTTAGA	GGGAGTCCTA	CCAGGTACTT	CTGTGATGCA	GGTGACAGCC	ACAGATGAGG	780
75	ATGATGCCAT	CTACACCTAC	AATGGGGTGG	TTGCTTACTC	CATCCATAGC	CAAGAACCAC	840
	AGGACCCACA	CGACCTCATG	TTCACAATTC	ACCGGAGCAC	AGGCACCATC	AGCGTCATCT	900
	CCAGTGGCCT	GGACCGGGAA	AAAGTCCCTG	AGTACACACT	GACCATCCAG	GCCACAGACA	960
	TGGATGGGGA	CGGCTCCACC	ACCACGGCAG	TGGCAGTAGT	GGAGATCCTT	GATGCCAATG	1020
80	ACAATGCTCC	CATGTTTGAC	CCCCAGAAGT	ACGAGGCCCA	TGTGCTGAG	AATGCACTGG	1080
	GCCATGAGGT	GCAGAGGCTG	ACGGTCACTG	ATCTGGACGC	CCCCAACTCA	CCAGCGTGGC	1140
	GTGGCACCTA	CCTTATCATG	GGCGGTGACG	ACGGGGACCA	TTTATCCATC	ACCACCCACC	1200
	CTGAGAGCAA	CCAGGGCATC	CTGACAACCA	GGAAGGGTTT	GGATTTTGAG	GCCAAAAACC	1260
	AGCACACCCT	GTACGTTGAA	GTGACCAACG	AGGCCCTTTT	TGTGCTGAAG	CTCCCAACCT	1320
	CCACAGCCAC	CATAGTGGTC	CACGTGGAGG	ATGTGAATGA	GGCACTGTG	TTTGTCCAC	1380

5 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440  
 CTGCAGAAAG CCCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCTCTG AGAGACCCAG 1500  
 CAGGGTGCGT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560  
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 ATGGAAGCCC TCCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680  
 ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC 1740  
 ACGTGCTGAA CATCACGGAC AAGGACCTGT CTCCCACAC CTCCTCTTC CAGGCCAGC 1800  
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 10 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG 1920  
 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
 ATGTCGAAAC CTGCGCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040  
 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100  
 TCAAGGAGCC CCTCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160  
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 15 AGGCCAGCGG GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280  
 TGTACCGTCC TAGGCCAGCC AACCAGATG AAATCGGCAA CTTTATAATT GAGAACCCTGA 2340  
 AGGGCGCTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TTCGACTATG 2400  
 AGGGCAGCGG TCCGACGCC GCGTCCCTGA GCTCCCTCAC CTCCTCCGCC TCCGACCAAG 2460  
 20 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520  
 ACGGTGGCGG GGAGGACGAC TAGGCGGCCCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC 2580  
 CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTCG GAGCTTGTC 2640  
 GGAAGTGGCC TTGACAACTT GGCGGAGACA GGCTATGAGT CTGACGTAG AGTGGTTGCT 2700  
 TCCTTAGCCT TTAGGATGAG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760  
 25 CACCTGGGCC AGGGTTGCCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820  
 TGCTCAACCC TGTGTCTGTG GCCTGGGCCCT GCTGTGACTG ACCTACAGTG GACTTCTCT 2880  
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940  
 TCAAAACGTT AGAGAAAGTT CTTCAAAGT GCAGCCAGCA GCTGCTGGGC CCATGGGCCG 3000  
 TCCTGCATTG CTGTTTCCA GACCCCAATG CCTCCCATC GGATGGATCT CTGCGTTTTT 3060  
 30 ATACTGAGTG TGCCTAGGTT GCCCTTATT TTTTATTTTC CCTGTTGCGT TGCTATAGAT 3120  
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAACTTTTT TATTAAAGAA A

**A178 Protein sequence:**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675

Cellular localization: plasma membrane

45 1 11 21 31 41 51  
 MGLPRGPLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEEQEPGQA LGKVFMGCPG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120  
 KGFFPQRLNQ LKSNKDRDTH IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREBIK 180  
 YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 50 DEDDAIYTYN GVVAYSIIHS EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TDMGDGSTT TAVAVVEILD ANDNAPMFD P KYEAHVPEP AVGHEVQRLT VTDLDAPNSP 360  
 AWRATYILIM GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPDKE NQKISYRILR 480  
 DPAGWLAMDP DSGQVTA VGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLTLID 540  
 55 VNDHGPVPEP RQTICNQSP VRHVLNITDK DLSPHSTSPFQ AQLTDDSDIY WTAEVNEEGD 600  
 TVVLSLKKFL KCCTYCTTAG LSDHGKNEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660  
 GAVLALLFL LVLLLLVRKK RKIKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720  
 GLEARPEVLL RNDVAPTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEED

**A179 DNA SEQUENCE**

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
 Unigene number: Hs.258583  
 Probeset Accession #: NM\_012152  
 65 Nucleic Acid Accession #: NM\_012152  
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51  
 CTCTCTTTAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60  
 GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGACTGGACA 120  
 GGAACAAGAG TTGTGATGTG TTTGTGTGTT GGGACGTTTT TCTGCCTGTT TATTTTTTTT 180  
 TCTAATCTCT TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC 240  
 75 TACCTGTGTG CTAATTTAGC TGCTGCCGAT TTCTTCGCTG GAATTGCCTA TGTATTCTCG 300  
 ATGTTTAAAC CAGGCCCACT TTCAAAAAC TTAGCTGTCA ACCGCTGGTT TCTCCGTCAG 360  
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420  
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480  
 CTGCTCATTT TGCTTGTCTG GGCATCGGCC ATTTTATGAG GGGCGGTCCC CACACTGGGC 540  
 80 TGAATTGCC TCTGCAACAT CTCTGCCTGC TCTTCCCTGG CCCCATTATA CAGCAGGAGT 600  
 TACCTTGTCT TCTGGACAGT GTCCAACCTC ATGGCCCTCC TCATCATGGT TGTGGTGATC 660  
 CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAACGTCT TGCTCCGCA TACAAGTGGG 720  
 TCCATCAGCC GCCGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780

GCGTTTGTGG TATGCTGGAC CCCGGGCCTG GTGGTTCTGC TCCTCGACGG CCTGAACTGC 840  
 AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCCCTG TGCTGGCGCT GCTCAACTCC 900  
 GTCGTGAACC CCATCATCTA CTCCTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960  
 ATGATCTGCT GCTTCTCTCA GGAGAACC CA GAGAGCGTC CCTCTCGCAT CCCCTCCACA 1020  
 GTCTCAGCA GAGTGCACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080  
 GTCTGCAATA AAAGCACTTC CTAAGCTCTG GATGCCTCTC GGCCACCCA GGTGATGACT 1140  
 GTCTTAGG

# A180 Protein sequence:

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7  
 Unigene number: Hs.258583  
 Probeset Accession #: NM\_012152  
 Protein Accession #: NP\_036284  
 Signal sequence: none found  
 Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIVLCVGTFF CLFIFFSNLS VIAAVIKNRK 60  
 FHFFFYLLA NLAAADFFAG IAYVFLMNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120  
 LVIAVERHMS IMRMVHNSL TKKRVTLLIL LVWAIAlFMG AVPTLGNCL CNISACSSLA 180  
 PIYSRSYLVF WTVSNLMAFL IMVVVYLRIY VYVKRKTNVL SPHTSGSISR RRTPMKLMKT 240  
 VMTVLGAFVW CWTPLVLL LDGLNCRQCG VQHVKRWFL LALNSVNP IISYKDEDM 300  
 YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

# A181 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.162859  
 Probeset Accession #: AA569531  
 Nucleic Acid Accession #: AA569531  
 Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGACCTACA GTTACTCATT TTTCAGGCCT GAGTTGATCG TTAATCATCT TAATTATGTT 60  
 CATTCTGAAG CCAACAGGAG AACCAAGACC AAAACTTTAT TGTCTCTGCT TTCATTTCCT 120  
 GATGAAACCT CTGGACTAAG CACACATCTT CCTTGTATTAT CTCTCTCAA GGAGTGTGGA 180  
 GTGCTTCATC TGGACATCCA CGGGAAGAAG GAAGACATGA GAATCACCCA ACAGTCTTCC 240  
 CAGCTATACC TGTGGGACAT GGGTGGTTTT ACAATATTTA AGAACCTGTG GATGAGCCTC 300  
 ATACCCAGAG GGAACAAACG CTCGCCAAAA AGAGTTACAG AAACCATCCT GAGAGATTTT 360  
 AAGCAGAAGC AAAGTTCAAA GATCCAAGAG GAGAGACGAA GAGAGTCTGC AGGACCAAAC 420  
 CTCTCTTCAT TCTGTTTGT GGGGAATGCT GGAAGAGGAG ACAGGCCCAA GATTGCGGCA 480  
 GGAAGTAAAC AGTTTTCAGG CTGAGGCCAA TCTGAGCAGG AACATTCCAA TATTCTTCA 540  
 GCTACGTTGT CCCAGCACTT CACTGGTTAA CCTTTTATGT CCACCATTTG TGGATTTCAC 600  
 AGCTACTTGT CAATGGTGAA TATTGATCAT CATCATTATC TACTGAGCTG CTACCATATC 660  
 CCAGCTACTC CTGTCATGTT GTTCATTATT TTCTCAACAC TCAGCATATT TGCAATATGT 720  
 TATGTAATAT CACAGACAAG GAAACTGAAC GCAGAAATGT TTTATTTCTT GCCAAACATC 780  
 ACATGAGGAT GAACAATGAA ACCGATTGTA AACAGGATT GTCTGATTCC AACATCTCTG 840  
 GGTCTTTTT CACTCTGATA TGCTGCAATT AAAAGCCAT TTCTAAGACT GT

# A182 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.162859  
 Probeset Accession #: AA569531  
 Protein Accession #: none found  
 Signal sequence: 1-46  
 Transmembrane domains: none found  
 Cellular Localization: not determined

1 11 21 31 41 51  
 MTYSYSFFRP ELIVNHLNYV HSEANRRTKT KTLSSLSSFL DETSGSLSTHL PCLSLSKECG 60  
 VLHLDIHGKK EDMRITQSS QLYLWDMGGF TIFKNLWMSL IPRGNKRSPK RVTETILRDF 120  
 KQKQSSKIQE ERRRESAGPN LSSFVFWGNA GRGDRPQIWA GSKQFSG

# A183 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.179809  
 Probeset Accession #: N95796  
 Nucleic Acid Accession #: XM\_050197  
 Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 TCACACGTGC CAAGGGGCTG GCTCAGCGGA ACCAGCCTGC ACGCGCTGGC TCCGGGTGAC 60  
 AGCCCGCGCG CTCGGCCAGG ATCTGAGTGA TGAGACGTGT CCCCACTGAG GTGCCCCACA 120  
 GCAGCAGGTG TTGAGCATGG GCTGAGAAGC TGGACCGGCA CCAAAGGGCT GGCAGAAATG 180  
 GGCGCCTGCG TGATTCCTAG GCAGTTGGCG GCAGCAAGGA GGAGAGGCGG CAGCTTCTGG 240  
 AGCAGAGCCG AGACGAAGCA GTTCTGGAGT GCCTGAACGG CCCCTGAGC CCTACCCGCC 300

TGGCCCACTA TGCTCCAGAG GCTGTGGGTG AGCCGCCTGC TGCGGCACCG GAAAGCCCAG 360  
 CTCTTGCTGG TCAACCTGCT AACCTTTGGC CTGGAGGTGT GTTTGGCCCG AGGCATCACC 420  
 TATGTGCCCG CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTTCATGAC CATGGTGCTG 480  
 GGCAATTGGT CAGTGTCTGG CCTGGTCTGT GTCCCGCTCC TAGGCTCAGC CAGTGACCAC 540  
 TGGCGTGGAC GCTATGGCCG CGCGCGGCC TFCATCTGGG CACTGTCCTT GGGCATCCTG 600  
 CTGAGCCTCT TTCTCATCCC AAGGGCCGGC TGGCTAGCAG GGCTGCTGTG CCCGGATCCC 660  
 AGGCCCTGG AGCTGGCACT GCTCATCTG GCGTGGGGC TGCTGGACTT CTGTGGCCAG 720  
 GTGTGCTTCA CTCCACTGGA GGCCCTGCTC TCTGACCTCT TCCGGGACCC GGACCACTGT 780  
 CGCCAGGCCT ACTCTGTCTA TGCCCTCATG ATCAGTCTTG GGGGCTGCCT GGGCTACCTC 840  
 CTGCCTGGCA TTGACTGGGA CACCAGTGCC CTGGCCCCCT ACCTGGGCAC CCAGGAGGAG 900  
 TGCCCTTTTG GCTCTCTAC CTCTATCTTC CTCACCTCGG TAGCAGCCAC ACTGCTGGTG 960  
 GCTGAGGAGG CAGCGCTGGG CCCCACCGAG CCAGCAGAAG GGCTGTCCGC CCCCTCCTTG 1020  
 TCGCCCACT GCTGTCCATG CGGGGCCCCG TTGGCTTTCC GGAACCTGGG CGCCCTGCTT 1080  
 CCCCCTGTC ACCAGCTGTG CTGCGCATG CCCCACCC TGCGCCGGCT CTTCGTGGCT 1140  
 GAGCTGTGCA GCTGGATGGC ACTCATGACC TTCACGCTGT TTTACACGGA TTTCGTGGGC 1200  
 GAGGGGCTGT ACCAGGCGGT GCCCAGAGCT GAGCCGGGCA CCGAGGCCCG GAGACACTAT 1260  
 GATGAAGGCG TTCGGATGGG CAGCCTGGGG CTGTTCTGTC AGTGCGCCAT CTCCCTGGTC 1320  
 TTCTCTCTGG TCATGGACCG GCTGGTGCGA CGATTGCGCA CTCGAGCAGT CTATTTGGCC 1380  
 AGTGTGGCAG CTTTCCCTGT GGCTGCCGGT GCCACATGCC TGTCCACAG TGTGGCCGTG 1440  
 GTGACAGCTT CAGCCGCCCT CACCGGGTTC ACCTTCTCAG CCTGCGAGAT CCTGCCCTAC 1500  
 AACTGGCCT CCCTCTACCA CCGGAGAGA CAGGTGTTCC TGCCCAAATA CCGAGGGGAC 1560  
 ACTGGAGGTG CTAGCAGTGA GGACAGCCTG ATGACCAGCT TCCTGCCAGG CCTTAAGCCT 1620  
 GGAGCTCCCT TCCCTAATGG ACACGTGGGT GCTGGAGGCA GTGGCCTGCT CCCACCTCCA 1680  
 CCGCGCTCT GCGGGGCCCT TGCTGTGAT GTCTCCGTAC GTGTGGTGGT GGGTGAGCCC 1740  
 ACCGAGGCCA GGGTGGTTC GGGCCGGGGC ATCTGCCTGG ACCTCGCCAT CTGGGATAGT 1800  
 GCCTTCCTGC TGTCCAGGT GGCCTCATCC CTGTTTATGG GCTCCATGT CCAGCTCAGC 1860  
 CAGTCTGTCA TGCCCTATAT GGTGTCTGCC GCAGGCCTGG GTCTGCTCGC CATTTACTTT 1920  
 GCTACACAGG TAGTATTGA CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAAACTTCC 1980  
 AGCACATTGG GGTGGAGGGC CTGCTCACT GGTGCCAGC TCCCGCTCC TGTAGCCCC 2040  
 ATGGGGCTGC CCGGGTGGCC GCCAGTTTCT GTTGTGCCA AAGTAATGTG GCTCTCTGCT 2100  
 GCCACCTGT GCTGCTGAGG TGCCTAGCTG CACAGCTGGG GGCTGGGGC TCCCTCTCCT 2160  
 CTCTCCCGAG TCTCTAGGGC TGCTGACTG GAGGCCTTCC AAGGGGGTTT CAGTCTGGAC 2220  
 TTATACAGG AGGCCAGAA GGCTCCATGC ACTGGAATGC GGGGACTCTG CAGGTGGATT 2280  
 ACCCAGGCTC AGGGTTAACA GCTAGCCTCC TAGTTGAGAC ACACCTAGAG AAGGGTTTTT 2340  
 GGGAGCTGAA TAAACTCAGT CACCTGGTTT CCCATCTCTA AGCCCTTAA CCTGCAGCTT 2400  
 CGTTTAATGT AGCTCTTGCA TGGGAGTTTC TAGGATGAAA CACTCTCCA TGGGATTGA 2460  
 ACATATGAAA GTTATTGTGA GGGGAAGAGT CTTGAGGGGC AACACACAAG AACAGGTCC 2520  
 CCTCAGCCCC ACAGGCACTG GTCTTTTTTG CTNGANTCCA CCCCCCCCCT CTTTACCCTT 2580  
 TT

#### A184 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.179809  
 Probeset Accession #: N95796  
 Protein Accession #: XP\_050197  
 Signal sequence: none  
 Transmembrane domains: 21-43, 53-75, 90-112, 125-147, 160-182, 199-221, 323-345, 350-372, 379-401  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MVQRLWVSRL LRHRKAQLLL VNLTFGLEV CLAAGITYVP PLLLEVGVVEE KFMTMVLGIG 60  
 PVLGLVCPVL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL 120  
 ELALLILGVG LLDFCGQVCF TPLEALLSDL FRDPDHCRAQ YSVYAFMISL GGCGLYLLPA 180  
 IDWTSALAP YLGTQEECLF GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH 240  
 CCPCRARLAF RNLGALLPRL HQLCCRMPT LRRLFVAELC SWMALMTFTL FYTDFVGEGL 300  
 YQGVPAEPG TEARRHYDEG VRMGSGLGLFL QCAISLVFSL VMDRLVQRFG TRAVYLASVA 360  
 AFPVAAATC LSHSVAVVTA SAALTGTFTS ALQILPYTLA SLVHREKQVF LPKYRGDTGG 420  
 ASSEDSLMTS FLPGPKPGAP FPNHVGAGG SGLLPPPPAL CGASACDVSV RVVVGPEPTEA 480  
 RVVPGRGICL DLAILDSAPL LSQVAPSLFM GSIVQLSQSV TAYMVSAAGL GLVAIYFATQ 540  
 VVPDKSLAK YSA

#### A185 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.11260  
 Probeset Accession #: R73640  
 Nucleic Acid Accession #: AK002126  
 Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGGTTCGCC GGGGGCTGCT TGCGTGGATT TCCCGGGTGG TGGTTTGTCT GGTGCTCCTC 60  
 TGCTGTGCTA TCTCTGTCTT GTACATGTTG GCCTGCACCC CAAAAGGTGA CGAGGAGCAG 120  
 CTGGCACTGC CCAGGGCCAA CAGCCCCACG GGAAGGAGG GGTACCAGGC CGTCTCTTCA 180  
 GAGTGGGAGG AGCAGACCG CAACTACGTG AGCAGCCTGA AGCGGCAGAT CGCACAGCTC 240  
 AAGGAGGAGC TGCAGGAGAG GAGTGAGCAG CTCAGGAATG GGCAGTACCA AGCCAGCGAT 300  
 GCTGCTGCCC TGGGTCTGGA CAGGAGCCCC CCAGAGAAAA CCCAGGCCGA CCTCTGGCC 360  
 TTCTGCACT CGCAGGTGGA CAAGGCAGAG GTGAATGCTG GCGTCAAGCT GGCCACAGAG 420  
 TATGCAGCAG TGCTTTTCTA TAGCTTTACT CTACAGAAGG TGTACCAGCT GGAGACTGGC 480  
 CTTACCCGCC ACCCCGAGGA GAAGCCTGTG AGGAAGGACA AGCGGGATGA GTTGGTGGAA 540  
 GCCATTGAAT CAGCCTTGGA GACCCTGAAC AATCTGCAG AGAACAGCCC CAATCACCGT 600

CCTTACACGG CCTCTGATTT CATAGAAGGG ATCTACCGAA CAGAAAGGGA CAAAGGGACA 660  
 TTGTATGAGC TCACCTTCAA AGGGGACCAC AAACACGAAT TCAAACGGCT CATCTTATTT 720  
 CGACCATTTCG GCCCCATCAT GAAAGTGAAA AATGAAAAGC TCAACATGGC CAACACGCTT 780  
 ATCAATGTGA TCGTGCCTCT AGCAAAAAGG GTGGACAAGT TCCGGCAGTT CATGCAGAAT 840  
 TTCAGGGAGA TGTGCATTGA GCAGGATGGG AGAGTCCATC TCACTGTGTG TTACTTTGGG 900  
 AAAGAAGAAA TAAATGAAGT CAAAGGAATA CTTGAAAACA CTTCCAAAGC TGCCAACTTC 960  
 AGGAACCTTA CCTTCATCCA GCTGAATGGA GAATTTTCTC GGGGAAAGGG ACTTGATGTT 1020  
 GGAGCCCGCT TCTGGAAGGG AAGCAACGTC CTTCTCTTTT TCTGTGATGT GGACATCTAC 1080  
 TTCACATCTG AATTCTCTCA TACGTGTAGG CTGAATACAC AGCCAGGGAA GAAGGTATTT 1140  
 TATCCAGTTC TTTTCAGTCA GTACAATCCT GGCATAATAT ACGGCCACCA TGATGCAGTC 1200  
 CCTCCCTTGG AACAGCAGCT GGTCAATAAG AAGGAAACTG GATTTTGAG AGACTTTGGA 1260  
 TTTGGGATGA CGTGTCACTA TCGGTTCAGC TTCATCAATA TAGGTGGGTT TGATCTGGAC 1320  
 ATCAAAGGCT GGGCGGAGA GGATGTGCAC CTTTATCGCA AGTATCTCCA CAGCAACCTC 1380  
 ATAGTGGTAC GCGCCCTGT GCGAGGACTC TTCCACCTCT GGCATGAGAA GCGCTGCATG 1440  
 GACGAGCTGA CCCCCGAGT GTACAAGATG TGCATGCAGT CCAAGGCCAT GAACGAGGCA 1500  
 TCCCACGGCC AGCTGGGCAT GCTGGTGTTC AGGCACGAGA TAGAGGCTCA CCTTCGCAA 1560  
 CAGAACAGA AGACAAGTAG CAAAAAACA TGA

# A186 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.11260  
 Probeset Accession #: R73640  
 Protein Accession #: NP\_060841  
 Signal sequence: 1-26  
 Transmembrane domains: none found  
 Cellular Localization: not determined

1 11 21 31 41 51  
 MVRRLGLAWI SRVVVLVLVLL CCAISVLYML ACTPKGDEEQ LALPRANSPT GKEGYQAVLQ 60  
 EWEEQHRNVY SSKLRQIAQL KEELQERSEQ LRNGQYQASD AAGLGLDRSP PEKTQADLLA 120  
 FLHSQVDKAE VNAGVKLATE YAAVPFDSFT LQKVYQLETG LTRHPEEKPV RKDKRDELVE 180  
 AIESALETLN NPAENSPNHR PYTASDFIEG IYRTERDKGT LYELTFKGDH KHEFKRLILF 240  
 RPFPGIMKVK NEKLNMANTL INVIVPLAKR VDKFRQFMQN FREMCIEQDG RVHLTVVYFG 300  
 KEELINEVKGI LENTSKAANF RNFTFIQLNG EFSRKGGLDV GARFWKGSNV LLFFCDVDIY 360  
 FTSEFLNTRC LNTQPGKKVF YPVLFSQYNP GIIYGHDAV PPLEQQLVIK KETGFWRDFG 420  
 FGMTCYRSD FINIGGFOLD IKWGGEVDVH LYRKYLSHNL IIVRTFVRGL FHLWHEKRCM 480  
 DELTPBQYKM CMQSKAMNEA SHGQLGMLVF RHEIEAHLRK QKQKTSKSKT

# A187 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Nucleic Acid Accession #: AF189723  
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGATTCCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
 ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
 TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTCTCTGGCT CTGCAGTCAT CAGTGTTTTA 240  
 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300  
 GCCTTTGTTC AGGAAATATCG TTCAAGAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360  
 CCAGAATGCC ATTGTGTGGC TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420  
 CCAGGTGATA CAGTTTGCCCT TTCTGTGGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTC 480  
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540  
 AAGGTGACAG CTCTTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600  
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCTT TGGAAACAGGA 660  
 GAAAATCTGT AATTGGGGGA GGTTTTAAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780  
 ATAGGAATCA TCACTGTGGT TGGCTGGTTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840  
 ATTAGTGTA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCCATTGT GGTCAAGTGT 900  
 ACGCTAGCTC TTGGTGTATG GAGAATGGTG AAGAAAAAGG CCATTGTGAA AAAGCTGCCT 960  
 ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTGAG AACACTGACG 1020  
 AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTACT 1080  
 GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATT 1140  
 TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200  
 AGAAACAATA CTCTAATGGG GAAGCCCAACA GAAGGGGCTT TAATTGCTCT TGAATGAAG 1260  
 ATGGGCTCTG ATGGACTTCA ACAAGACTAC ATCAGAAAAA CTGAATACCC TTTTAGCTCT 1320  
 GAGCAAAAGT GGTGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380  
 TGTTTTATGA AAGGTGCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440  
 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAGA GAAGGCACGC 1500  
 ATGGGCTCAG CGGACTCAG AGTTCTTGTCT TTGGCTTCTG GTCCTGAAC TGGACAGCTG 1560  
 ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACETAGAA CTGGGTGTA AGAAGCTGTT 1620  
 ACAACACTCA TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATT ACAGGAGACT 1680  
 GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCAAAAA CTTCCAGTC AGTCTCAGGA 1740  
 GAAGAAATAG ATGCAATGGA TGTTTCAGCAG CTTTCACAAA TAGTACCAAA GGTTCAGTA 1800  
 TTTTACAGAG CAGGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860  
 TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920  
 ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980  
 CTAGTGGATG ATGATTTTCA AACATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75

```

ATAACATTA AAAATTTTCGT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTA 2100
ATCTCATTGG CTACATTAAAT GAACTTTCTCT AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160
ATCAATATTA TTATGGATGG ACCCCACGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCATTG GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTTGATA 2280
CTTAAATAC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTTGT CTTCTGGCGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
TTTTTTGACA TGTTCAATGC ACTAAGTTC AGATCCCAGA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTCTCTG GATCCATCAT GGGACAATTA 2520
CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTTGT TCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT GA
  
```

**A188 Protein sequence:**

Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Protein Accession #: AAF27813  
 Signal sequence: none found  
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878  
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]  
 Cellular Localization: not determined

1 11 21 31 41 51  
 | | | | |  
 MIPVLTSKKA SELPVSEVAS ILQADLQNGL NKCEVSHHRA FHGWNEFDIS EDEPLWKKYI 60  
 SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQEYRSEK SLEELSKLVP 120  
 PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRFP EAVDLSIDES SLTGETTPCS 180  
 KVTAQPAAT NGDLASRSNI AFMGLTVRCG KAGGVVIGTG ENSEFGEVFK MMQAEAPKT 240  
 PLQKSMDLG KQLSFYSFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGPLIVVTV 300  
 TLALGVMRMV KKRAIVKKLP IVETLGCENV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360  
 GVGYNQFGEV IVDGDVVHGF YNPAVSRIE AGCVCNDAVI RNNTLMGKPT EGALIALAMK 420  
 MGLDGLQDDY IRKAEYPPSS EQKWMVAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480  
 GQTLTLTQQQ RDVYQQEKAR MGSAGLRVLA LASGPBLGQL TFLGLVGIIID PPRTGVKEAV 540  
 TFLIASGVSI KMITGDSQET AVAIA SRLGL YSKTSQSVSG EEDAMDVQV LSQIVPKVAV 600  
 FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGWAMQGTGT DVCKEADMI 660  
 LVDDDFQTIM SAIEEGKGIY NNIKNFVRFP LSTSIAALTL ISLATLMNFP NPLNAMQILW 720  
 INIIMDGPPA QSLGVEFVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780  
 ELRDNVITPR DTTMTFTCFV FDFMFNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840  
 LVYIFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVABIIK KVERSERKIQ KHVSTSSSF 900  
 LEV

**A189 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Nucleic Acid Accession #: N62096  
 Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGGGCTACC AGAGGCAGGA GCCTGTGCATC CCGCCGCAGA GAGGATTGCC TTATTCAATG 60  
 AAGCAAGCTG GGTTCCTTTT GGGAAATATTG CTTTATTCTT GGGTTTCATA TGTACAGAC 120  
 TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180  
 TTGGTCAATA AACTTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTCTT TCAGTTTGTG 240  
 TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300  
 TTTCAAAGAA TCCAGGAGT TGATCTCGAA AACGTGTTTA TTGGTCGCCA CTTCATTATT 360  
 GGACTTTCCA CAGTTACCTT TACTCTGCTT TATCTCTGT ACCGAAATAT AGCAAAGCTT 420  
 GGAAAGGTCT CCCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAA TGTAAATGGCA 480  
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG 540  
 CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTTGCCA CCATAACTCC 600  
 TTCTTAGTTT ACAGTTCTCT AGAAGAACC ACAGTAGCTA AGTGCTCCG CCTTATCCAT 660  
 ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATTCTTTG CTACATGTGG ATACTTGACA 720  
 TTTACTGGCT TCACCCAAGG GGAATTATTT GAAAATTACT GCAGAAATGA TGACCTGGTA 780  
 ACATTGGAA GATTTTGTTA TGGTGTCACT GTCATTTTGA CATACCCTAT GGAATGCTTT 840  
 GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC 900  
 ATTGTGTGTA CAGTGAATGT CATCACTGTA GCCACGCTTG TGTCTATGCT GATTGATTGC 960  
 CTCGGGATAG TTCTAGAAT CAATGGTGTG CTCTGTGCAA CTCCCTCAT TTTTATCATT 1020  
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080  
 TCTTGTGTCA TGCTTCCCAT TGGTGTCTGT GTGATGGTTT TTGGATTCTG CATGGCTATT 1140  
 ACAAACTACT AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTCC TGACAATTC 1200  
 TCTCTACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260  
 ATTAGTATCT TTCAACTCGA GTAA

**A190 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 28-50, 66-88-112-134, 142-164, 217-239, 260-282, 298-320, 327-348, 359-381



Cellular Localization: plasma membrane

5 1 11 21 31 41 51  
 | | | | |  
 MG YQRQEPVI PPQRGLPYSM KQAGFPLGIL LLEFWVS YVTD FSLVLLIKGG ALSGTD TYQS 60  
 LVNKT FGFPG YLLLSVLQFL YPFIAMISYN IIAGDTLSKV FORIPGVDPE NVFIGRHFII 120  
 GLSTV TFTLP LSLYRNIAKL GKVSLISTGL TTLILGIVMA RAISLGPHIP KTEDAWVFAK 180  
 PNAIQAVGVM SPAFICHHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240  
 10 FTGFTQGDLE ENYCRNDDL VTFGRFCYGV TILTYPMECF VTREVIANVF FGNLSSVFH 300  
 IVVTVMVITV ATLVSLIDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360  
 SCVMLPIGAV VMVFGFVMAI TNTQDCTHGQ EMFYCFPDNF SLTNTSESHV QQTQLSTLN 420  
 ISIFQLE

## A191 DNA SEQUENCE

15 Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Nucleic Acid Accession #: N62096  
 20 Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 | | | | |  
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGT TTTCCCTTGT TTTATTGATA 60  
 AAAGGAGGGG CCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTTCGGC 120  
 TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180  
 AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TTCAAAGAAT CCCAGGAGTT 240  
 30 GATCTGAAA ACGTGTATTAT TGGTCGCCAC TTCAATTATG GACTTTCCAC AGTTACCTTT 300  
 ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT 360  
 ACAGGTTTAA CAACCTCTGAT TCTTGAATT GTAATGGCAA GGGCAATTTC ACTGGGTCCA 420  
 CACATACCAA AACAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGCGGTC 480  
 GGGGTTATGT CTTTGTGATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA 540  
 35 GAAGAACCCA CAGTAGCTAA GTGGTCCGCG CTTATCCATA TGTCCATCGT GATTCTGTGA 600  
 TTTATCTGTA TATTCTTTCG TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660  
 GACTTATTTG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTGGAAG ATTTTGTAT 720  
 GGTGTCACTG TCAATTTGAC ATACCCCTATG GAATGCTTTG TGACAAGAGA GGTAAATTGCC 780  
 AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTTCCACA TTGTTGTAAC AGTGATGGTC 840  
 40 ATCACTGTAG CCACGCTTGT GTCATTGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC 900  
 AATGGTGTGC TCTGTGCAAC TCCCCTCATT TTTATCATTC CATCAGCCTG TTATCTGAAA 960  
 CTGTCTGAAG AACCAAGGAC ACACCTCGAT AAGATTATGT CTTGTGTCAT GCTTCCCATT 1020  
 GGTGCTGTGG TGATGTTTTC TGGATTGCTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080  
 CATGGGCAGG AAATGTTCTA CTGCTTTCCT GACAATTCT CTCTCACAAA TACCTCAGAG 1140  
 45 TCTCATGTTT AGCAGACAAC ACAACTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200  
 TAA

## A192 Protein sequence:

50 Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Protein Accession #: none found  
 Signal sequence: 1-26  
 55 Transmembrane domains: 45-61, 92-108, 117-132, 191-207, 274-290, 297-313, 335-351  
 Cellular Localization: plasma membrane

60 1 11 21 31 41 51  
 | | | | |  
 MG YQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYFFIAMI 60  
 SYNIIAGDTL SKVFQRIPGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLSI 120  
 TGLTTLILGI VMARAI SLGP HIPKTEDAV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL 180  
 EEPTVAKWSR LIHMSIVISV FICIFFATCG YLTFTGFTQG DLFENYCRND DLVTFGRFCY 240  
 65 GVTVILTYPM ECFVTREVI NVFFGGNLSS VFHIVVTVMV ITVATLVSLI IDCLGIVLEL 300  
 NGVLCATPLI FIIPSACYLK LSEEPRTSHD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360  
 HGQEMFYCFP DNFSLTNTSE SHVQQTQLS TINISIFQLE

## A193 DNA SEQUENCE

70 Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Nucleic Acid Accession #: N62096  
 Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51  
 | | | | |  
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGG TCAATAAAAC TTTCCGCTTT 60  
 CCAGGGTATC TGCTCCTCTC TGTTCCTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120  
 80 TACAATATAA TAGCTGGAGC TACTTTGAGC AAAGTTTTTC AAAGATCCC AGGAGTTGAT 180  
 CTTGAAAACG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTACT 240  
 CTGCCTTTAT CCTGTACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300  
 GGTTTAACAA CTCTGATTCT TGGAAATGTA ATGGCAAGGG CAATTTCAT GGGTCCACAC 360  
 ATACCAAAAA CAGAAGACGC TTGGGTATTG GCAAAGCCCA ATGCCATTCA AGCGGTCCGG 420

GTTATGTCTT TTGCATTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480  
 GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540  
 ATCTGTATAT TCTTTGTCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600  
 TTATTTGAAA ATTAAGTACAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTATGGT 660  
 5 GTCACGTCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATGCCAAT 720  
 GTGTTTTTTG GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCAATC 780  
 ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840  
 GGTGTGCTCT GTGCAACTCC CCTCATTITT ATCATTCCAT CAGCCTGTTA TCTGAAACTG 900  
 10 TCTGAAGAAC CAAGGACACA CTCCGATAAG ATTATGTCTT GTGTCATGCT TCCCATTGGT 960  
 GCTGTGGTGA TGGTTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020  
 GGGCAGGAAA TGTCTACTG CTTTCTGAC AATTCTCTCT TCACAAATAC CTGAGAGTCT 1080  
 CATGTTGAGC AGACAACACA ACTTCTACT TTAAATATTA GTATCTTTCA ACTCGAGTAA

**A194 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Protein Accession #: none found  
 20 Signal sequence: none found  
 Transmembrane domains: 24-40, 70-86, 95-111, 171-186, 253-269, 276-292, 314-330  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MGYQRQEPVI PPQVKNKTFGF PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIGVD 60  
 PENVFIGRHF IIGLSTVFTF LPLSLYRNIA KLKGVSLIST GLTTLILGIV MARAISLGPH 120  
 30 IPKTEDAWVF AKPNAIQAVG VMSFAFICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180  
 ICIFATCGY LTFTGFTQGD LFENYCRNDD LVTGFRFCYG VTVILTYPME CFVTVREVIAN 240  
 VFFGNNLSSV PHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCAATPLIF IIPSACYLKL 300  
 SEEPRTSHDK IMSCVMLPIG AVVMVGFVPM AITNTQDCTH QGEMFYCFPD NFSLNTNTSES 360  
 HVQQTQLST LNISIFQLE

**A195 DNA SEQUENCE:**

Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 40 Nucleic Acid Accession #: N62096  
 Coding sequence: 1-1389 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGA GAGATTAGA TGACAGAGAA 60  
 ACCCTTGTTT CTGAACATGA GTATAAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120  
 GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT 180  
 50 GGGTTTCCTT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTTACAGA CTTTCCCTT 240  
 GTTTTATTGA TAAAAGGAGG GGCCCTCTCT GGAACAGATA CCTACCAGTC TTTGGTCAAT 300  
 AAAACTTTTC GCTTTCCAGG GTATCTGCTC CTCTCTGTTT TTCAGTTTTC GTATCCTTTT 360  
 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAGT TTTTCAAAGA 420  
 ATCCCAGGAG TTGATCCTGA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC 480  
 ACAGTTACCT TTAATCTGCC TTTATCCTTG TACCGAAATA TAGCAAAGCT TGGAAAGGTC 540  
 55 TCCCTCATCT CTACAGTTT AACAACTCTG ATTCTTGGAA TTGTAATGGC AAGGGCAATT 600  
 TCACTGGGTC CACACATACC AAAAAACAGAA GACGCTTGGG TATTTGCAAA GCCCAATGCC 660  
 ATTCAAGCCG TCGGGGTTAT GTCTTTTGCA TTTATTTGCC ACCATAACTC CTTCTTAGTT 720  
 TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780  
 60 GTGATTCTCG TATTTATCTG TATATTCTTT GCTACATGTG GATACTTGAC ATTTACTGGC 840  
 TTCACCCAAG GGGACTTATT TGAAAATTAC TGCAGAAATG ATGACCTGGT AACATTGGGA 900  
 AGATTTTGTG ATGGTGTGAC TGTCATTTTG ACATACCCCTA TGGAAATGCTT TGTGACAAGA 960  
 GAGGTAATTC CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTTCCTA CATTGTTGTA 1020  
 ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATTGATTG CCTCGGGATA 1080  
 65 GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140  
 TGTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200  
 ATGCTTCCCA TTGGTGTCTG GGTGATGGTT TTTGGATTGC TCATGGCTAT TACAAATACT 1260  
 CAAGACTCGA CCCATGGGCA GGAAATGTTT TACTGCTTTC CTGACAATTT CTCTCTCACA 1320  
 70 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380  
 TTTCAATGA

**A196 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.293185  
 Probeset Accession #: N62096  
 Protein Accession #: none found  
 75 Signal sequence: none found  
 Transmembrane domains: 37-53, 66-82, 109-125, 155-172, 180-196, 255-271, 338-354, 361-377, 399-415  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60

GFPLGILLLF WVSYVTFDFSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPF 120  
 IAMISYNIIA GDILSKVFR IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIKLGKV 180  
 SLISTGLTTL ILGIVMARAI SLGPHIPKIE DAWVFAKPNA IQAVGVMSFA FICHHSNLFV 240  
 YSSLEETVA KWSRLIHMSI VISVFICIFF ATCGYLTFGT FTQGDLEFENY CRNDLDTFG 300  
 RFCEYGVTVIL TYPMECFVTR EVIANVFFGG NLSSVFHIV TVMVITVATL VSLIDLCLGI 360  
 VLELNGVLCA TPLIFIPSA CYLKLSEEP THSKIMSCV MLPIGAVVMV FGFVMAINT 420  
 QDCTHGQEMF YCFDPNFSLT NTSSEHVQQT TQLSTLNISI FQ

**A197 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.31608  
 Probeset Accession #: H18836  
 Nucleic Acid Accession #: NM\_017636  
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGGAGGATG CCTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACACGCGATG ACACACCACG 60  
 GAGAAGCCCA CCGATGCCTA CCGAGAGCTG GACTTCACGG GGGCCGGCCG CAAGCACAGC 120  
 AATTTCCTCC GGCTCTCTGA CCGAACGGAT CCAGCTGCAG TTTATAGTCT GGTCAACAGC 180  
 ACATGGGGCT TCCGTGCCCC GAACCTGGTG GTGTCACTGC TGGGGGGATC GGGGGGGCCC 240  
 GTCTCCAGA CCTGGCTGCA GGACCTGCTG CGTCGTGGGC TGGTGCGGCG TGCCAGAGC 300  
 ACAGGAGCCT GGATTGTAC TGGGGGTCTG CACACGGGCA TCGGCGCGCA GTTGGTGTG 360  
 GCTGTACGGG ACCATCAGAT GGCCAGCACT GGGGGCACCA AGGTGGTGGC CATGGGTGTG 420  
 GCCCCTGGG GTGTGGTCCG GAATAGAGAC ACCCTCATCA ACCCAAGGG CTCGTCCCT 480  
 GCGAGGTACC GTTGCGCGCG TGACCCGGAG GACGGGGTCC AGTTTCCCTT GGACTACAAC 540  
 TACTCGGCCT TCTTCTGGT GGACGACGGC ACACACGGCT CCCTGGGGGG CGAGAACCAG 600  
 TTCCGCTTGC GGCTGGAGTC CTACATCTCA CAGCAGAAGA CGGGCGTGGG AGGGACTGGA 660  
 ATTAGATACC CTGTCTGTCT CCTCTGATG GATGGTGTG AGAAGATGT GACGCGAATA 720  
 GAGAAGCCCA CCGAGGCTCA GCTCCCATGT CTCTCGTGG CTGGCTCAGG GGGAGCTGCG 780  
 GACTGCCTGG CGGAGACCCT GGAAGACACT CTGGCCCCAG GGAGTGGGGG AGCCAGGCAA 840  
 GGCGAAGCCC GAGATCGAAT CAGGCGTTTC TTTCCTCAAG GGGACCTTGA GGTCTCTCAG 900  
 GCCCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCCTGA CAGTCTATTC TTCTGAGGAT 960  
 GGGTCTGAGG AATTCGAGAC CATAGTTTTC AAGGCCCTTG TGAAGCCCTG TGGGAGCTCG 1020  
 GAGGCTCAG CCTACCTGGA TGAGCTGCGT TTGGCTGTGG CTTGGAACCG CGTGACATT 1080  
 GCCCAGAGTG AACTCTTTTC GGGGGACATC CAATGGCGGT CCTTCCATCT CGAAGCTTCC 1140  
 CTCATGGAGC CCCTGCTGAA TGACCGGCCT GAGTTCTGTC GCTTGTCTAT TTCCACGGC 1200  
 CTCAGCCTGG GGCACCTTCT GACCCGATG CGCCTGGCCC AACTCTACAG CGCGCGGCC 1260  
 TCCAACCTCG TCATCCGCAA CCTTTTGGAC CAGGCGTCCC ACACGCGAGG CACCAAGGCC 1320  
 CCAGCCCTAA AAGGGGGAGC TGCGGAGCTC CGGCCCTCCG ACGTGGGGCA TGTGCTGAGG 1380  
 ATGCTGCTGG GGAAGATGTG CGCGCCGAGG TACCCCTCCG GGGGCGCCTG GGACCTCAC 1440  
 CCAGGCCAGG GCTTCGGGGA GAGCATGTAT CTGCTCTCGG ACAAGGCCAC CTCGCCGCTC 1500  
 TCGCTGGATG CTGGCTCCGG GCAGGCCCCC TGGAGCGACC TGCTTCTTTG GGCAGTGTG 1560  
 CTGAACAGGG CACAGATGGC CATGTACTTC TGGGAGATGG GTTCCAATGC AGTTTCTCTA 1620  
 GCTCTTGGGG CCTGTTTGCT GCTCCGGGTG ATGGCACGCC TGGAGCCTGA CGCTGAGGAG 1680  
 GCAGCACGGA GGAAGACCTT GCGTTCAAG TTTAGGGGA TGGGCGTTGA CTTCTTTGGC 1740  
 GAGTGTCTAT GCAGCAGTGA GGTGAGGGCT GCCCGCCTCC TCCTCCGTCG CTGCCGCTC 1800  
 TGGGGGGATG CCACCTGGCT CCAGCTGGCC ATGCAAGCTG ACGCCCGTGC CTCTTTTGCC 1860  
 CAGGATGGGG TACAGTCTCT GCTGACACAG AAGTGGTGGG GAGATATGGC CAGCACTACA 1920  
 CCCATCTGGG CCTGTGTTCT GGCCTTCTTT TGCCCTCCAC TCATCTACAC CCGCCTCATC 1980  
 ACCTTCAGGA AATCAGAAGA GGAGCCACA CGGGAGGAGC TAGAGTTTGA CATGGATAGT 2040  
 GCTATTAATG GGAAGGGGCC TGTCCGGACG GCGGACCCAG CCGAGAAGAC GCCGCTGGGG 2100  
 GTCCCGCGCC AGTCGGGGCT TCCGGGTGTC TCGGGGGGCC GCTGCGGGGG GCGCCGGTGC 2160  
 CTACGCGCTG GGTTCACCTT CTGGGGCGCG CCGGTGACCA TCTTCATGGG CAACGTGGTC 2220  
 AGCTACCTGC TGTTCCTGCT GCTTTTCTCG CGGGTGTGTC TCGTGGATT TCAGCCGGCG 2280  
 CCGCCCGGCT CCTGGAGCT GCTGCTCTAT TTCTGGGCTT TCACGCTGCT GTGCGAGGAA 2340  
 CTGCGCCAGG CCTGTAGCGG AGGCGGGGGC AGCCTCGCCA GCGGGGGCCC CGGGCCTGGC 2400  
 CATGCTCTAC TGAGCCAGCG CCTGCGCTC TACCTCGCCG ACAGCTGGAA CCAGTGGCAG 2460  
 CTAGTGGCTC TCACCTGCTT CCTCCTGGGC GTGGGCTGCC GGCTGACCCC GGGTTTGTAC 2520  
 CACCTGGGCC GCACTGTCTT CTGATCGAC TTCTATGGTT TCACGGTGGC GCTGCTTAC 2580  
 ATCTTACCG TCAACAACA GCTGGGGCCC AAGATCGTCA TCGTGAGCAA GATGATGAAG 2640  
 GACGTGTTCT TCTTCTCTT CTTCCTCGGC GTGTGGCTGG TAGCCTATGG CGTGCCACG 2700  
 GAGGGGCTCC TGAGGCCACG GGACAGTGAC TTCCCAAGTA TCCTGCGCCG CGTCTTCTAC 2760  
 CGTCCCTACC TGCAGATCTT CCGGCAGATT CCCAGGAGG ACATGGACGT GGCCCTCATG 2820  
 GAGCACAGCA ACTGCTCGTC GGAGCCCGGC TTCTGGGCAC ACCCTCTGGG GGCCAGGGCG 2880  
 GGCACCTGCG TCTCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCTCTGT CATCTTCTGT 2940  
 CTGCTGGGCA ACATCTGCT GGTCAACTTG CTCATTGCCA TGTTCAAGTA CACATTGGGC 3000  
 AAAGTACAGG GCAACAGCGA TCTCTACTGG AAGGCGCAGC GTTACCGCCT CATCCGGGAA 3060  
 TTCCACTCTC GGGCCGCGCT GGGCCCGCCC TTTATCGTCA TCTCCACTT GCGCCTCTGT 3120  
 CTAGGCAAT TGTGCGGCG ACCCGGAGC CCCCAGCCGT CCTCCCGGCG CTTGAGCAT 3180  
 TTCCGGGTTT ACCTTTCTAA GGAAGCCGAG CGGAAGCTGC TAACGTGGGA ATCGGTGCAT 3240  
 AAGGAGAACT TTCTGCTGGC ACGCGTAGG GACAAGCGGG AGAGCGACTC CGAGCTGCTG 3300  
 AAGCGCACT CCCAGAAAGT GGACTTGGCA CTGAAACAGC TGGGACACAT CCGGAGTATC 3360  
 GAACAGCGCC TGAAGTGTCT GGAGCGGAG GTCCAGAGT GTAGCCCGCT CCTGGGGTGG 3420  
 GTGGCCGAGG CCCTGAGCCG CTCTGCCCTT CTGCCCCAG GTGGGCGGCC ACCCCCTGAC 3480  
 CTGCTGGGT CCAAGACTG A

**A198 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.31608  
 Probeset Accession #: H18836  
 Protein Accession #: none found

Signal sequence: none found  
 Transmembrane domains: 214-230, 537-556, 642-662, 730-752, 760-782, 815-837, 842-864, 877-899, 973-995  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MEDAFGAADV TVWSDAHTT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR 60
TWGFRAPNLV VSVLGGSGGP VLQTLWLDLL RRGLVRAAQS TGAWIVTGGL HTGIGRHVGV 120
AVRDHQMAST GGTKVVMGV APWGVVRNRD TLINPKGSFP ARYRWRGDPE DGVOFPLDYN 180
YSAFFLVDDG THGCLGGENR FRLRLSEYIS QQKTGVGGTG IDIPVLLLLI DGDEKMLTRI 240
ENATQAQLPC LLVAGSGGAA DCLAETLEDT LAPGSGGARQ GEARDRIIRF FPKGDLEVLQ 300
AQVERIMTRK ELLTVYSSD GSEEFETIVL KALVKACGSS EASAYLDEL R LAVAWNVRVDI 360
AQSELFGRDI QWRSFHLEAS LMDALLNDPR EFVRLLSHG LSLGHFLTPM RLAQLYSAAP 420
15 SNSLIRNLLD QASHSAGTKA PALKGGAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480
PGQFGESMY LLSDKATSP LSLDAGLGQAP WSDLLLWALL LNRAQMAMYF WEMGSNAVSS 540
ALGACLLLRV MARLEPDABE AARRKDLAFK FEGMGVDLFG EYRSSEVRA ARLLLRRCPL 600
WGDATCLQLA MQADARAFFA QDGVQSLLTQ KWWGDMASTT PIWALVLAFF CPPLIYTRLI 660
20 TFRKSEBEPT REELEFDMDS VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGGRCGGRRC 720
LRRWFHFWGA PVTIFMGNVV SYLLFLLLF S RVLLVDFQPA PPGSLELLLY FWAFTLLCEE 780
LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840
HLGRTVLCID FMVFTVRLH IFTVNKQLGP KIVIVSKMMK DVFFFLFFLG VWLVAYGVAT 900
BGLLRPRDS FPSILRRVFI RPYLQIFGQI PQEDMDVALM EHSNCSSEFG FWAHPGGAQA 960
25 GTCVSQYANW LVVLLLVIFL LVANILLVNL LIAMFSYTFG KVQGNSDLYW KAQRYRLIRE 1020
FHSRPALEAP FIVISHLRL LRQLCRRPRS PQSPSPALEH FRVYLSKEAE RKLLTWESVH 1080
KENFLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY BQRLKVLERE VQCSRVLGW 1140
VAEALSRSAL LPPGGPPPPD LPSGSKD

```

**A199 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.40808  
 Probeset Accession #: AA054237  
 Nucleic Acid Accession #: AA054237  
 Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCCTGGGG 60
CTGCTCGTCA CGGCATCTT CACCGACCAC TGGTACGAGA CCGACCCCGG GCGCCACAAG 120
40 GAGAGCTGCG AGCGCAGCCG CGCGGCGGCC GACCCCCCGG ACCAGAAGAA CCGCCTGATG 180
CCGCTGTCGC ACCTGCGCGT CGCGGACTCG CCCCCTGCTG GCGCGCGGCT GCTCCCGGGC 240
GGCCCGGGGG GCGCCGACCC CGAGTCTCGG CGCTCGCTCC TGGGGCTCGG CCGGCTGGAC 300
GCGAGTGCG GCGGCGCCCT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
45 CTGGGCATCG ACCGGGACAT CGACACCCCT ATCCTGAAAG GTATTGCGCA GCGATGCACG 420
GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCAGG ACATTCTTT TAATTTAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTTAA GAAGAATCAC TGCTGGCTTC 540
CTCGGCATGG CGGTAGCCGT CCTTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGACTCCTGT TCCTCATGAC AGGGATATTT 660
50 TGCAACATTT CCTCTGTAC TTATGCGGCC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCCTGCC TGCTGATGTG GAACATGGT ACAGCTGGTC CATCTTTTC 780
GCCTGGTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT 840
ATTAGCCGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA

```

**A200 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.40808  
 Probeset Accession #: AA054237  
 Protein Accession #: none found  
 Signal sequence: 1-18  
 Transmembrane domains: 179-201, 209-231, 257-279  
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DPPDQKNRLM 60
PLSHLPLRDS PPLGRRLLPG GPGRADPEW RSLGLGLGLD AECGRPLFAT YSGLWRKCYF 120
65 LGIDRDIDTL ILKGIAQRCT AIKYHFSQPI RLRNIPFNLT KTIQDEWHL LHLRRITAGF 180
LGMMAVAVLLC GCIVATVSFF WEESLTQHVA GLLFLMTGIF CTISLCTYAA SISYDLNRLP 240
70 KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

```

**A201 DNA SEQUENCE**

Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Nucleic Acid Accession #: NM\_016570  
 Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGAGGCGAC TGAATCGGAA AAAAAGTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTCCG 60
AAGGTTCTCT AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120

```

TTTACAACCTA TGGCTTTATT AACCATAATG GAATTCTCAG TATATCAAGA TACATGGATG 180  
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240  
 ACTGTTGCCA TGAAGTGTCA ATATGTTGGA GCGGATGTAT TGGATTAGC AGAAACAATG 300  
 GTTGCATCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360  
 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACTT 420  
 CAAGATGTGA TATTTAAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480  
 GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCAATAAA 540  
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600  
 CATTTGGCAG CAGTTGTCAA CCATGAATCT TACAATTTT CTATAGAAAT AGATCATTTG 660  
 TCTTTTGGAG AGCTTGTCTC AGCAATTATT AATCCTTTAG ATGGAACCTGA AAAAAATGCT 720  
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780  
 TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAA 840  
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTTATGA AATATGATCT CAGTTCTCTT 900  
 ATGGTGCAG TTACTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960  
 ATGTTGGAG GAATCTTTTC AACCAACAGG ATGTTACATG GAATTGGAAA ATTTATAGTT 1020  
 GAAATAATTT GCTGTCGTTT CAGACTTGGG TCCTATAAAC CTGTCAATTC TGTTCCTTTT 1080  
 GAGGATGGCC ACACAGACAA CCATTACCT CTTTATAGAAA ATAATACACA TTGA

# A202 Protein sequence:

Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Protein Accession #: NP\_057654  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Cellular Localization: nuclear

1 11 21 31 41 51  
 | | | | |  
 MRRLLNRKTL SLVKELDAFP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60  
 KYEYEDKDF SSKLRINIDI TVAMKQYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120  
 KEWQRMQLLI QSRLQEEHSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVNK 180  
 VAGNFHITVG KAIPHPRGHA HLAALVNHES YNFSHRIDHL SFGELVPAII NPLDGTETKIA 240  
 IDHNQMFQYF ITVVPKTLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300  
 MVTVTEEHMP FWQFFVRLCG IVGGIFSTTG MLHGIGKPIV EIICCRFRLG SYKPVNSVPF 360  
 EDGHTDNHLP LLENNTN

# A203 DNA SEQUENCE

Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)  
 Unigene number: Hs.44926  
 Probeset Accession #: S79876  
 Nucleic Acid Accession #: NM\_001935.1  
 Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CGCGCGTCTC CGCCGCCCGC GTGACTTCTG CCTGCGCTCC TTCTCTGAAC GCTCACTTCC 60  
 GAGGAGACGC CGACGATGAA GACACCGTGG AAGATTCTTC TGGGACTGCT GGGTGTGCT 120  
 GCGCTTGTC CCAATCATCAC CGTGCCCGTG GTTCTGCTGA ACAAGGCGAC AGATGATGCT 180  
 ACAGCTGACA GTCGCAAAAC TTACACTCTA ACTGATTACT TAAAAAATAC TTATAGACTG 240  
 AAGTTATACT CCTTAAGATG GATTTCAGAT CATGAATATC TCTACAAACA AGAAAAATAAT 300  
 ATCTTGGTAT TCAATGCTGA ATATGGAAAC AGCTCAGTTT TCTTGGAGAA CAGTACATTT 360  
 GATGAGTTTG GACATTCTAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTCTC 420  
 TTAGAATACA ACTACGTGAA GCAATGGAGG CATTCTTACA CAGCTTCATA TGACATTAT 480  
 GATTAAATACA AAAGGCAGCT GATTACAGAA GAGAGGATTC CAAACAACAC ACAGTGGGTC 540  
 ACATGGTCAC CAGTGGGTCA TAAATTGGCA TATGTTTGGG ACAAATGACAT TTATGTTAAA 600  
 ATTTGAACCA ATTTACCAAG TTACAGAATC ACATGGACGG GGAAGAAGA TATAATATAT 660  
 AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCTTCA GTGCCTACTC TGCTCTGTGG 720  
 TGGTCTCCAA ACGGCACATT TTTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCCTT 780  
 ATTTGAATCT CCTTCTACTC TGATGAGTCA CTGCAGTACC CAAAGACTGT ACGGGTTCCA 840  
 TATCCAAAGG CAGGAGCTGT GAATCCAAC GTAAAGTTCT TTGTGTGAAA TACAGACTCT 900  
 CTCAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCCTGCTTC TATGTTGATA 960  
 GGGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAAG AAAGAATTTC TTTGCAGTGG 1020  
 CTCAGGAGGA TTCAGAACTA TTCGGTCATG GATATTTGTG ACTATGATGA ATCCAGTGG 1080  
 AGATGGAAC GCTTAGTGGC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTGG 1140  
 AGATTAGGC CTTTCAAGAC TCATTTTACC CTTGATGGTA ATAGCTTCTA CAAGATCATC 1200  
 AGCAATGAAG AAGGTTACAG ACACATTTCG TATTTCCAAA TAGATAAAAA AGACTGCACA 1260  
 TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAAG CTCTAACCAG TGATTATCTA 1320  
 TACTACATTA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAATCCAA 1380  
 CTTATTGACT ATACAAAAGT GACATGCCTC AGTTGTGAGC TGAATCCGGA AAGGTGTCAG 1440  
 TACTATTCTG TGTCATTCTG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCCGGTCTC 1500  
 GGTCTGCCCC CTATACTCT ACACAGCAGC GTGAATGATA AAGGGCTGAG AGTCCTGGAA 1560  
 GACAAATCAG CTTTGGATAA AATGCTGCAG AATGTCCAGA TGCCCTCCAA AAACTGGGAC 1620  
 TTCATTATT TGAAATGAAC AAAATTTTGG TATCAGATGA TCTTGCTTCC TCATTTTGAT 1680  
 AAATCCAAGA AATATCTCTC ACTATTAGAT GTGTATGCAG GCCCATGTAG TCAAAAAGCA 1740  
 GACACTGTCT TCAGATGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATTATAGTA 1800  
 GCTAGCTTTG ATGGCAGAGG AAGTGTTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC 1860  
 AGAAGACTGG GAACATTTGA AGTTGAAGAT CAAATGAAG CAGCCAGACA ATTTTCAAAA 1920  
 ATGGGATTTG TGGACAACAA ACGAATTGCA ATTTGGGGCT GGTCAATAGG AGGGTACGTA 1980  
 ACCTCAATTG TCTGGGATC GGAAGTGCG GTGTTCAAGT GTGGAATAGC CGTGGCGCCT 2040

5  
 10  
 15  
 20  
 25  
 30  
 35

```

GTATCCCGGT GGGAGTACTA TGACTCAGTG TACACAGAAC GTTACATGGG TCTCCCAACT 2100
CCAGAAGACA ACCTTGACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAAAAATTTT 2160
AAACAAGTTG AGTACCTCCT TATTCATGGA ACAGCAGATG ATAACGTTCA CTTTCAGCAG 2220
TCAGCTCAGA TCTCCAAAGC CCTGGTCGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT 2280
ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG 2340
AGCCACTTCA TAAACAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCATTTA 2400
AAGCTTATTA AACTCATTT TTGTTTTTAT TATCTCAAAA CTGCACTGTC AAGATGATGA 2460
TGATCTTTAA AATACACACT CAATCAAGA AACTTAAGGT TACCTTTGTT CCCAAATTTT 2520
ATACCTATCA TCTTAAGTAG GGACTTCTGT CTTCACAACA GATTATTACC TTACAGAAGT 2580
TTGAATTATC CGTCCGGGTT TTATTGTTTA AAATCATTTT TGCATCAGCT GCTGAAACAA 2640
CAAAATAGGAA TTGTTTTTAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAATCTT 2700
TTTCTAACTG GACTGGTTCA AATGTTGTTT TCTTCTTTAA AGGGATGGCA AGATGTGGGC 2760
AGTGATGTCA CTAGGGCAGG GACAGGATAA GAGGGATTAG GGAGAGAAGA TAGCAGGGCA 2820
TGGCTGGGAA CCCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTGAG CTCCCTCGG 2880
AGAAGAGCTG TTCACCACGA GACTGGCACA GTTTCTGAG AAAGACTATT CAAACAGTCT 2940
CAGGAAATCA AATATCGAAA GCACTGACTT CTAAGTAAAC CACAGCAGTT GAAAGACTCC 3000
AAAGAAATGT AAGGGAAACT GCCAGCAACG CAGCCCCCAG GTGCCAGTTA TGGCTATAGG 3060
TGCTACAAAA ACACAGCAAG GGTGATGGGA AAGCATTGTA AATGTGCTTT TAAAAAATAA 3120
TACTGATGTT CCTAGTGAAG GAGGCAGCTT GAAACTGAGA TGTGAACACA TCAGCTTGCC 3180
CTGTTAAAGG ATGAAAATAT TTGTATCACA AATCTTAACT TGAAGGAGTC CTTGCATCAA 3240
TTTTTCTTAT TTCAATTTCT TGAGTGCTCT AATTAAGAAG ATATTTTAAAC TTCCTTGGAC 3300
TCATTTTAAA AAATGGAACA TAAATACAA TGTATATGAT TATTATTTCC ATTCTACATA 3360
CTATGGAATT TCTCCAGTC ATTAAATAAA TGTGCCCTCA TTTTTTC
  
```

**A204 Protein sequence:**

Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)  
 Unigene number: Hs.44926  
 Probeset Accession #: S79876  
 Protein Accession #: NP\_001926.1  
 Signal sequence: none found  
 Transmembrane domains: 6-28  
 DPPIV\_N\_term domain: 43-557  
 Peptidase\_S9 domain: 558-635  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 40 MKTPWKILG ILGAAALVTI ITVPVVLNKK GTDDATADSR KTYTLTDYK NTYRLKLYSL 60  
 RWISDHELYL QKQENILVFN AEYGNSSVFL ENSTFDEFH SINDYSISPD GQFILLEYN 120  
 VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVTWSEF GHKLAYVWNN DIYVKIEPNL 180  
 PSYRITWTGK EDIIYNGITD WYIEEVEFSA YSALWWSPNG TFLAYAQFND TEVPLIEYSF 240  
 45 YSDESLQYPK TVRVYPKAG AVNPTVKFFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300  
 CDVTWATQER ISLQWLRRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGWVGRFRPS 360  
 EPHFTLDGNS FYKIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYYISN 420  
 EYKGMFGGRN LYKIQIDYIT KVTCLSCELN PERCQYYSVS FSKEAKYYQL RCGSGPLPLY 480  
 TLHSSVNDKG LRVLENSAL DKMLQNVQMP SKKLDIFILN ETKFWYQML PPHFDKSKKY 540  
 50 PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFDF RSGGYQGDKI MHAINRRLGT 600  
 FEVEDQIEAA RQFSKMGFVD NKRIATWGS YGGYVISMVL GSGSGVFKCG IAVAPVSRWE 660  
 YDVSVTERY MGLPTPEDNL DHYRSTVMS RAENFKQVEY LLIHGTADDN VHFQQAQIS 720  
 KALVDVGVD FQAMWYDDEH GIASSTAHHQ IYTHMSHFIF QCFSLP

**A205 DNA SEQUENCE**

Gene name: predicted exon  
 Unigene number: none found  
 Probeset Accession #: none found  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-261 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 65 ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAATGACA ATGCCATCAG AGTTGACAAC 60  
 AGAAGTGTGA TTAAGTGC GCTAACCAAG TGTTCCTGCG ATGAGGCAGA AAGTGAATCC 120  
 AGAAACCCCTC AGGAGCTCTG GATGGGCTCG CTCCTCTTGA TGGGGGTCCT AGAAGCATGT 180  
 GTGGAATAGA GGCCTCTGTC AGTCTGTGTC CTGAGAGATG ACAAGGAGCA GAGCCCCCAC 240  
 CAGCCACAC TGGATGCTA A

**A206 Protein sequence:**

Gene name: predicted exon  
 Unigene number: none found  
 Probeset Accession #: none found  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 46-68  
 Cellular Localization: not determined

1 11 21 31 41 51  
 | | | | |  
 MALAKVREFN ANDNAIRVDN RSVIKVRANQ CSLHFAESSES RNPQELWMGL LLLMGVLEAC 60  
 VEMRPLSVWS LRDDKEQSPH QPTLDV

A207 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.222886  
 Probeset Accession #: AI672225  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTTGGAAGCA GTAAATGTTT AAAAACTGCT 60
CTCATACTTG CTGTATGTTG TGGATCAGCA AATATAGTCA GCCCTCTACT TGAGCAAAAT 120
ATTGATGTAT CTTCTCAAGA TCTGGACAGA CGGCCAGAGA GTATGCTGTT TCTAGTCATC 180
ATCATGTGGA CCAGTTTGTG GGAAGACAAT CTTTCCATGG GCTGGGGGAA GCTAGAAGAT 240
TTTATGGCTA TTGAAGAAGA AATGAAGAAG CACGGAAGTA CTCATGTGGG ATTCCCAGAA 300
AACTGACTA ATGGTGCCGC TGCTGGCAAT GGTGATGATG GATTAATTCC TCCAAGGAAG 360
AGCAGAACAC CTGAAAGCCA GCAATTTTCT GACACTGAGA ATGAAGAGTA TCACAGGTTT 420
GTCAAAGATC AGATAGTTGT AGATATGCGG CGTTATTTCT GA

```

A208 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.222886  
 Probeset Accession #: AI672225  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 16-38  
 Cellular Localization: not determined

```

1      11      21      31      41      51
|      |      |      |      |      |
MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPILLEQN IDVSSQDLDR RPESMLFLVI 60
IMWTSFVEDN LSMGWKLED FMAIEEMKK HGSTHVGFPE NLTNAAAAGN GDDGLIPPRK 120
SRTPEQQQFP DTENEYHHRF VKDQIVVDMR RYF

```

A209 DNA SEQUENCE

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1  
 Unigene number: Hs.23796  
 Probeset Accession #: NM\_014253  
 Nucleic Acid Accession #: NM\_014253  
 Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

```

45 1      11      21      31      41      51
|      |      |      |      |      |
GACTGCTTGC ATTAAAGGAC TTCCTCATCC TTTTTCATCAT GAAACTGAGC TTGCTTAATC 60
AGAGATGGAG CAAACTGACT GCAAACCCCTA CCAGCCTCTA CCAAAAGTCA AGCATGAAAT 120
GGATCTAGCT TACACCAGTT CTTCTGATGA GAGTGAAGAT GGAAGAAAAC CAAGACAGTC 180
ATACAACTCC AGGGAGACCC TGCACGAGTA TAACCAGGAG CTGAGGATGA ATTACAATAG 240
CCAGAGTAGA AAGAGGAAAG AAGTAGAAAA ATCTACTCAA GAGATGGAAT TCTGTGAAAC 300
CTCTCACACT CTGTGCTCTG GCTACCAAAC AGACATGCAC AGCGTTTCTC GGCATGGCTA 360
CCAGCTAGAG ATGGGATCTG ATGTGGACAC AGAGACAGAA GGTGCTGCCT CACCTGACCA 420
TGCACTAAGA ATGTGGATAA GGGGAATGAA ATCAGAGCAT AGTTCTGTGT TGTCCAGCCG 480
GGCCAACTCT GCATTATCCT TGACTGACAC TGACCATGAA AGGAAGTCTG ATGGGGAAAA 540
TGTTTCAAAA TTCTCTCTCT TTTGTTGTGA CATGGAGGCT CAAGCTGGGT CTACTCAAGA 600
TGTCGAGAGC AGCCCAACACA ACCAGTTCAC CTTACAGACC CTCCACCCGC CACCTCCGCC 660
TCCTCATGCC TGCACCTGTG CCAGGAAGCC ACCCCCTGCA GCGGACTCTC TTCAGAGGAG 720
ATCAATGACT ACCCGCAGCC AGCCAGCCCC AGCTGCTCCA GCTCCCCCAA CCAGCACGCA 780
GGATTGAGTC CATCTGCATA ACAGCTGGGT CCTGAACAGC AACATACCAT TGGAGACCCAG 840
GCATTCCCTG TTCAAAATATG GATCTGGTTC CTCTGCGATC TTCAGTGACG CCAGTCAGAA 900
CTACCCCTCTG ACATCCAATA CCGTGTACTC GCCCCCTCCC AGGCCTCTTC CTCGAAGCAC 960
CTTTTCCCAG CCTGCCTTTA CCTTTAACAA ACCTTACAGG TGCTGCAACT GGAAGTGCAC 1020
AGCATTGAGC GCCACTGCAA TCACAGTGAC TTTGGCCTTG TTAGTACGCT ATGTGATTGC 1080
AGTGCATTGT TTCGGCCTGA CTTGGCAGTT GCAACCAAGT GAAGGAGAGC TGTATGCAAA 1140
TGGAGTTAGC AAAGGGAACA GGGGGACCGA GTCCATGGAC ACTACTTACT CTCCAATTGG 1200
AGGAAAAGTT TCTGATAAAT CAGAGAAAAA AGTGTTCAG AAGGGACGGG CGATAGACAC 1260
TGGAGAAAGT GACATTGGTG CACAGGTATC GCAGACCATT CCACCTGGTT TATTCTGGCG 1320
TTTCCAGATT ACTATCCACC ATCCAATATA TCTGAAGTTC AATATTCTTT TAGCCAAGGA 1380
CTCTCTGCTG GGAATTTATG GCAGAAGAAA CATTCACCT ACACATACTC AGTTTGATT 1440
TGTAATACTA ATGGATGGCA AACAGCTGGT CAAGCAGGAC TCCAAGGGCT CTGATGATAC 1500
ACAGCACTCC CCTCGGAACC TGATCTTAAC TTCGCTTCAG GAGACAGGTT TCATAGAGTA 1560
TATGGATCAA GGACCTTGGT ATCTGGCGTT TTACAATGAT GGAATAAAGA TGGAGCAAGT 1620
ATTGCTGTGA ACTACAGCAA TTGAATAAAT GGATGACTGT TCAACCAATT GCAATGGAAA 1680
TGGAGAGTGT ATCTCTGGCC ATTGTCTATT TTTCCAGGA TTCCTTGGAC CTGACTGTGC 1740
TAGAGATTCC TGCCCTGTGC TGTGTGGTGG GAATGGAGAA TACGAGAAAG GACACTGTGT 1800
CTGCCGCGAT GGTCTGGAAG GGCAGAGTG TGACGTTCCG GAAGAACAAAT GCATTGATCC 1860
AACATGCTTT GGCCACGGCA CCTGCATCAT GGGAGTCTGC ATCTGTGTGC CAGGATACAA 1920
AGGAGAAATA TGCAGGAAAG AGGACTGCCT AGACCCAATG TGTCCAACC ATGGCATCTG 1980
TGTAAGAGTA GAATGTCACT GTTCTACTGG CTGGGGAGGA GTTAACTGTG AAACACCACT 2040
TCCTGTATGT CAAGAGCAGT GCTCAGGACA CGGAACCTTT CTTCTGGACG CTGGAGTATG 2100
CAGCTGTGAT CCCAAGTGA CAGGATCTGA CTGCTCAACA GAGCTGTGTA CCAATGGAGTG 2160
TGGTAGCCAT GGAGTCTGCT CAAGAGGAAT TTGCCAGTGT GAAGAAGGCT GGGTAGGACC 2220
AACATGTGAG GAACGCTCCT GTCATTCTCA TTGTACTGAG CATGGCCAAT GCRAAGATGG 2280

```

	AAAAATGTGAG	TGTAGCCCTG	GATGGGAGGG	CGACCACTGC	ACAATTGCTC	ACTACTTAGA	2340
	TGCTGTCCGA	GATGGCTGCC	CAGGGCTCTG	CTTTGGAAAT	GGACGATGTA	CCCTGGATCA	2400
	AAATGGTTGG	CACCTGTGTGT	GTCAGGTGGG	TTGGAGTGGG	ACAGGCTGCA	ATGTTGTTCAT	2460
	GGAAATGCTT	TGTGGAGATA	ACTTGGACAA	TGATGGAGAT	GGTTTAAACG	ACTGTGTGGA	2520
5	TCCTGACTGT	TGTCAACAAA	GCAACTGTTA	TATAAGTCCT	CTCTGCCAGG	GCTCACCAGA	2580
	TCCTCTTGAC	CTCATTACAG	AAAGCCAAAC	TCTCTTCTCT	CAGCACACTT	CAAGACTTTT	2640
	TTATGATCGA	ATCAAATTCC	TCATTGGCAA	GGACAGTACT	CATGTCAATC	CTCCTGAGGT	2700
	GTCATTTGAC	AGCAGGCGTG	CCTGTGTGAT	TCGAGGCCAA	GTGGTGGCCA	TAGATGGAAC	2760
10	TCCTCTAGTG	GGAGTGAATG	TCAGTTTCTT	GCACCACAGT	GATTATGGGT	TTACCATCAG	2820
	CCGGCAAGAT	GGAGCTTTG	ACCTCGTGGC	CATCGGTGGC	ATCTCTGTCA	TCTTAATCTT	2880
	CGACCGATCC	CCTTTCTCGC	CTGAGAAGAG	AACACTCTGG	TTGCCTTGGA	ATCAGTTTAT	2940
	TGTGGTAGAG	AAAGTACCCA	TGCAGAGAGT	TGTATCAGAC	CCGCCATCCT	GCGATATCTC	3000
	CAACTTTATC	AGCCCAAACC	CTATTGTGCT	TCCTTCACCG	CTCACATCAT	TTGGAGGGTC	3060
15	CTGTCCAGAG	AGGGGAACCT	TTGTTCTCTG	GCTGCAGGTT	GTACAGGAGG	AAATTCCCAT	3120
	TCCTCCAGC	TTTGTGAGGC	TGAGTTACCT	GAGCAGCCGC	ACCCCTGGGT	ATAAAACCTT	3180
	GCTACGGATC	CTTCTGACAT	ATTCAACGAT	TCCCGTAGGC	ATGATAAAAG	TACACCTCAC	3240
	AGTAGCTGTG	GAAGGGCGAC	TCACACAGAA	GTGGTTTCCC	GCCGCAATTA	ATCTTGTCTA	3300
	CACATTTGCT	TGGAACAAGA	CCGATATCTA	TGGACAGAAG	GTTTGGGGCC	TGGCAGAGGC	3360
20	TTTGGTATCT	GTGGGATATG	AATATGAAAC	GTGCCCTGAC	TTTATTCTCT	GGGAGCAAAG	3420
	GACAGTCGTT	TTACAAGGTT	TTGAGATGGA	TGCTTCTAAC	CTAGGAGACT	GGTCTTTGAA	3480
	TAAGCATCAC	ATTTTGAATC	CTCAAAGTGG	AATCATACAT	AAAGGGAATG	GAGAAAATAT	3540
	GTTCATTTCC	CAGCAGCCCC	CAGTCATATC	AACCATAATG	GGTAATGGAC	ACCAAAGGAG	3600
	TGTAGCCTGC	ACCAACTGCA	ATGGCCAGC	CCACAACAAC	AAACTCTTTG	CTCCTGTCGC	3660
25	CTTAGCTTCT	GGCCCTGATG	GCACTGTGTA	TGTTGGCGAC	TTCAATTTTG	TAAGGAGAAT	3720
	ATTTCCCTCG	GGAAACTCCG	TTAGTATTTT	GGAATTAAGC	ACAAGTCCTG	CTCACAATAA	3780
	CTATCTGGCT	ATGGACCTTG	TGCTGAATC	ACTCTATCTA	TCAGACACCA	ATACTCGCAA	3840
	AGTCTACAAG	TTGAAATCTC	TTTGGGAGAC	GAAAGATCTG	TCCAAGAATT	TTGAAGTGGT	3900
	GGCAGGAAGT	GGTGATCAGT	GCCTTCCCTT	TGACCAGAGT	CATTGTGGAG	ATGGTGGGAG	3960
30	AGCATCGGAA	GCTTCACTGA	ATAGCCCTCG	AGGCATCACA	GTTGATAGGC	ATGGATTAT	4020
	TTACTTTGTG	GATGGGACTA	TGATTTCGCA	AATTGATGAG	AATGCTGTGA	TCACAACITG	4080
	AATCGGCTCA	AATGGTCTGA	CTTCCACACA	ACCACTGAGC	TGTGACTCAG	GAATGGACAT	4140
	CACTCAGGTG	CGATTAGAGT	GGCCAACAGA	CCTTGCAGTA	AATCCTATGG	ACAATTTCAT	4200
	GTATGTCTTG	GATAACAACA	TTTGTCTGCA	AATTTCTGAG	AACAGGCGTG	TTCCGGATCAT	4260
35	CGCAGGACGC	CCCATTCTAC	GCCAGGTGCC	AGGCATCGAT	CATTTCTTGG	TCAGCAAGGT	4320
	AGCAATTAC	TCCACTCTAG	AGTCAGCGAG	GGCCATCAGT	GTCTCCACCA	GCGGCTGCT	4380
	CTTCATAGCT	GAACAGACG	AGAGGAAAGT	AAACCGCATT	CAGCAAGTAA	CCACCAATGG	4440
	GGAGATCTAC	ATCATCGCTG	GTGCCCCAC	TGACTGTGAC	TGCAAAATTG	ATCCAAACTG	4500
	TGACTGTTTT	TCAGGTGATG	GTGGCTATGC	CAAAGATGCA	AAGATGAAAG	CCCCCTCCTC	4560
40	CTTAGCAGTG	TGCCTGATG	GAACCTCTA	TGTGGCAGAC	CTCGGAAATG	TTCGAATTCTG	4620
	TACCATCAGC	AGGAACCAAG	CCCACCTGAA	TGACATGAAC	ATTTATGAGA	TTGCTTCCAC	4680
	CGCTGATCAG	GAACGTGACC	AGTTCACTGT	AAATGGAACC	CACCTACACA	CCCTGAACTT	4740
	GATAACAAGG	GACTATGTTT	ATAACTTCAC	CTACAATTCT	GAAGGTGACT	TGGGCGCGAT	4800
	TACCAGCAGC	AATGGCAATT	CAGTGCACAT	TCGCCGTGAT	GCAGGCGGAA	TGCCGCTATG	4860
45	GCTTGTGGTG	CCTGGCGGAC	AAGTATACTG	GCTGACTATA	AGCAGCAATG	GAGTCTCTGAA	4920
	AAGAGTGTCA	GCCCAAGGCT	ATAATCCGCG	CTTAATGACC	TATCCAGGAA	ACACAGGGCT	4980
	TCTGGCTACC	AAAAGTAAAG	AAAATGGATG	GACAACCGTT	TATGAGTATG	ACCCCGAGGG	5040
	ACACCTGACC	AATGCAACGT	TTCCCACTGG	AGAGTTCAGC	AGCTTCCACA	GTGACCTGGA	5100
	GAAAGTGTCA	AAAGTGGAGC	TAGATACTTC	CAACCGTGAA	AATGTCTCTA	TGTCAACCAA	5160
50	CTTGACGGCA	ACTAGTACCA	TATATATTTT	AAAAACAAGAA	AATACTCAAA	GTACCTATCG	5220
	GGTGAATCCA	GATGTTTCCC	TGCGTGTAC	TTTGGCCAGC	GGGATGGAGA	TGGGCTCAG	5280
	CTCAGAGCCC	CACATCCTGG	CAGGGGCACT	CAACCTTACC	CTGGGCAAT	GCAACATCTC	5340
	ATTGCCCGGA	GAGCACAATG	CAAACCTCAT	CGAGTGGCGG	CAGAGGAAGG	AGCAAAACAA	5400
	AGGCAATGTT	TCGGCTTTTG	AAAGGAGGCT	GAGGGCCAC	AACAGAAACC	TACTCTCCAT	5460
55	AGATTTTGAT	CATATAACCC	GCACAGGAAA	GATCTATGAT	GACCATCGAA	AATTCAACCT	5520
	TCGAATCTTT	TATGACCAGA	CTGGGCGACC	CATTCTGTGG	TCTCTGTGAA	GCAGATATAA	5580
	TGAAGTGAAC	ATCATATATT	CACCTTCGGG	ATTGGTGCAG	TTTATTCAAA	GAGGAACGTG	5640
	GAATGAAAAA	ATGGAATATG	ACCAGAGTGG	GAAAATTATT	TCAAGAACTT	GGGCTGATGG	5700
	GAAAAATTGG	AGCTATACCT	ACTTAGAAAA	ATCTGTGATG	CTTCTCTAC	ACAGCCAGCG	5760
60	GCGTTACATC	TTTGAATATG	ACCAATCAGA	TTGCCCTGCT	TCAGTTACCA	TGCCTAGCAT	5820
	GGTGCGCCAC	AGCTTACAAA	CCATGCTTTC	AGTGGGCTAC	TACCGTAATA	TCTACACCCC	5880
	ACCGGACAGT	AGCACTTCTT	TTATCCAAGA	CTATAGTCGA	GATGGCCGAT	TGCTACAGAC	5940
	CCTGCATCTG	GGGACAGGGC	GCAGAGTCTT	ATACAAGTAC	ACCAAGCAAG	CAAGGCTTTC	6000
	TGAGGTTCTC	TATGATACCA	CTCAGGTCAC	ATTAACATAT	GAGAGTCTT	CTGGAGTGAT	6060
65	TAAGACAATA	CACCTGATGC	ATGACGGATT	CATCTGCACA	ATCAGATACA	GGCAACACAG	6120
	ACCTCTTATT	GGACGCCAGA	TTTTCAGATT	CAGTGAAGAA	GGCCTTGTGA	ATGCACGGTT	6180
	CGACTACAGC	TACAACAATT	TCCGAGTCAC	AAGCATGCAA	GCTGTAATCA	ATGAAACCCC	6240
	TTTGCCCTATA	GATCTTTACC	GATATGTTGA	TGTCTCTGGC	AGAACAGAGC	AGTTTGGAAA	6300
	ATTTCAGTGA	ATTAATTACG	ATTAAATCA	GGTCATAACT	ACTACAGTGA	TGAAACACAC	6360
70	CAAAATCTTC	AGTGCCCAATG	GACAAGTCAT	TGAAGTCCAA	TATGAAATCC	TAAAGGCAAT	6420
	TGCCCTACTG	ATGACCAATC	AATATGATAA	TGTGGGCCGA	CATGGTAATA	TGTGCATAAG	6480
	GGTAGGAGTA	GATGCCAATA	TAAACAAGTA	CTTCTATGAA	TACGATGCTG	ATGGGCAACT	6540
	TCAGACTGTT	TCTGTAAATG	ACAAAACCCA	GTGGCGTTAT	AGTTACGATC	TGAATGGAGA	6600
	CATCAACCTC	TTAAGCCATG	GGAAAGAGTG	TCGCTTACT	CCTCTCCGAT	ATGACCTCCG	6660
75	AGACCGCATC	ACCAGATTAG	GAGAAATTCA	GTATAAAATG	GATGAAGATG	GCTTCTGAG	6720
	GCAGAGGGGA	AATGATATTT	TTGAATATAA	TTCTAATGGC	CTGCTGCAGA	AAGCCTACAA	6780
	TAAGGCTTCT	GGCTGGACTG	TGCAGTATTA	CTATGATGGG	CTTGGGCGAC	GTGTCGCGAG	6840
	TAAGTCCAGC	CTAGGGCAGC	ACCTTCAGTT	CTTTGTCGAC	CGCAGCCGCA	ACCCCATAG	6900
	AGTTACTACT	TTGTACAACC	ACACAAGCTC	GGAGATTACA	TCTCTGTATT	ATGATCTCCA	6960
80	AGGTCACCTT	ATTGCCATGG	AGTTAAGCAG	TGGTGAAGAA	TATTATGTAG	CCTGTGATAA	7020
	TACAGGTACC	CCACTAGCTG	TGTTACAGCAG	CCGAGGTCAG	GTCAATAAGG	AGATACTATA	7080
	CACACCTTAT	GGCGATATCT	ATCATGACAC	TTACCCTGAC	TTTCAGGTCA	TAATTGGTTT	7140
	TCATGGAGGA	CTCTATGATT	TCCTTACTAA	ATTAGTGAC	CTGGGGCAAA	GGGATTATGA	7200
	TGTTGTTGCT	GGCAGATGGA	CAACGGCCTA	TCATCACATA	TGAAACAGT	TGAACCTCCT	7260
	TCCTAAACCA	TTCAACCTCT	ACTCCTTTGA	AAATAACTAC	CCAGTTGGCA	AAATTCAAGA	7320



	TGTTGCAAAG	TATACCACAG	ACATCAGAAG	TTGGTTGGAG	CTATTTGGTT	TCCAATTACA	7380
	CAATGTACTA	CCTGGATTTC	CCAAACCTGA	ATTAGAAAAT	TTAGAATTAA	CTTACGAGCT	7440
	TCTACGGCTT	CAGACAAAAA	CTCAAGAGTG	GGATCCTGGA	AAGACTATCC	TGGGCATTCA	7500
5	GTGTGAACCT	CAGAAACAGC	TCAGGAATTT	CATTTCTCTG	GACCAACTAC	CTATGACTCC	7560
	CCGATACAAT	GATGGACGGT	GCCTTGAAGG	AGGGAAGCAA	CCAAGGTTTG	CTGCTGTCCC	7620
	TTCTGTTTTT	GGGAAAGGTA	TAAAAATTGC	CATCAAGGAT	GGCATAGTAA	CAGCTGATAT	7680
	TATAGGAGTA	GCCAAATGAAG	ATAGCAGGCG	GCTTGCTGCC	ATTCTCAATA	ATGCCCATTA	7740
	CCTGGAAAAA	CTACATTTTA	CCATAGAGGG	GAGGGACACT	CACTACTTCA	TTAAGCTTGG	7800
10	GTCTCTGGAG	GAAAGACCTGG	TGCTCATCGG	TAACACTGGG	GGGAGGCGGA	TTCTGGAGAA	7860
	TGGTGTCAAT	GTCACTGTGT	CCCAGATGAC	TTCTCTGTTG	AATGGGAGGA	CTAGACGGTT	7920
	TGCAGATATT	CAGCTCCAGC	ATGGAGCCCT	GTGCTTCAAC	ATCCGGTATG	GGACAACTGT	7980
	CGAAGAGGAA	AAGAATCACG	TGTTGGAGAT	TGCCAGACAG	CGCGCAGTGG	CCCAGGCCTG	8040
	GACTAAGGAA	CAAAGAAGGC	TGCAAGAGGG	GGAAGAGGGG	ATTAGGGCAT	GGACAGAAGG	8100
	GGAAAAGCAG	CAGCTTTTGA	GCACTGGGCG	GGTACAAGGT	TACGATGGGT	ATTTTGTTTT	8160
15	GTCTGTTGAG	CAGTATTTAG	AACTTTCTGA	CAGTGCCAAAT	AATATTCACT	TTATGAGACA	8220
	GAGCGAAATA	GGCAGGAGGT	AACAAAAATA	TCTCTGCCTT	TGCGTCACCA	AAGACTGCCT	8280
	GTTTTTAAAA	CATAAAATGG	TTTATTGTAT	TGTTTTTCTA	GATCAGAACT	CTGTATATGT	8340
	AAATATGGAG	GAAAAACATA	TCCAACCTGC	TTTCAATGTG	ACGGAAGATG	GTATTTTAAT	8400
	ATTGTTTTGT	TAAACTCTTT	AAGAAATGAC	AGAGATTTTT	AGTTCCTGTG	TGGCAGTATT	8460
20	CAAAATAACA	CAAGTAGAAC	TCAAACAGCT	AAAAACAGTT	TTCAGAAAAGC	ACCACCTTCA	8520
	ATTTGCCGAG	CCATGCATAT	GTTCCAATAT	CCAGAAAAGAA	CCCAAGGTTT	TCTATCTCTA	8580
	TTGTGAGAAG	CAGTTTCATC	CTTAACTGTT	GGCAGAACTT	ACGGGCTATT	TGAATAGGTG	8640
	TGTCAATAGT	ATCTGAAACT	TGCCCTTTCGA	AAGACTGCCA	GCCCTTTGAC	GTTTTCCAGA	8700
25	TCGTTTATAG	GAAACTTAAA	AACAGGTGTA	AAATGTCTTC	AGGCCACATC	TCCTAGAGTG	8760
	AGGACCCAAAT	TGCCCTTCTC	TCTTGATTAT	TCCTCCTTGC	TTGTTAAAGT	AAATGCCATA	8820
	TTGTTGTGCT	GTGTTTTTGGC	GTGTGGTGGC	TGGGTTCTGT	CTACCATGCT	TCCCTGTGGG	8880
	TGTGGTAACC	AGACTGTATA	GCCGCTATTT	GCTCGTGTGT	ACATGATACC	AAAGCAGCTG	8940
	GCCAGCGTGA	CCTCTCTCAC	ACGACCTGTT	TTGACTCAAT	TTTTTACTAA	AAGTTGTTCA	9000
30	GCTGTATTGG	TATCATGTAA	ACATAGCTTT	TATTAACCTG	GGTAGGAATT	TCTCATTATT	9060
	ATATAGGATG	TGTTTTGTGT	ATAGTTTCAC	ATTAGTGATT	CAGTATCTAT	ACACTGACCC	9120
	AATGGTTTTG	TGCACATGAA	CGGTAATTTA	CTTAAAAGTA	TGATTCTGGT	ACAAAAACAA	9180
	ACAAAGGCTT	TAGCAGGCAT	ACGTGTCTGG	GATGCCGATA	CATACATTAA	CTACTACTGC	9240
	AGAAATTCAT	AAGAGCCAAA	ACCTTAAAAA	AATAGACCTG	GTACTTAAAT	GAAAGTACTA	9300
35	AAGGGAAGAC	CAGACCAAA	ATCACAGCAG	TTGCTGCCAC	ATTGTTTCAG	CCCCTTAGA	9360
	TTTATCTTTC	AAATGTACAA	TTCTGTATTG	AACATCTCCC	AGCCATCTTC	AGGAAATCGA	9420
	ATCAAGTAAA	TCCTTTCCAA	CCGAAAACAT	TTCAACTAAC	TATAGAGAGG	CAGACTCATT	9480
	TTTACTAAAA	TAATTTATAC	AGTTAGTTAT	TTTCGTTCTC	CGTACTTACC	CATTATCTTT	9540
	TATTTAATCG	TCTCTACTGC	CTAGGAAAAAT	AACATTTTTC	CAGGACGGGT	TATTTGTTCT	9600
40	CGCATCATTT	AAAATTTTGA	GAAAGGTCAG	GATTAGTGTT	AATATCAGCT	GCAGTTTCTC	9660
	AATCTCTAGG	AATCCTGCAG	TAAAACAAGC	CCCTTGGTGA	GCTGGAAGAT	TGTGCCCAG	9720
	TGACAAAGAG	ATAGTTTGTA	AAATGCTGTG	TAATTTGTAAG	TTACACAAAA	TGAAAATACA	9780
	TGACAGCACA	ATGTGGCCCG	TAGAAAATTC	CCCTGAGCCA	GCTTCTGCAC	TTTCATCACC	9840
	GAATCTGAAC	ATTTGCTATG	TCGTAAGGCA	AATTTATGAT	GGAATGTTAG	TTTGGATTCT	9900
45	TTCCAGATGC	TACCTAAATG	CAGTGTGGGG	TCATTGCCCT	GCTTTGCGAT	GACAGTTTCT	9960
	TTGAAAATAT	GCAAGTCTAT	AAGCTCATGT	TAAGGTTTTT	CAAGAGTCTG	CCTCCTACTA	10020
	CACAAAGGAA	AGCAAGGGAA	AGGAAATGAC	CCTGGCAAAC	AGTAGGGAAG	GGTGTATTCA	10080
	AACATTTTCA	TTTCAAAACC	TTCCGGTTAG	AATACCACTT	ACACATGTAT	TCTGAGAGAC	10140
	AGAATTCATG	AGGAACTCAT	CTCTCTTTAT	AACTGGAAAC	ACACCAGCTT	GATATATTGC	10200
50	TAATCCATAC	TAAATTCATA	TTATTGGGTT	TTTTCTGAAT	CAGGCCCTGA	TTAATGGTAC	10260
	AGTATTATT	CAGAAATGGA	TTCTAAAATT	ACTAACAAAC	TTGTTGAAAA	TTTGAATACC	10320
	TCACACACAA	CCTAAAATATG	GACCTTAAAT	TCCTAGAAC	CTGTATGTTT	TTTTAAATTA	10380
	ATGGAAAAAT	AATTTGTGAA	CTGTATATAG	AGAGTGCATT	CATAAATGTG	ATTATGTATT	10440
	TTATCACAAC	TCCAAAATGT	CAATATTAGA	GTCTATTTTG	CTTATATTTT	AAGCAATTAT	10500
55	ACGTTTTTGC	AATTCATTGA	TGATGTATCA	TTTTCAAAC	GCTTTAAATA	TCCATTAGAA	10560
	ACAAATATT	GAAGCTTTTA	CTTAATAGTG	ATTACCTTGA	ACTGTGCATT	TCTAGTTTGT	10620
	AATACGTATT	TGGTTGGTTC	GTGCCCTTAG	TTTGTAAAG	TTACATTTGT	ATTATATTCA	10680
	GGAAATGCAC	TTTTTATTAC	TTACAGCTGT	GGTTTTAATA	CTGCCCTGAA	CTATTATTAT	10740
	TCTTTTTACA	ACTCCTAAG	CTTGAGGGAG	GAAAGAAAAA	AAAAACAAAA	CTACTAATCA	10800
60	GTAGTAAATC	GAAGAGAAAC	ATTTTGGCAT	TTCTTAAAG	GAAGATGGAG	ATATTGAGTA	10860
	TATCACTTCC	TATTCAGCTG	AATAGAAAGA	ATGCCCTCAT	TGACTTGCAG	TTCTGCAGTT	10920
	TAAATTATTG	AAAGAACAAT	TCGTTTGCAT	TTCTGTATGA	AAGTAAAGC	ATTTTTTCAG	10980
	GAAACATATG	AATTTCTCAT	ACCCAGCAGA	CAGATGGCTG	ACACTGCACA	GCCACACACC	11040
	ATTTCAGTAA	GTTAAAGTGA	GAGCATAGTA	GTTGGACTCT	CCTATGAAGA	ACATTCTGGG	11100
65	CTGGAGGCAG	GGAATACTCC	ATGTTTGTTC	CTTTTCTCTA	CTTAAGCCCA	TTTTGTTTGT	11160
	GCTTTTCTGT	TTTGTTTTGT	TTTCACTCTT	GCACTACAGT	CTAGAGATCC	AAATGAACCTG	11220
	AAAAGTTCAA	AGTTTAAAC	ATTTAAATAT	GTTTACTTTT	AGTTGTCACT	CTAATCGTTA	11280
	TTGATTAGAA	GCATGACTCC	TGAAGGAAAG	GGAAATAAAT	CTCAATTCAT	ACTAACTTGC	11340
	AAAAAACAC	TTTTACCATA	TAAATAAGTA	TATGATTAT	TTTTAACCCA	AAAAATGTAT	11400
70	AAAAAAGTG	TGTCCTTTAC	TGTCAATTTA	TCGAGAAGAT	CTATAATATA	TAGACTACAT	11460
	ATATATAATA	TATACAACAT	AGCCAAATGT	ATGAAAACCT	GACAATGTAT	AATTTGGAAT	11520
	TCACATGCTA	CCTATGTAGA	CAGGTATGAA	ATTAAGTTAT	AATTTTCATG	AGACATTTTC	11580
	ATCACTGTTG	ACACAGTTTC	AAGGCATTCC	ATCATGTTAT	TTTGACTCTT	TTTCTTTTTT	11640
	TTTTCTTTAA	AAATATATTT	TTAAGTAGAC	CAGGCCCCAC	TATAATATCA	CTTAAGAGAG	11700
75	TCAGGGCAAA	GTTTTTGCAT	TTATGAAGAT	GTGTTTCATG	AAGGGTGATT	GTAATGGAGT	11760
	TCATTGGTAA	TAGAAGCAAA	AGTACAGTAA	CGAAGTATTG	AAAAGAAAAA	TTTGGAGACA	11820
	TTGGAGCATA	TTATATATAG	CTTGTGGAAA	GACATAAGGC	TACAGATGGA	ATGGAACATT	11880
	CCTGTTTTCT	TGAAGAAATT	CACATACACA	TAGCTGACCT	GACTAGTACT	TCAGCTCTTC	11940
	CACAGCCTTC	TATAAAGGTT	CTTCTCTCTG	CAAAGAAAAA	AAAAACAAAA	AAAAACAAAA	12000
80	AAAAAAAAC	AAAAAAGCG	CAAAAAACAA	AAAAACAAA	AAAAAGCAAG	TAAATTTTAA	12060
	AAATACAGAA	AACAAACAC	AAAAAAGAA	TCAACCATAA	ATAGTGACTA	TTATTTTCAG	12120
	TGTGTCTTTC	ATGTGAAAGC	TATTAAGGAC	CAATATATCT	ACTGTTCATA	AGAAGAAATT	12180
	ACTTTCTAAA	CAGTAACTGA	AAATACCTAG	AGTTAAACTT	GCTGTGGATT	TTGTCTTGGC	12240
	AGTTGTCACT	TTACATTATT	TGTCAAAGGA	AATGTGTTTG	GCAGTTAAAA	ATCTTCTCTT	12300
	AGATTTAGTG	GTGGACTTTA	ACCTCTTAAA	TAAATGTTAG	TATATCAGAT	TGTGTCTCTG	12360

AAAAAATATTT TACTTGTATG AATCATGACA ACGTCTAAAT CTTTACTATT CTTCTGGCAA 12420  
 AAGCATCAGT AAGAAAGAAG GCGAAAAGA GAAGTATAGC CTTTATGTCA GAAAAACATT 12480  
 CTTTTTAGCT GCTTACTTTC TCATGAAAAG TAAAGATGTT TACAGTGTAT GCCAAGTTTT 12540  
 CAGTTTCTGT ATAACAACAG GTAGAGGTTT TAATCATATT GAAAATTGTG TTATAATGGT 12600  
 CTGAGCCATG TTGCTAGGAA ACAATAGGTT CCAATTTTGT ATTCCTGCTC TCCTGTGCTG 12660  
 AAAAGTGACT GGATACTGTA CAGGTTTCATG TTCTCTGGCT GCAGTTAAAT GGTCTTTTGC 12720  
 ATTTTGCTCT GGCTTTCAGG CCAGAAGCAT GCATTTTCT ACAAGAGCAT CACAACAACA 12780  
 TGCTGTAAAT ATTTAAAGTT AAACATTATG TGGTTGATATT TGAAAGAAAA GTACTTTGAA 12840  
 TATTTTCATT TTAATAAATA AAATTGCCAA TGAAAAAATA

**A210 Protein sequence:**

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1  
 Unigene number: Hs.23796  
 Probeset Accession #: NM\_014253  
 Protein Accession #: NP\_055068  
 Signal sequence: none found  
 Transmembrane domains: 318-340  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MEQTDCKPYQ PLPKVKHEMD LAYTSSSDS EDGRKPRQSY NSRETLHEYN QELRMNYSNQ 60  
 SKRKRKEVEKS TQEMFECETS HTLCGSGYQTD MHSVSRHGYQ LEMGSDVDTE TEGAASPDHA 120  
 LRMWIRGMKS EHSSCLSSRA NSALSITDIT HERKSDGENG FKFSFVCCDM EAQAGSTQDV 180  
 QSSPHNQFTF RPLPPPPPPP HACTCARKPP PAADSLQRRS MTRSQPSPA APAPPTSTQD 240  
 SVHLHNSWVL NSNIPLETRH SLFKHSGSS AIFSAASQNY PLTSNTVYSP PPRPLPRSTF 300  
 SRPAFTFNKP YRCNWKCTA LSATAITVTL ALLLAYVIAV HLFGLTWQLQ PVGEGLYANG 360  
 VSKGNRGTES MDTTYSPIGG KVSDEKSEKV FQKGRADITG EVDIGAQVMQ TIPPGLFWRF 420  
 QITIHHPYIL KPNISLAKDS LLGIYGRNNI PPHTQFDFV KLMDGKQLVK QDSKGSDDTQ 480  
 HSPRNILITS LQBTGPIEYM DQGPWYLAFY NDGKKMEQVF VLTATIEIMD DCSTNCNGNG 540  
 ECISGHCHCF PGFLGPDCA DSCPVLCCGN GEYKKGHCVC RHGWKGEPCD VPPEQCIDPT 600  
 CFGHGTICMG VCICVPGYKG EICEEEDCLD PMCSNHGICV KGECHCSTGW GGVNCETPLP 660  
 VCQEQCSGHG TFLLDAGVCS CDPKWTGSDC STELCTMECG SHGVCSRIGC QCEEGWVGPT 720  
 CEERSCHSHC TEHGQCKDGK CECSPGWEGD HCTIAHYLDA VRDGCPLCF GNGRCTLDQN 780  
 GWHCVQVGV SGTGCNVVME MLCGDNLNDND GDGLTDCVDP DCCQSQNCYI SPLCQGSPPD 840  
 LDLIQSQTL FSQHTSRIFY DRIKFLIGKD STHVIPPEVS FDSRRACVIR QGVVAIDGTP 900  
 LVGVNVSLFL HSDYGTITIS QDGSFDLVAI GGISVILIFD RSPFLPEKRT LWPWNQFIV 960  
 VEKVTMRQVV SDPPSCDISN FISPNIPLVP SPLTSFGGSC PERGTIVPEL QVVQEEIPI 1020  
 SSFVRLSYLS SRTPGYKTL RILLTHSTIP VGMIKVHLTV AVEGRLTQKW FPAAILNVYT 1080  
 FAWNKTDIYQ QKVGWLAEL VSVGYEYETC PDFILWEQRT VVLQGFEMDA SNLGDWLSNK 1140  
 HHILNPQSGI IHKNGENMNF ISQQPPVIST IMGNGHQRSV ACTNCSNGPAH NNKLFAPVAL 1200  
 ASGPDGSSVYV GDFNFVRIRF PSGNSVSILE LSTSPAHKYY LAMPVSESL YLSDTNRKV 1260  
 YKLKSLVETK DLSKNFVVA GTGDQCLPFD QSHCGDGGRA SEASLNSPRG ITVDRHGFIY 1320  
 FVDGTMIRKI DENAVITTVI GSNGLTSTQP LSCDSGMDIT QVRLEWPTDL AVNPMDSNLY 1380  
 VLDNNIVLQI SENRRVRRIA GRPIHCQVPG IDHFLVSKVA IHSTLESARA ISVSHSGLLF 1440  
 IATDERKVN RIQQVTNNGE IYIAGAPTD CDCKIDPNC DFGSDGGYAK DAKMKAPSSL 1500  
 AVSPDGTLYV ADLGNVRIR ISRNQALND MNIYEIASP DQELYQFTVN GTHLHTLNLI 1560  
 TRYVYVNTFY NSBGDLGAI TSSNGNSVHIR RDAGGMPLWL VVPGGQVYWL TISSNGVLKR 1620  
 VSAQGYNPAL MTPYGNLTGLL ATKSNENGWT TVYEYDPEGH LTNATFPTGE VSSFHSDLEK 1680  
 LTKVELDTSN RENVLMTNL TATSTIYILK QENTQSTYRV NPDGSLRVTF ASGMEIGLSS 1740  
 EFHILAGAVN PTLGKCNISL PGEHNNALIE WRQRKEQNGK NVSAFERRLR AHNRLNLSID 1800  
 FDHITRTGKI YDHRKFTLR ILYDQTRPI LWSPVSRVNE VNITYSPSL VTFIQRGTWN 1860  
 EKMEYDQSGK IISRTWADGK IWSYTYLEKS VMLLLHSQRR YIFEYDQSDC LLSVTMPMSV 1920  
 RHLQTMLSV GYRNIIYTPP DSSTSFIQDY SRDGRLLQTL HLGTGRRVLY KYTKQARLSE 1980  
 VLXDTQVTL TYESSGVV KTIHLMHDGFI CTIRYRQTGP LIGRQIFRFS BEGLVNARFD 2040  
 YSVNNFRVTS MQAVINETPL PIDLYRYVDV SGRTEQFGKF SVINYDLNQV ITTVMKHTK 2100  
 IFSANGQVIE VQYELKAI YWMTIQYDNV GRHGNMCIHV GVDANITRYF YEYDADGQLQ 2160  
 TVSVNDKTQW RYSYDLNGDI NLLSHGKSAR LTPRLYDLRD RITRLGEIQY KMDDEGFLRQ 2220  
 RGNDFEYNS NGLLQKAYNK ASGWTQVYV DGLGRRVASK SSLGQHLQFF VDATANPIRV 2280  
 THLYNHTSSE ITSYYDLQGG HLIAMELSSG BEYVYACDNT GTPLAVFSSR GQVIKEILYT 2340  
 PYGDIYHDTY PDFQVIIGFH GGLYDFLTKL VHLGQRDYDV VAGRWTAYH HIWKQLNLLP 2400  
 KPFNLVSFEN NYPVGKIQDV AKYTTDIRSW LELFGFQLHN VLPGFPPKPEL ENLELTIELL 2460  
 RLQTKTQEWL PGKTLIGIQC ELQQLRNFI SLDQLPMTPR YNDGRCLGEG KQPRFAAVPS 2520  
 VFGKGIKFAI KDGIVTADII GVANEDSRRL AAILNNAHYL ENLHFTIEGR DTHYFIKLG 2580  
 LEEDLVLIEN TGGRRILENG VNVTVSQMTS LLNGRTRRFA DIQLQHGLC FNIRYGTIVE 2640  
 EEKNHVLEIA RQRAVAQAWT KEQRLQEGE EGIRAWTEGE KQQLLSTGRV QGYDGYFVLS 2700  
 VEQYLELSDS ANNHIFMRQS EIGRR

**A211 DNA SEQUENCE:**

Gene name: Solute carrier family 26, member 4  
 Unigene number: Hs.159275  
 Probeset Accession #: AF030880  
 Nucleic Acid Accession #: NM\_000441  
 Coding sequence: 225-2567 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CTCAGCCTTC CCGGTTCGGG AAAGGGGAAG AATGCAGGAG GGGTAGGATT TCTTCTCTGA 60  
 TAGGATCCGT TGGGAAGAC CGCAGCCTGT GTGTGTCTTT CCCTTCGACC AAGGTGTCTG 120  
 TTGCTCCGTA AATAAACCT CCCACTGCCT TCTGAGAGCG CTATAAAGGC AGCGGAAGGG 180  
 TAGTCCGCGG GGCATTCCGG GCGGGGCGCG AGCAGAGACA GGTCTATGGCA GCGCCAGGCG 240  
 GCAGGTCCGA GCCGCGCGAG CTCCCAGAGT ACAGCTGCAG CTACATGGTG TCGCGGCCCG 300  
 TCTACACGGA GCTCGCTTTC CAGCAACAGC ACGAGCGGCG CCTGCAGGAG CGCAAGACGC 360

5 TGCGGGAGAG CCTGGCCAAG TGCTGCAGTT GTTCAAGAAA GAGAGCCTTT GGTGTGCTAA 420  
 AGACTCTTGT GCCCATCTTG GAGTGGCTCC CCAAATACCG AGTCAAGGAA TGGCTGCTTA 480  
 GTGACGTCAT TTCGGGAGTT AGTACTGGGC TAGTGGCCAC GCTGCAAGGG ATGGCATATG 540  
 CCCTACTAGC TGCAGTTCCT GTCGGATATG GTCTCTACTC TGCTTTTTTC CCTATCCTGA 600  
 CATACTTTAT CTTTGGAAACA TCAAGACATA TCTCAGTTGG ACCTTTTCCA GTGGTGAGTT 660  
 TAATGGTGGG ATCTGTTGTT CTGAGCATGG CCCCAGACGA ACACTTTCTC GTATCCAGCA 720  
 GCAATGGAAC TGTATTAAT ACTACTATGA TAGACACTGC AGCTAGAGAT ACAGCTAGAG 780  
 TCCTGATTGC CAGTGCCCTG ACTCTGCTGG TTGGAATTAT ACAGTTGATA TTTGGTGGCT 840  
 10 TGCAGATTGG ATTCATAGTG AGGTACTTGG CAGATCCTTT GGTGGTGGC TTCACACAG 900  
 CTGCTGCCTT CCAAGTGCTG GTCTCACAGC TAAAGATTGT CCTCAATGTT TCAACCAAAA 960  
 ACTACAATGG AGTTCTCTCT ATTATCTATA CGCTGGTTGA GATTTTCAA AATATTGGTG 1020  
 ATACCAATCT TGCTGATTTT ACTGCTGGAT TGCTCACCAT TGTCGTCTGT ATGGCAGTTA 1080  
 AGGAATTAAT TGATCGTTT AGACACAAAA TCCCAGTCCC TATTCCTATA GAAGTAATTG 1140  
 15 TGACGATAAT TGCTACTGCC ATTTCTATAT GAGCCAACTT GGAAAAAAT TACATGCTG 1200  
 GCATTGTTAA ATCCATCCCA AGGGGTTTTT TGCTCTCTGA ACTTCCACT GTGAGCTTGT 1260  
 TCTCGGAGAT GCTGGCTGCA TCAATTTTCCA TCGCTGTGGT GGCTTATGCT ATTGCAGTGT 1320  
 CAGTAGGAAA AGTATATGCC ACCAAGTATG ATTACACCAT CGATGGGAAC CAGGAATTCA 1380  
 TTGCCTTTGG GATCAGCAAC ATCTTCTCAG GATTCTTCTC TGTGTTTGTG GCCACCATG 1440  
 CTCTTTCCCG CACGGCCGTC CAGGAGAGCA CTGGAGGAAA GACACAGGTT GCTGGCATCA 1500  
 20 TCTCTGCTGC GATTGTGATG ATCGCCATTC TTGCGCTGGG GAAGCTTCTG GAACCTTGC 1560  
 AGAAGTCGCT CTGGCAGCT GTTGTAAATT CCAACCTGAA AGGGATGTTT ATGCAGCTGT 1620  
 GTGACATTCC TCGTCTGTGG AGACAGAATA AGATTGATGC TGTATCTGG GTGTTTACGT 1680  
 GTATAGTGTC CATCATCTG GGGCTGGATC TCGGTTTACT AGCTGGCCTT ATATTGGAC 1740  
 25 TGTGACTGT GGTCTGAGA GTTCAGTTTCT CTCTTGGAA TGGCCTTGA AGCATCCCTA 1800  
 GCACAGATAT CTACAAAAGT ACCAAGAATT ACAAAAACAT TGAAGAACCT CAAGGAGTGA 1860  
 AGATTCTTAG ATTTCCAGT CCTATTTTCT ATGGCAATGT CGATGGTTT AAAAAATGTA 1920  
 TCAAGTCCAC AGTTGATTTT GATGCCATTA GAGTATATAA TAAGAGGCTG AAAGCGCTGA 1980  
 GGAAAAATCA GAACTAATA AAAAGTGGAC AATTAAGAGC AACAAGAAT GGCATCATAA 2040  
 30 GTGATGCTGT TTCAACAAAT AATGCTTTTG AGCCTGATGA GGATATTGAA GATCTGGAGG 2100  
 AACTTGATAT CCCAACCAAG GAAATAGAGA TTCAAGTGA TTGGAACCTC GAGCTTCCAG 2160  
 TCAAGTGAA CGTTCACAAA GTGCCAATCC ATAGCCTTGT GCTTGACTGT GGAGCTATAT 2220  
 CTTTCTGGA CGTGTGGA GTGAGATCAC TCGGGTGAT TGTCAAAGAA TTCCAAGAA 2280  
 TTGATGTGAA TGTGATTTT GCATCACTTC AAGATTATGT GATAGAAAAG CTGGAGCAAT 2340  
 35 GCGGGTTCTT TGACGACAAC ATTAGAAAGG ACACATTCTT TTGACGGTC CATGATGCTA 2400  
 TACTCTATCT ACAGAACCAA GTGAAATCTC AAGAGGGTCA AGGTTCCATT TTAGAAACGA 2460  
 TCACTCTCAT TCAGGATTGT AAAGATACCC TTGAATTAAT AGAAACAGAG CTGACGGAAG 2520  
 AAGAACTTGA TGTCCAGGAT GAGGCTATGC GTACACTTGC ATCCTGAAAG TGGGTTCCGG 2580  
 AGGTCTCTAT GAGCAAGGAA TACAAGACAA AACTTCTCTA ATGCATTGAC TATTTCTTCA 2640  
 40 GACTCAAAAC ACCTATTCTT TTTTCTATTA AGCCATTGAA AGAGAAGCAC TAAGACTGCT 2700  
 TCTAGGCTTT ATTTATAAAA TAAACACCTT ATCCCTAACA TGGGCAAAAT GGCTAGAATT 2760  
 ATTCAGACGA TTGGCAGCG TCCAGGGTAA GCTGGTGTTA TAATACGCTG CTGATCTACA 2820  
 TCACAGATT GCTAATAATG TTCACGTGGG CCTGCGATA TCTCTGTTCA GTTAGAGTGA 2880  
 GTGCTGACCC AACAGCCTCT GTGGTCAAGC GAGTCACGAA TGATTATCA TAAAGAAAAA 2940  
 45 TCAGTTTTTG ACTGACCTGT ATATCCATGA GCTGCATGA TCACCATGTA AGGTCACATT 3000  
 TAGTAAATGC TGAATAAAAA TGATTAATGC ATTTATCAAT AAAAGCCTTT GAAAAACTT 3060  
 TGGATAATAA ATTGGAGTTT TAAAAATGCA AATTTGCTTA GTATCTAATA ATGAAGTGT 3120  
 ATTACATATA GCCGGAATTG AGGATCTCTT TGATCTGGA AATGGTTTAC CTAAAGCTA 3180  
 CAGAACCAAG CCAATATATT TTGAAATATT GATGCAGACA AATGAAATAA TAAAGAGATT 3240  
 50 TTTCATGGTT ATAAAAATCT TTTTGTATAT GATAATAATC ATGATCACAA CTGAGATCAA 3300  
 AAAAAATATAT GACAGATTAT TTTGTTAAA AATGCAGTTT TAATTATCTT AGTCTATAGA 3360  
 AATGATCATT GCATGGAGGC ATGTATAGGT ATGATCTGTG TAAATCTGA CATAAAAACA 3420  
 GTGCTATTCT GAGTGAATAA TTTTGTATG TGCTTACATA ACCATGGTGA TTAATAATGAG 3480  
 TTTATATTTT TTCTCAAAAA TTTTAGCAGT GTGTAAAGTA AGTAATCTTT AACTGAACTC 3540  
 55 TGACCACTTA AAAAAAATC TAAAAATTGA ACTACCTATA GTAGTCTGTG TTTAAAGTGA 3600  
 ATTTTAAAG ACAAGCAATT CTAAATGAAC TCAATATAAA AACATTCATT TGGAAATGTAC 3660  
 ATACTGAAA ATACAGGTTT TTTTGACCAA AAGTTTTTAT ATCTTTCTT TTTATTATT 3720  
 TTTTCTCTAA GTCCAAACA TTTTCTAGAT ATTATATACA ACACAGGCTT TGATCTGGG 3780  
 GACTTTTCCC ATGATTTTCA CACTGGAGTG AATGAAGTTG TACTTCAATT CTAGAGAAAA 3840  
 60 GTTATACCCA GGTCCCAAT TGAGAAATGTC TTGCTTGATT GAAAAACGACA TCATCCCTTG 3900  
 GTATACTCCA GGGATTGGTT TCAGGACCCC TGCATTTACC AAAATTGTG CACACTCAAG 3960  
 TCCTGCGATC ACCCTGCTT AAAGATAGAA TGGCTTCTCT GTTTTCTTTC TGAATACAA 4020  
 CCAGAAACAA TGTGCTATT TCTGAAAGAA TAGGATTAAT GATCATACAA ATGGGTTAAT 4080  
 CCTGAATCT GGTGTAAAT CTGTTACAG CATAACTAGG ATTATAATGC TGCCTCATTT 4140  
 65 TCACAGCACT ACTGCTTAT ATTGACAACA AATCATCTCG CTAAAGAGTG AATGTAGGCC 4200  
 AGGCGCGGTG GCTCATGCTT GTAATCCCAG CACTTTGGGA GGCCGAGGCG GGTGGATCAC 4260  
 GAGGTCAGGA GATCGAGACC ATCCTGGCTA ACATGGTAAA ACCCCGCTCT TACTAAAAAT 4320  
 AGAAAAAAG AAATTAGCCT AGCGTGGTGG CTGGCGGCGC CCTGTAGTCC CAGCTATTTG 4380  
 GGAGGCTAAG GCAGGAGAAT GGCCTGAACC CGGGAGGCGG AGCTTGCACT GAGCCGAGGT 4440  
 70 CGTGCCACTG CACTCCAGCC TGGGCGACAG AGCAAGACTC CGTCTCAAAA AAAAAAATAA 4500  
 AAAAAAATAA AGAGTGAATG TAATAGTCTT GCAGAAAATG AATGAATACC TTTGTTCAAT 4560  
 AAAGGAAATA TGACTGCTC ACTTTTGA AGGAAATGCC AAAGTTACGT TTTACACAA 4620  
 GGCTAGAGTT TGTAAATCT GGGTTCATTT GTGATGACAT AAGTCAGCAA ACTGCGGGAA 4680  
 TACTGTCTCT TTGTATGATT TTGTGAATAG TAAGCATAAT TTTAGTTTGT TATTATCAAT 4740  
 75 GAAAAATTCA CTTGAAATTA AAGCTGCCTT TTGTTATATT TTTAACCTAT AGGATAAGAT 4800  
 TCCAGTATTG TATATGAGTT TTAACAAAT AAAAAATCAA ATCATGTACA TTTGAAAAAT 4860  
 TTTGCACACA TTTAAATAA AATGTAAAGT TGTCTTTTAA ACTACTCGGA TGTGTCCTTT 4920  
 CTGAACAAA

**A212 Protein sequence:**

Gene name: Solute carrier family 26, member 4  
 Unigene number: Hs.159275  
 Probeset Accession #: AF030880  
 Protein Accession #: O43511  
 Signal sequence: none found

Transmembrane domains: 81-103, 109-131, 136-158, 185-207, 221-243, 245-267, 270-291, 295-317,  
347-369, 386-408, 420-442, 448-470, 486-508  
Cellular Localization: plasma membrane

5

10

15

20

```

1      11      21      31      41      51
|      |      |      |      |      |
MAAPGGRSEP PQLPEYSCSY MVSRPVYSEL AFQQQHERRL QERKTLRESL AKCCSCSRKR 60
AFGLVLTLPV ILEWLPKYRV KEWLLSDVIS GVSTGLVATL QGMAYALLAA VPVGYGLYSA 120
FFPILTYFIF GTSRHSISVGF FPVVSMLVGS VVLSMAPDEH FLVSSSNGTV LNTTMDTAA 180
RDSTARVLIA ALTLVLGIIQ LIFGGLQIGF IVRYLADPLV GGFTTAAAFQ VLVSQKLV 240
NVSTKNYNGV LSIITYLVEI FQNIGDTNLA DFTAGLLTIV VCMAYKELND RFRHKIPVPI 300
PIEVIVTIIA TAISYGANLE KNYNAGIVKS IPRGFLPPEL PPVSLFSEML AASFIAVVA 360
YAIASVGVKV YATKYDYTID GNQEFIAFGI SNIFSGFFSC FVATTALSRT AVQESTGGKT 420
QVAGIISAAI VMIAILALGK LLEPLQKSVL AAVVIANLKG MFMQLCDIPR LWRQNKIDAV 480
IWVFTCIVSI ILGLDLGLLA GLIFGLLTIV LRVQFPWSNG LGSIPSTDII KSTKNYKNIE 540
EPQGVKILRF SSPIFYGNVD GFKKCIKSTV GFDAIRVYNK RLKALRKIQK LIKSGQLRAT 600
KNGIISDAVS TNNAPFDEED IEDLEELDIP TKEIEIQVDW NSELPVKVNK PKVPIHSLVL 660
DCGAISFLDV VGVRSRLRVIV KEFQRIDVNV YFASLQDYVI EKLEQCGFFD DNIRKDTFFL 720
TVHDAIYLQ  NQVKSQEGQG SILETITLIQ DCKDTLELIE TELTEELDVL QDEAMRTLAS 780
QDEAMRTLAS

```

25

**A213 DNA SEQUENCE:**

Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]  
Unigene number: Hs.98280  
Probeset Accession #: AA418000  
Nucleic Acid Accession #: NM\_021614  
Coding sequence: 458-2197 (underlined sequences correspond to start and stop codons)

30

35

40

45

50

55

60

65

70

75

```

1      11      21      31      41      51
|      |      |      |      |      |
CGGCGGCAGC AGCCCATGCC TCCGGTGCAA CAGCTGCGCC TCCTCCGGTG CCCCAGCGGC 60
GGGGGCGGGA GATAACCTGT CCTGCTGCT CCGCACCTCC TCGCCCGCGG GCGCCTTCCG 120
GACCCCGCACC TCCTCGCCGC TGTCGGGCTC GTCTGCTGCT TGCTGCTGCT GCTCGTCGCG 180
CCGGGGGAGC CAGCTCAATG TGAGCGAGCT GACGCCGTCC AGCCATGCCA GTGCGCTCCG 240
GCAGCAGTAG CGCGCAGCAG CCGCGCAGCA GTCGGCGTCC GCCTCCAGT ACCACCAAGT 300
CCACAGCCTC CAGCCCGCCG CCAGCCCCAC GGGCAGCCTC GGCAGTCTGG GCTCCGCGCC 360
CCCGCTCTCG CACCACCACC ACCACCCGCA CCGGGCGCAC CACCAGCACC ACCAGCCCCA 420
GGCGCGCCCG GAGAGCAACC CCTTCAACCGA AATAGCCATG AGCAGCTGCA GGTACAACCG 480
GGCGGTCTAG CGGCCGTCTA GCAACTTGAG CGCGTCCCGC CGGAACCTCC ACGAGATGGA 540
CTCAGAGGCG CAGCCCTGCG AGCCCCCGCG GTCTGTGCGA GGAGGTGGCG GCGCGTCTCT 600
CCCGTCTGCA GAGCTGCGCG CCGCGCGCGC TGTTCGTGTC TCAGCCCCCG AGATCGTGGT 660
GTCTAAGCCC GAGCACAAACA ACTCCAACAA CCTGGCGCTC TATGGAACCG GCGGCGGAGG 720
CAGCACTGGA GGAGGCGGCG GCGGTGGAGG GAGCGGGCAC GGCAGCAGCA GTGGCACCAA 780
GTCCAGCAAA AAGAAAAACC AGAACATCGG CTACAAGCTG GGCACCCGCG GCGCCCTGTT 840
CGAAAAAGCG AAGCGGCTCA GCGACTACGC GCTCATCTTC GGCATGTTCT GCATCGTGGT 900
CATGGTCTAT GAGACCGAGC TGTCGTGGGG CGCCTACGAC AAGGCGTCTG TGTATTCTCT 960
AGCTCTGAAA TGCCCTTATC GTCTCTCCAC GATCATCTCT CTCGGTCTGA TCATCGTGTA 1020
CCACGCCAGG GAAATACAGT TGTTTCATGGT GGCAATGGA GCAGATGACT GGAGAATAGC 1080
CATGACTTAT GAGCGTATTT TCTTCATCTG CTTGGAATAA CTGGTGTGTG CTATTCATCC 1140
CATACCTGGG AATTATACAT TCACATGGAC GGCCCGGCTT GCCTTCTCCT ATGCCCATCC 1200
CACAAACACC GCTGATGTGG ATATTATTTT ATCTATACCA ATGTTCTTAA GACTCTATCT 1260
GATTGCCAGA GTCATGCTTT TACATAGCAA ACTTTTCACT GATGCCCTCT CTAGAAGCAT 1320
TGGAGCACTT AATAAGATAA ACTTCAATAC ACGTTTTGTT ATGAAGACTT TAATGACTAT 1380
ATGCCCAAGG ACTGATCTCT TGGTTTTTAG TATCTCATT TGGATAATTG CCGCATGGAC 1440
TGTCGAGCTT TGTGAAAGGT ACCATGATCA ACAGGATGTT ACTAGCAACT TCCTTGGAGC 1500
GATGTGGTTG ATATCAATAA CTTTTCTCTC CATTTGGTTAT GGTGACATGG TACCTAACAC 1560
ATACTGTGGA AAAGGAGTCT GCTTACTTAC TGAATATTAT GGTGCTGGTT GCACAGCCCT 1620
GGTGGTAGCT GTAGTGGCAA GGAAGCTAGA ACTTACCAAA GCAGAAAAAC ACGTGCACAA 1680
TTTTCATGAT GATACTCAGC TGACTAAAAG AGTAAAAAAT GCAGCTGCCA ATGTACTCAG 1740
GGAAACATGG CTAATTTTACA AAAATACAAA GCTAGTGAAG AAGATAGATC ATGCAAAAGT 1800
AAGAAAACAT CAACGAAAAT TCTTGCAAGC TATTCATCAA TTAAGAAGTG TAAAAATGGA 1860
GCAGAGGAAA CTGAATGACC AAGCAACAC TTTGGTGGAC TTGGCAAGA CCCAGAACAT 1920
CATGTATGAT ATGATTTCTG ACTTAAACGA AAGGAGTGAA GACTTCGAGA AGAGGATTGT 1980
TACCTTGAA ACAAACCTAG AGACTTTGAT TGGTAGCATC CACGCCCTCC CTGGGCTCAT 2040
AAGCCAGACC ATCAGGCAGC AGCAGAGAGA TTTCAATTGAG GCTCAGATGG AGAGCTACGA 2100
CAAGCACGTC ACTTACAATG CTGAGCGGTC CCGGTCCTCG TCCAGGAGGC GCGGTCCTC 2160
TTCCACAGCA CCACCAACTT CATCAGAGAG TAGCTAGAAG AGAATAAGTT AACCACAAAA 2220
TAAGACTTTT TGCCATCTAT TGGTCAATAT TTTAGCTTTT ATTGTAAGC CCCTATGGTT 2280
CTAATCAGCG TTATCCGGGT TCTGATGTCA GAATCCTGGG AACCTGAACA CTAAGTTTTA 2340
GGCCAAAATG AGTGAAAACCT CTTTTTTTTT CTTTCAGATG CACAGGGAAT GCACCTATTA 2400
TTGCTATATA GATTGTTTCT CCGTGAATTT CACTAACTTT TTATTCATGC ACTTCAACA 2460
AACTTTACTA CTACATTATA TGATATATAA TAAAAAAGT TAATTTCCGA

```

80

**A214 Protein sequence:**

Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]  
Unigene number: Hs.98280  
Probeset Accession #: AA418000  
Protein Accession #: NP\_067627  
Signal sequence: none found  
Transmembrane domains: 135-157, 168-190, 208-230, 254-276, 306-328, 342-364, 373-394

Calmodulin binding domain: 412-488  
Cellular Localization: plasma membrane

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
MSSCRYNGGV MRPLSNLSAS RRNLHEMDSE AQPLQPPASV GGGGGASSPS ADAAAAAAVS 60
SSAPEIVVSK PEHNNNSNLA LYGTGGGGST GGGGGGGGSG HGSSSGTKSS KKNQNIGYK 120
10    LGHRRALFEK RKRLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII 180
      LLGLIIVYHA REIQLFMVDN GADDWRIAMT YERIFFICLE ILVCAIHPIP GNYTFTWTAR 240
      LAFSYAPSTT TADVDIILSI PMFLRLYLIA RVMLLHSLKF TDASSRSIGA LNKINFNTRF 300
      VMKTLMTICP GTVLLVFSIS LWIIAAWTVR ACERYHDQDQD VTSNFLGAMW LISITFLSIG 360
      YGDMVPNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHNFN MDTQLTKRVK 420
15    NAAANVLRET WLIYKNTKLV KKIDHAKVRK HQRKFLQAIH QLRSVKMEQR KLNDQANTLV 480
      DLAKTONIMY DMISDLNERS EDFEKRIVTL ETKLETIGS IHALPGLISQ TIRQQQRDFI 540
      EAQMESYDKH VTYNAERSRS SSRRRRSST APPTSSESS

```

A215 DNA SEQUENCE:

Gene name: CGI-86 protein  
Unigene number: Hs.109201  
Probeset Accession #: AW161450  
Nucleic Acid Accession #: NM\_016029  
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

```

25      1      11      21      31      41      51
      |      |      |      |      |      |
CTGCGATCCC GCAGGGCAGC GACGCGACTC TGGTGCGGGC CGTCTTCTTC CCCCCGAGCT 60
30    GGGCGTGC GCAGCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCCGCG 120
      TGCTCCTGCT CTGTGGTGAG CTGCTGCGCT TCCTGAGGGC TGACGGCGAC CTGACGCTAC 180
      TATGGGCGGA GTGGCAGGGA CGACGCCAG AATGGGAGCT GACTGATATG GTGGTGTGGG 240
      TGACTGGAGC CTCGAGTGGG ATTGGTGAGG AGCTGGCTTA CCAGTTGTCT AACTAGGAG 300
      TTTCTCTTGT GCTGTACGCC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC 360
35    TAGAGAAATGG CAATTTAAAA GAAAAAGATA TACTTGTGTT GCCCCTTGAC CTGACCGACA 420
      CTGGTTCCCA TGAAGCGGCT ACCAAAGCTG TTCTCCAGGA GTTTGGTAGA ATCGACATTC 480
      TGGTCAACAA TGGTGGAATG TCCAGCGTTC CTCTGTGCAT GGATACCAGC TTGGATGTCT 540
      ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTC CTTGACAAAA TGTGTTCTGC 600
      CTCACATGAT CGAGAGGAAG CAAGGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA 660
40    TATCTGTACC TC'TTCCATT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGT'TTTT'TTA 720
      ATGCCTTCG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCAG 780
      GACCTGTGCA ATCAAAATATT GTGAGAAATT CCCTAGCTGG AGAAGTCACA AAGACTATAG 840
      GCATAATGG AGACCACTCC CACAAGATGA CAACCACTCG TTGTGTGCGG CTGATGTTAA 900
      TCAGCATGGC CAATGATTG AAGAAGTTT GGATCTCAGA ACAACCTTC TTGTTAGTAA 960
45    CATATTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAAG ATGGGGAAGA 1020
      AAAGGATTGA GAAC'TTAAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTAA 1080
      AGACAAAACA TGACTGAAAA GAGCACCTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA 1140
      AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200
50    ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260
      AGATTGCCAT GAATCTTGCA AA

```

A216 Protein sequence:

Gene name: CGI-86 protein  
Unigene number: Hs.109201  
Probeset Accession #: AW161450  
Protein Accession #: NP\_057113  
Signal sequence: 1-26  
Transmembrane domains: 183-206, 221-243  
Cellular Localization: plasma membrane

```

65      1      11      21      31      41      51
      |      |      |      |      |      |
MNWELLWLVL VCALLLLLV QLLRFLRADG DLTLWAEWQ GRRPEWELTD MVVWVTGASS 60
      GIGELAYQL SKLGVSLVLS ARRVHELERV KRRCLENGNL KEKDILVLPL DLTDTGSHEA 120
      ATKAVLQEFQ RIDILVNNGG MSQSLCMDT SLDVYRKLIE LNYLGTVSLT KCVLPHEMER 180
      KQGKIVTVNS ILGIISVPLS IGYCASKHAL RGFFNGLRTE LATYFGIIVS NICPGPVQSN 240
70    IVENSLAGEV TKTIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISEQP FLLVTVYLWQY 300
      MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD

```

A217 DNA SEQUENCE:

Gene name: Homo sapiens mRNA; cDNA DKFZp564O1763 (from clone DKFZp564O1763)  
Unigene number: Hs.27373  
Probeset Accession #: F13036  
Nucleic Acid Accession #: AC012478  
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

```

80      1      11      21      31      41      51
      |      |      |      |      |      |
ATGCGCGCGG TGCCGCTGCC CGCCCCGCTC CTGCCGCTGC TGCTGCTCGC GCTCCTGGCC 60
      GCTCCCGCGG CCCGCGCCAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120
      CGCGAGTCGC GGCCACCGCC CGGCCCGGGG CCCGGGAACA CCACCCGTT TGGGTCTGGG 180
      GCGGCGGGCG GCAGCGGCAG CTCAGCTCC AACAGCAGTG GCGACGCGTT GGTGACCCGC 240

```

ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAAGGCAG CCGTGATCGT GGCCTTCGCC 300  
 TTACCACCC TCCTCATCGC CTGCGTCTG CTGCGCGTCT TCAGGTCGGG AAAGAGGTTA 360  
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGA AATGGCGCCA 420  
 CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480  
 TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCTT 540  
 GTGCCCCAC CTTTCATCCT CGACATTGAC CTTCACGCAA GATGCAGTGG AAGGCCTGAT 600  
 GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCCTGT GGAAAGTTGG 660  
 TCAGCTGCAA CCTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGCCT CGGAGGTGTT 720  
 GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCCTGTC AGGCATCTGC 780  
 TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCACCACAA TGGAGTTGCT TCTGCCACCC 840  
 TTTGGGCATC CTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG 900  
 CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGCTCCATCT 960  
 GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020  
 CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAAACATG 1080  
 AGTACCTGG GCTTGGATGT TTTCTGTGGT GCCGGCCAGC GGGGCACCTT TGTGAAGAC 1140  
 AGAGCAGTGA CTAAGGTTC CTAGGGTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200  
 GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260  
 ACCCATCCTG TCAGGTTGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320  
 AGGGTGTTC GGCCTCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380  
 TGCTTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCCTC ACCTTGACCT CTCTACAAA 1440  
 ATCTGTCTCC CCGCTGTGTC CGTGGAAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500  
 GTCTTTCGCT CATTTAGCA GAGCCACAA AAGGCAGCTG CTGCCACGG GGAGCCTGTC 1560  
 AAACGAGGCG CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620  
 GCGAACCTGC AGACAATTC AGATACCCAA GGCCAGGAAG GCCCAGTGA GGATGTCAC 1680  
 CACCCCTGGAG GAGACTTGA TGGGGTGGCA AATTTCTATT TGGAGGAAGA GGGTTTCCAG 1740  
 GATGGCAGAT GCCAGAGTAT GGTCTGATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800  
 TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCTCT 1860  
 TCCCCCGAC AGCCCTGTT TCTGTCCAGG CCCTGA

**A218 Protein sequence:**

Gene name: Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)  
 Unigene number: Hs.27373  
 Probeset Accession #: F13036  
 Protein Accession #: PGENESH predicted  
 Signal sequence: 1-27  
 Transmembrane domains: 94-115, 448-469  
 Cellular Localization: not determined

1 11 21 31 41 51  
 | | | | |  
 MRAVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTRFRGSG 60  
 AAGSGSSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FTTLLIACLL LRVRFRSGKRL 120  
 KKTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGQTLTTPV 180  
 VPPFILDID LPARCSRPRD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV 240  
 ETKTNVMYKT PAPSVCVSGIC SDCHWQARFH VTTMELLPP FGHPFKVPPT STPHGFRQLQ 300  
 LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAAESDLFN PWWHFSATGS PIKTLTYQTM 360  
 STLGLDVFEG AGQRTFCED RAVTKVLQGS SFSQRLRWKP ALESGFPFHL RLLRECPPLS 420  
 THPVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480  
 ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHGEPV KRGPSSQLTR HTCPGWGITH 540  
 ANLQTIPTDQ QGEGPREDVT HPGGDLGVA NFYLEEGFQ DGRGQKMLVM SEEGPPSLTG 600  
 CERLTGSHHF SSHSKSWSFL SPRQPLFLSR P

**A219 DNA SEQUENCE**

Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAAGAGAGTGGGA 60  
 GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTTGT 120  
 CAGCAAAAGT ACACACACCT GGTTCGAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180  
 TCCATATTGA GCTATTACAC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240  
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAG CCAAGAACTG GGCTCCAGGT 300  
 GAACCCAACA ATAGGCAAAA AGATGAGGAC TGCCTGGAGA TCTACATCAA GAGAGAAAAA 360  
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420  
 GCTGGCTGTA CCAATACATC CTGCAGTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480  
 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAACCTGT 540  
 ACAGCCCTGG AATCCCTCTG GCATGGAAGC CTGGTTTGCA GTCACCCACT GGGAACTTC 600  
 AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660  
 ACCATGCAGT GTATGTCTTC TGGAGAATGG AGTGTCTCTA TTCCAGCCTG CAATGTGGTT 720  
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTTGGA 780  
 AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTTGA ACTAATGGGA 840  
 GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900  
 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960  
 CCTGTGGGAG AGTTACCTTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020  
 TTGCAGGGAC CAGCCAGGTT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAATCCCA 1080  
 GTTTGTGAAG TTCTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140  
 CTTCTAGTGT CTTCTGGCAG TTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200  
 GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

GAGAAGCCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
GTGAGGTGTG CTATTCCCC TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCCTTCAGC 1380
TGTGAGGAGG GATT'TGAATT ATATGGATCA ACTCAACTTG AGTGCACATC TCAGGGACAA 1440
TGGACAGAAG AGGTTCTCTC CTGCCAAGTG GTAAAAATGT CAAGCCTGGC AGTTCGGGA 1500
AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCCTGT 1560
CCTGAAGGAT GGCAGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
CTTTCTGCTG CTGACTCTC CCTCTGACA TTAGCACCAT TTCTCTCTG GCTTCGGAAA 1740
TGCTTACGGA AAGCAAAGAA ATTTGTTTCT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

```

A220 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Protein Accession #: NP\_000441  
 Signal sequence: 1-22  
 Transmembrane domains: 555-573  
 C-lectin domain: 23-139  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRTHLVAI QNKKEIEYLN 60  
 SILSYSPSY WIGIRKNNV WVWVGTKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120  
 DVMGNWDERC SKKKLALCYT AACTNTSCSG HGECEVETINN YTCKCDPGFS GLKCEQIVNC 180  
 TALESPHEGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240  
 ECDAVTNPAN GFVECFQNPFG SFPWNTTCTF DCEEGFELMG AQLSLQCTSSG NWDNEKPTCK 300  
 AVTCRAVRQP QNGSVRCSSH PAGEFTFKSS CNFTCEBGFMLQGPQVVECT TQGQWTQQIP 360  
 VCEAFQCTAL SNPERGYMNC LPSASGGSFRY GSSCEFSCEQ GFVLKGSKRL QCQFTGEWDN 420  
 EKPTCEAVRC DAVHQPPKGL VRCASPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480  
 WTEEVPSQCV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540  
 SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLWLRLK CLRKARKFVP ASSCQSLESD 600  
 GSQKPSYIL

Taxol ProstateA221 DNA SEQUENCE

Gene name: ESTs; Liprin A2  
 Unigene number: Hs.306480  
 Probeset Accession #: N51002  
 Nucleic Acid Accession #: N51002  
 Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ATGATGTGTG AAGTGATGCC CACGATTAAT GAGGACACCC CAATGAGCCA AAGGGGGTCC 60  
 CAAAGCAGTG GCTCGGACTC AGACTCCCAT TTTGAGCAGC TGATGGTGAA TATGCTAGAT 120  
 GAAAGGGATC GTCTTCTAGA CACCCTTCGG GAGACCCAGG AAAGCCTCTC ACTTGCCAG 180  
 CAAAGACTTC AGGATGTCAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTGAGCC 240  
 CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GGTGATCCA 300  
 CCGGAATTGT CTGCACTGAC AAAAGAATTA AATGCCTGCA GGGAAACAAC TCTAGAAAAG 360  
 GAAGAAAGAA TCCTCTGAAT TAAAGCTGAA AGAAACAACA CAAGACTATT ACTGGAGCAT 420  
 TTGGAGTGCC TTGTGTGTCAG ACATGAAAGA TCACTAAGAA TGACGGTGGT AAAACGGCAA 480  
 GCCCAGTCTC CCTCAGGAGT ATCCAGTGAA GTTGAAGTTC TCAAGGCACT GAAATCTTTG 540  
 TTTGAGCACC ACAAGGCCTT GGATGAAAAG GTAAGGGAGC GACTGAGGGT TTCTTTAGAA 600  
 AGAGTCTCTG CACTGGAAGA AGAACTAGCT GCTGCTAATC AGGAGATTGT TGCCTTGCGT 660  
 GAACAAAATG TTCATATACA AAGAAAATAT GCATCAAGCG AGGGATCCAC AGAGTCAGAA 720  
 CATCTTGAAG GGATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTTGTCT CAATGGTTCT 780  
 ATAGACTCAA CCGATGAAAC TAGTCAAATA GTTGAACCTAC AAGAATTGCT TGAAAAGCAA 840  
 AACTATGAAA TGGCCAGAT GAAAGAACGT TTAGCAGCCC TTCTTCCCG AGTGGGAGAG 900  
 GTGGAACAGG AAGCAGAGAC AGCAAGAAAG GATCTCATTA AAACAGAAGA AATGAACACC 960  
 AAGTATCAAA GGGACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAGAATT 1020  
 ACAACCTTG AAAAGCGTTA CCTCAGTGCT CAGAGAGAAT CTACCTCCAT ACATGACATG 1080  
 AATGATAAAC TAGAAAATGA GTTAGCAAAT AAAGAAGCTA TCCTACGGCA GATGGAAGAG 1140  
 AAAACAGAC AGTTACAAGA ACGTCTTGAG CTAGCTGAAC AAAAGTTGCA GCAGACCATG 1200  
 AGAAAGGCTG AAACCTTGCC TGAAGTAGAG GCTGAAGTGG CTCAGAGAAT TGCAGCCCTA 1260  
 ACCAAGGCTG AAGAGAGACA TGGAAATATT GAAGAACGTA TGAGACATTT AGAGGGTCAA 1320  
 CTTGAAGAGA AGAATCAAGA ACTTCAAAGA GCTAGGCAAA GAGAGAAAAA GAATGAGGAG 1380  
 CATACAAGA GATTATCGGA TACGGTTGAT AGACTTCTGA CTGAATCCAA TGAACGCCTA 1440  
 CACTACACT TAAAGGAAAG AATGGCTGCT CTAGAAGAAA AGAATGTTTT AATTCAAGAA 1500  
 TCAGAAACTT TCAGAAAGAA TCTTGAAGAA TCTTTACATG ATAAGGAAAG ATTAGCAGAA 1560  
 GAAATTGAAA AGCTGAGATC TGAACCTGAC CAATTGAAA TGAGAACTGG CTCTTTAATT 1620  
 GAACCCCAA TACCAAGAAC TCATCTAGAC ACCTCAGCTG AGTTGCGGTA CTGAGTGGGA 1680  
 TCCCTAGTGG ACAGCCAGTC TGATTACAGA ACAAATAAG TAATAAGAAG ACCAAGGAGA 1740  
 GGCCGCATGG GTGTGCGAAG AGATGAGCCA AAGGTGAAAT CTCTTGGGGA TCACGAGTGG 1800  
 AATAGAATC AACAGATTGG AGTACTAAGC AGCCACCCTT TTGAAAGTGA CACTGAAATG 1860  
 TCTGATATTG ATGATGATGA CAGAGAAACA ATTTTGTAGCT CAATGGATCT TCTCTCTCCA 1920  
 AGTGGTCATT CCGATGCCCA GACGCTAGCC ATGATGCTTC AGGAACAATT GGATGCCATC 1980  
 AACAAAGAAA TCAGGCTAAT TCAGGAAGAA AAAGAATCTA CAGAGTTGCG TGCTGAAGAA 2040  
 ATTGAAAATA GAGTGGCTAG TGTGAGCCTC GAAGGCCTGA ATTTGGCAAG GGTCCACCCA 2100

5 GGTACCTCCA TTAAGTGCCTC TGTTACAGCT TCATCGCTGG CCAGTTCATC TCCCCCAGT 2160  
 GGACACTCAA CTCCAAAGCT CACCCTCGA AGCCCTGCCA GGGAAATGGA TCGGATGGGA 2220  
 GTCATGACAC TGCCCAAGTGA TCTGAGGAAA CATCGGAGAA AGATTGCAGT TGTGGAAGAA 2280  
 GATGGTTCGAG AGGACAAAGC AACAATTAAT TGTGAACTT CTCCCTCTCC TACCCTTAGA 2340  
 GCCCTCAGAA TGACTCACAC TCTCCCTTCT TCCTACCACA ATGATGCTCG AAGTAGTTTA 2400  
 TCTGTCTCTC TTGAGCCAGA AAGCCTCGGG CTGTGTAGTG CCAACAGCAG CCAAGACTCT 2460  
 CTTCAAAAG CCCCCAAGAA GAAAGGAATC AAGTCTTCAA TAGGACGTTT GTTTGGTAAA 2520  
 10 AAAGAAAAAG CTCGACTTGG GCAGCTCCGA GGCTTTATGG AGACTGAAGC TGCAGCTCAG 2580  
 GAGTCCCTGG GGTTAGGCAA ACTCGGAAC CAAGCTGAGA AGGATCGAAG ACTAAAGAAA 2640  
 AAGCATGAAC TTCTTGAAGA AGCTCGGAGA AAGGGATTAC CTTTGGCCCA GTGGGATGGG 2700  
 CCAACTGTGG TCGCATGGCT AGAGCTTTGG TTGGGAATGC CTGCGTGGTA CGTGGCAGCC 2760  
 TGCCGAGCCA ACGTGAAGAG TGGTGCCATC ATGTCTGCTT TATCTGACAC TGAGATCCAG 2820  
 AGAGAAATTG GAATCAGCAA TCCACTGCAT CGCTTAAAC TTGATTAGC AATCCAGGAG 2880  
 15 ATGGTTTCCC TAACAAGTCC TTCAGTCTCT CCAACATCTC GAACTCCTTC AGGCAACGTT 2940  
 TGGGTGACTC ATGAAGAAAT GGAATATCTT GCAGCTCCAG CAAAAACGAA AGAATCTGAG 3000  
 GAAGGAAGCT GGGCCAGTGT TCCGGTTTTT CTACAGACCC TGGCTTATGG AGATATGAAT 3060  
 CATGAGTGGG TGGGAATGA ATGGCTTCCC AGCTTGGGGT TACCTCAGTA CAGAAGTTAC 3120  
 TTTATGGAAT GCTTGGTATG TGCAAGAATG TTAGATCACC TAACAAAAA AGATCTCCGT 3180  
 20 GTCCATTTAA AAATGGTGGG TAGTTTCCAT CGAACCAAGT TACAATATGG AATTATGTGC 3240  
 TTAAAGAGGT TGAATTTATG CAGAAAAGAA CTAGAAAGAA GACGGGAAGC AAGCCAACAT 3300  
 GAAATAAAG ACGTGTGGT GTGGAGCAAT GACCGAATTA TTGCTGGAT ACAAGCAAT 3360  
 GGACTTCGAG AATATGCAAA TAATATACTT GAGAGCGGTG TGCATGGCTC ACTTATAGCC 3420  
 CTGGATGAAA ACTTTGACTA CAGCAGCTTA ACTTTATTAT TACAGATTCC AACACAGAAC 3480  
 25 ACCCAGGCAA GGCAGATTCT TGAAGAGAAA TACAATAACC TCTTGGCCCT GGGAACTGAA 3540  
 AGGCGACTGG ATGAAAGTGA TGACAAGAAC TTGAGACGTG GATCAACCTG GAGAAGGCAG 3600  
 TTTCTCTCTC GTGAAATACA TGAATCAGC ATGATGCTCG GGTCTCAGA AACATTACCA 3660  
 GCTGGATTGA GGTAAACAC AACCTCTGGG CAATCAAGAA AAATGACAAC AGATGTTGCT 3720  
 30 TCATCAAGAC TGCAGAGGTT AGACAACCTC ACTGTTTCGCA CATACTCATG TCTCGAGTAA 3780  
 GCGGCGCTT TAA

A222 Protein sequence:

Gene name: ESTs; Liprin A2  
 Unigene number: Hs.306480  
 35 Probeset Accession #: N51002  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: none found  
 40 AAA domain: 286-539  
 SAM domains: 895-964, 1017-1084, 1105-1177  
 Cellular Localization: not determined

45 1 11 21 31 41 51  
 | | | | | |  
 MMCEVMPTIN EDTPMSQRGS QSSGSDSDSH FEQLMVNMLD ERDRLDLTLR ETQESLSLAQ 60  
 QRLQDVIYDR DSLQRQLNSA LPQDIESLTG GLAGSKGADP PEFAALTKEL NACREQLLEK 120  
 EEBISELKA E RNRRLRLLH LECLVSRHER SLRMTVVKRQ AQSPSGVSSE VEVLKALKSL 180  
 FEHHKALDEK VNRRLRVSL RVSALREELA AANQEIVLR EQNVHIQRKM ASSEGSTESE 240  
 50 HLEGMEPQK VHEKRLNSG IDSTDETSQI VELQELLEKQ NYEMAQMKER LAALSSRVGE 300  
 VEQEAETARK DLIKTEEMNT KYQDIREAM AQKEDMEERI TTLEKRYLSA QRESTSIHDM 360  
 NDKLENELAN KEAILRQME KNRQLQERLE LAEQKLQQT M RKAETLPEVE AELAQRIAL 420  
 TKABERHGN EERMRLHEGQ LEEKNQELQR ARQREKMNEE HNKRLSDTVD RLLTESNERL 480  
 QLHLKERMMA LEEKNVLIQE SETFRKNLEE SLHDKERLAE EIEKLRSLED QLMKRTGSLI 540  
 55 EPTTPRTHLD TSAELRYSVG SLVDSQSDYR TTKVIRRRPR GRMGVRRDEP KVKSLGDHEW 600  
 NRTQIGVLS SHPFESDTEM SDIDDDRET IFSSMDLLSP SGHSDAQTLA MMLQEQLDAI 660  
 NKEIRLIQEE KESTELRAEE IENRVASVSL EGLNLARVHP GTSITASVTA SSLASSPPPS 720  
 GHSTPKLTPR SPAREMDRMG VMTLPDLRK HRRKIIVVEE DGRDKATIK CETSPPPTPR 780  
 ALRMTHTLPS SYHNDARSSL SVSLEPESLG LGSANSSQDS LHKAPKKKGI KSSIGRLFGK 840  
 60 KEKARLQQLR GFMTETAAQA ESLGLGLGT QAEKDRRLKK KHELLEEAR KGLPFAQWDG 900  
 PTVVWALELW LGMPAWYVAA CRANVKSAGI MSALSDTEIQ REIGISNPLH RLKRLRAIQE 960  
 MVLSTSPSPS PSTRTPSGNV WVTHEEMENL AAPAKTKESE EGSWAQCPVF LQTLAYGDMN 1020  
 HEWIGNEWLP SLGLPQYRSY FMECLVDARM LDHLTKKDLR VHLKMVDSFH RTSLQYGYMC 1080  
 65 LKRLNYDRKE LERRREASQ EIKDVLVWSN DRIIRWIAI GLREYANNIL ESGVHGSLIA 1140  
 LDENFDYSSL TLLQIPTQN TQARQILERE YNNLLALGTE RRLDESDDKN FRRGSTWRRQ 1200  
 FPPREVHGIS MMPGSSETLP AGFRLTTTSG QSRKMTTDVA SSRLQRLDNS TVRTYSCLE

A223 DNA SEQUENCE

Gene name: CDA14  
 70 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Nucleic Acid Accession #: NM\_016570  
 Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51  
 | | | | | |  
 ATGAGGCGAC TGAATCGGAA AAAAACTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTCCG 60  
 AAGGTTCTCT AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120  
 80 TTACAACATA TGGCTTTATT AACCATAATG GAATTTCTCAG TATATCAAGA TACATGGATG 180  
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAT TAAGAATTAA TATAGATATT 240  
 ACTGTTGCCA TGAAGTGTC AATATGTTGA GCGGATGTAT TGGATTTAGC AGAAACAATG 300  
 GTTGATCTCG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360  
 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACCT 420  
 CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480



5 GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCAATAAA 540  
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600  
 CATTGTGGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTCATAGAAT AGATCATTTG 660  
 TCTTTTGGAG AGCTTGTTC AGCAATTATT AATCCTTTAG ATGGAACCTGA AAAAATTGCT 720  
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCCAACAAA ACTACATACA 780  
 TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAC 840  
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTTCTCTT 900  
 ATGGTGACAG TTACTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960  
 10 ATTGTGGAG GAATCTTTT AACAACAGGC ATGTTACATG GAATTGGAAA ATTTATAGTT 1020  
 GAAATAATT GCTGTCGTTT CAGACTTGA TCCTATAAAC CTGTCAATTC TGTTCCTTT 1080  
 GAGGATGGCC ACACAGACAA CCACTTACCT CTTTATAGAAA ATAATACACA TTGA

#### A224 Protein sequence:

15 Gene name: CDA14  
 Unigene number: Hs.26813  
 Probeset Accession #: N32912  
 Protein Accession #: NP\_057654  
 20 Signal sequence: none found  
 Transmembrane domains: none found  
 Cellular Localization: nuclear

25 1 11 21 31 41 51  
 MRLNLRKKTL SLVKELDAFP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60  
 KVEYEVVDKDF SSKLRINIDI TVAMKQYVVG ADVLDAETM VASADGLVYE PTVFDLSPQQ 120  
 KEWQRLMLQLI QSRLQBEHSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVVK 180  
 30 VAGNPHITVG KAIPHPRGHA HLAALVNHEB YNFSHRIDHL SFGELVPATII NPLDGTEDIA 240  
 IDHNQMFQYF ITVVPVTKLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300  
 MVTVTEEHMP FWQFFVRLCG IVGGIFSTTG MLHGIGKFIV EIICCRFRLG SYKPVNSVPF 360  
 EDGHTDNHLP LLENNTHT

#### Uterine

#### A225 DNA SEQUENCE:

35 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 40 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60  
 CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGCTCAGAG TTTCTTCCAA CCTTGCCATT 120  
 GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180  
 ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
 50 ATGGTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGCCC 300  
 CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
 GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420  
 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
 TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540  
 55 CAGTCAGAGC TATAAGAGAT GATAGAAAA AGCCTTCACT TCAAAGAGT CAAATTCAT 600  
 GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAA 660  
 TTACTATTTA GTTTTAA TGTGTTTGA ATAGTCTTAT TAAATAAAT GTTTTAA 720  
 TCTGAAAAA AAAAAA AAAAAA

#### A226 Protein sequence:

60 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 65 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

70 1 11 21 31 41 51  
 MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLRSGWGD DITWVQTYEE GLFYAQSKSK 60  
 PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM 120  
 75 FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

#### A227 DNA SEQUENCE

80 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Probeset Accession #: AA460530  
 Nucleic Acid Accession #: NM\_003667  
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GTGGCGGCAA	CCGGCACCTC	AGTCCCCGCC	GCGCTTCTCC	TCGCGGCCCA	CGCCGTGGGG	60
5	TCAGGAACGC	GGCGTCTGGC	GCTGCAGACG	CCCCGTAGGT	TGCAGAAGCC	CACGGAGCGG	120
	CGCCCGGCGC	GCCACGGGCC	GTAGCAGTCC	GGTGTCTGTC	TCCGCCGCGC	TCCGGCTCGT	180
	GGCCCCCTAC	TTCCGGGCACC	ATGGACACCT	CCCCGCTCGG	TGTGCTCCTG	TCCTTGCCCTG	240
	TGCTGTCTGA	GCTGGCGACC	GGGGGCAGCT	CTCCAGGTCC	TGGTGTGTGT	CTGAGGGGCT	300
	GCCCCACACA	CTGTCAATTGC	GAGCCCGACG	GCAGGATGTT	GCTCAGGGTG	GACTGCTCCG	360
10	ACCTGGGGCT	CTCGGAGCTG	CCTTCCAACC	TACAGGTCTT	CACCTCCTAC	CTAGACCTCA	420
	GTATGAACAA	CATCAGTCAG	CTGCTCCCGA	ATCCCTTGCC	CAGTCTCCGC	TTCTTGGAGG	480
	AGTTACGTCT	TGCGGGAAAC	GCTCTGACAT	ACATTCCCAA	GGGAGCATTC	ACTGGCCCTT	540
	ACAGTCTTAA	AGTTCTTTATG	CTGCAGAATA	ATCAGCTAAG	ACACGTACCC	ACAGAAGCTC	600
	TGCAGAAATT	GCGAAGCCTT	CAATCCCTGC	GTCTGGATGC	TAACCACATC	AGCTATGTGC	660
15	CCCCAAGCTG	TTTCAGTGGC	CTGCATTCCC	TGAGGCACCT	GTGGCTGGAT	GACAATGCGT	720
	TAACAGAAAT	CCCCGTCCAG	GCTTTTAGAA	GTTTATCGGC	ATTGCAAGCC	ATGACCTTGG	780
	CCCTGAACAA	AATACACCAC	ATACCAGACT	ATGCCTTTGG	AAACCTCTCC	AGCTTGGTAG	840
	TTCTACATCT	CCATAACAA	AGAAATCCACT	CCCTGGGAAA	GAAATGCTTT	GATGGGCTCC	900
	ACAGCCTAGA	GACTTTAGAT	TTAAATTACA	ATAACCTTGA	TGAATTCCTC	ACTGCAATTA	960
20	GGACACTCTC	CAACCTTAAA	GAACCTAGGAT	TTCATAGCAA	CAATATCAGG	TCGATACCTG	1020
	AGAAAGCATT	TGTAGGCAAC	CCTTCTCTTA	TTACAATACA	TTTCTATGAC	AATCCCATTCC	1080
	AATTTGTTGG	GAGATCTGCT	TTTCAACATT	TACCTGAACT	AAGAACACTG	ACTCTGAATG	1140
	GTGCCTCACA	AATAACTGAA	TTTCTGTATT	TAACTGGAAC	TGCAAACTCG	GAGAGTCTGA	1200
	CTTTAAGTGG	AGCAGAGATC	TCATCTCTTC	CTCAAACTCG	CTGCAATCAG	TTACCTAATC	1260
25	TCCAAGTGCT	AGATCTGTCT	TACAACCTAT	TAGAAGATT	ACCCAGTTT	TCAGTCTGCC	1320
	AAAAGCTTCA	GAAATTTGAC	CTAAGACATA	ATGAAATCTA	CGAAATTTAA	GTTGACACTT	1380
	TCCAGCAGTT	GCTTAGCCTC	CGATCGCTGA	ATTTGGCTTG	GAACAAAATT	GCTATTATTC	1440
	ACCCCAATGC	ATTTTCCACT	TTGCCATCCC	TAATAAAGCT	GGACCTATCG	TCCAACCTCC	1500
	TGTCGTCTTT	TCCCTAATCT	GGGTACATG	GTTTAACTCA	CTTAAATTA	ACAGGAAATC	1560
30	ATGCCTTACA	GAGCTTGATA	TCATCTGAAA	ACTTTCCAGA	ACTCAAGGTT	ATAGAAATGC	1620
	CTTATGCTTA	CCAGTGCTGT	GCATTGAGAG	TGTGTGAGAA	TGCCTATAAG	ATTTCTAATC	1680
	AATGAATAAA	AGGTGACAAC	AGCAGTATGG	ACGACCTTCA	TAAGAAAGAT	GCTGGAATGT	1740
	TTCAAGGCTCA	AGATGAACGT	GACCTTGAAG	ATTTCTGTCT	TGACTTTGAG	GAAGACCTGA	1800
	AAGCCCTTCA	TTCAGTGACG	TGTTACCTT	CCCCAGGCC	CTTCAAAACC	TGTGAACACC	1860
35	TGCTTGATGG	CTGGCTGATC	AGAATTGGAG	TGTGGACCAT	AGCAGTTCTG	GCACCTACTT	1920
	GTAATGCTTT	GGTGACTTCA	ACAGTTTTC	GATCCCTCT	GTACATTTCC	CCCATTAAAC	1980
	TGTTAATTGG	GGTCATCGCA	GCAGTGAACA	TGCTCACGGG	AGTCTCCAGT	GCCGTGCTGG	2040
	CTGGTGTGGA	TGCGTTCACT	TTTGGCAGCT	TTGCACGACA	TGGTGCCTGG	TGGGAGAAATG	2100
	GGGTGTTGTT	CCATGTCATT	GGTTTTTTGT	CCATTTTTC	TTCAGAATCA	TCTGTTTTCC	2160
40	TGCTTACTCT	GGCAGCCCTG	GAGCGTGGGT	TCTCTGTGAA	ATATTCTGCA	AAATTGTAAA	2220
	CGAAAGCTCC	ATTTTCTAGC	CTGAAAGTAA	TCATTTTGCT	CTGTGCCCTG	CTGGCCTTGA	2280
	CCATGGCCGC	AGTTCCCTCT	CTGGGTGGCA	GCAAGTATGG	CGCCTCCCCT	CTCTGCCTGC	2340
	CCTTGCCCTT	TGGGAGGCC	AGCACCATGG	GCTACATGGT	CGCTCTCATC	TTGCTCAATT	2400
	CCCTTTGCTT	CCTCATGATG	ACCATTGCC	ACACCAAGCT	CTACTGCAAT	TTGGACAAGG	2460
45	GAGACCTGGA	GAATATTGTT	GACTGCTCTA	TGGTAAACA	CATTGCCCTG	TTGCTCTTCA	2520
	CAACTGCAAT	CCTAAACTGC	CCTGTGGCTT	TCTTGCTCTT	CTCCTCTTTA	ATAAACCTTA	2580
	CATTTATCAG	TCTGAAGTA	ATTAAGTTTA	TCCTTCTGGT	GGTAGTCCCA	CTTCTGTCAT	2640
	GTCTCAATCC	CCTTCTCTAC	ATCTTGTTC	ATCCTCACTT	TAAGGAGGAT	CTGGTGAGCC	2700
	TGAGAAAGCA	AACCTACGAT	TGGACAAGAT	CAAAACACCC	AAGCTTGATG	TCAATTAAC	2760
50	CTGATGATGT	CGAAAAACAG	TCCTGTGACT	CAACTCAAGC	CTTGGTAAAC	TTTACCAGCT	2820
	CCAGCATCAC	TTATGACCTG	CCTCCAGTT	CCGTGCCATC	ACCAGCTTAT	CCAGTGACTG	2880
	AGAGCTGCCA	TCITTTCTCT	GTGGCATTTG	TCCCATGTCT	CTAATTAATA	TGTGAAGGAA	2940
	AATGTTTTCA	AAGGTTGAGA	ACCTGAAAT	GTGAGATTGA	GTATATCAGA	GCAGTAATTA	3000
	ATAAGAAAG	CTGAGGTGAA	ACTCGGTTTA	AA			

**A228 Protein sequence**

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Protein Accession #: NP\_003658.1  
 Signal sequence: 1-22  
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825  
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
65	MDTSRLGVLL	SLPVLLQLAT	GGSSPRSGVL	LRGCPHCHC	EPDGRMLLRV	DCSDLGLSEL	60
	PSNLSVFTSY	LDLSMNNISQ	LLPNPLPSLR	FLEELRLAGN	ALTYIPKGF	TGLYSLKVL	120
	LQNNQLRHVP	TEALQNLRLS	QSLRLDANHI	SYVPPSCFSG	LHSLRLHLWD	DNALTEIPVQ	180
70	AFRSLSALQA	MTLALNKIHH	IPDYAFGNLS	SLVVLHLHNN	RIHSLGKKCF	DGLHSLSETLD	240
	LNVNLDLDEF	TAIRTLNLK	ELGFHSNNIR	SIPEKAFVGN	PSLTIHFYD	NPIQFVGRSA	300
	FQHLPELRTL	TLNGASQITE	FPDLTGATNL	ESLTLTGAQI	SSLPQTVCNQ	LPNLQVLDLS	360
	YNLLEDLPF	SVQKQLKQID	LRHNEIYEIK	VDTFQQLLSL	RSNLNLANWKI	AIHPNAFST	420
	LPSLIKLDDL	SNLLSSFPIT	GLHGLTHLKL	TGNHALQSLI	SSNFPELKV	IEMFYAYQCC	480
75	AFGVCENAYK	ISNQWNKGDN	SSMDDLHKKD	AGMFQAQDER	DLEDFLDFFE	EDLKALHSVQ	540
	CSPSPGPFKP	CEHLLDGWLI	RIGVWTIAVL	ALTCNALVTS	TVFRSPLYIS	PIKLLIGVIA	600
	AVNMLTGVS	AVLAGVDAFT	PGSFARHGAW	WENGVGCHVI	GFLSIFASES	SVFLTLAAL	660
	ERGSFVKYSA	KFETKAPFSS	LKVIIILLCAL	LALTMVAVPL	LGGSKYGASP	LCLPLPFGE	720
	STMGYMLVAL	LLNSLCFALM	TIAYTKLYCN	LDKGDLENIW	DCSMVKHIAL	LLFTNCILNC	780
80	PVAFLSFSSL	LNLFISPEV	IKFILLVVP	LPACLNPLLY	ILFNPHFKED	LVSLRKQTYV	840
	WTRSKHPSLM	SINSDDVEKQ	SCDSTQALVT	FTSSSITYDL	PPSSVPSPAY	PVTESCHLSS	900
	VAFVPC						

Table 75: See Table 1

Table 76A depicts Seq ID No; UnigenelD; UnigeneTitle; PKey; Predicted Cellular Localization; and Exemplar Accession for each of the sequences in Table 78. The information in

Table 76A is linked by SeqID No to Table 78.

Seq ID No:	Sequence ID No for sequences in table				
Pkey:	Unique Eos probeset identifier number				
ExAccn:	Exemplar Accession number, Genbank accession number				
UnigenelD:	Unigene number				
Unigene Title:	Unigene gene title				
Pred Subcell Loc:	Predicted sub-cellular localization				
Seq ID No	Pkey	ExAccn	UnigenelD	Unigene Title	Pred Subcell Loc
Seq ID 1 & 2	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	plasma membrane
Seq ID 3 & 4	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	plasma membrane
Seq ID 5 & 6	429423	AI016712	Hs.287797	integrin, beta 1 (fibronectin receptor,	plasma membrane
Seq ID 7 & 8	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	secreted
Seq ID 9 & 10	419172	AW338625	Hs.22120	ESTs; similar to TRANSMEMBRANE 4 SUPERF	plasma membrane
Seq ID 11 & 12	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 13 & 14	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 15 & 16	407836	T79340	Hs.200272	B-cell CLL/lymphoma 6, member B, zinc fi	intracell
Seq ID 17 & 18	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	secreted
Seq ID 19 & 20	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	plasma membrane
Seq ID 21 & 22	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	secreted
Seq ID 23 & 24	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	secreted
Seq ID 25 & 26	429276	AF056085	Hs.198612	G protein-coupled receptor 51	plasma membrane
Seq ID 27 & 28	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	plasma membrane
Seq ID 29 & 30	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	secreted
Seq ID 31 & 32	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	intracell
Seq ID 33 & 34	418506	AA084248	Hs.85339	G protein-coupled receptor 39	plasma membrane
Seq ID 35 & 36	423961	D13666	Hs.136348	periostin (OSF-2os)	secreted
Seq ID 37 & 38	414812	X72755	Hs.77367	monokine induced by gamma interferon	secreted
Seq ID 39 & 40	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 41 & 42	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 43 & 44	424399	AI905687	AI905687:IL-BT095-190199-019 BT095 Homo	secreted	secreted
Seq ID 45 & 46	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	secreted
Seq ID 47 & 48	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	secreted
Seq ID 49 & 50	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	secreted
Seq ID 51 & 52	439569	AW602166	Hs.222399	CEGP1 protein	secreted
Seq ID 53 & 54	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 55 & 56	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	plasma membrane
Seq ID 57 & 58	411789	AF245505	Hs.72157	Adlcan	secreted
Seq ID 59 & 60	428698	AA852773	Hs.334838	KIAA1866 protein	plasma membrane
Seq ID 61 & 62	450098	W27249	Hs.8109	hypothetical protein FLJ21080	intracell
Seq ID 63 & 64	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	secreted
Seq ID 65 & 66	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	plasma membrane
Seq ID 67 & 68	415539	AI733881	Hs.72472	BMP-R1B	plasma membrane
Seq ID 69 & 70	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 71 & 72	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 73 & 74	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	plasma membrane
Seq ID 75 & 76	442082	R41823	Hs.7413	ESTs	plasma membrane
Seq ID 77 & 78	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	plasma membrane
Seq ID 79 & 80	451398	AI793124	Hs.144479	ESTs	intracell
Seq ID 81 & 82	429220	AW207206		ESTs	plasma membrane
Seq ID 83 & 84	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	plasma membrane
Seq ID 85 & 86	423242	AL039402	Hs.125783	DEME-6 protein	plasma membrane
Seq ID 87 & 88	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 89 & 90	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 91 & 92	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 93 & 94	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 95 & 96	325372			Phase 2 & 3 Exons	cytoplasmic
Seq ID 97 & 98	450375	AA009647		a disintegrin and metalloproteinase doma	plasma membrane
Seq ID 99 & 100	426215	AW963419	Hs.155223	stanniocalcin 2	secreted
Seq ID 101 & 102	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	secreted
Seq ID 103 & 104	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 105 & 106	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 107 & 108	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	plasma membrane
Seq ID 109 & 110	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	secreted
Seq ID 111 & 112	446163	AA026880	Hs.25252	prolactin receptor	plasma membrane
Seq ID 113 & 114	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	plasma membrane
Seq ID 115 & 116	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-li	intracell
Seq ID 117 & 118	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	plasma membrane
Seq ID 119 & 120	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 121 & 122	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 123 & 124	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 125 & 126	115522	BE614387	Hs.333893	c-Myc target JPO1	intracell
Seq ID 127 & 128	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	plasma membrane
Seq ID 129 & 130	446051	BE048061	Hs.37054	ephrin-A3	plasma membrane
Seq ID 131 & 132	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	secreted
Seq ID 133 & 134	410418	D31382	Hs.63325	transmembrane protease, serine 4	plasma membrane
Seq ID 135 & 136	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	plasma membrane
Seq ID 137 & 138	422260	AA315993	Hs.105484	regenerating gene type IV	secreted

5	Seq ID 139 & 140	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 141 & 142	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 143 & 144	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 145 & 146	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 147 & 148	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
10	Seq ID 149 & 150	104888	AW939591	Hs.5940	mucin 13, epithelial transmembrane	plasma membrane
	Seq ID 151 & 152	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ1245 fis, clone C	plasma membrane
	Seq ID 153 & 154	422330	D30783	Hs.115263	epiregulin	plasma membrane
	Seq ID 155 & 156	452461	N78223	Hs.108106	transcription factor	intracell
	Seq ID 157 & 158	413324	V00571	Hs.75294	corticotropin releasing hormone	secreted
15	Seq ID 159 & 160	412420	AL035668	Hs.73853	bone morphogenetic protein 2	secreted
	Seq ID 161 & 162	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	secreted
	Seq ID 163 & 164	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	secreted
	Seq ID 165	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	intracell
	Seq ID 166 & 167	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (	intracell
20	Seq ID 168 & 169	432829	W60377	Hs.57772	ESTs	intracell
	Seq ID 170 & 171	425721	AC002115	Hs.159309	uropalakin 1A	plasma membrane
	Seq ID 172 & 173	420370	Y13645	Hs.97234	uropalakin 2	plasma membrane
	Seq ID 174 & 175	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	plasma membrane
	Seq ID 176 & 177	402075			ENSP00000251056*:Plasma membrane calcium	secreted
25	Seq ID 178 & 179	421110	AJ250717	Hs.1355	cathepsin E	secreted
	Seq ID 180 & 181	451668	Z43948	Hs.326444	cartilage acidic protein 1	plasma membrane
	Seq ID 182 & 183	451668	Z43948	Hs.326444	cartilage acidic protein 1	secreted
	Seq ID 184 & 185	451668	Z43948	Hs.326444	cartilage acidic protein 1	intracell
	Seq ID 186 & 187	408243	Y00787	Hs.624	interleukin 8	secreted
30	Seq ID 188 & 189	422282	AF019225	Hs.114309	apolipoprotein L	secreted
	Seq ID 190 & 191	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	plasma membrane
	Seq ID 192 & 193	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	plasma membrane
	Seq ID 194 & 195	404875			NM_022819*:Homo sapiens phospholipase A2	intracell
	Seq ID 196 & 197	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	plasma membrane
35	Seq ID 198 & 199	404977			Insulin-like growth factor 2 (somatomedi	secreted
	Seq ID 200 & 201	420876	AA918425	Hs.177744	ESTs	plasma membrane
	Seq ID 202 & 203	427747	AW411425	Hs.180655	serine/threonine kinase 12	intracell
	Seq ID 204 & 205	420281	AI623693	Hs.323494	Predicted cation efflux pump	plasma membrane
	Seq ID 206 & 207	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	intracell
40	Seq ID 208	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 209 & 210	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 211 & 212	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 213 & 214	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 215 & 216	426900	AW163564	Hs.142375	ESTs	plasma membrane
45	Seq ID 217 & 218	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 219 & 220	405932			C15000305:gi 3806122 gb AAC69198.1  (AF0	intracell
	Seq ID 221 & 222	405932			C15000305:gi 3806122 gb AAC69198.1  (AF0	intracell
	Seq ID 223 & 224	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 225 & 226	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
50	Seq ID 227 & 228	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 229 & 230	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	secreted
	Seq ID 231 & 232	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	secreted
	Seq ID 233 & 234	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	secreted
	Seq ID 235 & 236	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
55	Seq ID 237 & 238	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 239 & 240	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 241 & 242	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	intracell
	Seq ID 243 & 244	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	secreted
	Seq ID 245 & 246	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	plasma membrane
60	Seq ID 247 & 248	430890	X54232	Hs.2699	glypican 1	plasma membrane
	Seq ID 249 & 250	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	plasma membrane
	Seq ID 251	429466	M85835	Hs.12827	ESTs	
	Seq ID 252	429466	M85835	Hs.12827	ESTs	
	Seq ID 253 & 254	419721	NM_001650	Hs.288650	aquaporin 4	plasma membrane
65	Seq ID 255 & 256	407034	U84540		gb:Human dystrobrein isoform DTN-3 (DTN	secreted
	Seq ID 257 & 258	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	plasma membrane
	Seq ID 259 & 260	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	secreted & plasma membrane
	Seq ID 261 & 262	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	secreted
	Seq ID 263 & 264	419704	AA429104	Hs.45057	ESTs	intracell
70	Seq ID 265 & 266	444471	AB020684	Hs.11217	KIAA0877 protein	plasma membrane
	Seq ID 267 & 268	409395	U46745	Hs.336678	dystrobrein, alpha	secreted
	Seq ID 269 & 270	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	secreted
	Seq ID 271 & 272	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	plasma membrane
	Seq ID 273	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
75	Seq ID 274	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 275 & 276	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	plasma membrane
	Seq ID 277 & 278	424998	U58515	Hs.154138	chitinase 3-like 2	secreted
	Seq ID 279 & 280	412709	AL022327	Hs.74518	KIAA0027 protein	plasma membrane
	Seq ID 281 & 282	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-lik	plasma membrane
80	Seq ID 283 & 284	404049			NM_018937*:Homo sapiens protocadherin be	plasma membrane
	Seq ID 285 & 286	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	plasma membrane
	Seq ID 287 & 288	404029			NM_018936*:Homo sapiens protocadherin be	plasma membrane
	Seq ID 289 & 290	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	intracell
	Seq ID 291 & 292	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 293 & 294	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 295 & 296	436895	AF037335	Hs.5338	carbonic anhydrase XII	plasma membrane
	Seq ID 297 & 298	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospho	plasma membrane

5	Seq ID 299 & 300	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	plasma membrane
	Seq ID 301 & 302	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	plasma membrane
	Seq ID 303 & 304	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter)	plasma membrane
	Seq ID 305 & 306	410407	X66839	Hs.63287	carbonic anhydrase IX	plasma membrane
	Seq ID 307 & 308	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	plasma membrane
	Seq ID 309 & 310	420737	L08096	Hs.99899	CD70 ; tumor necrosis factor (ligand) s	plasma membrane
	Seq ID 311 & 312	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	plasma membrane
10	Seq ID 313 & 314	412719	AW016610	Hs.816	ESTs	intracell
	Seq ID 315 & 316	417034	NM_006183	Hs.80962	neurotensin	secreted
	Seq ID 317 & 318	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	plasma membrane
	Seq ID 319 & 320	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	secreted
	Seq ID 321 & 322	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	plasma membrane
	Seq ID 323 & 324	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	secreted
15	Seq ID 325 & 326	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 327 & 328	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 329 & 330	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	secreted
	Seq ID 331 & 332	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	plasma membrane
	Seq ID 333 & 334	431846	BE019924	Hs.271580	uroplakin 1B	plasma membrane
20	Seq ID 335 & 336	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	secreted
	Seq ID 337 & 338	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane
	Seq ID 339 & 340	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	plasma membrane
	Seq ID 341 & 342	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	plasma membrane
	Seq ID 343 & 344	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	plasma membrane
25	Seq ID 345 & 346	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	secreted
	Seq ID 347 & 348	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	plasma membrane
	Seq ID 349 & 350	417542	J04129	Hs.82269	progesterone-associated endometrial prote	secreted
	Seq ID 351 & 352	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	plasma membrane
	Seq ID 353 & 354	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
30	Seq ID 355 & 356	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 357 & 358	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	secreted
	Seq ID 359 & 360	418462	BE001596	Hs.85266	integrin, beta 4	plasma membrane
	Seq ID 361 & 362	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	secreted
	Seq ID 363 & 364	439606	W79123	Hs.58561	G protein-coupled receptor 87	plasma membrane
35	Seq ID 365 & 366	404877			NM_005365:Homo sapiens melanoma antigen,	intracell
	Seq ID 367 & 368	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	plasma membrane
	Seq ID 369 & 370	109424	NM_005329	Hs.85962	hyaluronan synthase 3	plasma membrane
	Seq ID 371 & 372	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
40	Seq ID 373 & 374	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 375 & 376	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 377 & 378	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 379 & 380	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 381 & 382	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
45	Seq ID 383 & 384	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 385 & 386	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 387 & 388	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 389 & 390	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	secreted
	Seq ID 391 & 392	332180	AF134160	Hs.7327	claudin 1	plasma membrane
50	Seq ID 393 & 394	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 395 & 396	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 397 & 398	439223	AW238299	Hs.250618	UL16 binding protein 2	plasma membrane
	Seq ID 399 & 400	409757	NM_001898	Hs.123114	cystatin SN	secreted
	Seq ID 401 & 402	428969	AF120274	Hs.194689	artemin	secreted
55	Seq ID 403 & 404	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 405 & 406	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 407 & 408	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 409 & 410	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 411 & 412	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
60	Seq ID 413 & 414	414774	X02419	Hs.77274	plasminogen activator, urokinase	secreted
	Seq ID 415 & 416	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 417 & 418	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 419 & 420	428486	AW583497	Hs.184604	pancreatic polypeptide	secreted
	Seq ID 421 & 422	457489	AI693815	Hs.127179	cryptic gene	secreted
	Seq ID 423 & 424	432874	W94322	Hs.279651	melanoma inhibitory activity	secreted
65	Seq ID 425 & 426	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 427 & 428	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 429 & 430	404682			C9001188*:gi12738842[ref]NP_073725.1] p	secreted
	Seq ID 431 & 432	429547	AW009166	Hs.99376	ESTs	secreted
70	Seq ID 433 & 434	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter)	plasma membrane
	Seq ID 435 & 436	407242	M18728		gb:Human nonspecific crossreacting antig	plasma membrane
	Seq ID 437 & 438	407242	M18728		gb:Human nonspecific crossreacting antig	plasma membrane
	Seq ID 439 & 440	407242	M18728		gb:Human nonspecific crossreacting antig	plasma membrane
	Seq ID 441 & 442	432596	AJ224741	Hs.278461	matrilin 3	secreted
	Seq ID 443 & 444	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	plasma membrane
75	Seq ID 445 & 446	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	intracell
	Seq ID 447 & 448	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	secreted
	Seq ID 449 & 450	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 451 & 452	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 453 & 454	422109	S73265	Hs.1473	gastrin-releasing peptide	secreted
80	Seq ID 455 & 456	419235	AW470411	Hs.288433	neurotrophin	plasma membrane
	Seq ID 457 & 458	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	plasma membrane
	Seq ID 459 & 460	427333	AF067797	Hs.176658	aquaporin 8	plasma membrane
	Seq ID 461 & 462	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	secreted
	Seq ID 463 & 464	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	secreted

5	Seq ID 465 & 466	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	secreted
	Seq ID 467 & 468	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	secreted
	Seq ID 469 & 470	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10???	plasma membrane
	Seq ID 471 & 472	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10???	plasma membrane
	Seq ID 473 & 474	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	secreted
10	Seq ID 475 & 476	429010	Y18198	Hs.194725	one cut domain, family member 2	intracell
	Seq ID 477 & 478	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	secreted
	Seq ID 479 & 480	448243	AW369771	Hs.52620	integrin, beta 8	plasma membrane
	Seq ID 481 & 482	426427	M86699	Hs.169840	TTK protein kinase	intracell
	Seq ID 483 & 484	428187	AI687303	Hs.285529	G protein-coupled receptor 49	plasma membrane
15	Seq ID 485 & 486	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 487 & 488	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 489 & 490	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 491 & 492	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 493 & 494	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	secreted
20	Seq ID 495 & 496	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	plasma membrane
	Seq ID 497 & 498	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum corn	secreted
	Seq ID 499 & 500	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	secreted
	Seq ID 501 & 502	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	secreted
	Seq ID 503 & 504	420440	NM_002407	Hs.97644	mammaglobin 2	secreted
25	Seq ID 505 & 506	428450	NM_014791	Hs.184339	KIAA0175 gene product	intracell
	Seq ID 507 & 508	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	secreted
	Seq ID 509 & 510	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	secreted
	Seq ID 511 & 512	453392	U23752	Hs.32964	SRV (sex determining region Y)-box 11	secreted
	Seq ID 513	431989	AW972870	Hs.291069	ESTs	intracell
30	Seq ID 514	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	
	Seq ID 515 & 516	409178	BE393948	Hs.50915	kallikrein 5	secreted
	Seq ID 517 & 518	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	secreted
	Seq ID 519 & 520	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 521 & 522	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
35	Seq ID 523 & 524	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 525 & 526	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 527 & 528	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (	secreted
	Seq ID 529 & 530	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	secreted
	Seq ID 531 & 532	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	plasma membrane
40	Seq ID 533 & 534	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	plasma membrane
	Seq ID 535 & 536	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 537 & 538	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 539 & 540	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	secreted
	Seq ID 541 & 542	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	secreted
45	Seq ID 543 & 544	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	plasma membrane
	Seq ID 545 & 546	452792	AB037765	Hs.30652	KIAA1344 protein	plasma membrane
	Seq ID 547 & 548	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	plasma membrane
	Seq ID 549 & 550	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 551 & 552	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
50	Seq ID 553 & 554	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 555 & 556	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 557 & 558	400290	H18836	Hs.31608	hypothetical protein FLJ20041	plasma membrane
	Seq ID 559 & 560	410001	AB041036	Hs.57771	kallikrein 11	secreted
	Seq ID 561 & 562	418396	AI765805	Hs.26691	ESTs	plasma membrane
55	Seq ID 563 & 564	451027	AW519204	Hs.40808	ESTs	plasma membrane
	Seq ID 565 & 566	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	plasma membrane
	Seq ID 567 & 568	433466	AA508353	Hs.105314	relaxin 1 (H1)	secreted
	Seq ID 569 & 570	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 571 & 572	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
60	Seq ID 573 & 574	414569	AF109298	Hs.118258	prostate cancer associated protein 1	plasma membrane
	Seq ID 575 & 576	413435	X51405	Hs.75360	carboxypeptidase E	secreted
	Seq ID 577 & 578	426501	AW043782	Hs.293616	ESTs	plasma membrane
	Seq ID 579 & 580	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	plasma membrane
	Seq ID 581 & 582	408369	R38438	Hs.182575	solute carrier family 15 (H???) transport	plasma membrane
65	Seq ID 583 & 584	412628	AI972402	Hs.306051	hypothetical protein MGC2648	secreted
	Seq ID 585 & 586	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
	Seq ID 587 & 588	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
	Seq ID 589 & 590	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	plasma membrane
	Seq ID 591 & 592	445413	AA151342	Hs.12677	CGI-147 protein	secreted
70	Seq ID 593 & 594	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	intracell
	Seq ID 595 & 596	427958	AA418000	Hs.98280	potassium intermediate/small conductance	plasma membrane
	Seq ID 597 & 598	421887	AW161450	Hs.109201	CGI-86 protein	plasma membrane
	Seq ID 599 & 600	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	secreted
	Seq ID 601 & 602	432101	AI918950	Hs.123642	EphA3	plasma membrane
75	Seq ID 603 & 604	407786	AA687538	Hs.38972	tetraspan 1	plasma membrane
	Seq ID 605 & 606	416836	D54745	Hs.80247	cholecystokinin	secreted
	Seq ID 607 & 608	416539	Y07909	Hs.79368	epithelial membrane protein 1	plasma membrane
	Seq ID 609 & 610	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 611 & 612	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
80	Seq ID 613 & 614	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 615 & 616	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 617 & 618	422424	AI186431	Hs.296638	prostate differentiation factor	secreted
	Seq ID 619 & 620	428970	BE276891	Hs.194691	retinoic acid induced 3	plasma membrane
	Seq ID 621 & 622	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	secreted
	Seq ID 623 & 624	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 625 & 626	420610	AI683183	Hs.99348	distal-less homeo box 5	intracell
	Seq ID 627 & 628	425723	NM_014420	Hs.159311	dickkopf (Xenopus laevis) homolog 4	secreted

Seq ID 629 & 630	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	intracell
Seq ID 631 & 632	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	secreted
Seq ID 633 & 634	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	intracell

Table 76B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
424399	238961_1	AI905687 AI905624 AI905623 AA340069 R75793 W72837 BE074512 AI905633 W72838 BE092421 AI127172 BE186013 AW070916 AI139456 AW176044 AW291950
429220	301384_1	AW207206 AW341473 AA448195 AI951341
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

Table 76C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
403047	3540153	Minus	59793-59968
404029	7671252	Plus	108716-111112
404049	3688074	Minus	75765-78155
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404877	1519284	Plus	1095-2107
404977	3738341	Minus	43081-43229
405932	7767812	Minus	123525-123713
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 77 provides Pkey; Seq ID No; Disease Indications; and Preferred Utility for sequences in Table 78. Seq ID No links the information in Table 77 to Table 78.

5	Seq ID No:	Sequence ID No for sequences in table		
	Pkey:	Unique Eos probeset identifier number		
	Disease Indications:	Diseases designated for coverage as described in Table 1		
	Preferred Utility:	Preference of utility, based partly upon predicted localization (Ab is antibody; sm is small molecule target; CTL is vaccine target)		
	Seq ID No	Pkey	Disease Indications	Preferred Utility
10	Seq ID 1 & 2	425023	angiogenesis	Ab, sm, CTL, imaging
	Seq ID 3 & 4	424503	pancreas, prostate, angiogenesis, bladder, lung	Ab, sm, imaging
	Seq ID 5 & 6	429423	angiogenesis	Ab, sm
	Seq ID 7 & 8	400289	angiogenesis, bladder, lung, cervical, ovarian, head & neck	Ab, sm, CTL, diagnostic
15	Seq ID 9 & 10	419172	angiogenesis, renal	Ab, sm, CTL, imaging
	Seq ID 11 & 12	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 13 & 14	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 15 & 16	407836	angiogenesis	CTL
20	Seq ID 17 & 18	414577	angiogenesis	Ab, CTL, diagnostic
	Seq ID 19 & 20	418738	angiogenesis, lung, ovarian, bladder & stomach, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 21 & 22	428368	angiogenesis, head & neck, stomach	Ab, sm, diagnostic
	Seq ID 23 & 24	415138	angiogenesis, pancreas, stomach, lung, uterine	Ab, CTL, diagnostic
25	Seq ID 25 & 26	429276	angiogenesis, bladder, glioblastoma	Ab, sm, imaging
	Seq ID 27 & 28	418994	prostate, angiogenesis	Ab, CTL, imaging
	Seq ID 29 & 30	407975	angiogenesis, renal	Ab, CTL, diagnostic
	Seq ID 31 & 32	429113	angiogenesis, bladder and stomach	sm, CTL
30	Seq ID 33 & 34	418506	angiogenesis, ovarian, glioblastoma, uterine, lung, bladder, pancreas	Ab, sm, imaging
	Seq ID 35 & 36	423961	breast, colon, bladder, lung, fibrosis, pancreas, head and neck, ovarian	Ab, sm, diagnostic
	Seq ID 37 & 38	414812	breast, bladder, lung, Fibrosis, pancreas, colon, head and neck, cervical, stomach, renal, ovarian	Ab, CTL, diagnostic
	Seq ID 39 & 40	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
35	Seq ID 41 & 42	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
	Seq ID 43 & 44	424399	breast, uterine, head & neck	Ab, CTL, diagnostic
	Seq ID 45 & 46	422867	breast, ovarian, prostate, pancreas, lung, colon, uterine	Ab, CTL, diagnostic
	Seq ID 47 & 48	428227	breast, lung, bladder, ovarian, head & neck, fibrosis, colon, stomach, cervical	Ab, CTL, diagnostic
40	Seq ID 49 & 50	444381	breast, colon, bladder, lung, pancreas, head & neck, ovarian, stomach, uterine, renal, angiogenesis	Ab, CTL, diagnostic
	Seq ID 51 & 52	439569	breast, androgen withdrawal prostate, prostate, bladder	Ab, CTL, diagnostic
	Seq ID 53 & 54	411558	pancreas, prostate, stomach, breast, uterine, cervical, ovarian	Ab, sm, imaging
	Seq ID 55 & 56	400303	breast, ovarian, pros, stomach, uterine, bladder lung head & neck	Ab, sm, CTL, imaging
45	Seq ID 57 & 58	411789	pancreas, lung, breast, stomach, head & neck, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 59 & 60	428698	breast, colon, lung, pancreas, stomach, head & neck, ovarian	Ab, sm, imaging
	Seq ID 61 & 62	450098	breast, lung, stomach, uterine	CTL
	Seq ID 63 & 64	421552	breast, ovarian, pancreas, cervical, uterine, prostate, lung, stomach, head & neck	Ab, sm, CTL, diagnostic
50	Seq ID 65 & 66	452747	breast, bladder, lung, head & neck, ovarian, stomach, uterine, pancreas	Ab, imaging
	Seq ID 67 & 68	415539	breast, prostate, ovarian, cervical, uterine	Ab, sm, CTL, imaging
	Seq ID 69 & 70	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 71 & 72	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
55	Seq ID 73 & 74	409079	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 75 & 76	442082	breast, prostate, ovarian	Ab, imaging
	Seq ID 77 & 78	400297	breast, bladder, colon, prostate	Ab, sm, CTL, imaging
	Seq ID 79 & 80	451398	breast, ovarian	CTL
60	Seq ID 81 & 82	429220	breast, prostate, benign prostatic hyperplasia	Ab, CTL, imaging
	Seq ID 83 & 84	421524	breast	Ab, sm, CTL, imaging
	Seq ID 85 & 86	423242	breast, renal, ovarian, prostate, colon	Ab, CTL, imaging
	Seq ID 87 & 88	423242	breast, renal, ovarian, prostate, colon	CTL
65	Seq ID 89 & 90	423242	breast, renal, ovarian, prostate, colon	CTL
	Seq ID 91 & 92	452190	breast, stomach, pancreas	CTL
	Seq ID 93 & 94	452190	breast, stomach, pancreas	CTL
	Seq ID 95 & 96	325372	breast	CTL
70	Seq ID 97 & 98	450375	breast, ovarian, head & neck, pancreas, lung, colon	Ab, sm, CTL, imaging
	Seq ID 99 & 100	426215	breast, lung, renal, colon, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 101 & 102	425247	breast, ovarian, lung, colon, pancreas, head & neck, stomach, uterine, cervical, bladder	Ab, sm, CTL, diagnostic
	Seq ID 103 & 104	429353	breast, prostate	Ab, sm, CTL, imaging
75	Seq ID 105 & 106	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 107 & 108	432201	breast, colon, lung chemo, ovarian, stomach, pancreas, uterine, cervical	Ab, sm, CTL, imaging
	Seq ID 109 & 110	427585	breast, lung, head & neck, pancreas, stomach, colon, ovarian, cervical	CTL
	Seq ID 111 & 112	446163	breast, cervical, uterine	Ab, sm, imaging
80	Seq ID 113 & 114	442117	breast, lung, bladder, pancreas, head & neck, stomach, ovarian, prostate	Ab, CTL, imaging
	Seq ID 115 & 116	428179	breast	sm, CTL
	Seq ID 117 & 118	431211	colon, bladder, lung, pancreas, head & neck	Ab, sm, imaging
	Seq ID 119 & 120	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
75	Seq ID 121 & 122	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 123 & 124	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 125 & 126	115522	colon, lung, bladder, pancreas	CTL
	Seq ID 127 & 128	452679	prostate, colon, pancreas, Taxol prostate	Ab, CTL, imaging
80	Seq ID 129 & 130	446051	colon, breast	Ab, sm, CTL, imaging
	Seq ID 131 & 132	422048	colon, pancreas, prostate	diagnostic
	Seq ID 133 & 134	410418	colon, bladder, lung, ovarian, pancreas, head & neck	Ab, sm, CTL, imaging
	Seq ID 135 & 136	446342	uterine, colon, prostate	Ab, sm, CTL, imaging
80	Seq ID 137 & 138	422260	colon, ovarian mucinous	Ab, sm, CTL, diagnostic
	Seq ID 139 & 140	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 141 & 142	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 143 & 144	111929	colon, breast, fibrosis	Ab, sm, imaging
80	Seq ID 145 & 146	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 147 & 148	111929	colon, breast, fibrosis	Ab, sm, imaging



	Seq ID 149 & 150 104888	colon, stomach, uterine	Ab, imaging
	Seq ID 151 & 152 420159	bladder, stomach	Ab, sm, CTL, imaging
	Seq ID 153 & 154 422330	pancreas, colon, bladder	Ab, sm, CTL, imaging, diagnostic
5	Seq ID 155 & 156 452461	bladder, lung, head & neck, ovarian, glioblastoma, stomach, colon, cervical	CTL
	Seq ID 157 & 158 413324	bladder	Ab, sm, CTL, diagnostic
	Seq ID 159 & 160 412420	bladder, glioblastoma, lung, stomach	Ab, diagnostic
	Seq ID 161 & 162 416658	lung, ovarian, uterine, bladder	Ab, CTL, diagnostic
	Seq ID 163 & 164 407811	bladder, pancreas, stomach, uterine, lung	Ab, sm, diagnostic
10	Seq ID 165 402230	bladder	sm, CTL
	Seq ID 166 & 167 402230	bladder	sm, CTL
	Seq ID 168 & 169 432829	bladder	CTL
	Seq ID 170 & 171 425721	bladder	Ab, imaging
	Seq ID 172 & 173 420370	bladder	Ab, CTL, imaging
15	Seq ID 174 & 175 437852	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 176 & 177 402075	bladder, lung, head & neck, cervical	diagnostic
	Seq ID 178 & 179 421110	bladder, pancreas, stomach, ovarian, lung	Ab, sm, diagnostic
	Seq ID 180 & 181 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 182 & 183 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
20	Seq ID 184 & 185 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 186 & 187 408243	bladder, stomach, head & neck, cervical	Ab, diagnostic
	Seq ID 188 & 189 422282	bladder, lung, head & neck	CTL, diagnostic
	Seq ID 190 & 191 425852	bladder, lung, head & neck	Ab, sm, CTL, imaging
	Seq ID 192 & 193 439738	bladder, lung, cervical	Ab, sm, CTL, imaging
25	Seq ID 194 & 195 404875	bladder	sm, CTL
	Seq ID 196 & 197 425883	bladder, pancreas	Ab, CTL, imaging
	Seq ID 198 & 199 404977	bladder, ovarian	Ab, sm, CTL, diagnostic
	Seq ID 200 & 201 420876	pancreas, bladder	Ab, sm, CTL, imaging
	Seq ID 202 & 203 427747	bladder, lung, ovarian, stomach	sm, CTL
30	Seq ID 204 & 205 420281	lung, bladder, ovarian, pancreas	Ab, sm, imaging
	Seq ID 206 & 207 446673	bladder	sm, CTL
	Seq ID 208 437553	bladder	Ab, CTL, imaging
	Seq ID 209 & 210 437553	bladder	Ab, CTL, imaging
	Seq ID 211 & 212 437553	bladder	Ab, CTL, imaging
35	Seq ID 213 & 214 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 215 & 216 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 217 & 218 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 219 & 220 405932	bladder, lung, head & neck, cervical	sm
40	Seq ID 221 & 222 405932	bladder, lung, head & neck, cervical	sm
	Seq ID 223 & 224 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 225 & 226 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 227 & 228 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 229 & 230 444342	hepatitis C, lung, fibrosis, bladder	Ab, CTL, diagnostic
	Seq ID 231 & 232 421379	breast, pancreas, head & neck, lung, stomach, bladder, cervical, colon	Ab, CTL, diagnostic
45	Seq ID 233 & 234 417079	bladder, lung, head & neck, cervical	Ab, diagnostic
	Seq ID 235 & 236 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 237 & 238 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 239 & 240 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 241 & 242 447072	glioblastoma, pancreas	sm, CTL
50	Seq ID 243 & 244 419723	glioblastoma	Ab, CTL, diagnostic
	Seq ID 245 & 246 419723	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 247 & 248 430890	glioblastoma, lung, cervical, bladder	Ab, CTL, imaging, diagnostic
	Seq ID 249 & 250 456759	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 251 429466	glioblastoma, uterine	
55	Seq ID 252 429466	glioblastoma, uterine	
	Seq ID 253 & 254 419721	glioblastoma, lung	Ab, sm, CTL, imaging
	Seq ID 255 & 256 407034	glioblastoma	Ab, CTL, diagnostic
	Seq ID 257 & 258 413472	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 259 & 260 438380	glioblastoma	Ab, CTL, diagnostic, imaging
60	Seq ID 261 & 262 426271	glioblastoma	Ab, CTL, diagnostic
	Seq ID 263 & 264 419704	glioblastoma	sm, CTL
	Seq ID 265 & 266 444471	glioblastoma, lung, colon	Ab, sm, CTL, imaging
	Seq ID 267 & 268 409395	glioblastoma	Ab, CTL, diagnostic
	Seq ID 269 & 270 413063	glioblastoma, ovarian, bladder, lung	Ab, CTL, diagnostic
65	Seq ID 271 & 272 433800	glioblastoma, lung	Ab, CTL, imaging
	Seq ID 273 458435	glioblastoma	
	Seq ID 274 458435	glioblastoma	
	Seq ID 275 & 276 424343	glioblastoma, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 277 & 278 424998	glioblastoma	Ab, CTL, diagnostic
70	Seq ID 279 & 280 412709	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 281 & 282 435615	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 283 & 284 404049	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 285 & 286 418932	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 287 & 288 404029	glioblastoma	Ab, sm, CTL, imaging
75	Seq ID 289 & 290 436480	glioblastoma	sm, CTL
	Seq ID 291 & 292 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 293 & 294 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 295 & 296 436895	breast, renal, ovarian, glioblastoma	Ab, sm, imaging
	Seq ID 297 & 298 421471	renal	Ab, sm, CTL, imaging
80	Seq ID 299 & 300 428296	renal	Ab, sm, CTL, imaging
	Seq ID 301 & 302 423508	renal, colon	Ab, CTL, imaging
	Seq ID 303 & 304 450001	renal, lung	Ab, sm, CTL, imaging
	Seq ID 305 & 306 410407	renal, lung, colon, stomach, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 307 & 308 453496	renal, prostate	Ab, sm, CTL, imaging

	Seq ID 309 & 310 420737	renal	Ab,sm, CTL, imaging
	Seq ID 311 & 312 309931	lung	Ab,sm, CTL, imaging
	Seq ID 313 & 314 412719	lung, head & neck, bladder, glioblastoma, cervical	CTL
5	Seq ID 315 & 316 417034	lung, head & neck, a couple cervical	Ab, CTL, diagnostic
	Seq ID 317 & 318 430486	lung, bladder, head & neck, cervical	Ab,sm, imaging
	Seq ID 319 & 320 413753	lung, bladder, head & neck, pancreas, cervical, colon	CTL, diagnostic
	Seq ID 321 & 322 425650	lung, head & neck, cervical, bladder	Ab, imaging
	Seq ID 323 & 324 423673	bladder, lung, head & neck, ovarian, pancreas, colon, stomach, uterine, cervical	Ab, CTL, diagnostic
10	Seq ID 325 & 326 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 327 & 328 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 329 & 330 429610	lung	CTL, diagnostic
	Seq ID 331 & 332 406690	lung, head & neck, pancreas, stomach, bladder, colon, cervical	Ab, imaging
	Seq ID 333 & 334 431846	lung, bladder, head & neck, uterine, cervical, stomach, ovarian	Ab, imaging
	Seq ID 335 & 336 422158	head & neck, bladder, lung, cervical, stomach	diagnostic
15	Seq ID 337 & 338 431958	lung, bladder, cervical, head & neck, ovarian, colon, prostate, pancreas, breast	Ab, CTL, imaging
	Seq ID 339 & 340 437044	head & neck, cervical, lung, bladder, breast, prostate, ovarian, stomach	Ab, imaging
	Seq ID 341 & 342 428484	lung, glioblastoma, bladder, head & neck, colon, cervical	Ab, sm, imaging
	Seq ID 343 & 344 429211	lung, bladder, head & neck, cervical, stomach	Ab, imaging
20	Seq ID 345 & 346 417389	ovarian, lung, bladder, uterine, cervical, pancreas, stomach	Ab, diagnostic
	Seq ID 347 & 348 431009	lung, bladder, head & neck	Ab, sm, imaging
	Seq ID 349 & 350 417542	lung	CTL, diagnostic
	Seq ID 351 & 352 449230	lung, cervical, head & neck, bladder, ovarian, colon	Ab, imaging
	Seq ID 353 & 354 410555	lung	Ab, sm, imaging
25	Seq ID 355 & 356 410555	lung	Ab, sm, imaging
	Seq ID 357 & 358 424687	head & neck, pancreas, lung, uterine, cervical, colon, stomach	Ab, sm, diagnostic
	Seq ID 359 & 360 418462	lung, bladder	Ab, imaging
	Seq ID 361 & 362 410274	lung, renal	diagnostic
	Seq ID 363 & 364 439606	lung, bladder, head & neck, cervical	Ab,sm, imaging
30	Seq ID 365 & 366 404877	lung, bladder	CTL
	Seq ID 367 & 368 444781	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 369 & 370 109424	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 371 & 372 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 373 & 374 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
35	Seq ID 375 & 376 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 377 & 378 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 379 & 380 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 381 & 382 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 383 & 384 421817	lung, cervical, head & neck & bladder	CTL
40	Seq ID 385 & 386 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL, diagnostic
	Seq ID 387 & 388 418678	lung, bladder, stomach, ovarian, pancreas & cervical	Ab, sm, imaging
	Seq ID 389 & 390 409420	lung, head & neck, pancreas, stomach, cervical, bladder	Ab,sm, CTL, imaging
	Seq ID 391 & 392 332180	lung	Ab,sm, CTL, imaging
	Seq ID 393 & 394 408790	lung	Ab,sm, CTL, imaging
45	Seq ID 395 & 396 408790	lung	Ab, CTL, imaging
	Seq ID 397 & 398 439223	lung, head & neck, cervical, bladder & colon	Ab, CTL, diagnostic
	Seq ID 399 & 400 409757	pancreas, stomach, lung, bladder, stomach	Ab, CTL, diagnostic
	Seq ID 401 & 402 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 403 & 404 428969	lung, cervical	Ab, CTL, diagnostic
50	Seq ID 405 & 406 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 407 & 408 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 409 & 410 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 411 & 412 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 413 & 414 414774	lung, bladder, head & neck, pancreas, stomach, ovarian	Ab, sm, diagnostic
55	Seq ID 415 & 416 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 417 & 418 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 419 & 420 428486	pancreas	Ab, CTL, diagnostic
	Seq ID 421 & 422 457489	pancreas, prostate, lung	Ab, CTL, diagnostic
	Seq ID 423 & 424 432874	pancreas, stomach	Ab, CTL, diagnostic
60	Seq ID 425 & 426 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 427 & 428 445891	stomach, pancreas, ovarian	Ab, CTL, diagnostic
	Seq ID 429 & 430 404682	pancreas	Ab, CTL, imaging
	Seq ID 431 & 432 429547	pancreas, head & neck, lung, ovarian	Ab, CTL, diagnostic
	Seq ID 433 & 434 425921	stomach, pancreas	Ab,sm, CTL, imaging
65	Seq ID 435 & 436 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 437 & 438 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 439 & 440 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 441 & 442 432596	pancreas, breast	CTL
	Seq ID 443 & 444 444006	pancreas, colon, lung, ovarian & cervical	Ab, CTL, imaging
	Seq ID 445 & 446 423685	pancreas, uterine, colon	CTL
70	Seq ID 447 & 448 428392	pancreas	Ab, CTL, diagnostic
	Seq ID 449 & 450 429597	pancreas, colon, stomach, lung	Ab,sm, CTL, imaging
	Seq ID 451 & 452 448030	pancreas, renal and stomach,	Ab,sm, imaging
	Seq ID 453 & 454 422109	pancreas, lung, colon	Ab, CTL, diagnostic
	Seq ID 455 & 456 419235	pancreas, fibrosis, head & neck & lung	Ab, CTL, imaging
75	Seq ID 457 & 458 449048	pancreas, ovarian, uterine, glioblastoma, head & neck & lung	Ab, CTL, imaging
	Seq ID 459 & 460 427333	pancreas, colon	Ab, sm, imaging
	Seq ID 461 & 462 417931	ovarian, pancreas, stomach, colon, uterine, prostate	Ab, diagnostic
	Seq ID 463 & 464 419216	pancreas, lung, stomach, cervical, prostate, head & neck	Ab, CTL, diagnostic
80	Seq ID 465 & 466 431629	pancreas, uterine, cervical, stomach	Ab, CTL, diagnostic
	Seq ID 467 & 468 413554	pancreas, glioblastoma	Ab, CTL, diagnostic
	Seq ID 469 & 470 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 471 & 472 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 473 & 474 426322	pancreas, bladder, stomach	Ab, diagnostic

	Seq ID 475 & 476 429010	pancreas	sm, CTL
	Seq ID 477 & 478 431462	pancreas, lung, glioblastoma	Ab, diagnostic
	Seq ID 479 & 480 448243	ovarian, uterine, lung, stomach, head & neck, glioblastoma, pancreas	Ab, sm, imaging
5	Seq ID 481 & 482 426427	ovarian, lung, head & neck, cervical, colon, uterine, stomach	sm, CTL
	Seq ID 483 & 484 428187	ovarian, uterine, colon, stomach	Ab, sm, CTL, imaging
	Seq ID 485 & 486 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 487 & 488 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 489 & 490 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
10	Seq ID 491 & 492 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 493 & 494 445537	ovarian, bladder, uterine, breast, lung, head & neck, renal, fibrosis, pancreas, cervical	Ab, CTL, diagnostic
	Seq ID 495 & 496 422278	ovarian, head & neck, bladder, cervical, lung	Ab, sm, imaging
	Seq ID 497 & 498 424620	ovarian	Ab, CTL, diagnostic
	Seq ID 499 & 500 406400	ovarian, uterine	Ab, CTL, diagnostic
15	Seq ID 501 & 502 431130	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 503 & 504 420440	ovarian, uterine, cervical	Ab, CTL, diagnostic
	Seq ID 505 & 506 428450	ovarian, cervical, pancreas, lung	sm
	Seq ID 507 & 508 446619	ovarian, fibrosis, pancreas, head & neck, lung, colon	Ab, diagnostic
	Seq ID 509 & 510 436982	ovarian, fibrosis	Ab, CTL, diagnostic
20	Seq ID 511 & 512 453392	ovarian, lung, glioblastoma	CTL
	Seq ID 513 431989	ovarian	
	Seq ID 514 439820	ovarian, uterine, cervical, breast, prostate	
	Seq ID 515 & 516 409178	ovarian, breast	Ab, CTL, diagnostic
	Seq ID 517 & 518 426514	ovarian, colon, bladder, lung, cervical	Ab, CTL, diagnostic
25	Seq ID 519 & 520 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 521 & 522 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 523 & 524 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 525 & 526 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 527 & 528 452097	ovarian	Ab, sm, diagnostic
30	Seq ID 529 & 530 416530	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 531 & 532 431515	ovarian, prostate, lung	Ab, sm, CTL, imaging
	Seq ID 533 & 534 419452	ovarian, prostate, lung, breast, uterine	Ab, sm, CTL, imaging
	Seq ID 535 & 536 412078	ovarian	CTL
	Seq ID 537 & 538 412078	ovarian	CTL
35	Seq ID 539 & 540 411773	ovarian	Ab, sm, CTL, diagnostic
	Seq ID 541 & 542 407792	ovarian, uterine, cervical, pancreas	Ab, CTL, diagnostic
	Seq ID 543 & 544 431616	prostate, pancreas, colon	Ab, sm, CTL, imaging
	Seq ID 545 & 546 452792	prostate, uterine, breast	Ab, CTL, imaging
	Seq ID 547 & 548 400294	prostate, taxol prostate	Ab, sm, CTL, imaging
40	Seq ID 549 & 550 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 551 & 552 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 553 & 554 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 555 & 556 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 557 & 558 400290	prostate, colon	Ab, sm, CTL, imaging
45	Seq ID 559 & 560 410001	ovarian, prostate, uterine, cervical, lung	Ab, CTL, diagnostic
	Seq ID 561 & 562 418396	prostate	Ab, sm, CTL, imaging
	Seq ID 563 & 564 451027	prostate, uterine, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 565 & 566 446057	prostate	Ab, sm, CTL, imaging
	Seq ID 567 & 568 433466	prostate	Ab, CTL, diagnostic
50	Seq ID 569 & 570 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 571 & 572 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 573 & 574 414569	prostate	Ab, sm, CTL, imaging
	Seq ID 575 & 576 413435	prostate, glioblastoma, pancreas	Ab, sm, diagnostic
	Seq ID 577 & 578 426501	prostate, breast, glioblastoma, lung	Ab, CTL, imaging
55	Seq ID 579 & 580 448999	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 581 & 582 408369	prostate, lung, fibrosis, uterine, glioblastoma, cervical, ovarian	Ab, sm, CTL, imaging
	Seq ID 583 & 584 412628	prostate	Ab, CTL, diagnostic
	Seq ID 585 & 586 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
	Seq ID 587 & 588 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
60	Seq ID 589 & 590 408430	prostate	Ab, sm, CTL, imaging
	Seq ID 591 & 592 445413	prostate, colon, uterine, ovarian, lung, pancreas	diagnostic
	Seq ID 593 & 594 451982	prostate, bladder	CTL
	Seq ID 595 & 596 427958	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 597 & 598 421887	prostate	Ab, CTL, imaging
65	Seq ID 599 & 600 425071	prostate, colon, stomach, uterine, cervical, head & neck, pancreas	Ab, diagnostic
	Seq ID 601 & 602 432101	prostate, pancreas	Ab, sm, imaging
	Seq ID 603 & 604 407786	prostate, colon, uterine, stomach, inflammatory bowel disease, ovarian	Ab, sm, imaging
	Seq ID 605 & 606 416836	Prostate, Ewing, glioblastoma	Ab, CTL, diagnostic
70	Seq ID 607 & 608 416539	ZD1839 resistant cancers, head & neck	Ab, sm, CTL, imaging
	Seq ID 609 & 610 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 611 & 612 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 613 & 614 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 615 & 616 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 617 & 618 422424	bladder, pancreas, prostate, angiogenesis, colon, stomach, lung	Ab, CTL, diagnostic
75	Seq ID 619 & 620 428970	stomach, pancreas, colon	Ab, sm, imaging
	Seq ID 621 & 622 428330	uterine, ovarian, fibrosis, prostate, pancreas, lung, bladder, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 623 & 624 439018	uterine, stomach, prostate	Ab, sm, CTL, imaging
	Seq ID 625 & 626 420610	uterine, ovarian endometrioid, lung	CTL
	Seq ID 627 & 628 425723	ovarian endometrioid, uterine, colon	Ab, CTL, diagnostic
80	Seq ID 629 & 630 456662	uterine, ovarian	CTL
	Seq ID 631 & 632 418281	uterine, ovarian	Ab, CTL, diagnostic
	Seq ID 633 & 634 429903	lung	sm

Table 78

Seq ID NO: 1 DNA sequence  
Nucleic Acid Accession #: NM\_001400  
Coding sequence: 251..1399

	1	11	21	31	41	51	
10	TCTAAAGGTC	GGGCGCAGCA	GCAAGATGCG	AAGCGAGCCG	TACAGATCCC	GGGCTCTCCG	60
	AAAGCTACAC	AAAAAGCCTG	GATCACTCAT	CGAACCACCC	CTGAAGCCAG	TGAAGGCTCT	120
	CTCGCCTCGC	CCTCTAGCGT	TCGTCTGGAG	TAGCGCCACC	CCGGCTTCCT	GGGGACACAG	180
	GGTTGGCACC	ATGGGGCCCA	CCAGCGTCCC	GCTGGTCAAG	GCCCACCGCA	GCTCGGTCTC	240
15	TGACTACGTC	AACATAGATA	TCATCGTCCG	GCATTACAAC	TACACGGGAA	AGCTGAATAT	300
	CAGCGCGGAC	AAGGAGAACA	GCATTAAACT	GACCTCGGTG	GTGTTTCAATC	TCATCTGCTG	360
	CTTTATCATC	CTGGAGAACA	TCTTTGTCTT	GCTGACCATT	TGGAAAACCA	AGAAATTCCA	420
	CCGACCCATG	TACTATTTTA	TTGGCAATCT	GGCCCTCTCA	GACCTGTTGG	CAGGAGTAGC	480
	CTACACAGCT	AACCTGCTCT	TGCTCTGGGC	CACCACCTAC	AAGCTCACTC	CCGCCCAGTG	540
20	GTTTCTGCGG	GAAGGGAGTA	TGTTTGTGGC	CCTGTGAGCC	TCCGTGTTC	GTCTCCTCGC	600
	CATCGGCATT	GAGCGCTATA	TCACAATGCT	GAAAAAGAAA	CTCCACAACG	GGAGCAATAA	660
	CTTCCGCCTC	TTCCGTCTAA	TCAGCGCCTG	CTGGGTCAATC	TCCCTCATCC	TGGGTGGCCT	720
	GCCTATCATG	GGCTGGAACT	GCATCAGTGC	GCTGTCCAGC	TGCTCCACCG	TGCTGCCGCT	780
	CTACCACAAG	CACATATATCC	TCTTCTGCAC	CACGGTCTTC	ACTCTGCTTC	TGCTCTCCAT	840
25	CGTCATTCTG	TACTCGAGAA	TCTACTCCTT	GGTCAGGACT	CGGAGCGGCC	GCCTGACGTT	900
	CCGCAAGAAC	ATTTCACAGG	CCAGCCGCAG	CTCTGAGAAG	TGCTGGCGC	TGCTCAAGAC	960
	CGTAATTATC	GTCTGAGCG	TCTTCATCGC	CTGCTGGGCA	CCGCTCTTCA	TCCTGCTCCT	1020
	GCTGGATGTG	GGCTGCAAGG	TGAAGACCTG	TGACATCCTC	TTGAGAGCGG	AGTACTTCCT	1080
	GGTGTAGTAG	GTGCTCAACT	CCGGCACCAG	CCCCATCATT	TACACTCTGA	CCAACAAGGA	1140
30	GATGCGTCGG	GCCTTCATCC	GGATCATGTC	CTGCTGCAAG	TGCCGAGCG	GAGACTCTGC	1200
	TGGCAAAATC	AAGCGACCCA	TCATCGCCGG	CATGGAATTC	AGCCGCAGCA	AATCGGACAA	1260
	TTCTCTCCAC	CCCCAGAAAG	ACGAAGGGGA	CAACCCAGAG	ACCATTATGT	CTTCTGGAAA	1320
	CGTCAACTCT	TCCTCCTAGA	ACTGGAAGCT	GTCCACCCAC	CGGAAGCGCT	CTTACTTGG	1380
	TCGCTGGCCA	CCCCAGTGTT	TGGAAAAAAA	TCTCTGGGCT	TGCACTGCTG	CCAGGGAGGA	1440
35	GCTGCTGCAA	GCCAGAGGGA	GGAAGGGGGA	GAATACGAAC	AGCCTGGTGG	TGTCGGGTGT	1500
	TGGTGGGTAG	AGTTAGTTCC	TGTGAACAAT	GCACTGGGAA	GGGTGGAGAT	CAGGTCCCGG	1560
	CCTGGAATAT	ATATTCTACC	CCCCTGAGGC	TTTGATTTTG	CAGTGGAGCA	AAGGTCTAGC	1620
	ATTGTCAAGC	TCCTAAAGGG	TTTCAATTTG	CCCTCTCTCA	AGACTAATGT	CCCCATGTGA	1680
	AAGCGTCTCT	TTGTCTGGAG	CTTTGAGGAG	ATGTTTCTCT	TCATTTTAGT	TTCAAACCCA	1740
40	AGTGAGTGTG	TGCACTTCTG	CTTCTTTAGG	GATGCCCTGT	ACATCCCACA	CCCCACCTTC	1800
	CCTTCCCTTC	ATACCCCTCC	TCAACGTTCT	TTTACTTTAT	ACTTTAATCA	CCTGAGAGTT	1860
	ATCAGAGCTG	GGGTGTGGGA	ATGATCGATC	ATCTATAGCA	AATAGGCTAT	GTTGAGTACG	1920
	TAGGCTGTGG	GAAGATGAAG	ATGGTTTGGG	GGTGTAAAC	AATGTCCTTC	GCTGAGGCCA	1980
45	AAGTTTCCAT	GTAAGCGGGA	TCCGTTTTTT	GGAATTTGGT	TGAAGTCACT	TTGATTTCTT	2040
	TAAAAAATCT	CTTTTCAATG	AAATGTGTGA	CCATTTCATA	TCCATTGAAG	CCGAAATCTG	2100
	CATAAGGAAG	CCCCTTTTAT	CTAAATGATA	TTAGCCAGGA	TCCTTGGTGT	CCTAGGAGAA	2160
	ACAGACAAGC	AAAACAAAGT	GAAAAACGAA	TGGATTAACT	TTTGCAAACC	AAGGGAGATT	2220
	TCTTAGCAAA	TGAGTCTAAC	AAATATGACA	TCCGCTTTTC	CCACTTTTGT	TGATGTTTAT	2280
50	TTCAGAACTC	TGTTGTGATC	ATTTCAAGCA	ACAACATGTT	GTATTTTGTG	GTGTTAAAG	2340
	TACTTTTCTT	GATTTTGTAA	TGTATTTGTT	TCAGGAAGAA	GTCATTTTAT	GGATTTTCTT	2400
	AACCGTGTGT	AACCTTTTGA	GAATCCACCC	TCTTGTGCC	TTAAGCATTA	CTTTAACTGG	2460
	TAGGGAACGC	CAGAAGTTT	AAGTCCAGCT	ATTCATTAGA	TAGTAATTGA	AGATATGTAT	2520
	AAATATTACA	AAGATAAAAA	ATATATTACT	GTCTCTTTAG	TATGTTTTC	AGTGCAATTA	2580
55	AACCGAGAGA	TGCTTGTGTT	TTTTAAAAAG	AATAGTATTT	AATAGGTTTC	TGACTTTTGT	2640
	GGATCATTTT	GCACATAGCT	TTATCAACTT	TAAACATTA	ATAAAGTAT	TTTTTTAAAG	2700

Seq ID NO: 2 Protein sequence  
Protein Accession #: NP\_001391

	1	11	21	31	41	51	
60	MGPTSVPLVK	AHRSSVSDYV	NYDIIVRHYN	YTGKLNISAD	KENSIKLTSV	VFILICCFII	60
	LENIFVLLTI	WTKKFEHRPM	YFIGNLALS	DLLAGVAYTA	NLLLSGATTY	KLTPAQWFLR	120
	EGSMFVALSA	SVFSLLAIAI	ERYITMLKMK	LHNGSNFRL	FLLISACWVI	SLILGGLPIM	180
65	GWNCISALSS	CSTVLPYLYK	HYILFCTTVF	TLLLLLSIVL	YCRIYSLVRT	RSRRLTFRKN	240
	ISKASRSSEK	SLALLKTVII	VLSVFIACWA	PLFILLLLDV	GCKVKTCIDL	FRAEYFLVLA	300
	VLNSGTNPPI	YTLTNKEMRR	AFIRIMSCKK	CPSGDSAGKF	KRPPIAGMEF	SRSKSDNSSH	360
	PQKDEGDNPE	TIMSSGNVNS	SS				

Seq ID NO: 3 DNA sequence  
Nucleic Acid Accession #: NM\_002205.1  
Coding sequence: 1..3149

	1	11	21	31	41	51	
75	ATGGGGAGCC	GGACGCCAGA	GTCCCTCTCT	CACGCCGTGC	AGCTGCGCTG	GGGCCCCCGG	60
	CGCCGACCCC	CGCTSSGTCC	GCTGCTGTIG	CTGCTSSTGC	CGCCGCCACC	CAGGGTCGGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGTAGTTTAA	CCGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
80	CCCAAGGCTA	ATACCAAGCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGCTCT	300
	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAAGG	CTCTCGGCTC	360
	CTGGAGTCCT	CACGTGTCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCTTGCAG	420
	TGGTTCGGGG	CAACAGTTCG	AGCCCATGGC	TCCTCCATCT	TGGCATGCGC	TCCACTGTAC	480
	AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCCGCT	CAGATTTTCA	CTGGGCAGCA	600

5 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCGAGTTCA CCAAGACTGG CCGTGTGGTT 660  
 TAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720  
 ATTGCAGAAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780  
 CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGGTGGAA 840  
 10 TTCAGTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAAGGGAA CCTCACTTAC 900  
 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCGATCCC TCTACAACCT CTCAGGGGAA 960  
 CAGATGGCCT CCTACTTTGG CTATGCAGTG GCCGCCACAG ACGTCAATGG GGACGGGCTG 1020  
 GATGACTTGC TGGTGGGGGC ACCCCTGCTC ATGGATCGGA CCCCTGACGG GCGGCTCAG 1080  
 GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCG GCATAGAGCC CACGCCACCC 1140  
 15 CTTACCCCTA CTGGCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTGAC CCCCTGGGG 1200  
 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC 1260  
 CAGCAGGGAG TAGTGTTTGT ATTTCTGGG GCCCAGGAG GGCTGGGCTC TAAGCCTTCC 1320  
 CAGGTCTGCG AGCCCCGTG GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380  
 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCTTTGGT 1440  
 GTGGACAAGG CTGTGGTATA CAGGGGCCGC CCCATCGTGT CGCTAGTGC CTCCCTCACC 1500  
 ATCTTCCCGG CCATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1560  
 GCCTGCATCA ACCTTAGCTT CTGCTCAAT GCTTCTGGAA AACACGTTGC TGACTCCATT 1620  
 20 GGTTTCACAG TGGAACTTCA GCTGGAATGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1680  
 CTGTTCTCTG CCTCCAGGCA GGCAACCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740  
 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAATT TCGAGACAAA 1800  
 CTCTCGCCGA TTCACATCGC TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1860  
 CACGGGCTCA GGCACGCCCT ACATTATCAG AGCAAGAGCC GGATAGAGGA CAAGGCTCAG 1920  
 ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGT 1980  
 25 GGGGAGCAGA ACCATGTGTA CTGGGTGAC AAGAATGCC TGAACCTCAC TTTCATGCC 2040  
 CAGAATGTGT GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCCG CCCTCCAGAG 2100  
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2160  
 TTTGCCGTGA ACCAGAGCCG CTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGCAGGA 2220  
 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCGGGGACAC TAAGAAAACC 2280  
 30 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAG CGACGTGGTT 2340  
 TCCTTTCCGG TCCTCGTGGA GGCTCAGGCC CAGGTCAACC TGAACGCTGT CTCCAAGCCT 2400  
 GAGCCAGTGC TATTCCTAGT AAGCGACTGG CATCCCCGAG ACCAGCTCA GAAGGAGGAG 2460  
 GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520  
 AGCCAGGGTG TGTGGAACCT CAGCTGTCCC CAGGCTCTGG AAGGTGAGCA GCTCCTATAT 2580  
 35 GTGACCAAGG TTACGGGACT CAACTGCACC ACCAATCACC CCATTAACCC AAAGGGCCTG 2640  
 GAGTTGATC CCGAGGGTTC CCTGCACCAC CAGCAAAAAC GGGAACTCC AAGCCGCAGC 2700  
 TCTGCTTCCT CGGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGT 2760  
 TGTGAGCTCG GGGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAAGTGCA TTTCCGAGTC 2820  
 TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCCTGCAGTG TGAGGCTGTG 2880  
 40 TACAAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGCG AGCTGCCCA AAAAGAGCGT 2940  
 CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGCGT CCCACTGTGG 3000  
 ATCATCATCC TAGCCATCCT GTTGGGCTC CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060  
 TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCCATGGA AAAAGCTCAG 3120  
 CTCAGCCTC CAGCCACCTC TGATGCTCTGA

Seq ID NO: 4 Protein sequence  
 Protein Accession #: NP\_002196.1

50 1 11 21 31 41 51  
 MGSRTPESEPL HAVQLRWGPR RRPPLPLLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60  
 GFSVEFYRPG TDGVSVLVGA FKANTSQPGV LQGGAVYLCF WGSAPTQCTP IEFDSKGSRL 120  
 LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTXYLST 180  
 55 DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFKTGRV LGGPGSYFWQ GQILSATQEQ 240  
 IAESYYPEYL INLVQGLQRT RQASSIYDDS YLGYSVAVGE FSGDDTDFV AGVPKGNLTY 300  
 GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360  
 EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGET 420  
 QQGVVVFYFG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGRDLGNG YPDLIVGSFG 480  
 60 VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540  
 GFTVELQLDW QKQKGVRRRA LFLASRQATL TQTLTIQNGA REDCREMKIY LRNESEPRDK 600  
 LSPIHIALNF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660  
 GEQNHVYLG D KNALNLT FHA QNVGEGGAYE AELRVTAPE AEYSGLVRHP GNFSSLSCTDY 720  
 FAVNQSRLLV CDLGNPMKAG ASLWGGRLFT VPHLRDTKKT IQFDFQILSK NLNNSQSDVV 780  
 65 SFRLSVEAQA QVTILNGVSKP EAVLEFVSDW HPRDQFPKEE DLGPAVHHVY ELINQGPSSI 840  
 SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLSHH QKREAPSR 900  
 SASSGPQILK CPEABCFRLR CELGPLHQE SSQLHLFRV WAKTFLQREH QPFLQCEAV 960  
 YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFLGL LLLGLLIYIL 1020  
 YKLGFPRSL PYGTAMEKAQ LKPPATSDA

Seq ID NO: 5 DNA sequence  
 Nucleic Acid Accession #: NM\_002211.1  
 Coding sequence: 1..2397

75 1 11 21 31 41 51  
 ATGAATTTAC AACCAATTTT CTGGATTGGA CTGATCAGTT CAGTTTGCTG TGTGTTTGCT 60  
 CAAACAGATG AAAATAGATG TTTAAAAGCA AATGCCAAAT CATGTGGAGA ATGTATACAA 120  
 CGAGGCCCCA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT 180  
 80 TCTGCACGAT GTGATGATT AGAAGCCTTA AAAAAGAAGG GTTGCCCTCC AGATGACATA 240  
 GAAAAATCCA GAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAACCAA CCGTAGCAAA 300  
 GGAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCACA GCAGTTGGTT 360  
 TTGCGATTAA GATCAGGGCA GCCACAGACA TTTACATTAA AATTCAAGAG AGCTGAAGAC 420  
 TATCCCATTTG ACCTCTACTA CCTTATGGAC CTGTCTTACT CAATGAAAGA CGATTGGAG 480  
 AATGTAAGAA GTCTTGAAC AGATCTGATG AATGAAATGA GGAGGATTAC TTCGACTTC 540

5  
10  
15  
20  
25  
30

```

AGAATTGGAT TTGGCTCATT TGTGGAAAAG ACTGTGATGC CTTACATTAG CACAACACCA 600
GCTAAGCTCA GGAACCCCTTG CACAAGTGAA CAGAAGTGCA CCAGCCCATT TAGCTACAAA 660
AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTGG AAAACAGCGC 720
ATATCTGAAA ATTTGGATTTC TCCAGAAGGT GGTTCGATG CCATCATGCA AGTTGCAGTT 780
TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTTC CACAGATGCC 840
GGGTTTCACT TTGCTGGAGA TGGGAACTT GGTGGCATG TTTTACCAA TGATGGACAA 900
TGTCACCTGG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960
CACCTTGTCC AGAAACTGAG TGAAAATAAT ATTCAGACAA TTTTTCAGT TACTGAAGAA 1020
TTTCAGCCTG TTTCAAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
TCTGCAAAAT CTAGCAATGT AATTCACTTG ATCATTGATG CATACAATTC CCTTTCCTCA 1140
GAAGTCATTT TGGAAAACGG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200
TGCAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCAA TATTTCATT 1260
GGAGATGAGG TTCAATTTGA AATTAGCATA ACTTCAAATA AGTGTCCTCAA AAAGGATTCT 1320
GACAGCTTTA AAATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGGTAT TCTTCAGTAC 1380
ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGTG TCATGAAGGA 1440
AATGGGACAT TTGAGTGTGG CCGTGCAGG TGCAATGAAG GCGGTGTGG TAGACATTGT 1500
GAATCAGCAG CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAA 1560
AGTTCAGAAA TCTGAGTAA CAATGGAGAG TCGTCTGCG GACAGTGTGT TTGTAGGAAG 1620
AGGGATAATA CAAATGAAT TTATTCTGGC AAATTCTGCG AGTGTGATAA TTTCAACTGT 1680
GATAGATCCA ATGGCTTAAT TTGTGGAGGA AATGGTGTTC GCAAGTGTCT TGTGTGTGAG 1740
TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTCTCT TGGATACTAG TACTTGTGAA 1800
GCCAGCAACG GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTGGTGT CTGTAAGTGT 1860
ACAGATCCGA AGTTTCAAGG GCAAACGTGT GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
GCTGAGCATA TTGAGTGTGT TCAGTGCAGA GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980
TGCAACACAG AATGTTCCTA TTTTAACATT ACCAAGGTAG AAAGTCGGGA CAAATTACCC 2040
CAGCGGTGCC AACCTGATCC TGTGTCCCAT TGTAAGGAGA AGGATGTTGA CCACTGTTGG 2100
TTCTATTTTA CGTATTCAGT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAAT 2160
CCAGAGTGTG CCACCTGGTC AGACATCAT CCAATTGTAG CTGGTGTGGT TGCTGGAATT 2220
GTTCTTATTG GCCTTGCAAT ACTGCTGATA TGGAAAGCTT TAATGATAAT TCATGACAGA 2280
AGGGAGTTTG CTAATTTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAT 2340
CCTATTATTA AGAGTGCCGT AACAACTGTG GTCAATCCGA AGTATGAGGG AAAATGA

```

Seq ID NO: 6 Protein sequence  
Protein Accession #: NP\_002202.1

35  
40  
45  
50

```

1 11 21 31 41 51
| | | | |
MNLQPIFWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60
SARCDLEAL KKKGCPPDDI ENPRGSKDIK KNKNVNTNRSK GTAELKLPED ITQIQPQLV 120
LRLRSGEPT FTLKFKRAED YPIDLYLMD LSYMKDDLE NVKSLGTDLM NEMRRITSDF 180
RIGFGSFVEK TUMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTKNGE VFNELVGKQR 240
ISGNLDSPEG GFDAIMQVAV CGSLIGWRNV TRLLVFSSTA GFHFAGDGKL GGIVLPNDQO 300
CHLENNMYTM SHYVDYPSIA HLVQKLENN IQTIFAVTEE FQPVYKELKN LIPKSAVGT 360
SANSSNVIQL IIDAYNSLSS EVILENGKLS EGVVISYKSY CKNGVNGTGE NGRKCSNISI 420
GDEVQFEISI TSNKCPKIDS DSKIRPLGF TEEVEVILQY ICECEQSEGE IPESPKCHEG 480
NGTFECGACR KNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCGQCVCVK 540
RDNTNEYISY KFCECDNFNC DRNGLICGG NGVCKCRVCE CNPNYIGSAC DCSLDTSTCE 600
ASNGQICNGR GICEGVCKC TDPKFQGGTC EMCQTCLGVC AEHKECVQCR AFNKGKKKDT 660
CTQECYSFNI TKVESRDKLP QVPQDPVSH CKEKDVEDCW FYFTYSVNGN NEVMVHVVEN 720
PECPTEGPII PIVAGVVAGI VLIGLALLLI WKLLMIHHR REFAPKEKEK MNAKWDVTGEN 780
PIYKSAVTTV VNPKEGK

```

Seq ID NO: 7 DNA sequence  
Nucleic Acid Accession #: NM\_002425  
Coding sequence: 26..1453

55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCAATC CTTGTGCTGT TGTGTCIGCC 60
AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCCAAGCA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTT TTAATAAAT CCAAGGAATG CAGAAGTTC TGGGTTTGG 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT 420
TGAGAAAGCT CTGAAAGTCT GGGAGAGGTT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTGCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCACTTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCTT 660
CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACCTGAAGC 720
TTTGATGTAC CCACCTCTACA ACTCATTCAC AGAGCTCGCC CAGTTCGCCC TTTGCAAGA 780
TGATGTGAAT GGCATTCACT CTCTCTACGG ACCTCCCTCT GCCTCTACTG AGGAACCCCT 840
GGTGCCCAACA AAATCTGTTT CTTGCGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
GTCCTTCCAT GTCATCAGCA CTCGTAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT 960
TTGGCGAAGT TCCCACTGAG ACCCTGAACC TGAATTTTCT TTGATTTCTG CATTTTGGCC 1020
CTCTCTTCCA TCAATTTTGG ATGCTGCATA TGAAGTTAAC AGCAGGGACA CCGTTTTTAT 1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT ACCCTGGGTT TTCCTCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAAG AAGAAAACAT ACTTCTTTCG AGCGGACAAA TACTGGAGAT TTGATGAAA 1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGSATTTTTC TACTTCTTCA GTGGATCATC 1380
ACAGTTTGAAG TTTGAGCCCA ATGCCAGGAT GGTGACACAC ATATTAAGA GTAACAGCTG 1440
GTTACATTGC TAGCGGAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAAATT TTCTTGCATG TTCTGTGACT 1560

```

GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTCTTC 1620  
 ACTTGCTTTT GAATTGCCTT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680  
 ATGTATTTCCT ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740  
 CTT

Seq ID NO: 8 Protein sequence  
 Protein Accession #: NP\_002416

1 11 21 31 41 51  
 | | | | |  
 MHLAFLVLLC LPVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVQKF RPKDSNLIVK 60  
 KIQGMQKFLG LEVTGKGLD TD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTIRIVNYT 120  
 PDLPRDAVDS AIEKALKVWE EVTPLTF SRL YEGEADIMIS FAVKEHGDY SFDGPGHSLA 180  
 HAYPPGPGLY GDIHFDDDEK WTEDASGTNL FLVAAHELGH SLGLFHSANT EALMYPLYNS 240  
 FTFLAQFRLS QDDVNGIQSL YGPPPASTEE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300  
 RGEYLFFKDR YFWRSHWNP BPEFHLISAF WPSLPSYLD AYEVSNSRDV FIFKGNFWSA 360  
 IRGNEVQAGY PRGHTLGFPT PTIRKIDAAV SDKEKKKTYF FAADKYWRFD ENSQSMEQGF 420  
 PRLIADDFPG VEPKVDVAVLQ AFGFFYFFSG SSQFEFDPNA RMVTHILKSN SWLHC

Seq ID NO: 9 DNA sequence  
 Nucleic Acid Accession #: XM\_058189.2  
 Coding sequence: 169..774

1 11 21 31 41 51  
 | | | | |  
 GAAGACCAGC TCAGCTCTTC AGTTGTTGAT CATTGTCTAT TGTTCCTCAA ACAGTAAACC 60  
 AGTATTTTAC ACTGAGATTG TCGGCTGCGG GTATATTCCA ATTCCTCCGTC TCCTCATGAA 120  
 TATGAAGTGA AGGGCTCTGA CCCTGGAAGT GGTCTTAAGC AGGGCAAAAT GGGGTCTCGG 180  
 AAGTGTGGAG GCTGCTAAG TGTGTTGCTG ATTCGCTTG CACTTTGGAG TATAATCGTG 240  
 AACATATTAT TGTATTTCCC GAATGGGCAA ACTTCCTATG CATCCAGCAA TAAACTCACC 300  
 AACTACGTGT GGTATTTTGA AGGAATCTGT TTCTCAGGCA TCATGATGCT TATAGTAACA 360  
 ACAGTTCTTC TGGTACTGGA GAATAATAAC AACTATAAAT GTTGCCAGAG TGAAAACTGC 420  
 AGCAAAAAAT ATGTGACACT GCTGTCAATT ATCTTTTCTT CCCTCGGAAT TGCTTTTCT 480  
 GGATACTGCC TGGTCACTTC TGCCCTGGGT CTGTGCTCAAG GGCCATATTG CCGCACCCCT 540  
 GATGGCTGGG AGTATGCTTT TGAAGGCACT GCTGGACGTT TCCTTACAGA TTCTAGCATA 600  
 TGGATTCAGT GCCTGGAACC TGCACATGTT GTGGAGTGGA ACATCATTTT ATTTTCCATT 660  
 CTCATAACCC TCAGTGGGCT TCAAGTGATC ATCTGCCTCA TCAGAGTAGT CATGCAACTA 720  
 TCCAGATATC TGTGTTGAAG CTATTGATG ATCTTCCAGC CTGGAATCAT TTGAATAAGG 780  
 ACAAAATGTT TTCCATTATC AAGACATGGC CATCTATCTA AATATTATAT CAACGTGTGA 840  
 GACTTGAGGG CAATATTGAA ATGATGGTGC TTTCTGCATT TGGTGTATAT TTGTAAAAA 900  
 TTTGCACTCC TCAGTGCACA TGCAAGTATA CCACCCCTTC ATTTAGTATG TTTTAAAGT 960  
 AATATGCATC AGAAACTTCA GAAATACTTC TGCCCTTTGA TCAACAAAT CCATTCCAA 1020  
 GAATCTGTAC TAGGGAGTA AATAAGATA TGAGAGAAAC CTTTATGCAA ATATGTATAT 1080  
 TGCAACATTA TTTAATATTC TGGAAAATTG GAAACACCCC AAAATTTCTAA ACTCAGAGGA 1140  
 AGGATTAAGT AAAGATGGT ACATACGTGA AATGTTTCTT GATATTAAAA AAAAAATTAA 1200  
 ATAAAAAATA AAGAGTACTA CATGGTTGTA AAA

Seq ID NO: 10 Protein sequence  
 Protein Accession #: XP\_058189.1

1 11 21 31 41 51  
 | | | | |  
 MGSRKCGGCL SCLLIPLALW SIIVNILLYF PNGQTSYASS NKILNYVWYF EGICFSGIMM 60  
 LIVTTVLLVL ENNNNYKCCQ SENCSSKYVT LLSIIFSSLG IAFSGYCLVI SALGLVQGPY 120  
 CRTLDGWEYA FEGTAGRFLT DSSIWIQCLE PAHVVEWNII LFSILITLSG LQVIICLIRV 180  
 VMQLSKILCG SYSVIFQPGI I

Seq ID NO: 11 DNA sequence  
 Nucleic Acid Accession #: NM\_002421.2  
 Coding sequence: 1..1409

1 11 21 31 41 51  
 | | | | |  
 ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC 60  
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120  
 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCACTG 180  
 GTTGAAAAAT TGAAGCAATG GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCCAGT 240  
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT 300  
 GTCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT 360  
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCTCACTC 420  
 TGGAGTAATG TCACACCTCT GACATTCAAC AAGTCTCTG AGGGTCAAGC AGACATCATG 480  
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540  
 CTTGCTCATG CTTTCAACAT AGGCCAGGT ATTGGAGGGG ATGCTCATT TGTGAAGAT 600  
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC 660  
 GGCCATTCTC TTGCACTCTC CCACTTCTACT GATATCGGGG CTTTGTATGTA CCTAGCTAC 720  
 ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780  
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGGCCACAAA CCCCAGAAAGC ATGTGACAGT 840  
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAAG TGATGTTCTT TAAAGACAGA 900  
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCT TTCTGTTTCT 960  
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020  
 CGGTTTTTCA AAGGGAATA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080  
 CCAAGGACA TCTACAGATC CTTTGGCTTC CTTAGAACTG TGAAGCATAT CGATGCTGCT 1140  
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200  
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260

GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTA TTTCTTTCAT 1320  
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380  
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

5

Seq ID NO: 12 Protein sequence  
 Protein Accession #: NP\_002412.1

10 1 11 21 31 41 51  
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60  
 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120  
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180  
 LAHAFOQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSLGLSHST DIGALMYPST 240  
 15 TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300  
 FYMRTNPFYP EVELNFISVF WPQLPNGLEA AYEFAADRDEV RFPKGNKYWA VQGNVNLHGY 360  
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRY DEYKRSMDDPG YPKMIAHDFP 420  
 GIGHKVDVAVF MKDGFYFFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

20

Seq ID NO: 13 DNA sequence  
 Nucleic Acid Accession #: NM\_002421.2  
 Coding sequence: 1..1409

25 1 11 21 31 41 51  
 ATGCACAGTC TTCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTG ACACAGCTTC 60  
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120  
 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCACTG 180  
 GTTGAAAAAT TGAAGCAATC GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCCAGAT 240  
 30 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCCTGATG GGCTCAGTTT 300  
 GTCCCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAAT 360  
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACCTC 420  
 TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480  
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540  
 35 CTGTCTCATG CTTTTCAACC AGGCCCAGGT ATTTGAGGGG ATGCTCATTI TGATGAAGAT 600  
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC 660  
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720  
 ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780  
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCAAAA CCCCAGAAAGC ATGTGACAGT 840  
 40 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900  
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCAT TTCTGTTTTT 960  
 TGGCCCAACG TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020  
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080  
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140  
 45 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200  
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTCTCT 1260  
 GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTA TTTCTTTCAT 1320  
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380  
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

50

Seq ID NO: 14 Protein sequence  
 Protein Accession #: NP\_002412.1

55 1 11 21 31 41 51  
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60  
 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120  
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180  
 60 LAHAFOQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHAL GHSLGLSHST DIGALMYPST 240  
 TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300  
 FYMRTNPFYP EVELNFISVF WPQLPNGLEA AYEFAADRDEV RFPKGNKYWA VQGNVNLHGY 360  
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRY DEYKRSMDDPG YPKMIAHDFP 420  
 GIGHKVDVAVF MKDGFYFFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

65

Seq ID NO: 15 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 141..1580

70 1 11 21 31 41 51  
 TCTGCGTGTG CCGGGGCTAG GGGCTGGAAG TCCTGGCTCT AGTTGCACCT CGGAAGGAAA 60  
 AGGCACAAAG AGGAGGGGAG GCGTCTTAGG ACTGCCTGGA TCCAGAGCAC TTTCTCGGC 120  
 75 CTCTACAGGC CTGTGTGCGT ATGGGTTCCC CCGCGGCCCC GGAGGGAGCG CTGGGCTACG 180  
 TCCGCGAGTT CACTCGCCAC TCCTCCGACG TGCTGGGCAA CCTCAACGAG CTGCGCCTGC 240  
 GCGGGATCCT CACTGACGTC ACGCTGCTGG TTGGCGGGCA ACCCTCAGA GCACACAAGG 300  
 CAGTTCTCAT CGCCTGCGAT GGCTTCTTCT ATTCAATTTT CCGGGGCCGT GCGGGAGTCG 360  
 GGGTGGACGT GCTCTCTCTG CCCGGGGGTC CCGAAGCGAG AGGCTTCGCC CCTCTATTGG 420  
 80 ACTTCATGTA CACTTCGCGC CTGCGCCTCT CTCAGCCAC TGCACACGCA GTCCTAGCGG 480  
 CCGCCACCTA TTTGCAGATG GAGCACGTGG TCCAGGCATG CCACCGCTTC ATCCAGGCCA 540  
 GCTATGAACC TCTGGGCATC TCCCTGCGCC CCCTGGAAGC AGAACCCCCA ACACCCCAA 600  
 CGGCCCTCC ACCAGCTGAT CCGAAGGACA CCCAGACCCA CCTACTGAAT 660  
 CTCGAAGCTG CAGTCAAGGC CCCCCAGTC CAGCCAGCCC TGACCCCAAG GCCTGCAACT 720  
 GGAAGAGTA CAAGTACATC GTGCTAAACT CTCAGGCCTC CCAAGCAGGG AGCCTGGTCG 780



5	GGGAGAGAAG TTCTGGTCAA CCTTGCCCCC AAGCCAGGCT CCCCAGTGGG GACGAGGCCT 840
	CCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GTGAAGAAGG ACCCATTCCT GGTCCCCAGA 900
	GCAGGCTCTC TCCAACTGCT GCCACTGTGC AGTTCAAATG TGGGGCTCCA GCCAGTACCC 960
	CCTACCTCCT CACATCCCAG GCTCAAGACA CCTCTGGATC ACCCTCTGAA CGGGCTCGTC 1020
	CACTACCGGG AAGTGAATTT TTCAGCTGCC AGAACTGTGA GGCTGTGGCA GGGTGTCTAT 1080
	CGGGGCTGGA CTCTTGGTTC CTTGGGGACG AAGACAAACC CTATAAGTGT CAGCTGTGCC 1140
	GGTCTTCGTT CCGCTACAAG GGCAACCTTG CCAGTCATCG TACAGTGCAC ACAGGGGAAA 1200
	AGCCTTACCA CTGCTCAATC TGCAGGAGCC GTTTTAACCG GCCAGCAAAC CTGAAAACGC 1260
10	ACAGCCGCAT CCATTGCGGA GAGAAGCCGT ATAAGTGTGA GACGTGCGGC TCGCGCTTTG 1320
	TACAGGTGGC ACATCTGCGG GCGCACGTGC TGATCCACAC CGGGGAGAAG CCCTACCCCT 1380
	GCCCTACCTG CGGAACCCGC TTCCGCCACC TGCAGACCCT CAAGAGCCAC GTTCGCATCC 1440
	ACACCGGAGA GAAGCCTTAC CACTGCGACC CCTGTGSCCT GCATTTCGG CACAAGAGTC 1500
	AACTGCGGCT GCATCTGCGC CAGAAACACG GAGCTGCTAC CAACACCAA GTGCACTACC 1560
15	ACATTCTCGG GGGGCCCTAG CTGAGCGCAG GCCCAGGCCC CACTTGCTTC CTGCGGGTGG 1620
	GAAAGCTGCA GGGCCAGGCC TTGCTTCCCT ATCAGGCTTG GGCATAGGGG TGTGCCAGGC 1680
	CACCTTGGTA TCAGAAATTT CCACCCTCTT AATTTCTCAC TGGGGAGAGC AGGGGTGGCA 1740
	GATCCTGGCT AGATCTGCTT CTGTTTGTCT GGTCAAACCC TCTTCCCCAC AAGCCAGATT 1800
	GTCTCTGAGG AGAGAGCTAG CTAGGGGCTG GGAAGGSGGA GAGATTGGAG TCCTGGTCTC 1860
20	CCTAAGGGAA TAGCCCTCCA CCTGTGGCCC CCATTGCATT CAGTTTATCT GTAAATATAA 1920
	TTTATTGAGG CCTTTGGGTG GCACCGGGGC CTTCATTGCA TTGCATTTC CACTCCCCCT 1980
	TTCCACAAGT GCGATTAAAA GTGACCAGAA ACACAGAAGG TGAGATCACA GCTCTGTGG 2040
	CAGAGATTAC TAGCCCTTGG CTCTCTCGTT TGGCTTGGGT ATTTTATATT ATTTCTGTCA 2100
	TAACCTTTAT CTTTAGAATT GTTCTTTCTC CTGTTTGTCT GCTTGTAGT TGTGTTAAAA 2160
25	TGGAATAAGG GGTCTCTGTG GTTCTGCCCC TGTAATCTA GGTCTGGAAC CTTTATTTGT 2220
	TCTAGGGCAG CTCTGGGAAC ATGCGGGATT GTGGAATTGG GTGAGGAACC CTCTCTGGTA 2280
	TTCTGGATGT TGTAGGTTCT CTAGCAGTCT AGAAATGGAT ACAGACATTT CTCTGTCTCT 2340
	CAAGGGTGAT AGGAACCATT ATGTTGAGCC CAAAATGGAA GTAATAATAA ATGCCCTCTG 2400
	GAGGCTGTGG GTGTGGGGGA TTCTGTATCT GGATTCCGTA TCACTCCAAC TGTGAGGCTGT 2460
30	GGGTGTGGG GATTCTGTAT CTGGATTCCG TATCACTCCA AGTGAGGCTT GGCAGGTTTT 2520
	TCTGCAAGAT GGTCCAGAAT CTAAATGTC CCATTAATCT GGTCACTTGG GTTTGGCTCT 2580
	GCTGTATCCA TCTATAGTGG TAGAGACCCA CCAGGGCTCA AGTGGAGTCC ATCATCCTCC 2640
	CACGGGGGCC TGTTCTTAGC ACTGAGTTGA TCGCTCCATG GGGGAGAGAT CAGACATTCC 2700
	TTATCAGAGA TGATGTGACC TTTTCTGACT CTGCCCAGTC TCTATGAATG TTATGGCCTA 2760
35	GGGAAGAATC ATGAACCTCT TTAGCTTGAT TAGATGTTAA ACAGTGTAA CCCATCCTTT 2820
	ACTACAGAGG CATATGGGTT TGAATGTTAC CTGGGGTTCT CTCTATTGAG TTGAGCCCTT 2880
	TCTTCTTTTA GTGGGTTTTG GACATCTTCT GGCAAGTGTC CAGATGCCAG AACCTTCTTT 2940
	TCCTCTAGAA GGGATGGTGC TTGGTAACCT TACCTTTTAA AAGCTGGGTC TGTGACCTGG 3000
	TCTTCCCATC CTGTCAATTC TGTCTGGAAC CAGTGAATGC ATTAGAACCT TCCATAGGAA 3060
40	AAGAAAAGGG GCTGAGTTCC ATTCTGGGTT TGCTGTAGTT TGGTTGGGAT TATTGTTGGC 3120
	ATTACAGATG TAAAAGATTG ACTAGCCCAT AGGCCAAAGG CCTGTTCTAG TTGACCAAGT 3180
	TTCAAGTAGG ATTAAGAGGT TGGTTGAGGG GTGCAGTTTC TGGTGTAGGC CAGGTAGGTA 3240
	GAAAGTGAGG AACAGGGTTG CCTCTTGGCT GGGTGGAGTC TCTGAAATGT TAGAAGAAGC 3300
	GCTGAAGCCT TGATTGATAG TTCTGCCCTT TGTGCCCCTG GGGCTTATCT GATTATGGGA 3360
45	CGAGGGTAGA AAGTAAGAAG CACTTTTGAA TTTGTGGGGT AGAAGTTCAA CAATAAGTCA 3420
	GTTCTAGTGG CTGTGCGCTG GGGACTAGTG AGAAAGCTAC TCTTCTCCCT CTTCCTCTCT 3480
	TCTCCCCATG GCCCCACTGC AGAATTAAAG AAGGAAGAAG GGAAGGCGGA GGAGTCTATA 3540
	AGAAGGAATC ATGATTCTTA TTTAGCAGAT TGGATGGGCA GGTGGAGAAT GCCTGGGGGT 3600
50	AGAAATGTTA GATCTTGCAA CATCAGATCC TTGGAATAAA GAAGCCCTCT TGYGCWRAAA 3660
	AAAAAAAAA AAAAAA

Seq ID NO: 16 Protein sequence  
Protein Accession #: FGENESH predicted

55	1 11 21 31 41 51
	MGSPAPEGA LGYVREFTRH SSDVLGNLNE LRLRGILTDV TLLVGGQPLR AHKAVLIACS 60
	GFFYSIFRGR AGVGVDFVLSL PGGPEARFPA PLDFMYTSR LRLSPATAPA VLAAATYLMQ 120
	EHVQACHRF IQASYEPLGI SLRPLEAEPF TPPTAPPPGS PRRSEGHDPD PTESRSCSQG 180
60	PPSPASPPDK ACNWKYKYI VLNSQASQAG SLVGERSSGQ PCPQARLPSG DEASSSSSSS 240
	SSSSEEGPIP GPQSRSLPFA ATVQFKCGAP ASTPYLLTSQ AQDTSGPSSE RARPLPGSEF 300
	FSCQNCEAVA GCSSGLDSLIV PGDEDKPYKC QLCRSSFRYK GNLAHRTVH TGEKPYHCSI 360
	CGARENRPAN LKTHSRIHSG EKPYPKCTCG SRFVQVAHLR AHVLIHTGEK PYPCTCGTR 420
	FRHLQTLKSH VRIHTGEKPY HCDPCGLHFR HKSQRLRLHLR QKHGAATNTK VHYHILGGP

65 Seq ID NO: 17 DNA sequence  
Nucleic Acid Accession #: XM\_039209  
Coding sequence: 1..2049

70	1 11 21 31 41 51
	ATGCTGAAGA TGCTCTCCTT TAAGTGCTG CTGCTGGCCG TGGCTCTGGG CTTCTTTGAA 60
	GGAGATGCTA AGTTTGGGGA AAGAAACGAA GGGAGCGGAG CAAGGAGGAG AAGGTGCCTG 120
	AATGGGAACC CCCCAGAGCG CCTGAAAAGG AGAGACAGGA GGATGATGTC CCAGCTGGAG 180
75	CTGCTGAGTG GGGAGAGAGT GCTGTGCGGT GGCCTCTACC CTCGGCTGTC CTGCTGCGCTG 240
	CGGAGTGACA GCGCGGGGCT AGGGCGCCTG GAGAATAAGA TATTTTCTGT TACCAACAAC 300
	ACAGAATGTG GGAAGTTACT GGAGGAAATC AAATGTGCAC TTTGCTCTCC ACATTCTCAA 360
	AGCCTGTTCC ACTCACCTGA GAGAGAAGTC TTGGAAAGAG ACCTAGTACT TCCTCTGCTC 420
	TGCAAGACT ATTGCAAGA ATTCTTTTAC ACTTGCCGAG GCCATATTCC AGGTTTCTCT 480
80	CAAAACAACG CGGATGAGTT TTGCTTTTAC TATGCAAGAA AAGATGGTGG GTTGTGCTTT 540
	CCAGATTTTC CAAGAAAACA AGTCAGAGGA CCAGCATCTA ACTACTTGGA CCAGATGGAA 600
	GAATATGACA AAGTGGAAAG GATCAGCAGA AAGCACAAC ACAACTGCTT CTGTATTTCAG 660
	GAGGTGTGGA GTGGGCTGCG GCAGCCCGTT GGTGCCCTGC ATAGTGGGGA TGGCTCGCAA 720
	CGTCTCTTCA TTCTGAAAAA AGAAGGTTAT GTGAAGATAC TTACCCCTGA AGGAGAAAT 780
	TTCAAGGAGC CTTATTGGA CATTACAAA CTTGTTCAAA GTGGAATAAA GGGAGGAGAT 840

5  
10  
15  
20

```

GAAAGAGGAC TGCTAAGCCT CGCATTCAT CCAATTACA AGAAAAATGG AAAGTTGTAT 900
GTGTCTTATA CCACCAACCA AGAACGGTGG GCTATCGGGC CTCATGACCA CATTCTTAGG 960
GTTGTGGAAT ACACAGTATC CAGAAAAAAT CCACACCAAG TTGATTGAG AACAGCCAGA 1020
GTCTTTCTTG AAGTTGCAGA ACTCCACAGA AAGCATCTGG GAGGACAACT GCTCTTTGGC 1080
CCTGACGGCT TTTTGTACAT CATTCTTGGT GATGGGATGA TTACACTGGA TGATATGGAA 1140
GAAATGGATG GGTTAAGTGA TTTACAGGC TCAGTGCTAC GGCTGGATGT GGACACAGAC 1200
ATGTGTAACG TGCCTTATTC CATACCAAGG AGCAACCCAC ACTTCAACAG CACCAACCAG 1260
CCCCCGAAG TGTTCCTCA TGGGCTCCAC GATCCAGGCA GATGTGCTGT GGATAGACAT 1320
CCCACTGATA TAAACATCAA TTTAACGATA CTGTGTTTCA ACTCCAATGG AAAAAACAGA 1380
TCATCAGCCA GAATTTCTACA GATAATAAAG GGGAAAGATT ATGAAAGTGA GCCATCACTT 1440
TTAGAATTCA AGCCATTTCAG TAATGGTCCT TTGGTTGGTG GATTTGTATA CCGGGGCTGC 1500
CAGTCAGAAA GATTGTATGG AAGCTACGTG TTTGGAGATC GTAATGGGAA TTTCTTAAT 1560
CTCCAGCAAA GTCCCTGTGAC AAAGCAGTGG CAAGAAAAAC CACTCTGTCT CGGCACTAGT 1620
GGGTCTCTGA GAGGCTACTT TTCCGGTCAC ATCTTGGGAT TTGGAGAAAG TGAAC TAGGT 1680
GAAGTTTACA TTTTATCAAG CAGTAAAGT ATGACCCAGA CTCACAATGG AAAACTCTAC 1740
AAAATTGTAG ATCCCAAAAG ACCTTTAATG CCTGAGGAAT GCAGAGCCAC GGTACAACCT 1800
GCACAGACAC TGACTTCAGA GTGCTCCAGG CTCTGTGCGAA ACGGCTACTG CACCCCAACG 1860
GGAAAGTGCT GTGCGAGTCC AGGCTGGGAG GGGGACTTCT GCAGAACTGC AAAATGTGAG 1920
CCAGCATGTC GTCATGGAGG TGTCTGTGTT AGACCGAACA AGTGCCTCTG TAAAAAGGA 1980
TATCTTGGTC CTCAATGTGA ACAAGTGGAC AGAAACATCC GCAGAGTGAC CAGGGCAGAC 2040
ATCACCTAG

```

25 Seq ID NO: 18 Protein sequence  
Protein Accession #: XP\_039209

30  
35  
40

```

1 11 21 31 41 51
| | | | |
MLKMLSFKLL LLAVALGFFE GDAKFGERNE GSGARRRRCL NGNPPKRLKR RDRRMSQLE 60
LLSGGEMLCG GFYPRLSCLL RSDSPGLGRL ENKIFSVTNN TECGKLEEI KCALCSPHSQ 120
SLFHSPEREV LERDLVLPLL CKDYCKEFFY TCRGHIPGFL QTTADEFCFY YARKDGLCF 180
PDFPRKQVRG PASNYLDQME EYDKVEISR KHKHNCFCIQ EVVSGLRQPV GALHSGDGSQ 240
RLFILEKEGY VKILTPEGEI FKEPYLDIHK LVQSGIKGGD ERLLSLAFH PNYKKNKLY 300
VSYTTNQERW AIGPHDHILR VVEYTVSRKN PHQVDLRTAR VFLEVAELHR KHLGGQLLFG 360
PDGFLYIILG DGMITLDDME EMDGLSDFTG SVLRLDVDTD MCNVFYSIPR SNPHFNSTNQ 420
PPEVFAHGLH DPGRCVDRH PTDININLTI LCSDSNGKNR SSARILQIIK GKDYSEPSL 480
LEFKPFSNGP LVGGFVYRGC QSERLYGSYV FGDRNGNFLT LQQSPVTKQW QEKPLCLGTS 540
GSCRGYFSGH ILGFGEDELG EYVILSSSKS MTQTHNGKLY KIVDPKRPLM PEECRATVQP 600
AQTLTSECSR LCRNGYCTPT GKCCSPGWE GDFCRTAKCE PACRHGGVCV RPNKCLCKKG 660
YLGQPCEQVD RNIRRVTRAD IT

```

45 Seq ID NO: 19 DNA sequence  
Nucleic Acid Accession #: NM\_014331.2  
Coding sequence: 1..1506

50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
ATGGTCAGAA AGCCTGTGTG GTCCACCATC TCCAAAGGAG GTTACCTGCA GGGAAATGTT 60
AACGGGAGGC TGCCTTCCTT GGGCAACAAG GAGCCACCTG GGCAGGAGAA AGTGCAGCTG 120
AAGAGGAAAG TCACCTTTAT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTTGGAGCA 180
GGAATCTTCA TCTCTCCTAA GGGCGTGCTC CAGAACACGG GCAGCGTGGG CATGTCTCTG 240
ACCATCTGGA CGGTGTGTGG GGTCTGTGCA CTATTTGGAG CTTTGTCTTA TGCTGAATTG 300
GGAACAACATA TAAAGAAATC TGGAGGTGAT TACACATATA TTTTGGAAAT CTTTGTGTTCA 360
TTACCACTGA TTGTACAGAT CTGGGTGGAA CTCCTCATAA TACGCCCTGC AGCTACTGCT 420
GTGATATCCC TGGCATTTGG ACGCTACATT CTGGAACCAT TTTTATTACA ATGTGAAATC 480
CCTGAACCTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTGAT GGTCTCTAAT 540
AGCATGAGTG TACAGCTGAG CGCCCGGATC CAGATTTTCT TAACCTTTTG CAAGCTCACA 600
GCAATTTCTGA TAATTATAGT CCCTGGAGTT ATGCAGCTAA TTAAGGTGCA AACGCAGAAC 660
TTTAAAGACG CGTTTTCAGG AAGAGATTCA AGTATTACGC GGTGCGCACT GGCTTTTAT 720
TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTACTGTA AGAAGTAGAA 780
AACCTGAAA AAACCATTC CTTGCAATA TGTATATCCA TGGCCATTGT CACCATTGGC 840
TATGTGCTGA CAAATGTGGC CTACTTTACG ACCATTAATG CTGAGGAGCT GCTGCTTTCA 900
AATGCAGTGG CAGTGACCTT TTCTGAGCGG CTACTGGGAA ATTTCTCATT AGCAGTTCCG 960
ATCTTTGTTG CCTCTCCTG CTTTGGCTCC ATGAACGGTG GTGTGTTTGC TGTCTCCAGG 1020
TTATTTCTATG TTGCGTCTCG AGAGGGTCAC CTTCCAGAAA TCCTCTCCAT GATTCTATGTC 1080
CGCAAGCACA CTCCTCTACC AGCTGTTATT GTTTTGCAAC CTTTGACAAT GATAATGCTC 1140
TTCTCTGGAG ACCTCGACAG TCTTTTGAAT TTCTCTAGTT TTGCCAGGTG GCTTTTATTT 1200
GGGCTGGCAG TTGCTGGGCT GATTATCTT CGATACAAAT GCCCAGATAT GCATCGTCTT 1260
TTCAAGGTGC CACTGTTTCA CCCAGCTTTG TTTTCCTTCA CATGCCCTCT CATGGTTGCC 1320
CTTTCCCTCT ATTCGGACCC ATTTAGTACA GGGATTGGCT TCGTCATCAC TCTGACTGGA 1380
GTCCCTGGCT ATTAATCTCT TATTATATGG GACAAGAAAC CCAGGTGGTT TAGAATAATG 1440
TCAGAGAAA TAACCAGAAC ATTACAAATA ATACTGGAAG TTGTACCAGA AGAAGATAAG 1500
TTATGAACATA ATGGACTTGA GATCTTGGCA ATCTGCCCAA GGGGAGACAC AAAATAGGGA 1560
TTTTTACTTC ATTTTCTGAA AGTCTAGAGA ATTACAACCT TGGTGATAAA CAAAAGGAGT 1620
CAGTTATTTT TATTCATATA TTTTAGCATA TTCGAACATA TTTCTAAGAA ATTTAGTTAT 1680
AACTCTATGT AGTTATAGAA AGTGAATATG CAGTTATTCT ATGAGTCGCA CAATCTCTGA 1740
GTCTCTGATA CCTACCTATT GGGGTAGGA GAAAAGACTA GACAATTACT ATGTGGTCAT 1800
TCTCTACAAA ATATGTTAGC ACGGCAAGAA ACCTTCAAAAT TGAAGACTGA GATTTTCTG 1860
TATATATGGG TTTTATGAAAG ATGGTTTAC ACACTACAGA TGTCTATACT GTGAAAAGTG 1920
TTTTCAATTC TGAAGAAAAG CATACATCAT GATTATGGCA AAGAGGAGAG AAAGAAATTT 1980
ATTTTACATT GACATTGCAT TGCTTCCCCT TAGATACCAA TTTAGATAAC AAACACTCAT 2040
GCTTTAATGG ATTAATACCA GAGCACTTTG AACAAAGGTC AGTGGGGATT GTTGAATACA 2100
TTAAAGAAAG GTTTCTAGGG GCTACTGTTT ATGAGACACA TCCAGGAGTT ATGTTTAAAT 2160
AAAAATCCTT GAGAAATTTAT TATGTCAGAT GTTTTTTCAT TCATTATCAG GAAGTTTATG 2220

```

5  
 10  
 15

```

TTATCTGTCA TTTTCTTTT TCACATCAGT TTGATCAGGA AAGTGTATAA CACATCTTAG 2280
AGCAAGAGTT AGTTTGGTAT TAAATCCTCA TTAGAACAAC CACCTGTTTC ACTAATAACT 2340
TACCCCTGAT GAGTCTATCT AAACATATGC ATTTTAAGCC TTCAAATTAC ATTATCAACA 2400
TGAGAGAAAT AACCAACAAA GAAGATGTTC AAAATAATAG TCCCATATCT GTAATCATAT 2460
CTACATGCAA TGTAGTAAT TCTGAAGTTT TTTAAATTAT TGGCTATTTT TACACGATGA 2520
TGAATTTTGA CAGTTTGTGC ATTTTCTTTA TACATTTTAT ATTCTTCTGT TAAATATCT 2580
CTTCAGATGA AACTGTCCAG ATTAATTAGG AAAAGGCATA TATTAACATA AAAATTGCAA 2640
AAGAAATGTC GCTGTAAATA AGATTACAA CTGATGTTTC TAGAAAATT CCACCTCTAT 2700
ATCTAGGCTT TGTCACTAAT TTCCACACCT TAATTATCAT TCAACTTGCA AAAGAGACAA 2760
CTGATAAGAA GAAAATTGAA ATGAGAATCT GTGGATAAGT GTTTGTGTTC AGAAGATGTT 2820
GTTTTGCCAG TATTAGAAAA TACTGTGAGC CGGGCATGGT GGCTTACATC TGTAATCCCA 2880
GCACCTTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTCGG GAGTTCTAGA CCAGCCTGAC 2940
CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCACAT 3000
GCTGGTAATC TCAGCTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGGAGGCG 3060
GAGGTTGACG TGAGCCAAGA TTGCACCACT GTACTCCAGC CTGGGTGACA AAGTCAGACT 3120
CCATCTCCAA AAAAAA AAAA
  
```

Seq ID NO: 20 Protein sequence  
 Protein Accession #: NP\_055146.1

20  
 25  
 30

```

1      11      21      31      41      51
|      |      |      |      |      |
MVRKPVVSTI SKGGYLQGNV NGRPLSLGNK EPPGQEKVQL KRKVTLRGRV SIIIGTIIGA 60
GIFISPKGVL QNTGVSVMGL TIWTVCGVLS LFGALSYAEL GTTIKSGGH YTYILEVFGP 120
LPAFVRVWVE LLIIIRPAATA VISLAFGRYI LEFFFIQCEI PELAIKLITA VGITVVMVLN 180
SMSVSWASRI QIFLTFCKLT AILIIIVPGV MQLIKGTQON FKDAFSGRDS SITRLPLAFY 240
YGMAYAYAGWF YLNFVTEEEV NPEKTIPLAI CISMATITGV YVLTNVAYFT TINAEELLS 300
NAVAVTFSSR LIGNSLFAPV IFVALSCFSG MNGGVFAVSR LFYVASREGH LPEILSMIHV 360
RKHTPLPAVI VLHPLTIMML FSGDLDSLNL FLSFARWLFV GLAVAGLIYL RYKCPDMHRP 420
FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM 480
SEKITRTLQI ILEVVPEDDK L
  
```

Seq ID NO: 21 DNA sequence  
 Nucleic Acid Accession #: NM\_002422.2  
 Coding sequence: 64..1497

35  
 40  
 45  
 50  
 55  
 60  
 65  
 70

```

1      11      21      31      41      51
|      |      |      |      |      |
ACAAGGAGGC AGGCAAGACA GCAAGGCATA GAGACAACAT AGAGCTAAGT AAAGCCAGTG 60
GAAATGAAGA GTCTTCCAAT CCTACTGTTG CTGTGCGTGG CAGTTTGCTC AGCCTATCCA 120
TTGGATGGAG CTGCAAGGGG TGAGGACACC AGCATGAACC TTGTTCAAGT ATATCTAGAA 180
AACTACTACG ACCTCAAAAA AGATGTGAAA CAGTTTGTTA GGAGAAAGGA CAGTGGTCCT 240
GTTGTTAAAA AAATCCGAGA AATGCAGAAG TTCTTGGAT TGGAGGTGAC GGGGAAGCTG 300
GACTCCGACA CTCTGGAGGT GATGCGCAAG CCCAGGTGTG GAGTTCTCTG TGTGCTCAC 360
TTCAGAACCT TTCTTGGCAT CCCGAAGTGG AGGAAAACCC ACCTTACATA CAGGATTGTG 420
AATTATACAC CAGATTGGCC AAAAGATGCT GTTGATTCTG CTGTTGAGAA AGCTCTGAAA 480
GTCTGGGAAG AGGTGACTCC ACTCACATTC TCCAGGCTGT ATGAAGGAGA GGCTGATATA 540
ATGATCTCTT TTGCAGTTAG AGAACATGGA GACTTTTACC CTTTGTATGG ACCTGGAAAT 600
GTTTGGGCC ATGCTATGAC CCCTGGGCCA GGGATTAATG GAGATGCCCA CTTTGTATGAT 660
GATGAACAAT GGACAAAGGA TACAACAGGG ACCAATTAT TTTCTGTTGC TGCTCATGAA 720
ATTGGCCACT CCCTGGGTCT CTTTCACTCA GCCAACACTG AAGCTTTGAT GTACCCACTC 780
TATCACTCAC TCACAGACCT GACTCGGTTT CGCTGTCTC AAGATGATAT AAATGGCATT 840
CAGTCCCTCT ATGACCTTCC CCCTGACTCC CCTGAGACCC CCTGGTACC CACGGAACCT 900
GTCCTCCAG AACCTGGGAC GCCAGCCAAC TGTGATCTCT CTTTGTCTTT TGATGCTGTC 960
AGCACTCTGA GGGGAGAAAT CCTGATCTTT AAAGACAGGC ACTTTTGGCG CAAATCCCTC 1020
AGGAAGCTTG AACCTGAATT GCATTGTATC TCTTCATTTT GGCCATCTCT TCCTTCAGGC 1080
GTTGATGCGG CATATGAAGT TACTAGCAAG GACCTCGTTT TCATTTTAA AGGAAATCAA 1140
TTCTGGGCCA TCAGAGGAAA TGAGGTACGA GCTGGATACC CAAGAGGCAT CCACACCCTA 1200
GGTTTCCCTC CAACCGTGAG GAAAATCGAT GCAGCCATTT CTGATAAGGA AAAGAACAAA 1260
ACATATTCTT TTGTAGAGGA CAAATACTGG AGATTGTATG AGAAGAGAAA TTCCATGGAG 1320
CCAGGCTTTC CCAAGCAAAT AGCTGAAGAC TTTCCAGGGA TTGACTCAA GATTGATGCT 1380
GTTTTTGAAG AATTGGGTT CTTTATTTC TTTACTGGAT CTTACAGTT GGAGTTTGAC 1440
CCAAATGCAA AGAAAGTGAC ACACACTTTG AAGAGTAACA GCTGGCTTAA TTGTTGAAAG 1500
AGATATGTAG AAGGCACAAT ATGGGCACCT TAAATGAAGC TAATAATTCT TCACCTAAGT 1560
CTCTGTGAAT TGAATGTCT GTTTTCTCCT GCCTGTGCTG TGACTCGAGT CACACTCAAG 1620
GGAACCTGAG CGTGAATCTG TATCTTGCCG GTCATTTTAA TGTATTACA GGGCATTCAA 1680
ATGGGCTGCT GCTTAGCTTG CACCTTGTC CATAGAGTGA TCTTTCCCAA GAGAAGGGGA 1740
AGCACTCGTG TGCAACAGAC AAGTGACTGT ATCTGTGTAG ACTATTGTCT TATTTAATAA 1800
AGACGATTG TCAGTTGTTT T
  
```

Seq ID NO: 22 Protein sequence  
 Protein Accession #: NP\_002413

75  
 80

```

1      11      21      31      41      51
|      |      |      |      |      |
MKSLPILLLL CVAVCSAYPL DGAARGEDTS MNLVQKYLEN YYDLEKDVQK FVRRKDSGPV 60
VKKIREMQKF LGLEVTGKLD SDTLEVMRKP RCGVPDVGHF RTFPGIPKWR KTHLTYRIVN 120
YTPDLKDAV DSAVEKALKV WEEVTPLTFS RLYEGEADIM ISFAVREHGD FYPPDGPNGV 180
LAHAYAPGPG INGDAHFDDE EQWTKDITGT NLFLVAAHEI GHSLGLFHSA NTEALMYPLY 240
HSLTDLTRFR LSQDDINGIQ SLYGPPDPSP ETPLVPTEPV PPEPGTPANC DPALSFDVA 300
TLRGEILIFK DRHFWRKSLR KLEPELHLIS SFWPSLPSPV DAAYEVTSKD LVFIFKGNQF 360
WAIRGNVEVRA GYPRGIHTLG FPPTVRKIDA AISDKEKNKT YFFVEDKYWR FDEKRNMEP 420
GFFPKIAEDF PGIDSKIDAV FEEFGFFYFF TGSSQLEFDP NAKKVIHTLK SNSWLNC
  
```

Seq ID NO: 23 DNA sequence  
Nucleic Acid Accession #: NM\_006528  
Coding sequence: 57..764

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
GCCGCCAGCG GCTTTCTCGG ACGCCTTGCC CAGCGGGCCG CCCGACCCCC TGCACCATGG 60
ACCCCGCTCG CCCCTTGGGG CTGTCGATTC TGCTGCTTTT CCTGACGGAG GCTGCACTGG 120
GCGATGCTGC TCAGGAGCCA ACAGGAAATA ACGCGGAGAT CTGTCTCCTG CCCCTAGACT 180
ACGGACCCCTG CCGGGCCCTA CTTCTCCGTT ACTACTACGA CAGGTACACG CAGAGCTGCC 240
GCCAGTTCTT GTACGGGGGGC TGCAGGGGCA ACGCCAACAA TTTCTACACC TGGGAGGCTT 300
GCGACGATGC TTGCTGGAGG ATAGAAAAAG TTCCCAAAGT TTGCCGGCTG CAAGTGAGTG 360
TGGACGACCA GTGTGAGGGG TCCACAGAAA AGTATTTCTT TAATCTAAGT TCCATGACAT 420
GTGAAAAATT CTTTCCGGT GGGTGTCAAC GGAACCGGAT TGAGAACAGG TTTCCAGATG 480
AAGCTACTTG TATGGGCTTC TGCGCACCAG AGAAAATTCC ATCATTTTGC TACAGTCCAA 540
AAGATGAGGG ACTGTGCTCT GCCAATGTGA CTCGCTATTA TTTTAATCCA AGATACAGAA 600
CCTGTGATGC TTTACCTTAT ACTGGCTGTG GAGGGAATGA CAATAACTTT GTTAGCAGGG 660
AGGATTGCAA ACGTGCATGT GCAAAAGCTT TGAAAAAGAA AAAGAAGATG CCAAGCTTTC 720
GCTTTGCCAG TAGAATCCGG AAAATTCGGA AGAAGCAATT TTAACATTC TTAATATGTC 780
ATCTTGTTTG TCTTTATGGC TTATTGCTCT TTATGGTTGT ATCTGAAGAA TAATATGACA 840
GCATGAGGAA ACAATCATTT GGTGATTAT TACACAGTTT TTATTAATAC AAGTCACTTT 900
TTCAAAAAAT TGGATTTTTT TATATATAAC TAGCTGCTAT TCAATGTGA GTCTACCATT 960
TTTAATTAT GGTCAACTG TTTGTGAGAC GAATTCCTGC AATGCATAAG ATATAAAGC 1020
AAATATGACT CACTCATTTT TTGGGGTCGT ATTCCTGATT TCAGAAGAGG ATCATAACTG 1080
AAACAACATA AGACAATATA ATCATGTGCT TTAACATAT TTGAGAATAA AAAGGACTAG 1140
CC

```

Seq ID NO: 24 Protein sequence  
Protein Accession #: NP\_006519

35  
40  
45  
50  
55  
60  
65  
70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
MDPARPLGLS ILLFLTEAA LGDAAQEPTG NNAEICLLPL DYGPCRALLL RYYDYRYTQS 60
CRQFLYGGCE GNANNFYWE ACDDACWRIE KVPKVCRLQV SVDDQCEGST EKYFFNLSSM 120
TCEKFFSGGC HRNRIENRFP DEATCMGFCA PKKIPSFYCS PKDEGLCSAN VTRYFNFPRY 180
RTCDAFYTYG CCGNDNNFVS REDCKRCAK ALKKKKMKPK LRFASRIRKI RKKQF

```

Seq ID NO: 25 DNA sequence  
Nucleic Acid Accession #: NM\_005458.1  
Coding sequence: 1..2825

45  
50  
55  
60  
65  
70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGCTTCCC CGCGGAGGTC CGGGCAGCCA GGGCGGCGCG CGCCGCGGCC ACCGCGCGCC 60
GCGCGCTGCG TACTGCTACT GCTGCTGCCG CTGCTGCTGC CTCTGGCGCC CGGGGCTTGG 120
GGCTGGGCGC GGGGCGCCCC CCGGCGCGCG CCCAGCAGCC GCGCGCTCTC CATCATGGGC 180
CTCATGCCCG TCACCAAGGA GGTGGCCAAG GGCAGCATCG GGCAGCGGTG GCTCCCCGCC 240
GTGGAACTGG CCATCGAGCA GATCCGCAAC GAGTCACTCC TGCGCCCCTA CTTCCTCGAC 300
CTGCGGCTCT ATGACACGGA GTGCGACAAC GCAAAAGGGT TGAAGCCCTT CTACGATGCA 360
ATAAAATACG GGCCGAACCA CTGTATGGTG TTTGGAGGCG TCTGTCCATC CGTCACATCC 420
ATCATGCGAG AGTCCTCCA AGGCTGGAAT CTGGTGCAGC TTTCTTTTGC TGCAACCACG 480
CCTGTCTTAG CCGATAAGAA AAAATACCCT TATTTCTTTC GGACCGTCCC ATCAGACAAT 540
GGCGTGAATC CAGCCATTCT GAAGTTGCTC AAGCACTACC AGTGGGAGCG CGTGGGCACG 600
CTGACGCAAG ACGTTCAGAG GTTCTCTGAG GTGCGGAATG ACCTGACTGG AGTTCTGTAT 660
GGCGAGGACA TTGAGATTTC AGACACCGAG AGCTTCTCCA ACGATCCCTG TACCAGTGTC 720
AAAAAGCTGA AGGGGAATGA TGTGCGGATC ATCCTTGGCC AGTTTGACCA GAATATGGCA 780
GCAAAAGTGT TCTGTGTGCG ATACGAGGAG AACATGTATG GTAGTAAATA TCAGTGGATC 840
ATTCCGGGCT GGTACGAGCC TTCTTGGTGG GAGCAGGTGC ACACGGAAGC CAACTCATCC 900
CGCTGCCTCC GGAAGAATCT GCTTGTCTGC ATGGAGGGCT ACATTGGCGT GGATTTGCGAG 960
CCCCTGAGCT CCAAGCAGAT CAAGACCATC TCAGGAAAGA CTCCACAGCA GTATGAGAGA 1020
GAGTACAACA ACAAGCGGTC AGGCGTGGGG CCCAGCAAGT TCCACGGGTA CGCCTACGAT 1080
GGCATCTGGG TCATCGCCAA GACACTGCAG AGGGCCATGG AGACACTGCA TGCCAGCAGC 1140
CGGCACCAGC GGATCCAGGA CTTCACATAC ACGGACCACA CGCTGGGCAG GATCATCCTC 1200
AATGCCATGA ACGAGACCAA CTTCTTCGGG GTCACGGGTC AAGTTGTATT CCGGAATGGG 1260
GAGAGAAATG GGACATTAA ATTTACTCAA TTTCAAGACA GCAGGGAGGT GAAGGTGGGA 1320
GAGTACAACG CTGTGGCCGA CACACTGGAG ATCATCAATG ACACCATCAG GTTCCAAGGA 1380
TCCGAACCA CAAAGACAA GACCATCATC CTGGAGCAGC TGCGGAAGAT CTCCCTACCT 1440
CTCTACAGCA TCCTCTCTGC CCTCACATC CTGCGGATGA TCATGGCCAG TGCTTTTCTC 1500
TTCTTCAACA TCAAGAACCG GAATCAGAAG CTCATAAAGA TGTCGAGTCC ATACATGAAC 1560
AACTTATACA TCCTTGGAGG GATGCTCTCC TATGCTTCCA TATTTCTCTT TGGCCTTGAT 1620
GGATCCTTTG TCTCTGAAAA GACCTTTGAA ACACTTTGCA CCGTCAGGAC CTGGATTCTC 1680
ACCGTGGGCT ACACGACCGC TTTTGGGGCC ATGTTTGCAA AGACCTGGAG AGTCCACGCC 1740
ATCTTCAAAA ATGTGAAAAA GAAGAAGAAG ATCATCAAGG ACCAGAAACT GCTTGTGATC 1800
GTGGGGGGCA TGCTGCTGAT CGACCTGTGT ATCCTGATCT GCTGGCAGGC TGTGGACCCC 1860
CTCGAAGGA CAGTGGAGAA GTACAGCATG GAGCCGAGCC CAGCAGGACG GGATATCTCC 1920
ATCCGCCCTC TCCTGGAGCA CTGTGAGAAC ACCATATAGA CCATCTGGCT TGGCATCGTC 1980
TATGCCCTAC AGGCACTTCT CATGTTGTTC GGTGTTTCT TAGCTTGGGA GACCCGCAAC 2040
GTCAGCATCC CCGCACTCAA CGACAGCAAG TACATCGGGA TGAGTGTCTA CAACGTGGGG 2100
ATCATGTGCA TCATCGGGGC CGCTGTCTCC TTCTGACCC GGGACCAGCC CAATGTGCAG 2160
TTCTGCATCG TGGCTCTGGT CATCATCTTC TGCAGACCA TCACCCTCTG CTGGTATTTC 2220
GTGCCGAAGC TCATCACCCT GAGAACAAC CCAGATGCAG CAACGCAGAA CAGGCGATTTC 2280
CAGTTCACTC AGAATCAGAA GAAAGAAGAT TCTAAAACGT CCACCTCGGT CACCACTGTC 2340
AACAAGCCA GCATATCCCG CCTGGAGGGC CTACAGTCAG AAAACCATCG CTGCGAATG 2400

```

AAGATCACAG AGCTGGATAA AGACTTGGA GAGGTCACCA TGCAGCTGCA GGACACACCA 2460  
 GAAAAGACCA CCTACATTAA ACAGAACCAC TACCAAGAGC TCAATGACAT CCTCAACCTG 2520  
 GGAAACTTCA CTGAGAGCAC AGATGGAGGA AAGGCCATT TAAAAATCA CCTCGATCAA 2580  
 AATCCCCAGC TACAGTGGAA CACAACAGAG CCTCTCGAA CATGCAAGA TCCTATAGAA 2640  
 GATATAAAT CTCCAGAACA CATCCAGCGT CGGCTGTCCC TCCAGCTCCC CATCCTCCAC 2700  
 CACGCCTACC TCCCATCCAT CGGAGGCGTG GACGCCAGCT GTGTCAGCCC CTGCGTCAGC 2760  
 CCCACGCCCA GCCCCGCCA CAGACATGTG CCACCTCCT TCCGAGTCAT GGTCTCGGGC 2820  
 CTGTAA

Seq ID NO: 26 Protein sequence  
 Protein Accession #: NP\_005449.1

1 11 21 31 41 51  
 MASPRRSQGP GRPPPPPPPP ARLLLLLLLL LLLPLAPGAW GWARGAPRPP PSSPPLSIMG 60  
 LMPLTKEVAK GSIGRGVLP VELAIEQIRN BSLLRPYFLD LRLYDTECDN AKGLKAFYDA 120  
 IKYGNHLMV FGVCPVSVTS IIAESLQGNW LVQLSFAATT PVLADKKKYP YFFRTVPSDN 180  
 AVNPAILKLL KHYQWKRVGT LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SFSNDPCTSV 240  
 KKLKGNVRI ILGQFDQDMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWW EQVHTEANSS 300  
 RCLRNKLLAA MEGYIGVDFE PLSSKQIKTI SGKTPQQYER EYNKRSGVG PSKFHGYAYD 360  
 GIWVIKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRIL NAMNETNFFG VTGQVVRNG 420  
 ERMGTIKFTQ FQDSREVKVG EYNAVADILE IINDTIRFQG SEPPKDKTII LEQLRKISLP 480  
 LYSILSALTI LGMIMASAFI PFKIKNRNOK LKMSPPYMN NLILGGLMS YASIFLFLD 540  
 GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IFKNVKMKKK IKDQKLLVI 600  
 VGGMLLIDL ILICWQAVDP LRRTEVKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLIV 660  
 YAYKGLMLF GCFLAWETRN VSIPALNDSK YIGMSVYNVG IMCIIAASV FLTRDQPNVQ 720  
 FCIVALVIF CSTITLCLVF VPKLITLRTN PDAATQNRFF QFTQNKKEK SKTSTSVTSV 780  
 NQASTSRLEG LQSENHRLRM KITELDKDLE EVTMLQDTP EKTYYIKQNH YQELNDILNL 840  
 GNFTSTDDG KAILKNHLDQ NPQLQWNTPE PSRTCKDPIE DINSPEHIQR RLSLQLPILH 900  
 HAYLPSIGGV DASCVSPCVS PTASFRHRHV PPSFRVMVSG L

Seq ID NO: 27 DNA sequence  
 Nucleic Acid Accession #: NM\_000450.1  
 Coding sequence: 117..1949

1 11 21 31 41 51  
 CCTGAGACAG AGGAGCAGCT GATACCCACC TGAGAGATCC TGTGTTTGAA CAACTGCTTC 60  
 CCAAAACGGA AAGTATTTC AAGCTTAAAC TTTGGGTGAA AAGAACTCTT GAAGTCATGA 120  
 TTGCTTCACA GTTCTCTCTCA GCTCTCACTT TGGTGCTTCT CATTAAAGAG AGTGGAGCCT 180  
 GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT TATTGTGACG 240  
 AAAGGTACAC ACACCTGGTT GCAATTCCAA ACAAAGAAGA GATTGAGTAC CTAACCTCCA 300  
 TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG 360  
 TCTGGGTAGG AACCCAGAAA CCTCTGACAG AAGAAGCCAA GAAGCTGGCT CCAGGTGAAC 420  
 CCAACAATAG GCAAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG 480  
 TGGGCATGTG GAATGATGAG AGGTGCAGCA AGAAGAAGCT TGCCCTATGC TACACAGCTG 540  
 CCTGTACCAA TACATCCTGC AGTGGCCACG GTGAATGTGT AGAGACCATC AATAATTACA 600  
 CTTGCAAGTG TGACCTGGC TCAAGTGTGA GCAAAATTGT AACTGTACAG 660  
 CCCTGGAATC CCCTGAGCAT GGAAGCCTGG TTTGCACTCA CCCACTGGGA AACTTCAGCT 720  
 ACAATCTTTC CTGCTCTATC AGCTGTGATA GGGGTACCT GCCAAGCAGC ATGGAGACCA 780  
 TGCAGTGATG GTCTCTGGA GAATGGAGTG CTCCTATTCC AGCCTGCAAT GTGGTTGAGT 840  
 GTGATGCTGT GACAAATCCA GCCAATGGGT TCGTGAATG TTTCCAAAC CCTGGAAGCT 900  
 TCCATGGAA CACAACCTGT ACATTGACT GTGAAGAAGG ATTTGAACTA ATGGGAGCCC 960  
 AGAGCCTTCA GTGTACCTCA TCTGGGAATT GGGACAACGA GAAGCCAACG TGTAAAGCTG 1020  
 TGACATGACG GGCCGTCCGC CAGCCTCAGA ATGGCTCTGT GAGGTGCAGC CATTCCCCTG 1080  
 CTGGAGAGTT CACCTTCAA TCATCCTGCA ACTTCACCTG TGAGGAAGGC TTCATGTTGC 1140  
 AGGGACACAG CCAGGTGTA TGCACCACTC AAGGGCAGTG GACACAGCAA ATCCCACTTT 1200  
 GTGAAGCTTT CAGTGCACCA GCCTTGTTCCA ACCCCGAGCG AGGCTACATG AATTGTCTTC 1260  
 CTAGTGCTTC TGGCAGTTTC CGTTATGGGT CCAGCTGTGA GTTCTCCTGT GAGCAGGGTT 1320  
 TTGTGTTGAA GGGATCCAA AGGCTCCAAT GTGGCCCCAC AGGGGAGTGG GACAACGAGA 1380  
 AGCCCAATG TGAAGCTGTG AGATGCGATG CTGTCCACCA GCCCCGAAAG GGTGTTGGTGA 1440  
 GGTGTGCTCA TTCCCTATT GGAGAATCA CCTACAAGTC CTCTGTGTC TTAGCTGTG 1500  
 AGGAGGATT TGAATTATAT GGATCAACTC AACTTGAGTG CACATCTCAG GGACATGGA 1560  
 CAGAAGAGGT TCCTTCTGTC CAAGTGGTAA AATGTTCAAG CCTGGCAGTT CCGGGAAGA 1620  
 TCAACATGAG CTGCAGTGGG GAGCCCTGTG TTGGCACTGT GTGCAAGTTC GCCTGTCCCTG 1680  
 AAGGATGGAC GCTCAATGGC TCTGCAGCTC GGACATGTGG AGCCACAGGA CACTGTCTG 1740  
 GCCTGTACCT TACCTGTGAA GCTCCCACTG AGTCCAACAT TCCCTTGGTA GCTGGACTTT 1800  
 CTGCTGCTGG ACTCTCCCTC CTGACATTAG CACCATTCTT CCTCTGGCTT CGGAAATGCT 1860  
 TACGGAAGC AAAGAAATTT GTTCTGCTCA GCAGCTGCCA AAGCCTTGAA TCAGACGGAA 1920  
 GCTACCAAAA GCCTTCTTAC ATCCTTTAAG TTCAAAGAA TCAGAAACAG GTGCATCTGG 1980  
 GGAACATAGG GGATACAGT AAGTTAACAG AGACAGATAA CTCTCTCGG GTCTCTGGCC 2040  
 CTCTCTGCTT ACTATGCCAG ATGCCTTTAT GGCTGAAACC GCAACACCCA TCACCACCTT 2100  
 AATAGATCAA AGTCCAGCAG GCAAGGACGG CCTTCAACTG AAAAGACTCA GTGTTCCCTT 2160  
 TCTACTCTC AGGATCAAGA AAGTGTGGC TAATGAAGGG AAAGGATATT TTCTTCCAAG 2220  
 CAAAGGTGAA GAGACCAAGA CTCTGAAATC TCAGAAATCC TTTTCTAACT CTCCTTGCT 2280  
 CGCTGTAAAA TCTTGGCACA GAAACACAAT ATTTTGTGGC TTTCTTTCTT TTGCCCTTCA 2340  
 CAGTGTTCG ACAGCTGATT ACACAGTTGC TGTCAATAA ATGAATAATA ATTATCCAGA 2400  
 GTTATAGGGA AAAAATGAT TAAAAATATT ATAACCTAAA AAAATGACAG ATGTTGAATG 2460  
 CCCACGGCA AATGCAATGGA GGGTGTGTTA TGGTGCAAT CCACTGAAT GCTCTGTGCG 2520  
 AGGGTTACTA TGCACAATTT AATCACTTTC ATCCCTATGG GATTCACTGC TTCTTAAAGA 2580  
 GTTCTTAAAG ATTGTGATAT TTTTACTTGC ATTGAATATA TTATAATCTT CCATCTTCT 2640  
 TCATTCAATA CAGTGTGGT AGGGACTTAA AAAACTGTGA AATGCTGTCA ACTATGATAT 2700  
 GGTAAAAAGT ACTTATTCTA GATTACCCCC TCATTGTTTA TTAACAAATT ATGTTACATC 2760  
 TGTTTTAAAT TTATTTCAAA AAGGGAAACT ATTGTCCCCT AGCAAGGCAT GATGTTAACC 2820

AGAATAAAGT TCTGAGTGT TTTACTACAG TTGTTTTTGG AAAACATGGT AGAATTGGAG 2880  
 AGTAAAAAAT GAATGGAAGG TTTGTATATT GTCAGATATT TTTTCAGAAA TATGTGGTTT 2940  
 CCACGATGAA AAACCTCCAT GAGGCCAAAC GTTTTGAAC AATAAAGCA TAAATGCAAA 3000  
 CACACAAAGG TATAATTTTA TGAATGTCTT TGTTGGAAAA GAATACAGAA AGATGGATGT 3060  
 5 GCTTTGCATT CCTACAAAGA TGTTTGTGAG ATGTGATATG TAAACATAAT TCTTGTATAT 3120  
 TATGGAAGAT TTTAAATCCA CAATAGAAAC TCACCATGTA AAAGAGTCAT CTGGTAGATT 3180  
 TTTAACGAAT GAAGATGTCT AATAGTTATT CCCTATTTGT TTTCTTCTGT ATGTTAGGGT 3240  
 10 GCTCTGGAAG AGAGGAATGC CTGTGTGAGC AAGCATTAT GTTTATTAT AAGCAGATT 3300  
 AACAATTCCA AAGGAATCTC CAGTTTTCAG TTGATCACTG GCAATGAAAA ATTCTCAGTC 3360  
 AGTAATTGCC AAAGCTGCTC TAGCCTTGAG GAGTGTGAGA ATCAAAACTC TCCTACACTT 3420  
 CCATTAACCT AGCATGTGTT GAAAAAATAA GTTTCAGAGA AGTTCTGGCT GAACACTGGC 3480  
 AACGACAAAG CCAACAGTCA AAACAGAGAT GTGATAAGGA TCAGAACAGC AGAGGTTCTT 3540  
 15 TTAAAGGGGC AGAAAACTC TGGGAAATAA GAGAGAACA CTACTGTGAT CAGGCTATGT 3600  
 ATGGAATACA GTGTTATTTT CTTTGAATTT GTTTAAGTGT TGTAAATATT TATGTAAACT 3660  
 GCATTAGAAA TTAGCTGTGT GAAATACCAG TGTGGTTTGT GTTTGAGTTT TATTGAGAA 3720  
 20 TTTAAATTAT AACTTAAAT ATTTTATAAT TTTTAAAGTA TATATTATTT TAAGCTTATG 3780  
 TCAGACCTAT TTGACATAAC ACTATAAAGG TTGACAATAA ATGTGCTTAT GTTT

Seq ID NO: 28 Protein sequence  
 Protein Accession #: NP\_000441.1

1 11 21 31 41 51  
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRYLHLVAI QNKKEIEYLN 60  
 25 SILSYSPSY WIGIRKVMNV WVVVGTKPL TEEAKNWAPG EPNNRKDED CVEIYIKREK 120  
 DVGMMWDERC SKKKLALCYT AACTNTSCSG HGECVETINN YTKCDPFGS GLKCEQIVNC 180  
 TALESEPHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240  
 ECDAVTNPAN GFVECFQNGF SFPWNTTCTF DCEEGFELMG AQSLQCTSSG NWDNEKPTCK 300  
 30 AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEGFM LQGPQAVECT TQGWQWQIP 360  
 VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKGSKRL QCGFTGEWEN 420  
 EKPTCEAVRC DAVHQPPKGL VRCASPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480  
 WTTEEVPSCQV VKCSSLAAPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540  
 35 SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAFPLLWLRL CLRKAKEFVP ASSCQSLESD 600  
 GSYQKPSYIL

Seq ID NO: 29 DNA sequence  
 Nucleic Acid Accession #: NM\_007036  
 Coding sequence: 56..610

1 11 21 31 41 51  
 CTTCCACCA GCAAGACCA CGACTGGAGA GCCGAGCCGG AGGCAGCTGG GAAACATGAA 60  
 GAGCGTCTTG CTGCTGACCA CGCTCCTCGT GCCTGCACAC CTGGTGGCCG CTTGGAGCAA 120  
 45 TAATTATGCG GTGGACTGCC CTCAACACTG TGACAGCAGT GAGTGCAAAA GCAGCCCGCG 180  
 CTGCAAGAGG ACAGTGTCTG ACAGCTGTGG CTGCTGCCGA GTGTGCGCTG CAGGGCGGGG 240  
 AGAACTTGC TACCGCACAG TCTCAGGCAT GGATGGCATG AAGTGTGGCC CGGGGCTGAG 300  
 GTGTCAGCCT TCTAATGGGG AGGATCCTTT TGGTGAAGAG TTTGGTATCT GCAAAGACTG 360  
 50 TCCCTACGGC ACCTTCGGGA TGGATTGCAG AGAGACCTGC AACTGCCAGT CAGGCATCTG 420  
 TGACAGGGGG ACGGGAAAAA GCCTGAAATT CCCCTTCTTC CAATATTTCAG TAACCAAGTC 480  
 TTCCAACAGA TTTGTTTCTC TCACGGAGCA TGACATGGCA TCTGGAGATG GCAATATTGT 540  
 GAGAGAAGAA GTTGTGAAG AGAATGCTGC CGGCTCTCCC GTAATGAGGA AATGGTTAAA 600  
 TCCACGCTGA TCCCGGCTGT GATTCTGAG AGAAGGCTCT ATTTTCGTGA TTGTTCAACA 660  
 55 CACAGCCAAC ATTTTAGGAA CTTTCTAGAT ATAGCATAAG TACATGTAAT TTTTGAAGAT 720  
 CCAAATTGTG ATGCATGGTG GATCCAGAAA ACAAAGTA GGATACTTAC AATCCATAAC 780  
 ATCCATATGA CTGAACACTT GTATGTGTTT GTTAAATATT CGAATGCATG TAGATTTGTT 840  
 AAATGTGTGT GTATAGTAAC ACTGAAGAAC TAAAAATGCA ATTTAGGTAA TCTTACATGG 900  
 AGACAGGCTA ACCAAGAGG GAGCTAGGCA AAGCTGAAGA CCGCAGTGAG TCAAAATTAG 960  
 60 TCTTTGACTT TGATGTACAT TAATGTTGGG ATATGGAATG AAGACTTAAG AGCAGGAGAA 1020  
 GATGGGGAGG GGGTGGGAGT GGGAAATAAA ATATTAGCC CTTCTTGGT AGGTAGCTTC 1080  
 TCTAGAAATT AATTGTGCTT TTTTTTTTT TTTGGCTTGG GGAAGAGTCA AAATAAAACA 1140  
 ACCAGAAAAC CCCTGAAGGA AGTAAGATGT TTGAAGCTTA TGGAAATTG AGTAACAAAC 1200  
 AGCTTTGAAC TGAGAGCAAT TTCAAAGGC TGCTGATGCA GTTCCCGGT TACCTGTATC 1260  
 65 TGAAGGACGG TTTGGGGCA TAGGAAACAC ATACACTTCC ATAAATAGCT TTAACGTATG 1320  
 CCACCTCAGA GATAAATCTA AGAAGTATTT TACCCACTGG TGGTTTGTGT GTGTATGAAG 1380  
 GTAATAATTT ATATATTTT ATAAATAAAT GTGTAGTGC AAGTCATCTT CCCTACCCAT 1440  
 ATTTATCATC CTCTTGAGGA AGAAATCTA GTATTATTG TTGAAATGG TTAGAATAAA 1500  
 AACCTATGAC TCTATAAGGT TTTCAAACAT CTGAGGCATG ATAAATTTAT TATCCATAAT 1560  
 70 TATAGGAGTC ACTCTGGATT TCAAAAAATG TCAAAAAATG AGCAACAGAG GGACCTTTAT 1620  
 TAAACATAAG TGCTGTGACT TCGGTGAATT TCAATTTAA GGTATGAAAA TAAGTTTTTA 1680  
 GGAGGTTTGT AAAAGAAGAA TCAATTTTCA GCAGAAAACA TGTCAACTTT AAAATATAGG 1740  
 TGGAATTAGG AGTATATTG AAAGAATCTT AGCACAACA GGAAGTGTGT ACTAGATGTT 1800  
 CTTAGGAAAT ATCTCAGAAG TATTTTATTT GAAGTGAAGA ACTTATTTAA GAATTATTTT 1860  
 AGTATTTACC TGTATTTTAT TCTTGAAGTT GGCCAACAGA GTTGTGAATG TGTGTGGAAG 1920  
 75 GCCTTTGAAT GTAAAGCTGC ATAAGCTGTT AGGTTTGTGT TTAAAGGAC ATGTTTATTA 1980  
 TTGTTCAATA AAAAGAACA AGATAC

Seq ID NO: 30 Protein sequence  
 Protein Accession #: NP\_008967.1

1 11 21 31 41 51  
 MKSVLLLTLL LVPALHVAAW SNNYAVDCPQ HCDSSSECKSS PRCKRTVLDD CGCCRVCAAG 60  
 RGETCYRTVS GMDGMKCGPG LRCQPSNGED PFGEFEGICK DCPYGTFGMD CRETNCQSG 120  
 ICDRGTGKCL KPPFFQYSVT KSSNRFVSLT EHDMAAGDGN IVREEVVKEN AAGSPVMRKW 180

LNPR

Seq ID NO: 31 DNA sequence

Nucleic Acid Accession #: NM\_000963

Coding sequence: 135..1949

5	1	11	21	31	41	51	
	CAATTGTCAT	ACGACTTGCA	GTGAGCGTCA	GGAGCACGTC	CAGGAAGTCC	TCAGCAGCGC	60
10	CTCCTTCAGC	TCCACAGCCA	GACGCCCTCA	GACAGCAAAG	CCTACCCCGG	CGCCGCGCCC	120
	TGCCCGCCGC	TGGATGCTC	GCCCGCGCCC	TGCTGCTGTG	CGCGGTCTCT	GCGCTCAGCC	180
	ATACAGCAAA	TCCTTGCTGT	TCCCACCCAT	GTCAAAACCG	AGGTGTATGT	ATGAGTGTGG	240
	GATTTGACCA	GTATAAGTGC	GATTGTACCC	GGACAGGATT	CTATGGAGAA	AACTGCTCAA	300
	CACCGGAATT	TTTGACAAGA	ATAAAATTAT	TTCTGAAACC	CACCTCAAAC	ACAGTGCAC	360
15	ACATACTTAC	CCACTTCAAG	GGATTTTGA	ACGTTGTGAA	TAACATTCCT	TTCTTCGAA	420
	ATGCAATTAT	GAGTTATGTC	TTGACATCCA	GATCACATTT	GATTGACAGT	CCACCAACTT	480
	ACAATGCTGA	CTATGGCTAC	AAAAGCTGGG	AAGCCTTCTC	TAACCTCTCC	TATTATACTA	540
	GAGCCCTTCC	TTCTGTGCCT	GATGATTGCC	CGACTCCCTT	GGGTGTCAAA	GGTAAAAAGC	600
	AGCTTCTCTGA	TTCAAATGAG	ATTGTGGAAA	AATGTCTTCT	AAGAAGAAAG	TTCATCCCTG	660
20	ATCCCCAGGG	CTCAACATG	ATGTTTGCAT	TCCTTGCCCA	GCACCTCAGC	CATCAGTTTT	720
	TCAAGACAGA	TCATAAGCGA	GGGCCAGCTT	TCACCAACGG	GCTGGGCCAT	GGGGTGGATG	780
	TAAATCATAT	TACGGGTGAA	ACTCTGGCTA	GACAGCGTAA	ACTGCGCCTT	TTCAAGGATG	840
	GAAAAATGAA	ATATCAGATA	ATTGATGGAG	AGATGTATCC	TCCCACAGTC	AAAGATACTC	900
	AGGCAGAGAT	GATCTACCTC	CCTCAAGTCC	CTGAGCATCT	ACGGTTTGTCT	GTGGGGCAGG	960
25	AGGTCCTTGG	TCTGGTGCCT	GGTCTGATGA	TGTATGCCAC	AATCTGGCTG	CGGGAACACA	1020
	ACAGAGTATG	CGATGTGCTT	AAACAGGAGC	ATCCTGAATG	GGGTGATGAG	CAGTTGTTCC	1080
	AGACAAGCAG	GCTAAATACT	ATAGGAGAGA	CTATTAAGAT	TGTGATTGAA	GATTATGTGC	1140
	AACACTTGAG	TGGCTATCAC	TTCAAAGTGA	AATTTGACCC	AGAACTACTT	TTCAACAAAC	1200
	AATTCAGTA	CCAAAAATCGT	ATTGCTGCTG	AATTTAACAC	CCTCTATCAC	TGGCATCCCC	1260
30	TTCTGCTGTA	CACCTTTCAA	ATTCTGACCC	AGAAATACAA	CTATCAACAG	TTTATCTACA	1320
	ACAACCTCAT	ATTGCTGGAA	CATGGAATTA	CCCAAGTTGT	TGAATCATTC	ACCAGGCAAA	1380
	TTGCTGGCAG	GGTGTGCTGG	GGTAGGAATG	TTCCACCCGC	AGTACAGAAA	GTATCACAGG	1440
	CTTCCATTGA	CCAGAGCAGG	CAGATGAAAT	ACCAGTCTTT	TAATGAGTAC	CGCAAAACGCT	1500
	TTATGCTGAA	GCCTATGAA	TCATTTGAAG	AACTTACAGG	AGAAAAAGGAA	ATGCTCTCAG	1560
35	AGTTGGAAGC	ACTCTATGGT	GACATCGATG	CTGTGGAGCT	GTATCCTGCC	CTTCTGGTAG	1620
	AAAAGCCTCG	GCCAGATGCC	ATCTTTGGTG	AAACCATGGT	AGAAGTTGGA	GCACCATTCT	1680
	CCTTGAAAGG	ACTTATGGGT	AATGTTATAT	GTCTCTCTGC	CTACTGGAAG	CCAAGCACTT	1740
	TTGGTGGAGA	AGTGGGTGTT	CAAAATCATCA	ACACTGCCTC	AATTCAGTCT	CTCATCTGCA	1800
40	ATAACGTGAA	GGGCTGTCCC	TTTACTTCAT	TCAGTGTTC	AGATCCAGAG	CTCATTAAAA	1860
	CAGTCACCAT	CAATGCAAGT	TCTTCCCGCT	CCGACTAGA	TGATATCAAT	CCACAGTAC	1920
	TACTAAAAGA	ACGTTTCGACT	GAAGTGTAGA	AGTCTAATGA	TCATATTTAT	TTATTTATAT	1980
	GAACCATGTC	TATTAATTTA	ATTATTTAAT	AATATTTATA	TTAAACTCCT	TATGTTACTT	2040
	AACATCTTCT	GTAAACAGAAG	TCAGTACTCC	TGTTGCGGAG	AAAGGAGTCA	TACTTGTGAA	2100
	GACTTTTATG	TCACTACTCT	AAAGATTTTG	CTGTGTCTGT	TAAGTTTGGG	AAACAGTTTT	2160
45	TATTTCTGTT	TATAAACCCAG	AGAGAAATGA	GTTTTGACGT	CTTTTACTTT	GAATTTCAAC	2220
	TTATATTATA	AGAAGCAAAAG	TAAAGATGTT	TGAATACTTA	AACACTATCA	CAAGATGGCA	2280
	AAATGCTGAA	AGTTTATACA	CTGTCTGATG	TTCCAATGCA	TCTTCCATGA	TGCATTAGAA	2340
	GTAACATAAT	TTTGAAATTT	TAAAGTACTT	TTGTTATTTT	TTCTGTCTATC	AAACAAAAAC	2400
	AGGTATCAGT	GCATTATTTA	ATGAATATTT	AAATTAGACA	TTACCAGTAA	TTTCATGTCT	2460
50	ACTTTTAAAA	ATCAGCAATG	AAACAATAAT	TTGAAATTTT	TAAATTCATA	GGGTAGAAATC	2520
	ACCTGTAAAA	GCTTGTGTTGA	TTTCTTAAAG	TTATTAAGCT	TGTACATATA	CCAAAAAGAA	2580
	GCTGTCTTGG	ATTTAAATCT	GTAAATCAG	ATGAAATTTT	ACTACAATTG	CTTGTAAAAA	2640
	TATTTTATAA	GTGATGTTC	TTTTTCACCA	AGAGTATAAA	CCTTTTATAGT	GTGACTGTTA	2700
	AAACCTTCCTT	TTAAATCAAA	ATGCCAAATT	TATTAAGGTG	GTGGAGCCAC	TGCAGTGTTA	2760
55	TCTCAAAATA	AGAATATTTT	GTTGAGATAT	TCCAGAAATT	GTTTATATGG	CTGGTAACAT	2820
	GTAAAAATCA	TATCAGCAAA	AGGGTCTACC	TTTAAATATA	GCAATAACAA	AGAAGAAAAAC	2880
	CAAATATTAT	TTCAAATTTA	GGTTTAAACT	TTTGAAGCAA	ACTTTTTTTT	ATCCTTGTGC	2940
	ACTGCAGGCC	TGGTACTCAG	ATTTTGCTAT	GAGGTTAATG	AAGTACCAGG	CTGTGCTTGA	3000
	ATAACGATAT	GTTTCTCTCAG	ATTTTCTGTT	GTACAGTTTA	ATTTAGCAGT	CCATATCACA	3060
60	TTGCAAAAGT	AGCAATGACC	TCATAAAATA	CCTCTTCAAA	ATGCTTAAAT	TCATTTCCAC	3120
	CATTAAATTT	ATCTCAGTCT	TGAAGCCAAT	TCAGTAGGTG	CATTGGAATC	AAGCCTGGCT	3180
	ACCTGCATGC	TGTTCCCTTTT	CTTTTCTTCT	TTTAGCCATT	TTGCTAAGAG	ACACAGTCTT	3240
	CTCATCACTT	CGTTTCTCCT	ATTTTGTTTT	ACTAGTTTTA	AGATCAGAGT	TCACCTTCTT	3300
	TGGACTCTGC	CTATATTTTC	TTACCTGAAC	TTTTGCAAGT	TTTCAGGTAA	ACCTCAGCTC	3360
65	AGGACTGCTA	TTTAGCTCCT	CTTAAAGAAGA	TTAAAGAGA	AAAAAAAGG	CCCTTTTAAA	3420
	AATAGTATAC	ACTTATTTTA	AGTGAAAAGC	AGAGAATTTT	ATTTATAGCT	AATTTTAGCT	3480
	ATCTGTAACC	AAGATGGATG	CAAGAGGGCT	AGTGCCCTCAG	AGAGAAGTGT	ACGGGGTTTG	3540
	TGACTGGAAG	AAGTACGTT	CCCATTTCTAA	TTAATGCCCT	TTCTTATTTA	AAAACAAAAC	3600
	CAATGATAT	CTAAGTAGTT	CTCAGCAATA	ATAATAATGA	CGATAATACT	TCTTTTCCAC	3660
70	ATCTCATTGT	CACTGACATT	TAATGGTACT	GTATATTACT	TAATTTATTG	AAGATTATTA	3720
	TTTATGCTCT	ATTAGGACAC	TATGGTTATA	AACGTGTTTT	AAGCCTACAA	TCATTGATTT	3780
	TTTTTTGTTA	TGTCACAATC	AGTATATTTT	CTTTGGGGTT	ACCTCTCTGA	ATATTATGTA	3840
	AACAATCCAA	AGAAATGATT	GTATTAAAGAT	TTGTGAATAA	ATTTTGTAGAA	ATCTGATTGG	3900
	CATATTGAGA	TATTTAAGGT	TGAATGTTTG	TCCTTAGGAT	AGGCCATAGT	GCTAGCCAC	3960
75	AAAGATAACT	GTCTCATTTAG	CCTGAATGTG	CCATAAGACT	GACCTTTTAA	AATGTTTTGA	4020
	GGGATCTGTG	GATGCTTCTG	TAATTTGTTT	AGCCACAATT	TATTGAGAAA	ATATTCTGTG	4080
	TCAAGCAGCT	TGGGTTTTTA	TATTTTAAA	TCAAACGCTG	ATTACAGATA	ATAGTATTTA	4140
	TATAAATAAT	TGAAAAAAT	TTTCTTTTGG	GAAGAGGGAG	AAAAATGAAAT	AAATATCATT	4200
	AAAGATAACT	CAGGAGAATC	TTCTTTACAA	TTTTACGTTT	AGAATGTTTA	AGGTTAAGAA	4260
80	AGAAATAGTC	AATATGCTTG	TATAAAACAC	TGTTCACTGT	TTTTTTTAAA	AAAAAACTT	4320
	GATTTGTTAT	TAACATTGAT	CTGCTGACAA	AACCTGGGAA	TTTGGGTTGT	GTATGCGAAT	4380
	GTTCAGTGC	CTCAGACAAA	TGTGTATTTA	ACTTATGTAA	AAGATAAGTC	TGGAATAAAA	4440
	TGTCGTTTAA	TTTTGTACT	ATTTA				

Seq ID NO: 32 Protein sequence  
Protein Accession #: NP\_000954

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      MLARALLCA VLALSHTANP CCSHPCQNRG VCMSSVGFDQY KDCDTRTGFY GENCSSTPEFL 60
      TRIKLFLLKPT ENTVHYILTH FKGFWNVVMN IPFLRNAIMS YVLTSRSHLI DSPPTYNADY 120
      GYKSWAEAFSN LSYVTRALPP VPDDCPTPLG VKGKKQLPDS NEIVEKLLLR RKFIPTDPQGS 180
10     NMMAFFAQH FTHQFFKTDH KRGPFTNGL GHGVDLNHIY GETLARQRL RLFKDGKMKY 240
      QIIDGEMYP TVKDTPAEMI YPPQVPEHLR FAVGQEVFGL VPGLMMYATI WLRHNRVCD 300
      VLKQEHPEWG DEQLPQTSRL ILIGETIKIV IEDYVQHLSG YHFKLKFDPE LLFNKQFQYQ 360
      NRIAAEFNTL YHWHPLLPDT FQIHDQKYNQ QQFIYNNIL LEHGITQFVE SFTRQIAGRV 420
      AGGRNVPPAV QKVSQASIDQ SRQMKYQSFN EYRKRFLMKP YESFEELTGE KEMSAEAL 480
15     YGDI DAVELY PALLVEKPRP DAIFGETMVE VGAPPSLKGL MGNVICSPAY WKPSTFGGEV 540
      GFQINTASTI QSLICNNVKG CPFTSFSVPD PELIKTVTIN ASSSRSLDD INPTVLLKER 600
      STEL

```

Seq ID NO: 33 DNA sequence  
Nucleic Acid Accession #: NM\_001508.1  
Coding sequence: 1..1361

```

20     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAAA TCATTGATCA CAGTCATGTC 60
      CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCCTTA TTCTGGTGTA CCTGATCATC 120
      TTCTGATGCG GCCTTCTGGG GAACAGCGTC ACCATTCCGG TCACCCAGGT GCTGCAGAAG 180
      AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC 240
      TTGGTGTTCC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACCC 300
      ACGTCCAGCT ACACCTGTCT CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
30     GCTACGCTGC TGCACGTGCT GACGCTCAGC TTGAGCGCT ACATCGCCAT CTGTCAACCC 420
      TTCAGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
      GTCACCTCCG CCTTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTTG 540
      GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG 600
      CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660
35     CAGTCCAGCA TCTTCGGCGC CTCGTGGTTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720
      ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 780
      ACGCGGCTCT CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCCG CAGGAGGCAG 840
      ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCCAG 900
      ATTCGAGAGA TCATGGCTGC GGCCAAACCC AAGCAGGACT GGACGAGGTC CTACTCCCG 960
40     GCGTACATGA TCCTCTCTCC CTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCAACAAC 1020
      CCGCTCCTGT ACACGGTGTC CTGCGAGCAG TTTCCGGCGG TGTTCTGTGA GGTGCTGTGC 1080
      TGCCCGCTGT CGCTGCAGCA CGCCAACCCAG GAGAAGCGCC TGGCGGTACA TGGCACTCC 1140
      ACCACCGACA GCGCCGCTT TGTGCAGCGC CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC 1200
      TCTGCAAGGA GAAGTGAAGG GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
45     TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACAGGCC 1320
      AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

```

Seq ID NO: 34 Protein sequence  
Protein Accession #: NP\_001499.1

```

50     1      11      21      31      41      51
      |      |      |      |      |      |
      MASPSLPDSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLNSV TIRVTQVLQK 60
      KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120
55     ATLLHLVLTLS FERYIAIICH FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFMAGTEYPL 180
      VNVPSHRGLT CNRSSTRHHE QPETSNNMSIC TNLSSRWTVF QSSIFGAFVY YLVVLLSVAF 240
      MCWMMQVLM KSKQKSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRILIV TLAVCWMPNQ 300
      IRRIMAAAKP KPDWTRSYFR AYMILLPFSE TFFYLSSVIN PLYTVSSSQ FRRVFVQVLC 360
60     CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARTEKIFL STFQSEABPQ 420
      SKSQSLSLES LEPNSGAKPA NSAAENGFOE HEV

```

Seq ID NO: 35 DNA sequence  
Nucleic Acid Accession #: NM\_006475.1  
Coding sequence: 28..2538

```

65     1      11      21      31      41      51
      |      |      |      |      |      |
      AACAGAACTG CAACGGAGAG ACTCAAGATG ATTCCCTTTT TACCCATGTT TTCTCTACTA 60
      TTGCTGCTTA TTGTTAAACC TATAAACGCC AACAATCATT ATGACAAGAT CTGGGCTCAT 120
70     AGTCGTATCA GGGGTCGGGA CCAAGGCCCA AATGTCTGTG CCCTTCAACA GATTTTGGGC 180
      ACCAAAAAGA AATACTTCAG CACTTGTAAG AACTGGTATA AAAAGTCCAT CTGTGGACAG 240
      AAAACGACTG TTTTATATGA ATGTTGCCCT GGTATATGA GAATGGAAGG AATGAAAGGC 300
      TGCCCGACAG TTTTGCCCAT TGACCATGTT TATGGCACTC TGGGCATCGT GGGAGCCACC 360
75     ACAACGACAG GCTATTCTGA CGCCTCAAAA CTGAGGGAGG AGATCGAGGG AAAGGGATCC 420
      TTCATTACT TTGACCCGAG TAATGAGGCT TGGGACAACT TGGATTCTGA TATCCGTAGA 480
      GGTTTGAGGA GCAACGTGAA TGTGAATTA CTGAATGCTT TACATAGTCA CATGATTAAT 540
      AAGAGAATGT TGACCAAGGA CTTAAAAAAT GGCATGATTA TTCCTTCAAT GTATAACAAT 600
      TTGGGGCTTT TCATTAAACA TTATCCTAAT GGGGTGTGTA CTGTAAATG TGCTCGAATC 660
80     ATCCATGGGA ACCAGATTGC AACAAATGGT GTTGTCCATG TCATTGACCG TGTGCTTACA 720
      CAAATGGTGA CCTCAATTC AACTTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
      GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGA GAGACGGTCA CTTCACTC 840
      TTTGCTCCCA CCAATGAGGC TTTTGAGAAA CTTCCACGAG GTGCTCTAGA AAGGTTTCATG 900
      GGAGACAAAG TGGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
      TCTGAGTCTA TTATGGGAGG AGCAGTCTTT GAGACGCTGG AAGGAAATAC AATTGAGATA 1020

```



5 GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT 1080  
 GTGACAAATA ATGGTGTGAT CCATTTGATT GATCAGGTCC TAATTCCTGA TTCTGCCAAA 1140  
 CAAGTTATTG AGCTGGCTGG AAAACAGCAA ACCACCTTCA CGGATCTTGT GGCCCAATTA 1200  
 GGCTTGGCAT CTGCTCTGAG GCCAGATGGA GAATACACTT TGCTGGCACC TGTGAATAAT 1260  
 GCATTTCTCG ATGATACTCT CAGCATGGTT CAGCGCTCC TTAATAATAT TCTGCAGAAT 1320  
 CACATATTGA AAGTAAAGT TGGCCTTAAT GAGCTTTACA ACGGGCAAAT ACTGGAAACC 1380  
 ATCGGAGGCA AACAGCTCAG AGTCTTCTGA TATCGTACAG CTGTCTGCAT TGAAAATTCA 1440  
 10 TGCATGGAGA AAGGGAGTAA GCAAGGGAGA AACGGTGCGA TTCACATATT CCGCGAGATC 1500  
 ATCAAGCCAG CAGAGAAATC CCTCCATGAA AAGTTAAAC AAGATAAGCG CTTTAGCACC 1560  
 TTCTCTCAGC TACTTGAAGC TGCAGACTTG AAAGAGCTCC TGACACAACC TGGAGACTGG 1620  
 ACATTATTG TGCCAACCAA TGATGCTTTT AAGGGAATGA CTAGTGAAGA AAAAGAAATT 1680  
 CTGATACGGG AAAAAAATGC TCTTCAAAAC ATCATTCTTT ATCACCTGAC ACCAGGAGTT 1740  
 15 TTCAATTGGA AAGGATTGTA ACCTGGTGTT ACTAACATT TAAAGACCAC ACAAGGAAGC 1800  
 AAAATCTTTC TGAAGAAGT AAATGATACA CTTCTGGTGA ATGAATTGAA ATCAAAGAA 1860  
 TCTGACATCA TGACACAAA TGGTGTAAAT CATGTTGTAG ATAACTCCT CTATCCAGCA 1920  
 GACACACCTG TTGGAATGTA TCAACTGCTG GAAATACTTA ATAAATTAAT CAAATACATC 1980  
 CAAATTAAAT TTGTTCTGTT TAGCACCTTC AAAGAAATCC CCGTGACTGT CTATACAACT 2040  
 AAAATTATAA CCAAGTTGT GGAACCAAAA ATTAAAGTGA TTGAAGCGAG TCTTCAGCCT 2100  
 20 ATTATCAAAA CTGAAGGACC CACACTAACA AAAGTCAAAA TTGAAGGTGA ACCTGAATTG 2160  
 AGACTGATTA AAGAAGGTGA AACAATAACT GAAGTGATCC ATGGAGAGCC AATTATTAAA 2220  
 AAATACACCA AAATCATTTA TGGAGTGCTT GTGGAATAA CTGAAAAAGA GACACGAGAA 2280  
 GAACGAATCA TTACAGGTCC TGAATAAAAA TACACTAGGA TTTCTACTGG AGGTGGAGAA 2340  
 ACAGAAGAAA CTCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTCAC CAAATTCATT 2400  
 25 GAAGGTGGTG ATGGTCATT ATTGAAGAT GAAGAAATTA AAAGACTGCT TCAGGGAGAC 2460  
 ACACCCGTGA GGAAGTTGCA AGCCAACAAA AAAGTTCAAG GTTCTAGAAG ACGATTAAAG 2520  
 GAAGGTCGTT CTCACTGAAA ATCCAAAAAC CAGAAAAAAA TGTTTATACA ACCCTAAGTC 2580  
 AATAACCTGA CCTTAGAAAA TTGTGAGAGC CAAGTTGACT TCAGGAACCTG AAACATCAGC 2640  
 ACAAAAGAGC AATCATCAAA TAATCTGTAA CACAAATTTA ATATTTTTTT TTCTGAATGA 2700  
 30 GAAACATGAG GGAATTTGTG GAGTTAGCCT CCGTGGTAA AGGAATTGAA GAAAATATA 2760  
 CACCTTACAC CCTTTTTCAT CTTGACATTA AAAGTTCTGG CTAACCTTGG AATCCATTAG 2820  
 AGAAAAATCC TTGTCACCAG ATTCATTACA ATTCAAATCG AAGAGTTGTG AACTGTTATC 2880  
 CCATTGAAAA GACCGAGCCT TGTATGTATG TTATGGATA ATAAATGCA CGCAAGCCAT 2940  
 TATCTCTCCA TGGGAAGCTA AGTTATAAAA ATAGGTGCTT GGTGTACAAA ACTTTTTATA 3000  
 35 TCAAAAGGCT TTGCACATT CTATATGAGT GGGTTTACTG GTAAATTATG TTATTTTTTA 3060  
 CAACTAATTT TGTACTCTCA GAATGTTTGT CATATGCTTC TTGCAATGCA TATTTTTTAA 3120  
 TCTCAACGTT TCAATAAAA CCATTTTTCG GATATAAAGA GAATTACTTC AAATTGAGTA 3180  
 ATTCAGAAA ACTCAAGATT TAAGTTAAAA AGTGGTTGG ACTTGGGAA

Seq ID NO: 36 Protein sequence  
 Protein Accession #: NP\_006466.1

45 1 11 21 31 41 51  
 | | | | | |  
 MIPFLPMFSL LLLLVNPNIN ANHYDKILA HSRIRGRDQG PNVCALQQIL GTKKKYFSTC 60  
 KNWYKKSICG QKTTVLYECC PGYMRMEGMK GCPAVLPIDH VYGTGLGIVGA TTTQRYSDAS 120  
 KLREEIEGKG SFTYFAPSNE AWDNLDSDIR RGLSNVNVE LLNALHSHMI NKRMLTKDLK 180  
 NGMIIPSMYN NLGLFINHPY NGVVTVNCAR IIHGNQIATN GVVHVIDRVL TQIGTSIQDF 240  
 IEAEDDLSSY RAAAITSDIL EALGRDGHFT LFPATNEAFE KLPRGVLERF MGDKVASEAL 300  
 50 MKYHILNTLQ CSESIMGAV FETLEGNTIE IGCDDGSITV NGIKMVNKKD IVTNNGVIHL 360  
 IDQVLIPDSA KQVIELAGAQ QTTFTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLMS 420  
 VQRLKLILQ NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG 480  
 RNGAIHIFRE IIKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTQPGD WTLFVPTNDA 540  
 FKGMTSEEKE ILIRDKNALQ NIILYHLTPG VFICKGFEPG VTNILKTTQG SKIFLKEVND 600  
 55 TLLVNELKSK ESDIMTTNGV IHVVDKLLYP ADTPVGNQDL LEILNKLKLY IQIKFVRGST 660  
 FKEIPVTYVT TKIITKVVEP KIKVIEGSLQ PIKTEGPTL TKVKIEGEPE FRLIKEGETI 720  
 TEVIHGEPII KKYTKIIDGV PVEITEKETR EERIITGPEI KYTRISTGGG ELETBLKKLL 780  
 QEEVTKVTKF IEGGDGHLFE DBEIKRLLQG DTPVRKIQAN KKVQGSRRRL REGRSQ

Seq ID NO: 37 DNA sequence  
 Nucleic Acid Accession #: NM\_002416  
 Coding sequence: 40..417

65 1 11 21 31 41 51  
 | | | | | |  
 ATCCAATACA GGAGTGACTT GGAATCCAT TCTATCACTA TGAAGAAAAG TGGTGTCTCT 60  
 TTCCTCTTGG GCATCATCTT GCTGGTTCTG ATTGGAGTGC AAGGAACCCC AGTAGTGAGA 120  
 AAGGGTCGCT GTTCTGTCAT CAGCACCAAC CAAGGAGCTA TCCACCTACA ATCCTTGAAA 180  
 GACCTTAAAC AATTTGCCCC AAGCCCTTCC TGCAGAAAAA TTGAATCAT TGCTACACTG 240  
 70 AAGAATGGAG TTCAAACATG TCTAAACCCA GATTGAGCAG ATGTGAAGGA ACTGATTAAA 300  
 AAGTGGGAGA AACAGGTCAG CCAAAAGAAA AAGCAAAAGA ATGGGAAAAA ACATCAAAAA 360  
 AAGAAAGTTC TGAAGTTCG AAAATCTCAA CGTTCTCGTC AAAAGAAAGAC TACATAAGAG 420  
 ACCACTTCAC CAATAAGTAT TCTGTGTTAA AAATGTTCTA TTTTAATTAT ACCGCTATCA 480  
 TTCCAAAGGA GGATGGCATA TAATACAAAG GCTTATTAAAT TTGACTAGAA AATTATAAAC 540  
 75 ATTACTCTGA AATTGTAAGT AAAGTTAGAA AGTTGATTIT AAGAATCCAA ACGTTAAGAA 600  
 TTGTTAAAGG CTATGATTGT CTTTGTCTCT CTACACCCA CCAGTTGAAT TTCATCATGC 660  
 TTAAGGCCAT GATTTTAGCA ATACCCATGT CTACACAGAT GTTCACCCAA CCACATCCCA 720  
 CTCAACAACG CTGCCCTGGAA GAGCAGCCCT AGGCTTCCAC GTACTGCAGC CTCAGAGAG 780  
 TATCTGAGGC ACATGTCAGC AAGTCCTAAG CCTGTTAGCA TGCTGGTGAG CCAAGCAGTT 840  
 80 TGAATTGAG CTGGACCTCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TTGAATCAGC 900  
 CTACAGGCCT CACACACAAT GTGTCTGAGA GATTGATGCT GATTGTTATT GGGTATCACC 960  
 ACTGGAGATT ACCAGTGTGT GGCTTTTCTG GCCTCCTTTC TGGCTTTGGA AGCCATGTGA 1020  
 TTCCATCTTG CCCGCTCAGG CTGACCACTT TATTTCTTTT TGTTCCTCTT TGCTTCATTC 1080  
 AAGTCAGCTC TTCTCCATCC TACCACAATG CAGTGCCTTT CTCTCTCTCA GTGCACCTGT 1140  
 CATATGCTCT GATTTATCTG AGTCAACTCC TTTCTCATCT TGTCCCCAAC ACCCCACAGA 1200

5 AGTGCTTTCT TCTCCCAATT CATCCTCACT CAGTCCAGCT TAGTTCAGT CCTGCCTCTT 1260  
 AAATAAACCT TTTTGGACAC ACAAAATTATC TTAACACTCC TGTTCACCTT GGTTCACTAC 1320  
 CACATGGGTG AACACTCAAT GGTAACTAA TTCTGGGTG TTTATCCTAT CTCTCCAACC 1380  
 AGATTGTGAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC 1440  
 CTAATAATAC TGTGGAACATA GGTTTAATA ATTTTAAAT TGATGTTGTT ATGGGCAGGA 1500  
 TGGCAACCAG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560  
 CTAGCCTCTG GTAACCTCTT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT 1620  
 10 GATGCAACAT CCTTGTCTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680  
 GCACGTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740  
 AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800  
 CCAACCATAC AAAAAATTCCT TTTCCGAAG GAAAAGGGCT TTCTCAATAA GCCTCAGCTT 1860  
 TCTAAGATCT AACAAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAAATAG 1920  
 AGTTTTATTG TCCGTTTACT TGTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980  
 15 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040  
 TAGTGGAAAG ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAAACC TCCTTCCAGG 2100  
 GGAGGTTGAG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160  
 CTTTCCCAAA TTGAATCACT GCTCACAATG CTGATGATTT AGAGTGCTGT CCGGTGGAGA 2220  
 TCCCACCCGA ACGTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280  
 20 AAAAAATCTAA GTGTTTCATA AATTTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340  
 GTAGACAGTA TATAACTAAC AACCAGAGAC TACATATTGT CACTGACACA CACGTTATAA 2400  
 TCATTATACA TATATATACA TACATGCATA CACTCTCAA GCAAATAATT TTTCACTTCA 2460  
 AAACAGTATT GACTTGTATA CCTTGTAAAT TGAAATATTT TCTTTGTTAA AATAGAATGG 2520  
 TATCAATAAA TAGACCATTA ATCAG

Seq ID NO: 38 Protein sequence  
 Protein Accession #: NP\_002407

30 1 11 21 31 41 51  
 MKKSGVFLFL GIILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCEK 60  
 IEIIATLKNQ VQTCNLNPSA DVKELIKKWE KQVSQKKKQK NGKKHQKKKV LKVRKSQRSR 120  
 QKKT

Seq ID NO: 39 DNA sequence  
 Nucleic Acid Accession #: NM\_006670  
 Coding sequence: 85..1347

40 1 11 21 31 41 51  
 CCGGCTCGCG CCCTCCGGGC CCAGCCTCCC GAGCCTTCGG AGCGGGCGCC GTCCACGCC 60  
 AGCTCCGGGG AAACCGCAGC CGCGATGCCT GGGGGGTGCT CCCGGGGCCC CGCCGCCGGG 120  
 GACGGGCGTC TGGCGCTGGC GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCTCGTCT 180  
 TCTCCACCT CCTCGGCATC CTCCTTCTCC TCCTCGGCGC CGTTCCTGGC TTCGCCGTG 240  
 45 TCCGCCAGC CCCTCGTGGC GGACCACTGC CCGCGCTGT GCGAGTGCTC CGAGGCAGCG 300  
 CGCACAGTCA AGTGCCTTAA CCGCAATCTG ACCGAGGTGC CCACGGACCT GCCCGCTAC 360  
 GTGCGCAACC TCTTCTTAC CGGCAACCAG CTGGCCGTGC TCCTTGCCTG CGCCTTCGCC 420  
 CGCCGGCCGC CGCTGGCGGA GCTGGCCGCG CTCAACCTCA GCGGCAGCCG CCTGGACGAG 480  
 GTGCGCGCGG GCGCCTTCGA GCATCTGCCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC 540  
 50 CCCTGCGCGC ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTCGGCCCCC 600  
 AGTCCCTTGG TGGAACTGAT CCTGAACCAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660  
 CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCCGTGCACT GCAGGGGCTC 720  
 CGCCGCTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGGATGT GCTGGCCCAA 780  
 CTGCCAGCC TCAGGCACCT GGACTTAAAT AATAATTGCG TGGTGAGCCT GACCTACGTG 840  
 55 TCCTTCGCA ACCTGACACA TCTAGAAAGC CTCACCTGG AGGACAATGC CCTCAAGGTC 900  
 CTTCAAAATG GCACCTTGGC TGAGTTGCAA GGTCTACCCC ACATTAGGCT TTTCTGGAC 960  
 AACAAATCCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020  
 GAGGTAGTGC AGGGCAAGAA CCGGCTCACC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080  
 GTCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG 1140  
 60 CAAACCTCTT ATGCTTCTCT GGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200  
 GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC 1260  
 AGGGATCACA TGGAAAGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAAAC 1320  
 AACCTCAGTT CTAACCTCGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380  
 CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440  
 65 TAGATACAAC GGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCCTTG TTATGTAAAG 1500  
 TTTCTCGGTG TGTTCGTGTA ATGTAAGACG ATGAACAGTT GTGTATAGTG TTTTACCCTC 1560  
 TTCTTTTCT TGGAACTCCT CAACACGTAT GGAGGGATTT TTCAGGTTTC AGCATGAACA 1620  
 TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680  
 ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTTCGAG AAAAAACTT TATTATAAAA 1740  
 70 TATCAGTTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAAA AATTGCATCC TATAAACTGC 1800  
 CTGCAGACGT TAGCAGGCTC TTCAAATAAA CTCATGTTG CACAGGAGCA CCTGCATCCA 1860  
 AGAGCATGCT TACATTTTAC TGTTCGTCAT ATTACAAAAA ATAACCTTGA ACTTCATAAC 1920  
 TTCTTTGACA AAGTAAATTA CTTTTTGTAT TGCAGTTTAT ATGAAATGT ACTGATTTT 1980  
 TTTTAATAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040  
 ATTTTAAAA GAA

Seq ID NO: 40 Protein sequence  
 Protein Accession #: NP\_006661

80 1 11 21 31 41 51  
 MPGGCSRGA AGDGRRLRLR LALVLLGWVS SSSPTSSASS FSSSAFFLAS AVSAQPPLPD 60  
 QCPALCECSE AARTVKCVNR NLTEVPTDLF AYVRNLFLTG NQLAVLPAGA FARRPPLAEL 120  
 AALNLSGSR LDEVRAFAEH LPSLRQLDLS HNPLADLSPF AFSGSNASVS APSPLVELIL 180  
 NHIVPPEDER QNRSFEGMVV AALLAGRALQ GLRRLLEASN HFLYLPRDVL AOLPSLRHL 240

LSNNSLVSLT YVSRNLTHL ESHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWVDCD 300  
 HMADMVTLWK ETEVVOGKDR LTCAYPEKMR NRVLLELNSA DLDCDPILPP SLQTSYVFLG 360  
 IVLALIGAIF LLVLYLNRKG IKKWMHNIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

Seq ID NO: 41 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..927

1	11	21	31	41	51	
ATGCGTGGGG	GGTGTCTCCG	GGGCCCCGCC	GCCGGGGACG	GGCGTCTGCG	GCTGGCGCGA	60
CTAGCGCTGG	TACTCTCTGG	CTGGGTCTCC	TGCTCTTCTC	CCACCTCTCT	GGCATCCTCC	120
TTCTCTCTCT	CGGCGCCGTT	CCTGGCTTCC	GCCGTGTCCG	CCCAGCCCCC	GCTGCCGGAC	180
CAGTGCCCCG	CGCTGTGCCA	GTGCTCCGAG	GCAGCGCGCA	CAGTCAAGTG	CGTTAACCGC	240
AATCTGACCG	AGGTGCCAC	GGACCTGCCC	GCCTACGTGC	GCAACCTCTT	CCTTACCGGC	300
AACCAAGTGG	CCAGCAACCA	CTTCCTTTAC	CTGCCGCGGG	ATGTGCTGGC	CCAACCTGCC	360
AGCCTCAGCG	ACCTGGACTT	AAGTAATAAT	TGCTGGTGA	GCCTGACCTA	CGTGTCTTTC	420
CGCAACCTGA	CACATCTAGA	AAGCCTCCAC	CTGGAGGACA	ATGCCCTCAA	GGTCTCTCAC	480
AATGGCACCC	TGGCTGAGTT	GCAAGGTCTA	CCCCACATTA	GGGTTTTCTC	GGACAACAAT	540
CCCTGGGTCT	GCGACTGCCA	CATGGCAGAC	ATGGTGACCT	GGCTCAAGGA	AACAGAGGTA	600
GTGCAGGGCA	AAGACCGGCT	CACCTGTGCA	TATCCGGAAA	AAATGAGGAA	TCCGGTCTCT	660
TTGGAACCTA	ACAGTGCTGA	CCTGGACTGT	GACCCGATTG	TCCCCCATC	CCTGCAAAAC	720
TCTTATGTCT	TCTTGGGTAT	TGTTTTAGCC	CTGATAGGCG	CTATTTTCTC	CCTGGTTTTG	780
TATTTGAACC	GCAAGGGGAT	AAAAAAGTGG	ATGCATAACA	TCAGAGATGC	CTGCAGGGAT	840
CACATGGAAG	GGTATCATTA	CAGATATGAA	ATCAATGCGG	ACCCAGATT	AACAAACCTC	900
AGTTCTAACT	CGGATGTCTT	CGAGTGA				

Seq ID NO: 42 Protein sequence  
 Protein Accession #: Eos sequence

1	11	21	31	41	51	
MPGGCSRGA	AGDGRRLAR	LALVLLGWVS	SSSPTSSASS	FSSSAPFLAS	AVSAQPPLPD	60
QCPALCECSE	AARTVKCVNR	NLTVPTDLP	AYVRNLFLTG	NQLASNHFLY	LPRDVLAQLP	120
SLRHLDSLN	SLVSLTYVSF	RNLTHLESLH	LEDNALKVLH	NGTLAELQGL	PHIRVFLDNN	180
PWVCDCHMAD	MVTWLKETEV	VQGDRLTCA	YPEKMRNRVL	LELNSADLDC	DPILPPSLQT	240
SYVFLGIVLA	LIGAIFLLVL	YLNKRGIKKW	MHNIRDACRD	HMEGYHYRYE	INADPRLTNL	300
SSNSDVLE						

Seq ID NO: 43 DNA sequence  
 Nucleic Acid Accession #: NM\_058173  
 Coding sequence: 68..340

1	11	21	31	41	51	
AGCGCCTTGC	CTTCTCTTAG	GCCTTGAAGC	ATTTTGTCT	GTGCTCCCTG	ATCTTCAGGT	60
CACACCATAG	AAGTTCTTAG	CAGTCTGGT	ACTCTTGGGA	GTTCCTATCT	TTCTGGTCTC	120
TGCCCAGAAT	CCGACAACAG	CTGCTCCAGC	TGACACGTAT	CCAGCTACTG	GTCCGTCTGA	180
TGATGAAGCC	CCTGATGCTG	AAACCACTGC	TGCTGCAACC	ACTGCGACCA	CTGCTGCTCC	240
TACCACTGCA	ACCACCGCTG	CTTCTACCAC	TGCTCGTAAA	GACATTCCAG	TTTACCCTAA	300
ATGGGTGGG	GATCTCCCGA	ATGGTAGAGT	GTGTCCCTGA	GATGGAATCA	GCTTGAGTCT	360
TCGCAATTG	GGTCACAAC	ATTCATGCTT	CCGTGTGATT	CATCCAAC	CTTACCTTGC	420
CTACGATATC	CCCTTTATCT	CTAATCAGTT	TATTTTCTTT	CAAATAAAAA	ATAACTATGA	480
GCGAGCTAAC	AT					

Seq ID NO: 44 Protein sequence  
 Protein Accession #: NP\_477521

1	11	21	31	41	51	
MKFLAVLVLL	GVSIFLVSAQ	NPTTAAPADT	YPATGPADDE	APDAETTAAA	TTATTAAPTT	60
ATTAASTTAR	KDIPVLPKWV	GDLPNGRVCP				

Seq ID NO: 45 DNA sequence  
 Nucleic Acid Accession #: NM\_000095.1  
 Coding sequence: 26..2299

1	11	21	31	41	51	
CAGCACCCAG	CTCCCCGCCA	CCGCCATGGT	CCCCGACACC	GCCTGCGTTC	TTCTGCTCAC	60
CCTGGCTGCC	CTCGGCGCGT	CCGGACAGGG	CCAGAGCCCG	TTGGGCTCAG	ACCTGGGCCC	120
GCAGATGCTT	CGGGAACATG	AGGAAACCAA	CGCGGCGCTG	CAGGACGTGC	GGGACTGGCT	180
GCGGCAGCAG	GTCAGGGAGA	TCACGTTCTT	GAAAAACACG	GTGATGGAGT	GTGACGCGTG	240
CGGATGACAG	CAGTCAAGTAC	GCACCGGCCT	ACCCAGCGTG	CGGCCCCGTC	TCCACTGCGC	300
GCCCGGCTTC	TGCTTCCCGG	GCGTGGCCTG	CATCCAGACG	GAGAGCGGCG	GCCGCTGCGG	360
CCCTTGCCCC	GCGGGCTTCA	CGGGCAACGG	CTCGCACTGC	ACCGACGTCA	ACGAGTGCAA	420
CGCCACCCCC	TGCTTCCCCC	GAGTCCGCTG	TATCAACACC	AGCCCCGGGT	TCCGCTGCGA	480
GGCTTGCCCC	CCGGGGTACA	GCGGCCCCAC	CCACCAGGGC	GTGGGGCTGG	CTTTCGCCAA	540
GGCCAACAAG	CAGTTTGTGA	CGGACATCAA	CGAGTGTGAG	ACCGGGCAAC	ATAACTGCGT	600
CCCCAATCTC	GTGTGCATCA	ACACCCGGGG	CTCCTTCCAG	TGCGGCCCCG	GCCAGCCCGG	660
CTTCGTGGGC	GACCAGGCGT	CCGGCTGCCA	GCGCGGCGCA	CAGCGCTTCT	GCCCCGACGG	720
CTCGCCAGC	GAGTGCCACG	AGCATGCAGA	CTCGTCTCTA	GAGCGCGATG	GCTCGCGGTC	780
GTGCGTGTGT	CGCGTTGGCT	GGGCGGGCAA	CGGGATCCTC	TGTGGTCCGC	ACACTGACCT	840
AGACGGCTTC	CCGGACGAGA	AGCTGCGCTG	CCCGAGCCCG	CAGTGCCGTA	AGGACAACCT	900

CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCCTG 960  
 CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAAG GACAACCTGCC CGCTGGTGCG 1020  
 GAACCCAGAC CAGCGCAACA CCGACGAGGA CAAGTGGGGC GATGCGTGCG ACAACTGCCG 1080  
 GTCCCAAGAG AACGACGACC AAAGAGCAC AGACCAGGAC GGCCGGGGCG ATGCGTGCGA 1140  
 5 CGACGACATC GACGCGGACC GATCCGCAA CCAGGCGGAC AACTGCCCTA GGTACCCAA 1200  
 CTCAGACCCAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA 1260  
 GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT TTGGGAGATG CTTGTGACAG 1320  
 CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACCTGT CCACGGTGCC 1380  
 10 TAACAGTGCC CAGGAGGACT CAGACCAGGA TGGCCAGGGT GATGCCTGCG ACACGACGGA 1440  
 CGACAATGAC GGAGTCCCTG ACAGTCCGGG CAACTGCCCG CTGGTGCCCTA ACCCCGGCCA 1500  
 GGAGGACGCG GACAGGGGAC GCGTGGGCGA CGTGTGCCAG GACGACTTGG ATGCAGACAA 1560  
 GGTGGTAGAG AAGATCGACG TGTGTCCGGA GAACGCTGAA GTACACGCTCA CCGACTTCAG 1620  
 GGCCTTCCAG ACAGTCGTGC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680  
 15 GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT 1740  
 GGGTTACACT GCCTTCAATG GCGTGGGACT CGAGGGGACG TTCCATGTGA ACACGGTCAC 1800  
 GGATGACGAG TATGCGGGCT TCACTTTTGG CTACGAGGAC AGCTCCAGCT TCTACGTGGT 1860  
 CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA 1920  
 GCCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGCGGAA 1980  
 20 CGCTCTGTGG CATAACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040  
 AAACGTGGGT TGGAGGACA AGAAGTCTTA TCGTTGGTTC CTGACGACCC GGCCCCAAGT 2100  
 GGGCTACATC AGGTGCGGAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAACGTGGT 2160  
 CTTGGACACA ACCATGCGGG GTGGCCGCTT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220  
 CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280  
 25 TCAGCTGCGG CAAGCTAGG GACCAGGGTG AGGACCCGCC GGATGACAGC CACCCTCACC 2340  
 GCGGCTGGAT GGGGGCTCTG CACCAGCCC AAGGGGTGGC CGTCTGAGG GGAAGTGAG 2400  
 AAGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGACGGG

Seq ID NO: 46 Protein sequence  
 Protein Accession #: NP\_000086.1

1 11 21 31 41 51  
 | | | | |  
 MVPDTACVLL LTLAALGASG QQSPLGSDL GPQMLRELQE TNAALQDVDR WLRQQVREIT 60  
 35 FLKNTVMECD ACGMQSVRT GLPSVRPLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG 120  
 NGSHCTDVNE CNAHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180  
 INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDAQSG CQRGAQRFCP DGSPSECHEH 240  
 ADCVLERDGS RSCVCRVGWA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSSGQ 300  
 EDVDRDGIAD ACDPDADGDG VPNEKDNCPL VRNPDQRNTD EDKWDACDN CRSQKNDQDK 360  
 40 DTDQDGRGDA CDDIDIDGRI RNQADNCPRV PNSDQKDSG DGIGDACDNC PQKSNPDQAD 420  
 VDHDVFVGDA DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVPS 480  
 RDNCRVLPNP GQEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAETVLT D FRAQTUVLD 540  
 PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDYAGFI 600  
 FGYQDSSSFY VVMWKQMEQT YWQANPFRV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT 660  
 45 ESQVRLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTMRGG 720  
 RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA

Seq ID NO: 47 DNA sequence  
 Nucleic Acid Accession #: NM\_001565.1  
 Coding sequence: 67..363

1 11 21 31 41 51  
 | | | | |  
 GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60  
 55 AGCACCATGA ATCAAATGCG GATTCTGATT TGTCGCCTTA TCTTCTGAC TCTAAGTGGC 120  
 ATTCAAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180  
 CCTGTTAATC CAAGGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240  
 CGTGTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300  
 TCGAAGGCCA TCAAGAATT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360  
 60 TAAACCAGA GGGGAGCAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420  
 CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTT TTAGTTTGCA 480  
 GTTACACTAA AAGGTGACCA ATGATGGTCA CCAAATCAGC TGCTACTACT CCTGTAGGAA 540  
 GGTAAATGTT CATCATCTTA AGCTATTGAG TAATACTCT ACCCTGGCAC TATAATGTAA 600  
 GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTTCTGACC CTGCTTCAA TATTTCCTC 660  
 65 ACCTTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAATTC 720  
 TCAGAATCTC AAATAACTAA AAGGTATGCA ATCAAATCTG CTTTTTAAAG AATGCTCTTT 780  
 ACTTCATGGA CTCTCACTGC CATCTCCCA AGGGGCCCAA ATTCTTTCAG TGGCTACCTA 840  
 CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT 900  
 CTTATTTAAT GAAAGACTGT ACAGAGTATA AGTCTTAGAT GTATATATTT CCTATATTGT 960  
 70 TTTCAAGTGA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020  
 TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080  
 TTTTCAAATA AAAATGAGGT ACTCTCTCTG AAATATTAAG

Seq ID NO: 48 Protein sequence  
 Protein Accession #: NP\_001556.1

1 11 21 31 41 51  
 | | | | |  
 MNQTAILICC LIFLTLSGIQ GVPLSRTVRC TCISISNQPV NPRSLEKLEI IPASQFCPRV 60  
 80 EIIATMKKKK EKRCINPESK AIKNLLKAVS KEMSKRSP

Seq ID NO: 49 DNA sequence  
 Nucleic Acid Accession #: XM\_057014  
 Coding sequence: 143..874

1 11 21 31 41 51  
 5 GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60  
 CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCCTCCGCC TCCAGCTCCG 120  
 CGCTGCCCGG CAGCCGGGAG CCATGCGACC CCAGGGCCCC GCCGCCTCCC CGCAGCGGCT 180  
 CCSCGCGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT 240  
 CCCCAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGAGCC TGTATAATGG 300  
 AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360  
 CATTCCGGGT ACACCTGGGA TCCCAGGTGCG GGATGGATT CAAAGAGAAA AGGGGGAATG 420  
 10 TCTGAGGAA AGCTTTGAGG AGTCCTGGAC ACCCAACTAC AAGCAGTGT CATGGAGTTC 480  
 ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540  
 AAATAGTGCT CTAAGAGTTT TGTTCACTGG CTCACTTCGG CTAAAATGCA GAAATGCATG 600  
 CTGTACGCGT TGGTATTTCA CATTCAATGG AGCTGAATGT TCAGGACCTC TCCCATTGA 660  
 15 AGCTATAATT TATTTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG 720  
 CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780  
 CTGGGTTGCG ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840  
 TTCTCGCATC ATTATGAAG AACTACCCAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900  
 TTTTITTTAT ATGCCCTTGA ATGGTTCAC TAAATGACAT TTTAAATAAG TTTATGTATA 960  
 20 CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020  
 TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCATAT TTTTITTTAGT 1080  
 TGTTTAAAT ACTTTCTTCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140  
 GGTCITTTTGT TTTTCTCTCT AGTATAGCAT TTTTAAAAA ATATAAAAGC TACCAATCTT 1200  
 TGTACAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260  
 CAACCTTAAA AAAAAA AAAA

Seq ID NO: 50 Protein sequence  
 Protein Accession #: XP\_057014

1 11 21 31 41 51  
 30 MRPQGPAAAP QRLRGLLLLL LLQLPAPSSA SEIPKKGKQA QLRQREVVDL YNGMCLQGPA 60  
 GVPGRDGSFG ANGIPGTGPI PGRDGFKEK GECLRESFEE SWTFNYKQCS WSSLNYGIDL 120  
 GKIAECTFTK MRSNSALRLV FSGSLRLKCR NACCQRWYFT FNGAECGSL PIAIILYLDQ 180  
 35 GSPENNSTIN IHRITSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240  
 LPK

Seq ID NO: 51 DNA sequence  
 Nucleic Acid Accession #: NM\_020974  
 Coding sequence: 81..3080

1 11 21 31 41 51  
 40 GCGCTCCGCG CACACCTCCC CGCGCGCGCG CCGCCACCGC CCGCACTCCG CCGCCTCTGC 60  
 CCGCAACCGC TGAGCCATCC ATGGGGGTGCG CCGGCCGCAA CCGTCCCGGG GCGGCCTGGG 120  
 45 CGGTGCTGCT GCTGCTGCTG CTGCTGCGCG CACTGCTGCT GCTGGCGGGG GCCGTCCCCG 180  
 CCGGTGCGGG CCGTGC CGCG GGGCCG CAGG AGGATGTAGA TGAGTGTGCC CAGAGGCTAG 240  
 ATGACTGCCA TGCCGACGCG CTGTGTGAGA ACACACCCAC CTCCTACAAG TGCTCTGCA 300  
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAATGAGC 360  
 50 TCATAGGAGG CTGTGTCCAT GACTGTTTGA ATATTCAGG CAATTATCGT TGCACTTGT 420  
 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG 480  
 AGAACAAATG CGGCTGCCAG CATACCTGTG TCAACGTCAT GGGGAGCTAT GAGTGTCTGCT 540  
 GCAAGGAGGG GTTTTTCTG AGTGACAATC AGCACACCTG CATTCACCGC TCGGAAGAGG 600  
 GCCTGAGCTG CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGG 660  
 55 GCAGCGTCGC CTGTGAGTGG AGGCCTGGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720  
 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780  
 GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840  
 AGCGAGAGGA CACTGTCTCT GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGG 900  
 60 ATAAACGGGT GAAACGGCGG CTGCTCATGG AAACGTGTGC TGTCAACAAT GGAGGCTGTG 960  
 ACCGCACCTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGCTCTGTT GGATTCACCT 1020  
 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT 1080  
 GTGATCATTT CTGCAAAAAC ATCGTGGGCA GTTTTGACTG CCGCTGCAAG AAAGGATTTA 1140  
 AATTATTAAC AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT 1200  
 GTGACCACAG CTGCATCAAC CACCCTGGCA CATTGCTTGT TGCTTGCAAC CGAGGGTACA 1260  
 65 CCCTGTATGG CTTACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320  
 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAGTGCCAC CCTGGGTACA 1380  
 AGCTCCACTG GAATAAAAAA GACTGTGTGG AAGTGAAGGG GCTCCTGCC ACAAAGTGTG 1440  
 CACCCCGTGT GTCCCTGCAC TGCAGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT 1500  
 70 GTCACCTGCG CATTCACCTC TCTTCAGATG TCACCAACAT CAGGACAAGT GTAACCTTTA 1560  
 AGCTAAATGA AGGCAAGTGT AGTTTGAAAA ATGCTGAGCT GTTTCCCGAG GGTCTGCGAC 1620  
 CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT 1680  
 GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCACCCCT AAGGAAATGT 1740  
 TTATCACTGT TGAGTTTGAG CTTGAACTA ACCAAAGGA GGTGACAGCT TCTTGTGACC 1800  
 TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCATCCGC ACGCTCAGAA 1860  
 75 AGGCCGTCCA CAGGGAGCAG TTTCACTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA 1920  
 AAAAGCCTCC CAGAATCATCT GAACGCCAGG CAGAGTCCTG TGGAGTGGGC CAGGGTCACTG 1980  
 CAGAAAACCA ATGTGTCACT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT 2040  
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAAATGACT TGTGAACCAT 2100  
 GCCCCAAGAC AGGAAATTTCT GGGGCCCTGA AGACCCAGCA AGCTTGGAAAT ATGCTCGAAT 2160  
 80 GTGGAGGTCT GTGTCAACCT GGTGAATATT CTGCAGATGG CTTTGACACT TGCCAGCTCT 2220  
 GTGCCCTGGG CACGTTCAG CTTGAAGCTG GTCGAACCTC CTGCTTCCCC TGTGGAGGAG 2280  
 GCCTTGCCAC CAAACATCAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT 2340  
 GTTCACTGCG ACATTTCTCA AACACACCA CTCACCGATG TATTCGTTGC CCAAGTGGGA 2400  
 CATACAGGCC TGAATTTGGA AAAAAATAAT GTGTTTCTTG CCCAGGAAAT ACTACGACTG 2460  
 ACTTTGATGG CTCCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520

GAGATTTTCAC TGGGTACATT GAATCCCCAA ACTACCCAGG CAATTACCCA GCCAACACCG 2580  
 AGTGATACGTG GACCATCAAC CCACCCCCCA AGCGCCGCAT CCTGATCGTG GTCCTGAGA 2640  
 TCTTCTTGCC CATAGAGGAC GACTGTGGGG ACTATCTGGT GATGCGGAAA ACCTCTTCAT 2700  
 CCAATTTCTGT GACAACATAT GAAACCTGCC AGACCTACGA ACGCCCCATC GCCTTCACCT 2760  
 CCAGGTCAAA GAAGTGTGG ATTCAAGTCA AGTCCAATGA AGGGAACAGC GCTAGAGGGT 2820  
 TCCAGGTCCC ATACGTGACA TATGATGAGG ACTACCAGGA ACTCATTGAA GACATAGTTC 2880  
 GAGATGGCAG GCTCTATGCA TCTGAGAACC ATCAGGAAAT ACTTAAGGAT AAGAACTTA 2940  
 TCAAGGCTCT GTTTGATGTC CTGGCCCATC CCCAGAACTA TTTCAAGTAC ACAGCCCAGG 3000  
 AGTCCCAGGA GATGTTTCCA AGATCGTTCA TCCGATTGCT ACGTTCCAAA GTGTCCAGGT 3060  
 TTTTGAGACC TTACAAATGA CTCAGCCAC GTGCCACTCA ATACAAATGT TCTGCTATAG 3120  
 GGTGGTGGG ACAGAGCTGT CTTCTTCTG CATGTCAGCA CAGTCGGGTA TTGCTGCCTC 3180  
 CCGTATCAGT GACTCATTAG AGTTCAATTT TTATAGATAA TACAGATATT TTGTTAAATT 3240  
 GAACTTGTT TTTCTTTCCC AGCATCGTGG ATGTAGACTG AGAATGGCTT TGAGTGGCAT 3300  
 CAGCTTCTCA CTGCTGTGGG CGGATGTCTT GGATAGATCA CGGGCTGGCT GAGCTGGACT 3360  
 TTGGTCAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTAATCTCTC TCAAGGAGTC 3420  
 TGTAGTGAAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACTTCAGC TTCCTCTAGC 3480  
 CCGGCCCTCT CTAAGGGAGC CCTCTGCACT CGTGTGCAGG CTCTGACCAG GCAGAACAGG 3540  
 CAAGAGGGGA GGGAGGAGA CCCCTGCAGG CTCCTCCAC CCACCTTGAG ACCTGGGAGG 3600  
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACITG 3660  
 AGTTCTAAGC AGTGCTCGTG AAAAAAATAA GCAGAAAGAA TTAGAAATAA ATAAAACTA 3720  
 AGCACTTCTG GAGACAT

Seq ID NO: 52 Protein sequence  
 Protein Accession #: NP\_066025

1 11 21 31 41 51  
 | | | | |  
 LGVAGRNRPF AAWAVLLLLL LLPLLLLLAG AVPPGRGRRA GPQEDVDECA QGLDDCHADA 60  
 LCQNTPTSYK CSCKPGYQGE GRQCEDIDEC GNELNGGCVH DCLNIPGNR CTCFDGFMFLA 120  
 HDGHNCLDVD ECLENNNGCG HTCVNMVMSY ECCCKEGFFL SDNQHTCIHR SEEGLSMCMNK 180  
 DHGCSHICKE APRGSVACBC RPFELAKNQ RDCILTCNHG NGGCQHSCHD TADGPECSCH 240  
 PQYKMTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCDRTCKDT 300  
 STGVHCSCPV GFTLLQDQKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLLTDEK 360  
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCQVVCVN 420  
 TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480  
 SSDVTITRTS VTFKLNEGKC SLKNAELFPE GLRPLALPEKH SSVKESFRYV NLTCSGSKQV 540  
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600  
 FHLQLSGMNL DVAKKPPRTS ERQAESCQVG QGHAENQCVS CRAGTYDGA RERCILCPNG 660  
 TFQNEEGQMT CEPCPRPGNS GALKTPEAWN MSECGLCQF GEYSADGFAP QQLCALGTFQ 720  
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHFY NTTTHRCIRC PVGTYQPEFG 780  
 KNKNCVSCPN TTTDFDGSFN ITQCKNRRCG BELGDFGTGYI ESPNYPGNYP ANTECTWTIN 840  
 PPPKRRLIV VPEIFLPIED DCGDYLVMRK TSSNSVTTYI ETCQTYERPI AFTSRSKKLW 900  
 IQFKSNEGNS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLIALKFDV 960  
 LAHPQNYFKY TAQESREMF FRSFIRLLRSK VSRFLRPYK

Seq ID NO: 53 DNA sequence  
 Nucleic Acid Accession #: NM\_014211  
 Coding sequence: 157..1479

1 11 21 31 41 51  
 | | | | |  
 GGGACAGGGC TGAGGATGAG GAGAACCTTG GGGACCCAGA AGACCGTGCC TTGCCCGGAA 60  
 GTCTGCCTG TAGGCTGAA GGACTTGCCC TAACAGAGCC TCAACAACCTA CCTGGTGATT 120  
 CCTACTTCAG CCCCTTGGT TGAGCAGCTT CTCAACATGA ACTACAGCCT CCACCTGGCC 180  
 TTCGTGTGTG TGAATCTCTT CACTGAGAGG ATGTGCATCC AGGGGAGTCA GTTCAACGTC 240  
 GAGGTGCGCA GAAGTGACAA GCTTTCCTTG CCTGGCTTTG AGAACCTCAC AGCAGGATAT 300  
 AACAAATTTT TCAGGCCCAA TTTTGGTGGA GAACCCGTAC AGATAGCGCT GACTCTGGAC 360  
 ATTGCAAGTA TCTCTAGCAT TTCAGAGAGT AACATGGACT ACACAGCCAC CATATACCCT 420  
 CGACACGCTG GGATGGACCA CGCGCTGGTG TTTGAAGGCA ACAAGAGCTT CACTCTGGAT 480  
 GCCCGCCTCG TGGAGTCTCT CTGGGTGCCA GATACTTACA TTGTGGAGTC CAAGAAGTCC 540  
 TTCCTCCATG AAGTCACTGT GGGAAACAGG CTCATCCGCC TCTTCTCCAA TGGCAGGTC 600  
 CTGTATGCCC TCAGAATCAC GACAACTGTT GCATGTAACA TGGATCTGTC TAAATACCCC 660  
 ATGGACACAC AGACATGCAA GTTGACGCTG GAAAGCTGGG GCTATGATGG AAATGATGTG 720  
 GAGTTCACCT GGCTGAGAGG GAACGACTCT GTGCGTGGAC TGAACACCT GCGGCTTGCT 780  
 CAGTACACCA TAGAGCGGTA TTTACCTTA GTACACAGAT CGCAGCAGGA GACAGGAAAT 840  
 TACACTAGAT TGGTCTTACA GTTTGAGCTT CGGAGGAATG TTCTGTATTT CATTTTGGAA 900  
 ACCTACGTTT CTTCCACTTT CCTGGTGGTG TTGTCTGGG TTTTATTTT GATCTCTCTC 960  
 GATTCACTG CTGCAAGAAC CTGCAATTGGA GTGACGACCG TGTATCAAT GACCACACTG 1020  
 ATGATCGGGT CCCGCACTTC TCTTCCCAAC ACCAAGTCTT TCATCAAGGC CATCGATGTG 1080  
 TACCTGGGGA TCTGCTTTAG CTTTGTGTTT GGGGCCTTGC TAGAATATGC AGTTGCTCAC 1140  
 TACAGTTCTT TACAGCAGAT GGCAGCCAAA GATAGGGGGA CAACAAGGA AGTAGAAGAA 1200  
 GTCAGTATTA CTAATATCAT CAACAGCTCC ATCTCCAGCT TTAACAGGAA GATCAGCTTT 1260  
 GCCAGCATTG AATTTTCCAG CGACAACGTT GACTACAGTG ACTTGACAAT GAAAACCAGC 1320  
 GACAAGTTCA AGTTTGTCTT CCGAGAAAAG ATGGGCAGGA TTGTGTGATTA TTTCACAATT 1380  
 CAAACCCCA GTAATGTTGA TCACTATTC AACTACTGT TTCTTTGAT TTTTATGCTA 1440  
 GCCAATGTAT TTTACTGGG ATACTACATG TATTTTGGAG TCAATGTAA ATTTCTTGCA 1500  
 TGCCATAGGT CTTCAACAGG ACAAGATAAT GATGTAAATG GTATTTTAGG CCAAGTGTGC 1560  
 ACCACATCC AATGGTGCTA CAAGTGACTG AAATAATATT TGAGTCTTTC TGCTCAAAGA 1620  
 ATGAAGCTCC AACCATGTT TAAAGCTGTG TAGAAGTCTT AGCATTATAG GATCTGTGTA 1680  
 TAGAAACATC AGTCCATTC TCTTTCATCT TAATCAAGGA CATTCCTATG GAGCCCAAGA 1740  
 TTACAAATGT ACTCAGGCT GTTTATTCGG TGGCTCCCTG GTTTGCATTT ACCTCATATA 1800  
 AAGAAATGGGA AGGAAGACCT TGGGTAACCC TCAAGTGTCG GAAGTTGTTT CTAAGTAAC 1860  
 TATACATGTT TTTTACTAAA TCTCTGCAGT GCTTATAAAA TACATTGTTG CCTATTTAGG 1920  
 GAGTAACATT TTCTAGTTTT TGTTCCTGGT TAAATGAAA TATGGGCTTA TGTCAATTCA 1980

TTGGAAGTCA ATGCACTAAC TCAATACCAA GATGAGTTTT TAAATAATGA ATATTATTTA 2040  
 ATACCACAAC AGAATTATCC CCAATTTCCA ATAAGTCCTA TCATTGAAAA TTCAAATATA 2100  
 AGTGAAGAAA AAATTAGTAG ATCAACAATC TAAACAAATC CCTCGGTTCT AAGATACAAT 2160  
 GGAATCCCCA TACTGGAAGG ACTCTGAGGC TTTATTTCCC CACTATGCAT ATCTTATCAT 2220  
 TTTATTATTA TACACACATC CATCCTAAAC TATACTAAAG CCCTTTTCCC ATGCATGGAT 2280  
 GGAATGGAA GATTTTTTTG TAACCTGTTC TAGAAGTCTT AATATGGGCT GTTGCCATGA 2340  
 AGGCTTGCGA AATTGAGTCC ATTTTCTAGC TGCCTTTATT CACATAGTGA TGGGGTACTA 2400  
 AAAGTACTGG GTTGACTCAG AGAGTCGCTG TCATTCTGTC ATTGCTGCTA CTCTAACACT 2460  
 GAGCAACACT CTCCCGATGG CAGATCCCTT GTATCATTC CAGAGGAGCA TTCTCCCTT 2520  
 TGCTCTAATG ATCAGGAATG ATGCTTATTA GAAAACAAAC TGCTTGACCC AGGAACAAGT 2580  
 GGCTTAGCTT AAGTAAACTT GGCTTTGCTC AGATCCCTGA TCCTTCCAGC TGGTCTGCTC 2640  
 TGAGTGGCTT ATCCCGCATG AGCAGGAGCG TGCTGGCCCT GAGTACTGAA CTTTCTGAGT 2700  
 AACAAATGAGA CACGTTACAG AACCTATGTT CAGGTGCGG GTGAGCTGCC CTCTCCAAAT 2760  
 CCAGCCAGAG ATGCACATTC CTCGGCCAGT CTCAGCCAAC AGTACCAAAA GTGATTTTTG 2820  
 AGTGTGCCAG GGTAAGAGCT TCCAGTTTCT CCTCAGTTAT TTTAGACAAAT CTCGCCATCT 2880  
 TTAATTTCTT AGCTTCTGTT TCTAATAAAT GCACGGCTTT ACCTTTCCTG TCAGAAATAA 2940  
 ACCAAGGCTC TAAAGATGTA TTTCCCTTCT GTAACCTCCT AGAGCCACAG GTTCTCATTC 3000  
 CTTTCCCAT TATACTTCTC ACAATTCAGT TTCTATGAGT TTGATCACCT GATTTTTTTA 3060  
 ACAAATATTT TCTAACGGGA ATGGGTGGGA GTGCTGGTGA AAAGAGATGA AATGTGGTTG 3120  
 TATGAGCCAA TCATATTTGT GATTTTTTAA AAAAAGTTTA AAAGGAAATA TCTGTTCTGA 3180  
 AACCCCACTT AAGCATTTGT TTTATATAAA ACAAATGATA AAGATGTGAA CTGTGAAATA 3240  
 AATATACCAT ATTAGCTACC CACC

Seq ID NO: 54 Protein sequence  
 Protein Accession #: NP\_055026

1 11 21 31 41 51  
 MNYSLHLAFV CLSLFTERMC IQGSQFNVEV GRSDKLSLPG FENLTAGYNK FLRPNFGGEP 60  
 VQIALTLDDIA SISSISESNM DYTATIYLRQ RWMQRLVFE GNKSFTLDAR LVEFLWVPDT 120  
 YIVESKKSPFL HEVTVGNRLI RLFSNGTVLY ALRITTTVAC NMDLSKYPMD TQTKQLQLES 180  
 WGYDGNDFEF TWLRGNDVSR GLEHLRLAQY TIERYFTLVLT RSQQETGNYT RLVLQFELRR 240  
 NVLYFILETY VPSTFLVLVS WVSFWISLDS VPARTCIGVT TVLSMTTLM I GSRTSLPNTN 300  
 CFIKADIVLY GICFSEVFPA LLEYAVAHYS SLQQMAAKDR GTTKEVEEVS ITNIINSSIS 360  
 SPKRKISFAS IEISSDNVDY SDLTMTSDK FKFVFREKMG RIVDYFTIQN PSNVHDHYSKL 420  
 LFPLIFMLAN VFYWAYMYF

Seq ID NO: 55 DNA sequence  
 Nucleic Acid Accession #: XM\_084007  
 Coding sequence: 138..2405

1 11 21 31 41 51  
 CTCGTGCCGA ATTCGGCAGC AGACCGCGTG TTCGCGCCTG GTAGAGATTT CTCGAAGACA 60  
 CCAGTGGGCC CGTGTGGAAC CAAACCTGCG CGCGTGCGCG GGCCGTGGGA CAACGAGGCC 120  
 CGCGAGACGA AGCGCGCAAT GCGAGGAAGT TATCTGTAAT CTGTGATCCTG ACCTTTGCCC 180  
 TCTCTGTAC AAATCCCTT CATGAACTAA AAGCAGCTGC TTTCCCCAG ACCACTGAGA 240  
 AAATTAGTCC GAATTGGGAA TCTGGCATT AATGTTGACTT GGCAATTTC ACACGGCAAT 300  
 ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT 360  
 TCAGAAAATT ACTTCAAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420  
 ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480  
 AGCATCACTC AGACCACGAG CATCACTCTG ACCATGATCA TCACTCCAC CATAATCATG 540  
 TCGCTTCTGG TAAAAATAAG CGAAAAGCTC TTTGCCGAGA CCATGACTCA GATAGTTTCA 600  
 GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660  
 GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCAACTGTG TACAACACTG 720  
 TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTTCTC 780  
 CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCACATC AAAGAGCCGG GTGAGCCGGC 840  
 TGGCTGGTAG GAAAACAAAT GAATCTGTGA GTGAGCCCGG AAAAGGCTTT ATGTATTCCA 900  
 GAAACACAAA TGAATAATCT CAGGAGTGT TCAATGCATC AAAGCTACTG ACATCTCATG 960  
 GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATCA 1020  
 TCAACCAAT TGAATGCTAGA TCTTGTCTGA TTCATACAAG TGAAAAGAAG GCTGAAATCC 1080  
 CTCCAAAGAC CTATTCATTA CAAATAGCCT GGGTTGGTGG TTTTATAGCC ATTTCCATCA 1140  
 TCAGTTTCTT GTCTCTGCTG GGGGTTATCT TAGTGCCTCT CATGAATCGG GTGTTTTTCA 1200  
 AATTTCTCTT GAGTTTCTTT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTTT 1260  
 TACACCTTCT TCCACATTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCAG 1320  
 CAATGGAAAT GAAAAGAGGA CCACTTTTCA GTCATCTGTC TTCTCAAAAC ATAGAAGAAA 1380  
 GTGCCTATTT TGATTTCCAG TGGAAAGGTC TAACAGCTCT AGGAGGCTCT TATTTCTATG 1440  
 TTCTTGTTGA ACATGTCTCT ACATTGATCA ACAAATTAA AGATAAGAAG AAAAAGAATC 1500  
 AGAAGAAACC TGAATATGAT GATGATGTGG AGATTAAGAA GCAGTTGTCC AAGTATGAAT 1560  
 CTCACATTTT ACACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCATTATTAC 1620  
 GAGCAGACTC ACAAGAGCCC TCCCACTTGG ATCTCTAGCA GCCTGCGAGT TTGGAAGAA 1680  
 AAGAGGTCTT GATAGCTCAT GCTCATCCAC AGGAAGTCTA CAATGAATAT GTACCCAGAG 1740  
 GGTGCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA 1800  
 TTCACCACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCACCAA AACCAACATC 1860  
 CTCACAGTCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCCGGC GTCGCCACTT 1920  
 TGGCTGGTAG GGTGATAATG GGTGATGGCC TGCACAAATT CAGCGATGGC CTAGCAATTG 1980  
 GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTTGCT GTGTTCTGTC 2040  
 ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTTCTACT AAAGGCTGGC ATGACCGTTA 2100  
 AGCAGGCTGT CTTTATAAT GCATGTGTCAG CCATGCTGGC GTATCTTGA ATGGCAACAG 2160  
 GAATTTTCAT TGGTCATTAT GCTGAAAATG TTTCTATGTG GATATTTGCA CTTACTGCTG 2220  
 GCTTATTCAT GTATGTTGCT CTGTTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280  
 GTGACCATGG ATGATAGCGC TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340  
 GTTTTGGAAT TATGTACTT ATTTCCATAT TTGAACATAA AATCGTGTTC CGTATAAATT 2400  
 TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAAAGTTG TCATAGTTTC AGTAGGTCA 2460

AGGGAGATGA GTTGTGATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATTT 2520  
 TTGTATTGAA TATTGCTGTC TGTACAAAG TCAGTTAAAG GTACGTTTAA ATATTTAAGT 2580  
 TATTCTATCT TGGAGATAAA ATCTGTATGT GCAATTCACC GGTATTACCA GTTTATTATG 2640  
 TAAACAAGAG ATTTGGGCATG ACATGTTCTG TATGTTTCAG GGAATAATGT CTTTAATGCT 2700  
 TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTTTA GGTCTCTGAA GAACTGCTGG 2760  
 TGTTTAGGAA TAAGAATGTG CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820  
 AGCAAGAGAA TAAAGGAGAA AAGAGAAGAA TCTGAGAATT GGGGAGGCAT AGATTCTTAT 2880  
 AAAAATCACA AAATTTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAG TATAAAAAGG 2940  
 CAGAATTAGT ATAGAGTACA TTCATTAAAC ATTTTGTGCA GGATTATTTC CCGTAAAAAC 3000  
 GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT 3060  
 AAATATATTT AATGAATTCA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG 3120  
 TTCGTGCGGG TTATATACCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT 3180  
 TATTGCCAAG TTATATATCA CCAAAGCTG TATGACTGGA TGTCTGTTT ACCTGGTTTA 3240  
 CAAAATTATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAGT ACACATAAGTA 3300  
 TCATTGTATT CGATTTCAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATGTT 3360  
 GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGCTGTG GCATTCTCTA 3420  
 GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

Seq ID NO: 56 Protein sequence  
 Protein Accession #: XP\_084007

1 11 21 31 41 51  
 | | | | |  
 MARKLSVILI LTFALSVTNP LHELKAAAFP QTTEKISPNN ESGINVDLAI STRQYHLQQL 60  
 FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHDSHS DHEHSDHER HSDHEHSDH 120  
 EHSDHDSHS HHNHAASGN KKKALCPDHD SDSSGKDPNN SQKGGAHRPE HASGRRNVKD 180  
 SVSASEVTST VYNTVSEGT FLETIETPRP KGLFPKDVSS STPPSVTSKS RVSRLAGRKT 240  
 NESVSEPRKG FMYSRNTNEN PQECFNASKL LSHGGMGIQV PLNATEFNLY CPAIINQIDA 300  
 RSCLIHTSEK KAEIIPKTY S LQIAWVGGSF AISIISFLSL LGVILVPLMN RVFFKFLLSF 360  
 LVALAVGTLS GDAFLHLLPH SHASHHSHS HEPEAMEMKR GFLFSLSSQ NIEESAYFDS 420  
 TWKGLTALGG LYFMFLVEHV LTLIKQFKDK KKKNQKKPEN DDDVEIKQL SKYESQLSTN 480  
 BEKVDTDDRT EGYLRADSQE PSHFDSQQPA VLEEEVEMIA HAHPQEVYNE YVPRGCKNKC 540  
 HSHFHDTLGQ SDDLIIHHHD YHHILHHHH QNHHPHSHSQ RYSREELKDA GVATLAWMVI 600  
 MGDGLHNFSD GLAIGAAFTF GLSSGLSTSV AVFCHLPHE LGDFAVLLKA GMTVKQAVLY 660  
 NALSAMLAYL GMATGIFIGH YAENVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS 720  
 RWGYFFLQNA GMLLGFGIML LISIFEHKIV FRINF

Seq ID NO: 57 DNA sequence  
 Nucleic Acid Accession #: NM\_015419.1  
 Coding sequence: 1..8487

1 11 21 31 41 51  
 | | | | |  
 ATGCCCAAGC GCGCGCACTG GGGGGCCCTC TCCGTGGTGC TGATCCTGCT TTGGGGCCAT 60  
 CCGCGAGTGG CGCTGGCCTG CCGCATCCTT TGTGCCTGCT ACGTCCCCAG CGAGGTCCAC 120  
 TGCACGTTCC GATCCCTGGC TCCGTGCCCC GCTGGCATTG CTAGACACGT GGAAGAATC 180  
 AATTTGGGGT TTAATAGCAT ACAGGCCCTG TCAGAAACCT CATTTCAGG ACTGACCAAG 240  
 TTGGAGCTAC TTATGATTCA CGGCAATGAG ATCCCAAGCA TCCCGATGG AGCTTTAAGA 300  
 GACCTCAGCT CTCTTCAGGT TTTCAAGTTC AGCTACAACA AGCTGAGAGT GATCAGAGGA 360  
 CAGACCTCC CAGGTCCTCT TAACTTAATG AGGCTGCACA TTGACCAACA CAAGATCGAG 420  
 TTTATCCACC CTCAAGCTTT CAACGGCTTA ACGTCTCTGA GGCTACTCCA TTTGGAAGGA 480  
 AATCTCTCTC ACCAGCTGCA CCCCAGCACC TTCTCCACGT TCACATTTT GGTATTATTTC 540  
 AGACTCTCCA CCATAAGGCA CCTCTACTTA GCAGAGAACA TGGTTAGAAC TCTTCTGCCC 600  
 AGCATGCTTC GGAACATGCC GCTTCTGGAG AATCTTTACT TGCAGGGAAT TCCGTGGACC 660  
 TGCAGATTGT AGATGAGATG GTTTTGGAA TGGGATGCAA AATCCAGAG AATTCTGAAG 720  
 TGTAAAAGAG ACAAGGCTTA TGAAGGCGGT CAGTTGTGTG CAATGTGCTT CAGTCCAAAG 780  
 AAGTTGTACA AACATGAGAT ACACAAGCTG AAGGACATGA CTGTCTGTA GCCTTCAATA 840  
 GAGTCCCTCT TGAGACAGAA CAGGAGCAGG AGTATTGAGG AGGAGCAAGA ACAGGAAGAG 900  
 GATGGTGGCA GCCAGCTCAT CCTGGAGAAA TTCCAATGCG CCCAGTGGAG CATCTCTTTG 960  
 AATATGACCG ACGAGCACCG GAACATGGTG AACTTGGTCT GTGACATCAA GAAACCAATG 1020  
 GATGTGTACA AGATTCACCT GAACCAACG GATCCTCCAG ATATTGACAT AAATGCAACA 1080  
 GTTGCTTGG ACTTGTAGTG TCCAATGACC CGAGAAAAC ATGAAAAGCT ATGGAATTTG 1140  
 ATAGCATACT ACAGTGAAGT TCCGTGAAG CTACACAGAG AGCTCATGCT CAGCAAGAGC 1200  
 CCCAGAGTCA GCTACCAGTA CAGGCAGGAT GCTGATGAGG AAGCTCTTTA CTACACAGGT 1260  
 GTGAGAGCCC AGATCTTTCG AGAACCAGAA TGGGTCTATG AGCCATCCAT AGATATCCAG 1320  
 CTGAACCGAC CTCAGAGTAG GGCACAGAA GTGCTACTTT CACTACTAC CAGTATTCT 1380  
 CAAACAATAT CCACCAAGA TACAAGGCAG GCTCGGGGCA GAAGCTGGGT AATGATTGAG 1440  
 CCTAGTGGAG CTGTGCAAG AGATCAGACT GTCCTGGAAG GGGGTCCATG CCAGTTGAGC 1500  
 TGCAACGTGA AAGCTTCTGA GAGTCCATCT ATCTTCTGGG TGCTTCCAGA TGGCTCCATC 1560  
 CTGAAAGCGC CCATGGATGA CCCAGACAGC AAGTTCTCCA TTCTCAGCAG TGGCTGGCTG 1620  
 AGGATCAAGT CCAATGGAGC ATCTGACTCA GGCTGTGACC AGTGCATTGC TCAAGTGAGG 1680  
 GATGAAATGG ACCGCATGGT ATATAGGGTA CTTGTGCACT CTCCTCCAC TCAGCCAGCC 1740  
 GAGAAAGACA CAGTGACAAT TGGCAAGAAC CCAGGGGAGT CGGTGACATT GCCTTGCAAT 1800  
 GCTTTAGCAA TACCCGAAAG CCACCTTAGC TGGATTCTTC CAAACAGAA GATAATTAAT 1860  
 GATTGCGCTA ACACATCACA TGTATACATG TTGCCAAATG GAACCTCTTC CATCCCAAAG 1920  
 GTCCAAGTCA GTGATAGTGG TTAATACAGA TGTGTGGCTG TCAACCAGCA AGGGGCAGAC 1980  
 CATTTTACGG TGGGAATCAC AGTGACCAAG AAAGGGTCTG GCTTGCCATC CAAAAGAGGC 2040  
 AGACGCCAG GTGCAAGGCG TCTTTCCAGA GTCAAGAGAG ACATCGTGGG GGTGAGAGG 2100  
 GGCTCGGACA TGGGAGATGA AGAGAACACT TCAAGGAGAC TTCTGCATCC AAAGGACCAA 2160  
 GAGGTGTTC TCAAAACAAA GGATGATGCC ATCAATGGAG ACAAGAAAGC CAAGAAAGGG 2220  
 AGAAGAAAGC TGAAACTCTG GAAGCATTCG GAAAAAGAAC CAGAGACCAA TGTGTCAGAA 2280  
 GGTGCGAGAG TGTTCGAATC TAGACGAAGG ATAAACATGG CAAACAAACA GATTAATCCG 2340  
 GAGCGCTGGG CTGATATTTT AGCCAAAGTC CGTGGGAAAA ATCTCCCTAA GGGCACAGAA 2400  
 GTACCCCGGT TGATTAAGAC CACAAGTCCT CCATCCTTGA GCCTAGAAGT CACACCACCT 2460



	TTTCTGCTG	TTTCTCCCC	CTCAGCATCT	CCTGTGCAGA	CAGTAACCAG	TGCTGAAGAA	2520
	TCCTCAGCAG	ATGTACCTCT	ACTTGGTGAA	GAAGAGCACG	TTTGGGGTAC	CATTTCCTCA	2580
	GCCAGCATGG	GGCTAGAACA	CAACCACAAT	GGAGTTATTC	TTGTTGAACC	TGAAGTAACA	2640
5	AGCACACCTC	TGGAGGAAGT	TGTTGTATGAC	CTTTCCTGAGA	AGACTGAGGA	GATAACTTCC	2700
	ACTGAAGGAG	ACCTGAAGGG	GACAGCAGCC	CCTACACTTA	TATCTGAGCC	TTATGAACCA	2760
	TCTCTACTCT	TGCACACATT	AGACACAGTC	TATGAAAAGC	CCACCCATGA	AGAGACGGCA	2820
	ACAGAGGGTT	GGTCTGCAGC	AGATGTTGGA	TCGTCAACAG	AGCCCAATC	CAGTGAGTAT	2880
	GAGCCTCCAT	TGGATGCTGT	CTCCTTGGCT	GAGTCTGAGC	CCATGCAATA	CTTTGACCCA	2940
10	GATTTGGAGA	CTAAGTCACA	ACCAGATGAG	GATAAGATGA	AAGAAGACAC	CTTTGCACAC	3000
	CTTACTCCAA	CCCCACCAT	CTGGGTTAAT	GACTCCAGTA	CATCACAGTT	ATTTGAGGAT	3060
	TCTACTATAG	GGGAACCAAG	TGTCCCAAGC	CAATCACATC	TACAAGGACT	GACAGACAAC	3120
	ATCCACCTTG	TGAAAAGTAG	TCTAAGCACT	CAAGACACCT	TACTGATTAA	AAAGGGTATG	3180
	AAAGAGATGT	CTCAGACACT	ACAGGGAGGA	AATATGCTAG	AGGGAGACCC	CACACACTCC	3240
15	AGAAGTTCTG	AGAGTGAGGG	CCAAGAGAGC	AAATCCATCA	CTTTGCCTGA	CTCCACACTG	3300
	GGTATAATGA	GCAGTATGTC	TCCAGTTAAG	AAGCCTGCGG	AAACCACAGT	TGGTACCCTC	3360
	CTAGACAAAG	ACACCACAAC	AGTAACAACA	ACACCAAGGC	AAAAAGTTGC	TCCGTCATCC	3420
	ACCATGAGCA	CTCACCTCTT	TCGAAGGAGA	CCCAACGGGA	GAAGGAGATT	ACGCCCAAC	3480
	AAATTCCGCC	ACCGGCACAA	GCAAAACCCCA	CCCAACAATT	TTGCCCATC	AGAGACTTTT	3540
20	TCTACTCAAC	CAACTCAAGC	ACCTGACATT	AAGATTTCAA	GTCAAGTGGG	GAGTTCTCTG	3600
	GTTCTCTACG	CTTGGGTGGA	TAAACACAGT	AATACCCCA	AACAGTTGGA	AATGGAGAAG	3660
	AATGCAGAAC	CCACATCCAA	GGGAACACCA	CGGAGAAAAC	ACGGGAAGAG	GCCAAACAAA	3720
	CATCGATATA	CCCCTCTTAC	AGTGAGCTCA	AGAGCGTCCG	GATCCAAGCC	CAGCCCTTCT	3780
	CCAGAAAATA	AACATAGAAA	CATTGTTACT	CCCAGTTTCA	AAACTATACT	TTTGCCCTAG	3840
25	ACTGTTTCTC	TGAAAACCTG	GGGCCCTTAT	GATTCTTTAG	ATTACATGAC	AACCACCAAG	3900
	AAAAATATAT	CATCTTACCC	TAAAGTCCAA	GAGACACTTC	CAGTCACATA	TAAACCCACA	3960
	TCAGATGGAA	AAGAATTTAA	GGATGATGTT	GCCACAAATG	TTGACAAAAC	TAAAAGTGAC	4020
	ATTTTAGTCA	CTGGTGAATC	AATTACTAAT	GCCATACCAA	CTTCTCGCTC	CTTGGTCTCC	4080
	ACTATGGGAG	AATTTAAGGA	AGAATCCTCT	CCTGTAGGCT	TTCACGGAAC	TCCAACCTGG	4140
30	AATCCCTCAA	GACGGCCCA	GCCTGGGAGG	CTACAGACAG	ACATACCTGT	TACCCTTCT	4200
	GGGGAATAAT	TTACAGACCC	TCCCTTCTT	AAAGAGCTTG	AGGATGTGGA	TTTCACTTCC	4260
	GAGTTTTTGT	CCTCTTTGAC	AGTCTCCACA	CCATTTACCC	AGGAAGAAGC	TGGTTCTTCC	4320
	ACAACCTCTC	CAAGCATAAA	AGTGGAGGTG	GCTTCAAGTC	AGGCAGAAAC	CACCACCTT	4380
	GATCAAGATC	ATCTTGAAC	CACCTGTGGCT	ATTTCTCTTT	CTGAACACTAG	ACCACAGAAT	4440
35	CACACCCCTA	CTGCTGCCCG	GATGAAGGAG	CCAGCATCCT	CGTCCCCATC	CACAATTCTC	4500
	ATGCTTTTGG	GACAAACCAC	CACCCTAAG	CCAGCACTTC	CCAGTCCAAG	AATATCTCAA	4560
	GCATCTAGAG	ATTCCAAGGA	AAATGTTTTT	TTGAATTATG	TGGGGAATCC	AGAAACAGAA	4620
	GCAACCCCA	TCAACAATGA	AGGAACACAG	CATATGTCTG	GGCCAAATGA	ATTATCAACA	4680
	CCCTCTTCCG	ACCGGATGTC	ATTAACTTGG	TCTACAAAGC	TGGAATTGGA	AAAGCAAGTA	4740
40	TTTGGTAGTA	GGAGCTTACC	ACGTGGCCCA	GATAGCCAAC	GCCAGGATGG	AAGAGTTCTT	4800
	GCTTCTCATC	AACATAACCA	AGTCCCTGCC	AAACCCATCC	TACCAACAGC	AACAGTGAGG	4860
	CTACCTGAAA	TGTCCACACA	AAGCGCTTCC	AGATACTTGG	TAACTTCCCA	GTCACTCTGT	4920
	CACCTGGACCA	ACAAACCGGA	AATAACTACA	TATCCTTCTG	GGGCTTTGCC	AGAGAACAAA	4980
	CAGTTTACAA	CTCCAAGATT	ATCAAGTACA	ACAATTCTCT	TCCCATTGCA	CATGTCCAAA	5040
45	CCCAGCATTC	CTAGTAAGTT	TACTGACCGA	AGAACTGACC	AATTTCAATGG	TTACTCCAAA	5100
	GTGTTTGGAA	ATAACAACAT	CCTTGAGGCA	AGAAACCCAG	TTGGAAGGCC	TCCAGTCCA	5160
	AGAATTCTCT	ATTATTCCAA	TGGAAGACTC	CCTTTCTTTA	CCAACAAGAC	TCCTTCTTTT	5220
	CCACAGTTGG	GAGTCAACCG	GAGACCCCA	ATACCCACTT	CTCTTGCCCC	AGTAATGAGA	5280
	GAGAGAAAAG	TTATTCCAGG	TTCTTACCA	AGGATACATT	CCCATAGCAC	CTTCCATCTG	5340
50	GACTTTGGCC	CTCCGGCACC	TCCGTTGTTG	CACACTCCGC	AGACCACGGG	ATCACCTCTA	5400
	ACTAACTTAC	AGAAATATCC	TATGGTCTCT	TCCACCCAGA	GTCTATCTCT	CTTTATAACA	5460
	TCCTCTGTCC	AGTCTCTAGG	AAGCTTCCAC	CAGAGCAGCT	CAAAGTTCTT	TGCAGGAGGA	5520
	CCTCCIGCAT	CCAAATCTGT	GTCTCTTGGG	GAAAAGCCCC	AAATCCTCAC	CAAGTCCCCA	5580
	CAGACTGTGT	CCGTCAACCG	TGAGACAGAC	ACTGTGTTCC	CCTGTGAGGC	AACAGGAAAA	5640
55	CCAAAGCCTT	TCGTTACTTG	GACAAAGGTT	TCCACAGGAG	CTCTTATGAC	TCCGAATACC	5700
	AGGATACAAC	GGTTTGAAGT	TCTCAAGAAC	GGTACCTTAG	TGATACGGAA	GGTTCAAGTA	5760
	CAAGATCGAG	GCCAGTATAT	GTGCACCGCC	AGCAACCTGC	ACGGCCTGGA	CAGGATGGTG	5820
	GTCTTGCTTT	CGGTCAACGT	GCAGCAACCT	CAAATCCTAG	CCTCCCACTA	CCAGGACGCT	5880
	ACTGTCTACT	TGGGAGACAC	CATTGCAATG	GAGTGTCTGG	CCAAAGGGAC	CCGAGCCCCC	5940
60	CAATTTCTCT	GGATCTTCCC	TGACAGGAGG	GTGTGGCAAA	CTGTGTCCCC	CGTGGAGAGC	6000
	CGCATCACCC	TGCACGAAAA	CCGGACCCCT	TCCATCAAGG	AGGCGTCTTT	CTCAGACAGA	6060
	GGCGTCTATA	AGTGCGTGGC	CAGCAATGCA	GCCGGGGCGG	ACAGCCTGGC	CATCCGCTGT	6120
	CACGTGGCGG	CACCTGCCCC	CGTTATCCAC	CAGGAGAAGC	TGGAGAACAT	CTCGTGGCCC	6180
	CCGGGGCTCA	GCATTCACAT	TCACTGCACT	GCCAAGGCTG	CGCCCCCTGC	CAGCGTGGCG	6240
65	TGGGTGCTCG	GGGACGCTAC	CCAGATCCGC	CCCTCGCAGT	TCCTCCACGG	GAACCTGTTT	6300
	GTTTTCCTCA	ACGGGACGCT	CTACATCCGC	AACCTCGCGC	CCAAGGACAG	CGGGCGCTAT	6360
	GAGTGGCTGG	CCGCCAACCT	GGTAGGCTCC	GCGGCGAGGA	CGGTGCAAGT	GAACGTGCAG	6420
	CGTGACGAGC	CCAACGCGCG	CATCACGGGC	ACCTCCCGCG	GGAGGACGGA	CGTCAGGTAC	6480
	GGAGGAACCC	TCAAGCTGGA	CTGCAGCGCC	TCGGGGGACC	CCTGGCCGCG	CATCCTCTGG	6540
70	AGGCTGCCGT	CCAAGAGGAT	GATCGACGCG	CTCTTCAGTT	TTGATAGCAG	AATCAAGGTG	6600
	TTTGCCAAAT	GGACCTGGT	GGTGAAATCA	GTGACGGACA	AAGATGCGCG	AGATTACCTG	6660
	TGCGTAGCTC	GAAATAAGGT	TGGTGATGAC	TACGTGGTGC	TCAAAGTGA	TGTGGTGATG	6720
	AAACCGGCCA	AGATTGAACA	CAAGGAGGAG	AACGACCACA	AAGTCTTCTA	CGGGGGTGAC	6780
	CTGAAAGTGG	ACTGTGTGGC	CACCGGGCTT	CCCAATCCCG	AGATCTCCTG	GAGCCTCCCA	6840
75	GACGGGATGC	TGGTGAACCT	CTTCATGACG	TCGGATGACA	CGGGTGAGAC	CACCAAGCGC	6900
	TATGTCTGCT	TCAACAATGG	GACACTCTAC	TTTAACGAAG	TGGGGATGAG	GGAGGAAGGA	6960
	GACTACACTT	GCCTTGCTGA	AAATCAGGTC	GGGAAGGACG	AGATGAGAGT	CAGAGTCAAG	7020
	GTGGTGACAG	GCCCCGCCAC	CATCCGGAAC	AAGACTTACT	TGGCGGTTCA	GGTGCCCTAT	7080
	GGAGACGTTG	TCACTGTAGC	CTGTGAGGCC	AAAGGAGAAC	CCATGCCCAA	GGTGACTTGG	7140
80	TTGTCCCAAA	CCAACAAGGT	GATCCCCACC	TCCTCTGAGA	AGTATCAGAT	ATACCAAGAT	7200
	GGCACTCTCC	TTATTTCAGAA	AGCCACGCGT	TCTGACAGCG	GCAACTACAC	CTGCCTGGTC	7260
	AGGAACAGCG	CGGGAGAGGA	TAGGAAGACG	GTGTGGATTTC	ACGTCAACGT	CCAGCCACCC	7320
	AAGATCAACG	GTAACCCCAA	CCCCATCAC	ACCGTGCGGG	AGATAGCAGC	CGGGGGCAGT	7380
	CGGAACTGTA	TTGACTGCAA	AGCTGAAGGC	ATCCCCACCC	CGAGGGTGT	ATGGGCTTTT	7440
	CCCAGGGGTG	TGGTCTTGCC	AGCTCCATAC	TATGGAACCC	GGATCACTGT	CCATGGCAAC	7500

5	GGTTCCCTGG	ACATCAGGAG	TTTGAGGAAG	AGCGACTCCG	TCCAGCTGGT	ATGCATGGCA	7560
	CGCAACGAGG	GAGGGGAGGC	GAGGTGATC	GTGCAGCTCA	CTGTCTCGGA	GCCCATGGAG	7620
	AAACCCATCT	TCCACGACCC	GATCAGCGAG	AAGATCACGG	CCATGGCGGG	CCACACCATC	7680
	AGCCTCAACT	GCTCTGCCGC	GGGGACCCCG	ACACCCAGCC	TGGTGTGGGT	CCTTCCCAAT	7740
	GGCACCAGTC	TGCAGAGTGG	ACAGCAGCTG	CAGCGCTTCT	ACCAACAAGC	TGACGGCATG	7800
	CTACACATTA	GGGTCCTCTC	CTCGGTGGAC	GCTGGGGCCT	ACCGCTGCGT	GGCCCGCAAT	7860
	GCCGCTGGCC	ACACGGAGAG	GCTGGTCTCC	CTGAAGGTGG	GACTGAAGCC	AGAAGCAAAC	7920
	AAGCAGTATC	ATAACCTGGT	CAGCATCATC	AATGGTGAGA	CCCTGAAGCT	CCCCTGCACC	7980
	CCTCCCGGGG	CTGGGCAGGG	ACGTTTCTCC	TGGACGCTCC	CCAATGGCAT	GCATCTGGAG	8040
10	GGCCCCAAAC	CCCTGGGACG	CGTTTCTCTT	CTGGACAATG	GCACCTCTAC	GGTTCGTGAG	8100
	GCCTCGGTGT	TTGACAGGGG	TACCTATGTA	TGCAGGATGG	AGACGGAGTA	CGGCCCTTCG	8160
	GTCACCAGCA	TCCCCGTGAT	TGTGATCGCC	TATCCTCCCC	GGATCACCAG	CGAGCCCAAC	8220
	CCGGTCATCT	ACACCCGGCC	CGGGAACACC	GTGAACTGA	ACTGCATGGC	TATGGGGATT	8280
	CCCAAAGCTG	ACATCACGTG	GGAGTTACCG	GATAAGTCGC	ATCTGAAGGC	AGGGGTTCAG	8340
15	GCTCGTCTGT	ATGGAACACG	ATTTCTTCAC	CCCCAGGGAT	CACTGACCAT	CCAGCATGCC	8400
	ACACAGAGAG	ATGCCCGTCT	CTACAAGTGC	ATGGCAAAAA	ACATTCTCGG	CAGTGACTCC	8460
	AAAACAACTT	ACATCCACGT	CTTCTGAAAT	GTGGATTCCA	GAATGATTGC	TTAGGAACTG	8520
	ACAACAAGAG	GGGTTTGTGA	AGGGAAGCCA	GGTTGGGGAA	TAGGAGCTCT	TAAATAATGT	8580
20	GTCACAGTGC	ATGGTGGCCT	CTGGTGGGTT	TCAAGTTGAG	GTTGATCTTG	ATCTACAATT	8640
	GTTGGGAAAA	GGAAGCAATG	CAGACACGAG	AAGGAGGGCT	CAGCCTTGCT	GAGACACTTT	8700
	CTTTTGTGTT	TACATCATGC	CAGGGGCTTC	ATTCAGGGTG	TCGTGTCTCT	GACTGCAATT	8760
	TTTCTTCTTT	TGCAAAATGCC	ACTCGACTGC	CTTCATAAGC	GTCCATAGGA	TATCTGAGGA	8820
	ACATTTCATCA	AAAAAAGCC	ATAGACATGA	ACAACACCTC	ACTACCCCAT	TGAAGACGCA	8880
25	TCACCTAGTT	AACCTGCTGC	AGTTTTTACA	TGATAGACTT	TGTTCCAGAT	TGACAAGTCA	8940
	TCCTTCAGTT	ATTTCCTCTG	TCACCTCAAA	ACTCCAGCTT	GCCCAATAAG	GATTTAGAAC	9000
	CAGAGTGACT	GATATATATA	TATATATTTT	AATTCAGAGT	TACATACATA	CAGCTACCAT	9060
	TTTATATGAA	AAAAGAAAAA	CATTTCTTCC	TGGAACCTAC	TTTTTATATA	ATGTTTTATA	9120
	TATATATTTT	TTCTTTTCAA	ATCAGACGAT	GAGACTAGAA	GGAGAAATAC	TTTCTGTCTT	9180
30	ATTAAATATA	ATAAAATATT	GGTCTTTACA	AGACTTGGAT	ACATTACAGC	AGACATGGAA	9240
	ATATAATTTT	AAAAAATTTT	TCTCCAACCT	CCTTCAAATT	CAGTCACCAC	TGTTATATTA	9300
	CCTTCTCCAG	GAACCCCTCA	GTGGGGAAGG	CTGCGATATT	AGATTTCTCT	GTATGCAAAAG	9360
	TTTTTGTGTA	AAGCTGTGCT	CAGAGGAGGT	GAGAGGAGAG	GAAGGAGAAA	ACTGCATCAT	9420
	AACTTTACAG	AATTGAATCT	AGAGTCTTCC	CCGAAAAGCC	CAGAACTTTC	TCTGCAGTAT	9480
35	CTGGCTTGTC	CATCTGGTCT	AAGGTGGCTG	CTTCTTCCCC	AGCCATGAGT	CAGTTTGTGC	9540
	CCATGAATAA	TACACGACCT	GTTATTTCCA	TGACTGCTTT	ACTGTATTTT	TAAGGTCAAT	9600
	ATACTGTACA	TTTGATAATA	AAATAATATT	CTCCCAAAAA	AAAAA		

Seq ID NO: 58 Protein sequence  
Protein Accession #: NP\_056234.1

40	1	11	21	31	41	51	
	MPKRAHWGAL	SVVLILLWGH	PRVALACPHP	CACYVPSEVH	CTFRSLASVP	AGIARHVERI	60
45	NLGFNSIQAL	SETSFAGLTK	LELLMIHNE	IPSIPDGALR	DLSSLQVFKF	SYNKLRVITG	120
	QTLQGLSNLM	RLHIDHNKIE	FIHPQAFNGL	TSRLRLHLEG	NLLHQLHPST	FSTFTFLDYF	180
	RLSTIRHLYL	AENMVRTLPA	SMLRNMPLLE	NLYLQGNPWT	CDCEMRWFLE	WDAKSRGILK	240
	CKKDKAYEGG	QLCAMCFSPK	KLYKHEIHKL	KDMTCLKPSI	ESPLRQNRSR	SIEEEQEQEE	300
	DGGSQLILEK	FQLPQWSISL	NMTDEHGNMV	NLVCDIKKPM	DVYKIHLNQT	DPPDIDINAT	360
50	VALDFECFMT	RENYEKLWKL	IAYSEVPVK	LHRELMLSKD	PRVSYQYRQD	ADEALYYTG	420
	VRAQILAEPE	WVMQAGTIDQ	LNRRQSTAKK	VLLSYTYQYS	QTISTKDTRO	ARGRSWVMIE	480
	PSGAVQRDQT	VLEGGPQQLS	CNVKASESPS	IFWVLPDGS	LKAPMDPDSD	KFSILSSGWL	540
	RIKSMEPSDS	GLYQCIQAVR	DEMDRMVYRV	LVQSPSTQPA	EKDTVTIGKN	PGESVTLPCN	600
	ALAIPEAHLS	WILPNRRIIN	DLANTSHVYM	LPNGTSLIPK	VQVSDSGYYR	CVAVNQGGAD	660
55	HFTVGITVTK	KGSLPLSKRG	RRPGAKALSR	VREDIVEDEG	GSNGMDEENT	SRRLHLPKDQ	720
	EVFLTKDDA	INGDKKAKKG	RRKLKLWKHS	EKEPETNVAE	GRRVFESRRR	INMANKQINP	780
	ERWADILAKV	RGKNLPGKTE	VPPLIKTTSP	PSLSLEVTPP	PPAVSPSPAS	PVQVTTSAAE	840
	SSADVPLLGE	EEHVLGTISS	ASMGLEHNHN	GVILVEPEVT	STPLEEVVDD	LSEKTEEITS	900
	TEGDLKGTAA	PTLLSEPEYR	SPTLHLDTV	YEKPHEETA	TEGWSAADVG	SSPEPTSSEY	960
60	BPPLDAVSLA	ESEPMQYFDP	DLETKSQPD	DKMKEDTFAH	LTPTPTIWN	DSSTSOLFED	1020
	STIGEPGVPG	QSHLQLFDN	IHLVKSSLST	QDTLLIKKGM	KEMSQTLQGG	NMLEGDPHST	1080
	RSSESEGQES	KINTLPDSTL	GIMSSMSPVK	KPAETTVGTL	LDKDTTIVTT	TPRQKVAPSS	1140
	TMSTHPSRRR	PNGRRRLRPN	KFRHRHKQTP	PTTFAPSETF	STQPTQAPDI	KISSQVESSL	1200
	VPTAWVDNTV	NTPKQLEMEK	NAEPTSKGTP	RRKHGKRPNK	HRYTPSTVSS	RASGSKPSPS	1260
65	PENKHRNIVT	PSSETILLPR	TVSLKTEGPE	DSLDMYMTTR	KIYSSYPKVQ	ETLPVTVKPT	1320
	SDGKEIKDDV	ATNVDKHKSD	ILVTGESITN	AIPTSRSLVS	TMGEFKEESS	PVGFPFGPTW	1380
	NPSRTAQVGR	LQTDIPVPTS	GENLTDPPLL	KELEDVDFTS	EFLSSLTVST	PFHQEEAGSS	1440
	TTLSIKVEV	ASSQAETTTQ	DQDHLLETTVA	ILLSETRPQN	HTPTAARMKE	PASSSPSTIL	1500
	MSLGQTTTTK	PALPSPRISQ	ASRDSKENVF	LNRYGNPTE	ATPVNNEGTO	HMSGPNELST	1560
70	PSSDRDAFNL	STKLELEKQV	FGSRSLPRGP	DSQRQDGRVH	ASHQLTRVPA	KPILPTATVR	1620
	LPSTSTQAS	RYFVTSQSPR	HWTNKPEITT	YPSGALPENK	QFTTPRLSST	TIPPLHMSK	1680
	PSIPSKFTDR	RTDQFNGYSK	VFGNNNIEPA	RNPVGKPPSP	RIPHYSNRGL	PPFTNKTLSP	1740
	PQLGVTRRRQ	IPTSPAPVMR	ERKVIKPSYN	RIHSHSTFHL	DFGPPAPPLL	HTPQTGSPS	1800
	TNLQNIPTMS	STQSSISFT	SSVQSSGSPH	QSSSKFFAGG	PPASKFWSLG	EKPQILTKSP	1860
75	QTVSVTAETD	TVFPCEATGK	PKPFVTWTKV	STGALMTPTN	RIQRFEVLKN	GTLVIRKQVP	1920
	QDRGQYMCFA	SNLHGLDRMV	VLLSVTVQQP	QILASHYQDV	TVYLGDTIAM	ECLAKGTAP	1980
	QISWIFPDPR	VWQTSVPVES	RITLHENRTL	SKEASFSDR	GVIKCVASNA	AGADSLAIRL	2040
	HVAALPPVIH	QEKLENISLP	PGLSIHIHCT	AKAAPLPSVR	WVLGDTQIR	PSQFLHGNLF	2100
	VFPNGTLYIR	NLAPKDSGRY	ECVAANLVGS	ARRTVQLNVQ	RAAANARITG	TSPRRTDVRY	2160
80	GGTLKLDCA	SGDPWPRLIW	RLPSKRMIDA	LFSFDSRIKV	FANGTLVVK	VTDKADAGDYL	2220
	CVARNKVGDD	YVVLKVDVVM	KPAKIEHKKE	NDHKVFYGGD	LKVDVCVATGL	PNPETISWLP	2280
	DGSLVNSFMQ	SDDSGGRTKR	YVVFNNGTLY	FNEVGMREBG	DYTCFAENQV	GKDEMRVRVQ	2340
	VVTAPATIRN	KTYLAVQVFP	GDVVTVACEA	KGEPMKPVTV	LSPTNKVIPT	SSEKYQIYQD	2400
	GTLILQKAGR	SDSGNYTCLV	RNSAGEDRKT	VWIHVNQVPP	KINGNENPIT	TVREIAAGGS	2460
	RKLIDCKABG	IPTPRVLWAF	PEGVVLPAFY	YGNRITVHGN	GSLDIRSLRK	SDSVQLVCMA	2520

RNEGGEARLI VQLTVLEPME KPIFHDPISE KITAMAGHTI SLNCSAAGTP TPSLVWVLPN 2580  
 GTDLQSQQL QRFYHKADGM LHISGLSSVD AGAYRCVARN AAGHTERLVS LKVGLKPEAN 2640  
 KQYHNLVSI NGETLKL PPGAGQGRFS WTLPMHLE GPQTLGRVSL LDNGTLTVRE 2700  
 ASVFDRGTIV CRMTEYGPS VTSIPVIVIA YPPRITSEPT PVIYTRPNT VKLNCMAMGI 2760  
 PKADITWELP DKSHLKAGVQ ARLYGNRFLH PQGSLTIQHA TQRDAGFYKC MAKNILGSDS 2820  
 KTTYIHVF

Seq ID NO: 59 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..5001

	1	11	21	31	41	51	
15	ATGCCAGGCA	CAAAACTAAC	CCGAACAGGC	GCCCCAGCAG	ACTACAGAGT	GATATTGAAG	60
	ACCTCTCAAG	AGGACGAATT	GGATGTACCT	GACGACATCA	GCGTCCGGGT	TATGTCTATCT	120
	CAGTCTGTGC	TTGTGTCCCT	GGTGGATCCT	GTTCTGGAAA	AACAGAAAGAA	AGTTGTTGCA	180
	TCAAGACAGT	ACACCGTGGC	CTATCGAGAG	AAGGGGGAAT	TGGCCAGGTG	GGATTATAAG	240
	CAGATCGCTA	ACAGGCGTGT	GCTGATTGAG	AACTTGATTG	CAGACACTGT	GTATGAATTT	300
20	GCAGTCCGTA	TTTCACAGGG	TGAAAGAGAT	GGCAAATGGA	GTACGTCAGT	CTTCCAAAGA	360
	ACACCAGAA	CTGCCCTTAC	CACAGCTCCT	GAAGAACTTGA	ACGTCTGGCC	AGTCAATGGC	420
	AAACCTACAG	TTGTGCTGTC	ATCTTGGGAT	GCGCTACCAG	AGACTGAGGG	GAAAGTGAAA	480
	GTCTGTCTGC	TGGACACAGG	ACTGTTTTCA	GTTTCTCCTC	TCCAACCATC	TGCCAAATCA	540
	TTTCAGAATA	CATTCTTTCA	TACGCCCCGG	CTCTCAAACC	ATTTGGAGCA	AAGTCCCTCA	600
25	CCTATCCTGG	AGACACTACT	TCTGCCCTGG	TGGATGGTCT	GCAGCCTGGG	GAACGCTATC	660
	TTTTCAAAAT	CCGGGCCACA	AACAGGAGAG	GCCTGGGACC	TCACTCCAAA	GCCTTCATGT	720
	TGCTATGCTG	AACAAGAATG	CAGCTGTACC	CAGAAGGATT	TCAGTTGTCT	AGCTTACCTG	780
	ATCGATATCC	AAACCAAAAC	AGTTAATAAA	GATCCACAAC	TGGAAGGGAG	TGTTTTTGGA	840
	CCATGTTTTG	TTTTCTACTT	CCTCACATTT	ATGCTGGATA	TTGGCGGCTT	TTCTTTCATT	900
30	ATGTGCTATG	AAGACCAANN	TGTTTTCTCT	TTGACAGGCA	ATTCTTTAAA	ATCTGTTGCA	960
	GCCAGTAAGG	CGGATGTTCA	GCAGAACACG	GAGGACAATG	GGAACCCCGA	AAAACCTGAG	1020
	CCTTCTCTAC	CTTCTCCAG	AGCTCCAGCT	TCTCTCCAAC	ACCCCTCTGT	GCCTGCTTCT	1080
	CCCCAAGGGA	GAAATGCCAA	GGACCTTCTT	CTTGACTTGA	AGAACAAAAT	ATTGGCTAAT	1140
	GGTGGGGCGC	CCCGAAACC	CCAGCTTCGC	GCCAAGAAAG	CAGAGGAGCT	GGATCTTCAG	1200
35	TCGACAGAAA	TCACTGGGGA	GGAGGAGCTG	GGTTCCCGGG	AGGACTCGCC	CATGTCACCC	1260
	TCAGACACCC	AAGACCAGAA	ACGGACCCCT	AGGCCGCCAA	GTAGACACGG	CCACTCGGTG	1320
	GTGTCTCCCG	GCAGGACTGC	AGTGAGGGCC	CGGATGCCAG	CGCTGCCCCG	AAGGGAAGGC	1380
	GTAGATAAGC	CTGGCTTTTC	CCTGGCCACG	CAGCCCGGCC	CAGGGGCGCC	CCCCTCGGCT	1440
	TCGGCCTCTC	CTGCCACCA	CGCGTCCACC	CAGGGCACCT	CTCATCGTCC	TTCCCTGCCT	1500
40	GCCAGCTTGA	ATGACAACGA	CTTGGTGGAC	TCAGACGAAG	ATGAGCGCGC	TGTGGGCTCC	1560
	CTCCACCCCA	AGGGCCGCTT	CGCCACGCC	CGGCCAGCCC	TGTCCTCCAG	CGCCAGTCC	1620
	CCGTCCAGCG	TTCTCCGCGA	CAGAAGCTCT	GTGCACCCCG	CGCACAAGCC	AGCCTCGCCG	1680
	CGCGGAGGGA	CCCCCATTT	AGGGCCGCA	GAGGAAGATT	CCAGTGCCTC	AGCCCCACCC	1740
	TCAAGACTTT	CTCCACCCCA	TGGGGGATCA	TCTCGGCTGC	TGCCACCCCA	GCCACACCTG	1800
45	AGCTCTCCAC	TTTCCAAGGG	CGGGAAGGAT	GGTGAGGACG	CCCCAGCCAC	CAACTCCAAT	1860
	CGGCCATCAC	GGTCCACCAT	GTCTCTCTCT	ATCTCTCGTC	CAGGACGCGA		1920
	GTCTCTGAGG	GAGCGGAGGC	TTCTGATGGT	GAAAGCCACG	GTGACGCGCA	TAGGGAAGAC	1980
	GGCGGAAGGC	AGGCGGAGGC	CACGGCCCGG	ACGCTGCGGG	CCGGGCGCTG	CTCTGGACAC	2040
	TTCCATTGTC	TCAGACACAA	ACCCTTTGCT	GCCAACGGGA	GGTCTCCAAG	CAGGTTTCAG	2100
	ATTGGGCGGG	GAGCTCGGCT	GCAGCCCTCC	AGCTCCCCAC	AGTCGACTGT	GCCTTCCCGA	2160
50	GCCACACCCA	GGGTTCCTCT	TCACCTGAT	TCCCAACCTA	AGCTTAGCTC	AGGTATCCAT	2220
	GGAGACGAGG	AGGATGAGAA	GCCGCTTCTT	GCCACCGTTG	TCAATGACCA	CGTGCCTTCC	2280
	TCCTCCAGGC	AGCCCATCTC	CCGGGGCTGG	GAGGACTTAA	GGAGAAGCCC	GCAGAGAGGG	2340
	GCCAGCCTGC	ATCGGAAGGA	ACCCATCCCA	GAGAACCCCA	AATCCACAGG	GGCAGATACA	2400
	CATCTCAGG	GCAAGTACTC	CTCCCTGGCC	TCCAAGGCTC	AGGATGTTCA	ACAGAGCACA	2460
55	GACGCGGACA	CGGAGGGTCA	TTCTCCCAAA	GCACAGCCAG	GGTCCACAGA	CCGCCACGCG	2520
	TCCCTGTCTC	GTCTTCCCG	AGCACGGTCA	CAGCAGCATC	CCAGTGTTC	CAGAAGGATG	2580
	ACACCCGGCC	GGGCCCCAGA	ACAGCAGCCC	CCTCTCCCG	TGCGCCAGTC	CCAGCACCAC	2640
	CCGGGACCCC	AGAGCAGAGA	CGCGGTTCGG	TCACCTTCCC	AGCCAGGCT	CTCACTGACC	2700
	CAGGCCGGGC	GGCCCCGGCC	CACGTCGCAG	GGCGGCTCCC	ACTCTCTCTC	GGACCCTTAC	2760
60	ACGGCGAGCT	CCAGAGGGAT	GCTCCCCACG	GCCCTCCAGA	ACCAGGACGA	GGATGCCCGG	2820
	GGCAGTACG	ACGACGACAG	CACAGAAGTC	GAGGCCAGG	ATGTGCGGGC	CCCCGCGCAC	2880
	GCCGCGCGCG	CCAAGGAGGC	AGCTGCGTCC	CTTCCCAAGC	ACCAGCAGGT	GGAGTCTCCC	2940
	ACAGGCGCAG	GGGCGAGTGG	CGACCACAGG	TCCCAGCGCG	GACATGCGGC	CTCCCCCGCC	3000
65	AGGCCACGCC	GACCCGCGCG	CCCCCAGTCC	CGCGCCCGGG	TCCCCAGCAG	GGCAGCGCCG	3060
	GGGAAGTCGG	AGCCTCCTTC	CAAGCGGGCC	CTGTCTTCCA	AGTCCCAGCA	GTCCGTCTCA	3120
	GCCGAGGACG	AGGAGGAGGA	GGACGCGGGG	TTTTTTAAAG	GCGGGAAGAA	AGACCTTCTG	3180
	TCTTCTCTCT	TGCCAAAGTG	GCCCTCTTCC	TCCACTCCCA	GGGGCGGCAA	AGACGCGGAT	3240
	GGGAGCTCTG	CCAAGGAAGA	GAGGGAGCCT	GCCATCGCGC	TTGCCCCCTG	CGGAGGGAGG	3300
70	CTGGCTCTCT	TGAAGCGACC	TCTCCCCCCA	CCTCCAGGCA	GCTCCCCCAG	GGCTCCCCAC	3360
	GTCCCTTCCC	GACCGCGGCC	TCGCAGCGCT	GCCACCGTGA	GCCCCGTGCG	GGGCACCCAC	3420
	CCCTGGCGCG	GGTACACCAC	GCGCGCCCV	CCTGGCCACT	TCTCCACCAC	CCCGATGCTG	3480
	TCCTTGCCTG	AGAGGATGAT	GCATGCCAGA	TTCCGTAACC	CTCTCTCCCG	ACAGCCTGCC	3540
	AGACCCTCTT	ACAGACAAGG	TTATAATGGC	AGACCAATAT	TAGAAGGGAA	AGTCTTCTCT	3600
75	GGTAGTAATG	GAAACCCGAA	TGGACAGAGA	ATTATCAATG	GCCCTCAAGG	AACAAAGTGG	3660
	GTTGTGAGAC	TTGATCGTGG	GTTAGTATTG	AATGCAGAAG	GAAGGTACCT	CCAAGATTCA	3720
	CATGGAATAT	CTCTTCGGAT	TAAACTAGGA	GGAGATGGTC	GAACCATGTG	AGATCTGGAA	3780
	GGGACCCCGG	TGGTGAGTCC	TGACGGCCTC	CCACTCTTTG	GGCAGGGGCG	ACATGGCACA	3840
	CCTCTGGCCA	ATGCCCAAGT	TAAGCCAATT	TTGAGTCTTG	GAGGAAAGCC	GCTGGTGGGC	3900
80	TTGGAGGTCA	TCAAAAACAC	CACCATCCC	CCTACCACTA	CCATGCAGCC	CACCACTACT	3960
	ACGACGCCCC	TGCCATACCAC	TACAACCCCG	AGGCCACCA	CTGCCACCAC	CATGCAGCCC	4020
	ACCACCTACT	CGACGCCCTT	GCCTACCACT	ACACCGAGGC	CCACCACTGC	CACCAACCCG	4080
	CGCAGCACCA	CCAGGCTCCC	AACAACCA	GTCCGAACCA	CTACGCGGAC	AACCAACCCG	4140
	ACCACCCCCA	AACCCACCAC	TCCATCCCC	ACCTGTCCCC	CTGGGACCTT	GGAACGGCAC	4200
	GACGATGATG	GCAACCTGAT	AATGAGCTCC	AATGGGATCC	CAGAGTGCTA	CGCTGAAGAA	4260

	GATGAGTTCT	CAGGCTTGGG	GACTGACACT	GCAGTACCTA	CGGAAGAGGC	CTACGTTATA	4320
	TATGATGAAG	ATTATGAATT	TGAGACGTCA	AGGCCACCAA	CCACCACTGA	GCCTTCGACC	4380
	ACTGCTACCA	CACCGAGGGT	GATCCCAGAG	GAAGGCGCCA	TCAGTTCCTT	TCCTGAAGAA	4440
5	GAATTTGATC	TGGCTGGAAG	GAAACGATTT	GTTGCTCCTT	ACGTGACGTA	CCTAAATAAA	4500
	GACCCATCAG	CCCCGTGCTC	TCTGACTGAT	GCACTGGATC	ACTTCCAAGT	GGACAGCCTG	4560
	GATGAAATCA	TCCCAATGA	CCTGAAGAAG	AGTGATCTGC	CTCCCCAGCA	TGCTCCCCGC	4620
	AACATCACCG	TGGTGGCCGT	GGAAGGTTGC	CACCTATTTC	TCATTGTGGA	TGCGGACAAA	4680
	GCCACCCAG	GAGATTTGGT	CACAGGTTAT	TGTTGTTTACA	GTGCATCCTA	TGAAGATTTC	4740
10	ATCAGGAACA	AGTTTTCCAC	TCAAGCTTCA	TCAGTAACTC	ACTTGCCCAT	TGAGAACCTA	4800
	AAGCCCAACA	CGAGGTATTA	TTTTAAAGTG	CAAGCACAAA	ATCCTCATGG	CTACGGACCT	4860
	ATCAGCCCTT	CGGTCTCATT	TGTCACCGAA	TCAGATAATC	CTCTGCTTGT	TGTGAGGCC	4920
	CCAGGCGGTG	AGCTATCTGG	ATCCCATTCG	CTTTCAAACA	TGATCCCAGC	TACACGGACT	4980
	GCCATGGACG	GCAATATGTG	AAGCGCACGT	GGTATCGAAA	GTTTGTGGGA	GTTTGTCTTT	5040
15	GTAATTCAC	TGAGGTATAA	ATCTACCTCA	GTGACAACCT	GAAAGATACA	TTCTACAGCA	5100
	TGAGGAGACG	CTGGGGAAGA	GGTGAAGACC	ATTGCCAATT	TGTGGATTCA	CACCTTGATG	5160
	GAAGAACAGG	GCCTCAGTCC	TATGTAGAAG	CCCTCCCTAC	TATTCAGGCG	TACTATCGCC	5220
	AGTATCGTCA	GGAGCCTGTC	AGGTTTGGGA	ACATCGGCTT	CGGAACCCCC	TACTACTATG	5280
	TGGGCTGGTA	CGAGTGTGGG	GTCCTCCATC	CTGGAAGTGT	GTAATCACAG	GACCGTCATG	5340
20	CTGCAAGCTT	GCCCTGCCCA	GCCCCACCAA	CTAAGTCGCA	CTAGGGGCTG	TGAGCAAAGA	5400
	CAGCCAGCAT	GCTCAGCCCC	GCTGCCCTAG	GTGCCAGGAA	GGTCACAGAT	GGACACTGGC	5460
	ATCTCTGGTC	ATCTCAGTCT	GGAACCTCAG	CCCACTTCTT	GGCCTGGACA	ATGAACAGGA	5520
	TTCACTTTTG	CTGTTAACTT	TGCTTCTCTA	CTTTTTTTTG	TTTGTGTTGA	ATAGCACATC	5580
	CCAGAGACAT	CAGAAACGAG	CAACTGATTG	AGTGTGATTT	CCCAGACTTT	TAGGCATGA	5640
25	AATTCGGACA	CTTCAGTATT	TCCAGGAATA	GCATATGCAC	GCTGTCTCTG	CTTCATGGAA	5700
	TGCTACATCG	TTCTCTGTTT	TCTCATTTTG	GATTTCTCCA	AAACTAACTG	AATTTAAGCT	5760
	TCAGGTCCCT	TGTTATGTCG	TAGAAAGGAA	TTATTAAAAA	CACCACCAA	GAAAAATAAT	5820
	ATATCTACT	TGAAATTTAC	TCTATGGACT	TACCCACTGC	TAGAATAAAT	GTATCAAATC	5880
	TTATTTGTAA	ATTCTCAATT	TTGATATATA	TATGTATATA	TGCATATACA	TATCCACACT	5940
30	TGCTGCAAG	AATATTGATT	AAAATTGCTA	AATTTGTACT	TGTTTACCAC	AAAAAATAAT	6000

Seq ID NO: 60 Protein sequence  
Protein Accession #: Eos sequence

35	1	11	21	31	41	51	
	MPGTLKTRTG	APADYRVILK	TSQEDELDPV	DDISVRVMSS	QSVLVSVDV	VLEKQKVVVA	60
	SRQYTVRYRE	KGBELARWDYK	QIANRRVLIE	NLIPDVTYEF	AVRISQGERD	GKWTSTVFQR	120
40	TPESAPTTAP	ENLNVWVING	KPTVVAASWD	ALPETEGKVK	VCLLDLTGLFS	VSSFQPSAKS	180
	FQNTFFHTPR	LSNHLQSPS	PILETLPLPW	WMVCSLGNAI	FSKSGPQTGE	AWDLTPKPSL	240
	SLCQEQCSCT	QKDFSLAYL	IDITKQVVK	DPQLGSSVFG	PCFLFYFLTF	MLDIGGFSFI	300
	MCYEDPVSSL	TGNSLKSVA	SKADVQONTE	DNGKPEKPEP	SSPSRAPAS	SOHPSVPASP	360
	QGRNAKDLLL	DLKNKILANG	GAPRKPQLRA	KKAEELDLQS	TEITGEEELG	SREDSPPMS	420
45	DTQDQKRTL	PPSRHGHVS	APGRTAVRAR	MPALPRREGV	DKPGFSLATQ	PRPGAPPSAS	480
	ASPAHASTQ	CTSHRSLPLA	SLNDNDLVDS	DEDERAVGSL	HPKGAFAPQR	PALSPSRQSP	540
	SSVLRDRSSV	HPGAKPASPA	RRTPHSGAAE	EDSSASAPPS	RLSPPHGGSS	RLLPQTQPHLS	600
	SPLSKGGKDG	EDAPATNSNA	PSRSTMSSSV	SSHLSSRTQV	SEGAESDGE	SHGDGDREDG	660
	GRQAEATAQT	LRARPASGHF	HLLRHKPFPA	NGRSPSRFSI	GRGPRLQPSS	SPQSTVPSRA	720
50	HPRVPSHSDS	HPKLSSSIHG	DEEDEKPLPA	TVVNDHVPSS	SRQPISRGWE	DLRRSPQRGA	780
	SLHRKEPIPE	NPKSTGADTH	PQKYSLLAS	KAQDVQOSTD	ADTEGHSPKA	QPGSTDRHAS	840
	PARPPAARSQ	QHSVSVPRMT	PGRAPQEQPP	PPVATSQHHP	GPQSRDAGRS	PSQPRLSLTQ	900
	AGRPRPTSQG	RSHSSSDPYT	ASSRGMPLPTA	LQNQDEDAQG	SYDDDDSTEVE	AQDVRAFAHA	960
	ARAKEAASL	PKHQGVESPT	GAGAGGDHRS	QRGHAASPAR	PSRPGGPQSR	ARVPSRAAPG	1020
55	KSEPPSKRPL	SSKQSQSVSA	EDEEEEDAGF	FKGKEDLLS	SSVPKWPSSS	TPRGGKADAG	1080
	SLAKEEREPA	IALAPRGGS	APVKRPLPPP	PGSSPRASHV	PSRPPPSRAA	TVSPVAGTHP	1140
	WPRYTTRAPP	GHFSTTPMLS	LRQRMHARF	RNPLSRQPAR	PSYRQGYNGR	PNVEGKVLPG	1200
	SNKPNQGR	INGPQGTQW	VDLDRGLVLN	AEGRYLQDSH	GNPLRIKLG	DGRITVDLEG	1260
	TPVVPDGLR	LFGQGRGPT	LANAQDKPIL	SLGGKPLVGL	EVIKKTHPP	TTTMTQPTTT	1320
60	TPLETTTTPR	PTTATTMQPT	TTTTPLPTTT	PRPTTATRR	TTTRRPTTTV	RTTTRTTTTT	1380
	TPKPTTPIPT	CPPGTLERHD	DDGNLIMSSN	GIPECYAEED	EFGLETDTA	VPTEEAIVYI	1440
	DEDEYEFETR	PPTTTEPSTT	ATTPRVIEPE	GAISSFPPEE	FDLAGRKRFR	APYVTYLNKD	1500
	PSAPCSLTDA	LDHFQVDSL	EIIPNDLKKS	DLPPQHAPRN	ITVVAVEGCH	SFVIVDWDKA	1560
	TPGDLVTGYL	VYSASYEDFI	RNKFSTQASS	VTHLPIENLK	PNTRYFYKQV	AQNPHGYGPI	1620
65	SPSVSVFTES	DNPLLVVRPP	GGELSGSHSL	SNMIPATRTA	MDGNM		

Seq ID NO: 61 DNA sequence  
Nucleic Acid Accession #: NM\_022743  
Coding sequence: 128..1237

70	1	11	21	31	41	51	
	GTGGATTTTA	GAGATACCTC	CCCTCCTTCT	GCTCAGCTGC	CTTGCACTAA	TTAAACTCTT	60
	TCTCTGCTGC	AACACCCCTA	CTGTTCTCCG	TGTATTGGCT	TTTCTGGGCA	GCAGGAAGGA	120
75	AAAGCTGATG	CGATGCTCTC	AGTGCCGCGT	CGCCAAATAC	TGTAGTGCTA	AGTGTGAGAA	180
	AAAAGCTTGG	CCAGACCAAC	AGCGGGAATG	CAAAATGCCTT	AAAAGCTGCA	AACCCAGATA	240
	TCCTCCAGAC	TCCGTTCGAC	TTCTTGGCAG	AGTTGTCTTC	AACTTATGG	ATGGAGCACC	300
	TTCAAGATCA	GAGAAGCTTT	ACTCATTTTA	TGATCTGGAG	TCAAATATTA	ACAAACTGAC	360
	TGAAGATAAG	AAAGAGGGCC	TCAGGCAACT	CGTAATGACA	TTTCAACATT	TCATGAGAGA	420
80	AGAAATACAG	GAGGCTCTC	AGCTGCCACC	TGCCTTTGAC	CTTTTGAAG	CCTTTGCAAA	480
	AGTGATCTGC	AACTCTTTCA	CCATCTGTAA	TGCGGAGATG	CAGGAAGTTG	GTGTTGGCCT	540
	ATATCCCAGT	ATCTCTTTCG	TCAATCACAG	CTGTGACCCC	AACTGTTCGA	TTGTGTTCAA	600
	TGGGCCCCAC	CTCTACTTGC	GAGCAGTCCG	AGACATCGAG	GTGGGAGAGG	AGCTCACCAT	660
	CTGCTACCTG	GATATGCTGA	TGACCACTGA	GGAGCGCCGG	AAGCAGCTGA	GGGACCAAGT	720
	CTGCTTTGAA	TGTGACTGTT	TCCGTGCCCA	AACCCAGGAC	AAGGATGCTG	ATATGCTAAC	780

TGGTGATGAG CAAGTATGGA AGGAAGTTCA AGAATCCCTG AAAAAAATG AAGAACTGAA 840  
 GGCACACTGG AAGTGGGAGC AGGTTCTGGC CATGTGCCAG GCGATCATAA GCAGCAATTC 900  
 TGAACGGCTT CCCGATATCA ACATCTACCA GCTGAAGGTG CTCGACTGCG CCATGGATGC 960  
 CTGCATCAAC CTCGGCCTGT TGGAGGAAGC CTTGTTCTAT GGTACTCGGA CCATGGAGCC 1020  
 ATACAGGATT TTTTCCCGAG GAAGCCATCC CGTCAGAGGG GTTCAAGTGA TGAAAGTTGG 1080  
 CAAACTGCAG CTACATCAAG GCATGTTTCC CCAAGCAATG AAGAATCTGA GACTGGCTTT 1140  
 TGATATTATG AGAGTGACAC ATGGCAGAGA ACACAGCCTG ATTGAAGATT TGATTCTACT 1200  
 TTTAGAAAGAA TGCAGCGCCA ACATCAGAGC ATCCTAAGGG AACGCAGTCA GAGGGAAATA 1260  
 CGGCGTGTGT CTTTGTGAA TGCCTTATG AGGTCACACA CTCTATGCTT TGTTAGCTGT 1320  
 GTGAACCTCT CTTATTGAA ATTCTGTTCC GTGTTTGTGT AGGTAAATAA AGGCAGACAT 1380  
 GGTGTCAAA CCACAAGAA CATTAGTTGT AGAGAAGCAC GATTATAATA AATTCAAAAC 1440  
 ATTTGGTTGA GGATGCCAAA AAAAAAATAA AAAAAA

Seq ID NO: 62 Protein sequence  
 Protein Accession #: NP\_073580

1 11 21 31 41 51  
 | | | | |  
 MRCSQCRVAK YCSAKCQKKA WPDHKRECKC LKSKCKPRYP DSVRLGLRVV FKLMGAPSE 60  
 SEKLYSFYDL ESNINKLTED KKEGLRQLVM TFQHFMRBEE QDASQLPPAF DLFEAFKVI 120  
 CNSFTICNAE MQEVGVGLYP SISLLNHSCD PNCISVFNFG HLLLRVRDI EVGEELTICY 180  
 LDMLMTSEER RQQLRDQYCF ECDPCRCQTQ DKDADMLTGD EQVWKEVQES LKKIEELKAH 240  
 WKWEQVLAMC QAIISNSNER LPDINIYQLK VLDCAMDACI NLGLLEEALF YGTRTMEPYR 300  
 IFFPGSHPRV GVQVMKVGLK QLHQGMFPQA MKNLRLAFDI MRVTHGREHS LIEDLILLLE 360  
 ECDANIRAS

Seq ID NO: 63 DNA sequence  
 Nucleic Acid Accession #: NM\_003014.2  
 Coding sequence: 238..648

1 11 21 31 41 51  
 | | | | |  
 GCGGGGTTCC GCGCCCGAAG GCTGAGAGCT GCGCTGCTC GTGCCCTGTG TGCCAGACGG 60  
 CGGAGCTCCG CGGCCGGACC CCGCGGCCCC GCTTTGCTGC CGACTGGAGT TTGGGGGAAG 120  
 AAACCTCTCT GCGCCCGAGA AGATTCTTTC CTCGGCGAAG GGACAGCGAA AGATGAGGGT 180  
 GGCAGGAAGA GAAGGCGCTT TCTGTCTGCC GGGGTGCGAG CGCGAGAGGG CAGTGCCATG 240  
 TTCTCTCCA TCTTAGTGGC GCTGTGCCCTG TGGCTGCACC TGGCGCTGGG CGTGCGCGGC 300  
 GCGCCCTGCG AGCGGTGCG CATCCCTATG TGCCGCGACA TGCCCTGGAA CATCACGCGG 360  
 ATGCCCAACC ACCTGCACCA CAGCACGCAG GAGAACGCCA TCCTGGCCAT CGAGCAGTAC 420  
 GAGGAGCTGG TGGACGTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTCTG TGCCATGTAC 480  
 GCGCCCATTT GCACCTGGA GTTCTGTGAC GACCCTATCA AGCCGTGCAA GTCCGTGTGC 540  
 CAACGCGCGC GCGACGACTG CGAGCCCTC ATGAAGATGT ACAACCACAG CTGGCCCGAA 600  
 AGCCTGGCCT GCGACGAGCT GCCTGTCTAT GACCCTGGCG TGTGCATTTT GCCTGAAGCC 660  
 ATCGTCAAGG ACCTCCCGGA GGATGTTAAG TGGATAGACA TCACACCAGA CATGATGGTA 720  
 CAGGAAAGGC CTCTTGATGT TGACTGTAAA CGCCTAAGCC CCGATCGGTG CAAGTGTAAA 780  
 AAGGTGAAGC CAACTTTGGC AACGTATCTC AGCAAAAACT ACAGCTATGT TATTCTATGCC 840  
 AAAATAAAAG CTGTGCAGAG GAGTGGCTGC AATGAGGTCA CAACGGTGGT GGATGTAAAA 900  
 GAGATCTTCA AGTCTCTATC ACCCATCCCT CGAACTCAAG TCCCGCTCAT TACAAATTCT 960  
 TCTTGCCAGT TGCACACATC CCTGCCCATC CAAGATGTTT TCATCATGTG TTACGAGTGG 1020  
 CGTTCAAGGA TGATGCTTCT TGAAATTTGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080  
 AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG 1140  
 AAGAAAACAG CCGGGCGCAC CAGTCGTAGT AATCCCCCCA AACCAAGGGG AAAGCCTCCT 1200  
 GCTCCCAAAC CAGCCAGTCC CAAGAAGAAC ATTAATAACT GAGATGCCCA GAAGAGAAC 1260  
 AACCAGAAA GAGTGTGAGC TAACTAGTTT CCAAGCGGA GACTTCCGAC TTCTTACAG 1320  
 GATGAGGCTG GGCATTGCTT GGGACAGCCT ATGTAAGGCC ATGTGCCCTT TGCCCTAACA 1380  
 ACTCACTGCA GTGCTCTTCA TAGACACATC TTGCAGCATT TTTCTTAAGG CTATGCTTCA 1440  
 GTTTTTCTTT GTAAGCCATC ACAAGCCATA GTGGTAGGTT TGCCCTTTGG TACAGAAGGT 1500  
 GAGTTAAAGC TGGTGGAAAA GGCTTATTGC ATTGCATTCA GAGTAACCTG TGTGCATACT 1560  
 CTAGAAGAGT AGGGAAAAATA ATGCTGTGTA CAATTGACAC TAATATGTGC ATTGTAAAA 1620  
 AAATGCCATA TTTCAACAA AACACGTAAT TTTTTTACAG TATGTTTTAT TACCTTTTGA 1680  
 TATCTGTTGT TGCAATGTTA GTGATGTTT AAAATGTGAT GAAAATATAA TGTTTTAAAG 1740  
 AAGGAACAGT AGTGAATGA ATGTTAAAG ATCTTTATGT GTTTATGGTC TGCAGAAGGA 1800  
 TTTTGTGAT GAAAGGGGAT TTTTGAATA ATTAGAGAAG TAGCATATGG AAAATTATAA 1860  
 TGTGTTTTTT TACCAATGAC TTCAGTTTCT GTTTTATGCT AGAACTTAA AAACAAAAT 1920  
 AATAATAAAG AAAATAAAT AAAAGGAGA GGCAGACAAT GTCTGGATTC CTGTTTTTTG 1980  
 GTTACCTGAT TTCCATGATC ATGATGCTTC TTGTCAACAC CCTCTTAAGC AGCACCAGAA 2040  
 ACAGTGAGTT TGTCTGTACC ATTAGGAGTT AGTACTAAT TAGTTGGCTA ATGCTCAAGT 2100  
 ATTTTATACC CACAAGAGAG GTATGCTACT CATCTTACTT CCCAGGACAT CCACCTGAG 2160  
 AATAATTTGA CAAGCTTAAA AATGGCCTTC ATGTGAGTGC CAAATTTTGT TTTTCTTCAT 2220  
 TTAATATTT TCTTTGCCATA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG 2280  
 AAAGTTGATG TCCACTCTG AATGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA 2340  
 AAAAAGAAT TATTTGCAGC ATTTTATCAA CAAATTTTAT AATTGTGGAC AATTGGAGGC 2400  
 ATTTATTTTA AAAACAAT TTATTGGCCT TTGCTAACA CAGTAAGCAT GTATTTTATA 2460  
 AGGCATTCAA TAAATGCACA ACGCCCAAAG GAAATAAAT CCTATCTAAT CCTACTCTCC 2520  
 ACTACACAGA GGTATCACT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580  
 GCACTTATGA AATGATTTGA ACATAAATA CTAGGAACCT GTATACATGT GTTTCATAAC 2640  
 CTGCTCTCTT TGCTTGGCCC TTTATTGAGA TAAGTTTTCC TGTCAAGAAA GCAGAAACCA 2700  
 TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760  
 TATTGGATAC TTAGGTGTT TCTTCACTGA CAATACTGAA TAAACATCTC ACCGGAATTC

Seq ID NO: 64 Protein sequence  
 Protein Accession #: NP\_003005.1

1 11 21 31 41 51

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60

MPLSILVALC	LWLHLALGVR	GAPCEAVRIP	MCRHMPWNIT	RMPNHLHHST	QENAILAIEQ	60
YEELVDVNC	AVLRRFFCAM	YAPICTLEFL	HDPIKPKSV	CQRARDCEP	LMKMYNHSWP	120
ESLACDELTV	YDRGVCISPE	AVTDLPELV	KWIDITPDM	VQERPLDVC	KRLSPDRCKC	180
KVKKPTLATY	LKKNYSYVIH	AKIKAVQRSG	CNEVTTVVDV	KEIFKSSSPI	PRTQVPLITN	240
SSCQCCHILP	HQDVLIMCYE	WRSRMMLLEN	CLVEKWRDQL	SKRSIQWEER	LQEQRRRTVQD	300
KKKTAGRTSR	SNPPKPKGKP	PAPKPASPKK	NIKTRSAQKR	TNPKRV		

Seq ID NO: 65 DNA sequence  
 Nucleic Acid Accession #: BC010423  
 Coding sequence: 248..1780

1  
 11  
 21  
 31  
 41  
 51

CACAGCGTGG	GAAGCAGCTC	TGGGGGAGCT	CGGAGCTCCC	GATCACGGCT	TCTTGGGGGT	60
AGCTACGGCT	GGGTGTGTAG	AACGGGGCCG	GGGCTGGGGC	TGGGTCCCTT	AGTGGAGACC	120
CAAGTGCAGG	AGGCAAGAAG	TCTGCAGCTT	CCTGCCTTCT	GGGTACAGTT	CTTATTCAAG	180
CTGTGACGGG	GCTCCACAGG	AGATCTCGGT	GGAACCTTCAG	AAACGCTGGG	CAGTCTCGCT	240
TTCAACCATG	CCCCTGTCCC	TGGGAGCCGA	GATGTGGGGG	CCTGAGGCCT	GGCTGTGTCT	300
GCTGTACTGT	CTGGCATCAT	TTACAGGCCG	GTGCCCCGCG	GGTGAGCTGG	AGACCTCAGA	360
CGTGGTAAC	GTGGTGTCTG	GCCAGGACGC	AAAACCTGCC	TGCTTCTACC	GAGGGGACTC	420
CGGCGAGCAA	GTGGGGCAAG	TGGCATGGGC	TCGGGTGGAC	GCGGGCGAAG	GCGCCACAGG	480
ACTAGCGCTA	CTGCATCCCA	AATACGGGCT	TCATGTGAGC	CCGGCTTACG	AGGGCCCGCT	540
GGAGCAGCCG	CCGCCCCAC	GCAACCCCTT	GGACGGCTCA	GTGCTCCTGC	GCAACGCAGT	600
GCAGGCGGAT	GAGGGCCAGT	ACGAGTGCCG	GGTCAGCACC	TTCCCCCGCG	GCAGCTTCCA	660
GGCGCGGCTG	CGGCTCCGAG	TGCTGGTGCC	TCCCCTGCC	TCATGAATC	CTGGTCCAGC	720
ACTAGAAGAG	GGCCAGGGCC	TGACCCCTGG	AGCCTCCTGC	ACAGCTGAGG	GCAGCCAGC	780
CCCCAGCGTG	ACCTGGGACA	CGGAGGTCAA	AGGCACAACG	TCCAGCCGTT	CCTTCAAGCA	840
CTCCCGCTCT	GCTGCGCTCA	CCTCAGAGTT	CCACTTGGTG	CCTAGCCGCA	GCATGAATGA	900
GCAGCCACTG	ACTTGTGTGG	TGTCCCATCC	TGGCTGTCTC	CAGGACCAAA	GGATCACCCA	960
CATCCTCCAC	GTGTCTTCC	TTGCTGAGGC	CTCTGTGAGG	GGCCTTGAAG	ACCAAAATCT	1020
GTGGCAGATT	GGCAGAGAAG	GAGCTATGCT	CAAGTGCTCT	AGTGAAGGGG	AGCCCTCTCC	1080
CTCATACAAC	TGGACACGGC	TGGATGGGCC	TCTGCCAGT	GGGTACGAG	TGGATGGGGA	1140
CACCTTGGCG	TTTCCCCAC	TGACCACTGA	GCACAGCGGC	ATCTACGCT	GCCATGTGAG	1200
CAATGAGTTC	TCCTCAAGGG	ATTCTCAGGT	CACTGTGGAT	GTCTTGAGC	CCCAGGAAGA	1260
CTCTGGGAAG	CAGGTGAGCC	TAGTGTGAGC	CTCGGTGGTG	GTGGTGGGGT	TGATCGCCGC	1320
ACTCTTGTTC	TGCTTCTTGG	TGGTGGTGGT	GGTGCTCATG	TCCCGATACC	ATCGGCGCAA	1380
GGCCAGCAG	ATGACCCAGA	AATATGAGGA	GGAGCTGACC	CTGACCAAGG	AGAACTCCAT	1440
CCGGAGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CCGGAGGAGA	GTGTAGGGCT	1500
GAGAGCCGAG	GGCCACCTCG	ATAGTCTCAA	GGACAACAGT	AGCTGCTCTG	TGATGAGTGA	1560
AGAGCCCGAG	GGCCGCGAGT	ACTCCACGCT	GACCACGGTG	AGGGAGATAG	AAACACAGAC	1620
TGAACTGCTG	TCTCCAGGCT	CTGGCGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAAGGCAT	1680
CAAAACAGGCC	ATGAACCAT	TTGTTCAGGA	GAATGGGACC	CTACGGGCCA	AGCCACCGGG	1740
CAATGGCATC	TACATCAATG	GGCGGGGACA	CCTGGTCTGA	CCCAGGCCGT	CCTCCCTTCC	1800
CTAGGCGCTG	CTCCTTCTGT	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GCCTCCTTAA	1860
ACACCCCATC	TTCTTGCAGG	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACCTCC	1920
AACCTTCTG	TTTCATCGGA	GGGCTCCACC	AATTGAGTCT	CTCCACCAT	GCATGCAGGT	1980
CACGTGTGTG	GTGCATGGGT	GCCTGTGTGA	GTGTGACTG	ACTGTGTGTG	TGTGGAGGGG	2040
TGACTGTCCG	TGGAGGGGTG	ACTGTGTCCG	TGGTGTGTAT	TATGCTGTCA	TATCAGAGTC	2100
AAGTGAAC	TGGTGTATGT	GCCACGGGAT	TTGAGTGGTT	GCGTGGGCAA	CACGTGCAGT	2160
GTTTGGCGTG	TGTGTATGT	GGCTGTGTGT	GACCTCTGCC	TGAAAAGCA	GGTATTCTCT	2220
CAGACCCAG	AGCAGTATTA	ATGATGCAGA	GGTTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
CAGACCCAG	TGTGCGGGAG	TAGCTGGAGC	TGGAATCTGC	CTCCGGTGTG	AGGGAACCTG	2340
TCTCTACAA	CTTGGAGGCC	ATGGGGGCAA	GTGTGAAGCA	GCCAGTCCCT	GGGTGAGCTA	2400
GAGGCTTGA	CTGTATACGA	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGCATGT	2460
ACATATTTTC	TGTAAATATA	CATGCGCCGG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
ACTTTTAATT	TTTTTCTTTT	TTTTTCTTTG	CCCTTCTCAT	TAGTTGTATT	TTTTATTAT	2580
TTTTATTTT	ATTTTCTTTT	AGAGTTTGAG	TCCAGCCTGG	ACGATATAGC	CAGACCTCTG	2640
CTGTAAAAA	ACCAAAACCC	AAAAAATAA	AAAAAATAA			

Seq ID NO: 66 Protein sequence  
 Protein Accession #: AAH10423

65  
 70  
 75

MPLSLGAEMW	GPEAWLLLLL	LLASFTGRCP	AGELETSADV	TVVLGQDAKL	PCFYRGDSGE	60
QVQGVAVARV	DAGEGAQELA	LLHSKYGLHV	SPAYEGRVEQ	PPPPRNPLDG	SVLLRNAVQA	120
DEGEYECRVS	TFPAGSFQAR	LRLRLVLPPL	PSLNPGPALE	EGQGLTLAAS	CTAEGSPAPS	180
VTWDETVKGT	TSSRSFKHSR	SAAVTSEFHL	VPSRSMNGQP	LTCVVSHPLG	LQDQRITHIL	240
HVSFLAEASV	RGLEDQNLWH	IGREGAMLC	LSEGGPPPSY	NWTRLDGFLP	SGVRVDGDTL	300
GFPPLTTEHS	GIYVCHVSNE	FSSRDSQVT	DVLDPQEDSG	KQVDLVASAV	VVVGIVIAALL	360
FCLLVVVVVL	MSRYHRRKAQ	QMTQKYEEEL	TLTRENSIRR	LHSHHTDPRS	QPEESVGLRA	420
EGHPDLSLKN	SSCSVMSEEP	EGRSYSTLT	VREIETQTEL	LSPFGSRAEE	EEDQDEGIKQ	480
AMNHVQENG	TLRAKPTGNG	IYINGRHLV				

Seq ID NO: 67 DNA sequence  
 Nucleic Acid Accession #: NM\_001203  
 Coding sequence: 274..1782

80

CGCGGGGCGC	GGAGTCGGCG	GGGCCTCGCG	GGACGCGGCG	AGTGCAGAGA	CGCGGCGGCT	60
GAGGACGCGG	GAGCCGGGAG	CGCACGCGCG	GGGTGGAGTT	CAGCCTACTC	TTTCTTAGAT	120
GTGAAAGGAA	AGGAAGATCA	TTTCATGCC	TGTTGATAAA	GGTTCAGACT	TCTGCTGATT	180

CATAACCAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240  
 TGCCATAAGT GAGAAGCAAA CTTCCCTTGAT AACATGCTTT TGCAGAGTGC AGGAAATTA 300  
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC 360  
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420  
 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTGCGCTGT GGTCACTTCT 480  
 GGTGCGCTAG GACTAGAAGG CTCAGATTTT CAGTGTCTGG ACACCTCCAT TCCTCATCAA 540  
 AGAAGATCAA TTGAATGCTG CACGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600  
 CTGCTCCCAT TGAAAAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCTTTACTT 660  
 ATATCTGTGA CTGTCTGTAG TTTGCTCTGT GTCCTTATCA TATTATTTTG TTACTTCCGG 720  
 TATAAAAGAC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780  
 ATTCTCCTG GAGAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840  
 TCAGGCCTCC CTCTGCTGGT CCAAGGACT ATAGCTAAGC AGATTTCAGAT GGTGAAACAG 900  
 ATTGAAAAAG GTCGCTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGGCGA AAAGGTAGCT 960  
 GTGAAAGTGT TCTTACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020  
 ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080  
 GGGTCTGGA CCGAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140  
 TATCTGAAGT CCACCACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTCTGTCT 1200  
 AGTGGCTTAT GTCATTTACA CACGAAATC TTAGTACTC AAGGCAACC AGCAATTGCC 1260  
 CATCGAGATC TGAAAGTAA AAAACATTCTG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320  
 GACCTGGGCC TGGCTGTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380  
 ACTCGAGTTG GCACCAAGC CTATATGCCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440  
 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500  
 GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560  
 CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620  
 CGCCCTCAT TCCCAAAACG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAACTC 1680  
 ATGACAGAA GCTGGGCTCA CAATCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740  
 ACACCTGCCA AAATGTGCA GTCCCAGGAC ATTAACCTCT GATAGGAGAG GAAAAGTAAG 1800  
 CATCTCTGCA GAAAGCCAA AGGTACTCTT CTGTTGTGG GCAGAGCAAA AGACATCAA 1860  
 TAAGCATCCA CAGTACAAGC CTTGAACATC GTCCTGCTTC CCAGTGGGT CAGACCTCAC 1920  
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCA GAAGGAGAGA TTGATCCGTG 1980  
 TCTGTTTGA GCGCGAGAAA CCGTTGGGTA ACTTGTTCAC GATATGATGC AT

Seq ID NO: 68 Protein sequence

Protein Accession #: NP\_001194

1 11 21 31 41 51  
 | | | | |  
 MLLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHHCPE DSVNNICSTD GYCFMIEED 60  
 DSGLPVVTSGLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECNKDLHPTL PPLKNRDFVD 120  
 GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180  
 EQSQSSGSGS GLPLLVQRTI AKQIQMVQKI GKGRYGEVWM GKWRGEKVAV KVFFTEEAS 240  
 WPRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
 MLKLAYSSVS GLCHLHTEIF STQKGPAAIH RDLKSKNIV KKNGTCCIA D LGLAVKFISD 360  
 TNEVDIPPNT RVGTTRYMPP EVLDESINRN HFQSYIMADM YSFLGLLWEV ARRCVSGGIV 420  
 BEYQLPYHDL VPSDPSYEDM REIVCIKKLR PSPPNRWSSD ECLRQMGKLM TECWAHNPAS 480  
 RLTAALRVKKT LAKMSSEQDI KL

Seq ID NO: 69 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 166..1737

1 11 21 31 41 51  
 | | | | |  
 TTGGGGGTTT ATTCTCTTCC CTTCTAAGTT GACAGGGTCT TGCTCTGTCA TTCAGGCAAG 60  
 AGTGCAGTAG TGATGATCACT TCTTACTGCC GCCTCAAGCT TCCAGCTCA ACTCAAGCAA 120  
 TCCTCCACAC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAATGAC CCAAAATAAA 180  
 TTAAGACTTT GTTCCAAGAC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240  
 GCGGTAGCTT TTTCAATTTT CTTCTGTTGA GTCTTCACT ACGGCATCAT CAAGACATT 300  
 GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360  
 ATAATCTCAA TCTGTGTGTT TGTCTTAAAC TTTTCAGCTC CCCTCGCCAC AGTCTGAGC 420  
 AATCGTTTCG GACACCGTCT GGTAGTGATG TTGGGGGGGC TACTTGTTCAG CACCGGGATG 480  
 GTGGCCGCTC CTTCTCTACA AGAGGTTTCT CATATGTACG TCGCCATCGG CATCATCTCT 540  
 GGTCTGGGAT ACTGCTTTAG TTTTCTCCCA ACTGTAACCA TCCTATCACA ATATTTTGGC 600  
 AAAAGACGTT CCATAGTCAC TGCAGTTGCT TCCACAGGAG AATGTTTCGC TGTGTTTGCT 660  
 TTCGCACCAG CAATCATGGC TCTGAAGGAG CGCATTGGCT GGAGATACAG CCTCCTCTTC 720  
 GTGGGCTTAC TACAGTTAAA CATTGTATC TTCGGAGCAC TGCTCAGACC CATCTTTATC 780  
 AGAGGACCAG CGTCACCGAA AATAGTCATC CAGGAAATC GGAAGAAGC GCAGTATATG 840  
 CTTGAAAATG AGAAAACAG AACCTCAATA GACTCCATTG ACTCAGGAGT AGAACTAACT 900  
 ACCTCACCTA AAAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCCGACATG 960  
 CAGCAGGTCC TGGTGAAGAC CAGCCCCAGG CCAAGCGAAA AGAAAGCCCC GCTATTAGAC 1020  
 TTCTCATTTT TGAAGAAGAA AAGTTTATTT TGTATGTCAT TATTGCTCT CTTGCAACA 1080  
 CTGGGATTCT TTGCACCTTC CTTGTATATC ATTCTCTGG GCATTAGTCT GGGCATTGAC 1140  
 CAGGACCGCG CTGCTTTTTT ATTATCTACG ATGGCCATTG CAGAAGTTT CCGAAGGATC 1200  
 GGAGCTGTTT TTGTCTCTCA CAGGAGCCCC ATTGTAAGA TTTACATTGA GCTCATCTGC 1260  
 GTCATCTTAT TGACTGTGTC TCTGTTTGCC TTTACTTTTG CTACTGAATT CTGGGGTCTA 1320  
 ATGTCATGCA GCATATTTT TTGGGTTTATG GTTGAACAA TAGGAGGGAC TCACATTCCA 1380  
 CTGCTTGCTG AGGATGATGT CGTGGGCATT GAGAAGATGT CTTCTGCAGC TGGGGTCTAC 1440  
 ATCTTCATTC AGACATATAG AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC 1500  
 CAAAGTAAGA TCTACAGCAG GGCCTTCTAC TCTGCGCAG CTGGCATGGC CTTGGCTGCT 1560  
 GTGTGCTCG CCCTGGTGAG ACCGTGTAG ATGGGACTGT GCCAGCATCA TCACTCAGGT 1620  
 GAAACAAAGG TAGTGAGCCA TCGTGGGAAG ACTTTACAGG ACATACCTGA AGACTTTCTG 1680  
 GAAATGGATC TTGCAAAAAA TGAGCACAGA GTTCACGTGC AAAATGGAGCC GGTATGACAC 1740  
 ACTTTCTTAC AACACAGGCC ACTGTGTTGG CTGGAGAGGG ATGGGGTGGG CCCAACGGGG 1800  
 ACACAAGGAG GCAGAGGAGC TAACCCCTCT ACTCCACTTT CAAAACATA TTTTAAAGGG 1860

AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGTGT TGTTTTGTGT TGTTTTAAGC 1920  
 TTTTGTGTGT TGTGTGTGT TAAAGCCAAA ACAAAAAACA ACCAAGCACT CTTCATATA 1980  
 TAAATCTGGC TGTATTAGT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTCACA 2040  
 TTCCGATATT AAAATAGTGA CATGAAGTGG CAAAGTGGTT TTAAGAGCTT TCACGTGGGA 2100  
 TAAATGATT TCTTTTGTCT TTTTCTTTCT TCCTATGGTC TTGTCTGAAT AAACACTCT 2160  
 CCTGAATAAA ACAACATCCA ACCCAGGTCA TTGAAATGAA ATTGGCCAGT C

Seq ID NO: 70 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 MTQNKLLKCS KANVYTEVPD GGWGWAVAVS FFFVEVFTYG IIKTFGVFFN DLMDSFNESH 60  
 SRISWIISIC VFVLTFSAPL ATVLSNRFHG RLVVMLGGLL VSTGMVAASF SQEVSHMYVA 120  
 IGIISGLGYC FSFLPTVTIL SQYFGKRRSI VTAVASTGEC FAVFAFAPAI MALKERIGWR 180  
 YSLLFVGLLQ LNIIVFGALL RPIFIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240  
 GVLELTSPKN VPHTHNLLELE PKADMQQVLV KTSRPPSEKK APLLDIFSILK EKSFCYALF 300  
 GLFATLGGFA PSLYIIPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360  
 IELICVILLT VSLFAFTFAT EFWGLMSCSI FFGFMVGTIG GTHIPLAED DVVGIEKMSS 420  
 AAGVYIFIQS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480  
 HHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 71 DNA sequence  
 Nucleic Acid Accession #: NM\_004694  
 Coding sequence: 166..1737

1 11 21 31 41 51  
 | | | | |  
 TTGGGGGTTT ATTCTCTTCC CTTCTAACTT GACAGGGTCT TGCTCTGTCA TTCAGGCAAG 60  
 AGTGCGTAGT TGTGATCACT TCTTACTGCC GCCTCAAGCT TCCAGCCTCA ACTCAAGCAA 120  
 TCCTCCACAC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAATGAC CCAAAATAAA 180  
 TTAAGAGCTT GTTCCAAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240  
 GCGGTAGCTG TTTTCAATTT CTTCTGTGAA GTCTTTCACCT ACGGCATCAT CAAGACATTT 300  
 GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360  
 ATAATCTCAA TCTGTGTGTT TGTCTTAACA TTTTCAGCTC CCTCGCCAC AGTCTGAGC 420  
 AATCGTTTCG GACACCGTCT GGTAGTGTAT TTGGGGGGGC TACTTGTGAG CACCGGGATG 480  
 GTGGCCGCCCT CCTTCTCACA AGAGGTTTCT CATATGTACG TCGCCATCGG CATCATCTCT 540  
 GGTCTGGGAT ACTGCTTTAG TTTTCTCCCA ACTGTAACCA TCCTATCACA ATATTTTGGC 600  
 AAAAGACGTT CCATAGTCAC TGCAGTTGCT TCCACAGGAG AATGTTTCGC TGTGTTTGCT 660  
 TTCGCACCAG CAATCATGGC TCTGAAGGAG CGCATTGGCT GGAGATACAG CCTCCTCTTC 720  
 GTGGGCCCTAC TACAGTTAAA CATGTGCATC TTCGGAGCAC TGCTCAGACC CATCATATAT 780  
 AGAGGACCAG CGTACCAGAA AATAGTCATC CAGGAAATC GGAAGAAGC GCAGTATATG 840  
 CTTGAAAATG AGAAACACG AACCTCAATA GACTCCATTG ACTCAGGAGT AGAACTAACT 900  
 ACCTCACCTA AAAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCCGACATG 960  
 CAGCAGGTCC TGGTGAAGAC CAGCCCCAGG CCAAGCGAAA AGAAAGCCCC GCTATTAGAC 1020  
 TTCTCCATTG TGAAGAGAAA AAGTTTATAT TGTATGTGAT TATTGTGCTT CTTTGCAACA 1080  
 CTGGGATCTT TGCACCTTC CTTGTACATC ATTCCTCTGG GCATTAGTCT GGGCATTGAC 1140  
 CAGGACCGCG CTGCTTTTTT ATTATCTACG ATGGCCATTG CAGAAGTTT CCGAAGGATC 1200  
 GGAGCTGGTT TTGTCTCAA CAGGGAGCCC ATTCGTAAGA TTTACATTGA GCTCATCTGC 1260  
 GTCATCTTAT TGACTGTGTC TCTGTTTGCC TTTACTTTTG CTACTGAATT CTGGGGTCTA 1320  
 ATGTCATGCA GCATATTTT TGGGTTTATG GTTGGAAACA TAGGAGGACT CACATTCCAC 1380  
 TGCTTGCTGA AGATGATGTC GTGGGCATTG CAGAAGATGT CTTCTGCAGC TGGGGTCTAC 1440  
 ATCTTCATTG AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC 1500  
 CAAAGTAAGA TCTACAGCAG GGCCTTCTAC TCCTGCGCAG CTGGCATGGC CCTGGCTGCT 1560  
 GTGTGCTTCG CCTGGTGAG ACCGTGTAAG ATGGGACTGT GCCAGCGTCA TCACACAGGT 1620  
 GAAACAAAGG TAGTGAGCCA TCGTGGGAAG ACTTTACAGG ACATACCTGA AGACTTTCTG 1680  
 GAAATGGATC TTGCAAAAAA TGAGCACAGA GTTCACGTGC AAATGGAGCC GGTATGACAC 1740  
 ACTTTCTTAC AACACAGGCC ACTGTGTTGG CTGGAGAGGG ATGGGGTGGG CCCAACGGGG 1800  
 ACACAGGAGC GCAGAGGAGC TAACCCCTCT ACTCCACTTT CAAACTACA TTTTAAAGGG 1860  
 AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGTGT TGTTTTGTGT TGTTTTAAGC 1920  
 TTTTGTGTGT TGCTTGTGTT TAAAGCCAAA ACAAAAAACA ACCAAGCACT CTTCATATA 1980  
 TAAATCTGGC TGTATTCAGT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTCACA 2040  
 TTCCGATATT AAAATAGTGA CATGAAGTGG CAAAGTGGTT TTAAGAGCTT TCACGTGGGA 2100  
 TAAATGATT TCTTTTGTCT TTTTCTTTCT TCCTATGGTC TTGTCTGAAT AAACACTCT 2160  
 CCTGAATAAA ACAACATCCA ACCCAGGTCA TTGAAATGAA ATTGGCCAGT C

Seq ID NO: 72 Protein sequence  
 Protein Accession #: NP\_004685

1 11 21 31 41 51  
 | | | | |  
 MTQNKLLKCS KANVYTEVPD GGWGWAVAVS FFFVEVFTYG IIKTFGVFFN DLMDSFNESH 60  
 SRISWIISIC VFVLTFSAPL ATVLSNRFHG RLVVMLGGLL VSTGMVAASF SQEVSHMYVA 120  
 IGIISGLGYC FSFLPTVTIL SQYFGKRRSI VTAVASTGEC FAVFAFAPAI MALKERIGWR 180  
 YSLLFVGLLQ LNIIVFGALL RPIIIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240  
 GVLELTSPKN VPHTHNLLELE PKADMQQVLV KTSRPPSEKK APLLDIFSILK EKSFCYALF 300  
 GLFATLGGFA PSLYIIPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360  
 IELICVILLT VSLFAFTFAT EFWGLMSCSI FFGFMVGTIG GLTFHCLLM MSWALQKMSS 420  
 AAGVYIFIQS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480  
 RHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 73 DNA sequence  
 Nucleic Acid Accession #: NM\_002184.1  
 Coding sequence: 256..3012



```

1      11      21      31      41      51
|      |      |      |      |      |
5  GAGCAGCCAA AAGGCCCGCG GAGTCGCGCT GGGCCGCCCC GGCAGCAGCTG AACCGGGGGC 60
   CGCGCCTGCC AGGCCGACGG GTCTGGGCCA GCCTGGCGCC AAGGGGTTCTG TGCCTGTGG 120
   AGACGCGGAG GGTGAGGCG GCGCGGCTTG AGTGAAACCC AATGGAAAAA GCATGACATT 180
   TAGAAGTAGA AGACTTAGCT TCAAATCCCT ACTCCTTCAC TTACTAATTT TGTGATTTGG 240
   AAATATCCCG GCAAGATGTT GACGTTGCAG ACTTGGGTAG TGCAAGCCTT GTTTATTTTC 300
   CTCACCACTG AATCTACAGG TGAACCTCTA GATCCATGTG GTTATATCAG TCCTGAATCT 360
   CCAGTTGTAC AACTTCATTC TAATTTCACT GCAGTTTGTG TGCTAAAGGA AAAATGTATG 420
10 GATTATTTTC ATGTAATGTC TAATTACATT GTCTGAAAAA CAAACCATT TACTATTCTT 480
   AAGGAGCAAT ATACTATCAT AAACAGAACA GCATCCAGTG TCACCTTTAC AGATATAGCT 540
   TCATTAAATA TTCAGCTCAC TTGCAACATT CTTACATTCG GACAGCTTGA ACAGAATGTT 600
   TATGGAATCA CAATAATTTC AGGCTTGCCCT CCAGAAAAAC CTAAAAATTT GAGTTGCATT 660
   GTGAACGAGG GGAAGAAAAAT GAGGTGTGAG TGGGATGGTG GAAGGGAAAC ACCTTGGAG 720
15 ACAAACTTCA CTTTAAAAAT TGAATGGGCA ACACACAAGT TTGCTGATTG CAAAGCAAAA 780
   CGTGACACCC CCACCTATG CACTGTGTAT TATTCTACTG TGTATTTTGT CAACATTGAA 840
   GTCTGGGTAG AAGCAGAGAA TGCCCTTGGG AAGGTTACAT CAGATCATAT CAATTTTGAT 900
   CCTGTATATA AAGTGAAGCC CAATCCGCCA CATAATTTAT CAGTGATCAA CTCAGAGGAA 960
20 CTGTCTAGTA TCTTAAAAAT GACATGGACC AACCACAGTA TTAAGAGTGT TATAATACTA 1020
   AAATATAACA TTCAATATAG GACCAAGAT GCCTCAACTT GGAGCCAGAT TCCTCCTGAA 1080
   GACACAGCAT CCACCCGATC TTCAATTCAT GTCCAAGACC TTAAACCTTT TACAGAATAT 1140
   GTGTTTAGGA TTCGTGTAT GAAGGAAGAT GGTAGGGGAT ACTGGAGTGA CTGGAGTGAA 1200
   GAAGCAAGTG GGATCACCTA TGAAGATAGA CCATCTAAG CACCAAGTTT CTGGTATAAA 1260
25 ATAGATCCAT CCCATCTCA AGGCTACAGA ACTGTACAAC TCGTGTGGAA GACATTGCCT 1320
   CCTTTTGAAT CCAATGGAAA AATCTTGGAT TATGAAGTGA CTCTACAAG ATGGAAATCA 1380
   CATTTACAAA ATTACACAGT TAATGCCACA AACTGACAG TAAATCTCAC AAATGATCGC 1440
   TATCTAGCAA CCCTAACAGT AAGAAATCTT GTTGGCAAAT CAGATGCAGC TGTTTTAACT 1500
   ATCCCTGCCT GTGACTTTCA AGCTACTCAC CCTGTAATGG ATCTTAAAGC ATTCCTCCAA 1560
   GATAACATCG TTTGGGTGGA ATGGACTACT CCAAGGGAAT CTGTAAAGAA ATATATACTT 1620
30 GAGTGGTGTG TGTATCAGA TAAAGCACCC TGTATCACAG ACTGGCAACA AGAAGATGGT 1680
   ACCGTGCATC GCACCTATTT AAGAGGGAAC TTAGCAGAGA GCAAATGCTA TTTGATAACA 1740
   GTTACTCCAG TATATGCTGA TGGACCAGGA AGCCCTGAAT CCATAAAGGC ATACCTTAAA 1800
   CAAGCTCCAC CTTCCAAAGG ACCTACTGTT CGGACAAAAA AAGTAGGGAA AAACGAAGCT 1860
   GTCTTAGAGT GGGACCAACT TCCTGTTGAT GTTCAGAATG GATTTATCAG AAATTATACT 1920
35 ATATTTTATA GAACATCAT TGGAAATGAA ACTGCTGTGA ATGTGGATTCT TCCCACACA 1980
   GAATATACAT TGCTCTCTTT GACTAGTGAC ACATTGTACA TGGTACGAAT GGCAGCATAC 2040
   ACAGATGAAG GTGGGAAGGA TGGTCCAGAA TTCACTTTTA CTACCCCAA GTTGTCTCAA 2100
   GGAGAAATTG AAGCCATAGT CGTGCCCTGT TGTCTAGCAT TCCTATTGAC AACTCTTCTG 2160
   GGAGTGTCTG TCTGCTTTAA TAAGCGAGAC CTAATTAAAA AACACATCTG GCCTAATGTT 2220
40 CCAGATCCCT CAAAGAGTCA TATTGCCAG TGGTCACCTC ACCTCTCTCC AAGGCACAAT 2280
   TTTAATTCAA AAGATCAAA GTATTTCAGT GGCATTTTCA CTGATGTAAG TGTGTGGAA 2340
   ATAGAAGCAA ATGACAAAAA GCCTTTTCCA GAAGATCTGA AATCATTGGA CCTGTTCAA 2400
   AAGGAAAAAA TTAATACTGA AGGACACAGC AGTGGTATTG GGGGCTCTC ATGCATGTCA 2460
   TCTTCTAGGC CAAGCATTTC TAGCAGTGAT GAAAAATGAAT CTTACAAAA CACTTCGAGC 2520
45 ACTGTCCAGT ATTCTACCT GGTACACAGT GGCTACAGAC ACCAAGTTCC GTCACTCCAA 2580
   GTCTTCTCAA CAGTCCGAGT TACCCAGCCC TTGTTAGATT CAGAGGAGCG GCCAGAAGAT 2640
   CTACAATTAG TAGATCATGT AGATGGCGGT GATGTTATT TGCCAGGCA ACAGTACTTC 2700
   AAACAGAACT GCAGTCAGCA TGAATCCAGT CCAGATATTT CACATTTTGA AAGGTCAAAG 2760
   CAAGTTTCAT CAGTCAATGA GGAAGATTT GTTAGACTTA AACAGCAGAT TTCAGATCAT 2820
50 ATTTCAACA CTGTGGATG TGGCAAATG AAAATGTTT AGGAAGTTTC TGCAGCAGAT 2880
   GCTTTTGGTC CAGGTACTGA GGGACAAGTA GAAAGATTG AAACAGTTG CATGGAGGCT 2940
   GCGACTGATG AAGGCATGCC TAAAGTTAC TTACCACAGA CTGTACGGCA AGGCGGCTAC 3000
   ATGCCTCAGT GAAGGACTAG TAGTTCCTGC TACAACCTCA GCGATACCTA TAAAGTAAAG 3060
55 CTAATATGAT TTTATCTGTG AATTC

```

Seq ID NO: 74 Protein sequence  
Protein Accession #: NP\_002175.1

```

60 1      11      21      31      41      51
   |      |      |      |      |      |
   MLTLQTWVQV ALFIFLTTE TGEILDPCGY ISPESPVVQL HSNFTAVCVL KEKCMDYFHV 60
   NANYIVWKTN HFTIPKEQYT IINRTASSVT FTDIASLNIQ LTCNLTFGQ LEQNVYGITI 120
   ISGLPPEKPK NLSIVNEGK KMRCEWDGGR ETHLETNFTL KSEWATHKFA DCAKRDTP 180
65 SCTVDYSTVY FVNIEVWVEA ENALGKVTS D HINFDVYKV KPNPPHNSLV INSEELSSIL 240
   KLTWTNPSIK SVIILKYNIQ YRTKDASTWS QIPPEDTAST RSSFTVQDLK PFTEYVFRIR 300
   CMKEDGKGYW SDWSEASGI TYEDRPSKAP SFWYKIDPSH TQGYRTVQLV WKTLPPEFAN 360
   GKILDYEVTL TRWKSHLQNY TVNATKLTVN LTNDRYLATL TVRNLVGKSD AAVLTIPACD 420
   FQATHFVMDL KAFPKDMLW VEWTTPRESV KKYILEWCVL SDKAPCITDW QQEDGTVHRT 480
70 YLRGNLAESK CYLITVTPVY ADGPGSPESI KAYLKQAPPS KGPTVRTKKV GKNEAVLEWD 540
   QLPVDVQNGF IRNYTIFYRT IIGNETAVNV DSSHTYTLS SLTSDTLXV RMAAYTDEGG 600
   KDGPFTFTT PKFAQGEIEA IVVPVCLAF LTTLLGVLC FNRDLIKKH IWPNVDPDSK 660
   SHIAQWSPH PPRHNFNSKD QMYSNGNFTD VSVVEIAND KKPFPEDLKS LDLFKKEKIN 720
   TEGHSSGIGG SSCMSSSRPS ISSDENESS QNTSSTVQYS TVVHSGYRHQ VPSVQVFSRS 780
75 ESTQPLDSE ERPELDQLVD HVDGGDILP RQQYFKQNC QHESPDSH FERSKQVSSV 840
   NEEDFVRLKQ QISDHISQSC GSGQMKMFQE VSAADAFGFG TEGQVERFET VGMEAATDEG 900
   MPKSYLPQTV RQGGYMPQ

```

Seq ID NO: 75 DNA sequence  
Nucleic Acid Accession #: NM\_022131  
Coding sequence: 11..2878

```

80 1      11      21      31      41      51
   |      |      |      |      |      |
   TGCTGCGAGG ATGCTGCCTG GCGGCTGTG CTGGGTGCCG CTCCTGCTGG CGCTGGGCGT 60

```

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75

GGGGAGCGGC AGCGGCGGTG GCGGGGACAG CCGGCAGCGC CGCCTCCTCG CCGCTAAAGT 120  
 CAATAAGCAC AAGCCATGGA TCGAGACTTC ATATCATGGA GTCATACTG AGAACAATGA 180  
 CACAGTCATT TTGGACCCAC CACTGGTAGC CCTGGATAAA GATGCACCGG TTCCTTTTGC 240  
 AGGGGAAATC TGTGCGTTCA AGATCCATGG CCAGGAGCTG CCCTTTGAGG CTGTGGTGCT 300  
 CAACAAGACA TCAGGAGAGG GCCGGCTCCG TGCCAAGAGC CCCATTGACT GTGAGTTGCA 360  
 GAAGGAGTAC ACATTTCATCA TCCAGGCCCTA TGACTGTGGT GCTGGGCCCC ACGAGACAGC 420  
 CTGGAAAAAG TCACACAAGG CCGTGGTCCA TATACAGGTG AAGGATGTCA ACGAGTTTGC 480  
 TCCCACCTTC AAAAGAGCCAG CCTACAAGGC TGTGTGACG GAGGGCAAGA TCTATGACAG 540  
 CATTTCTGAC GTGGAGGCCA TTGACGAGGA CTGCTCCCCA CAGTACAGCC AGATCTGCAA 600  
 CTATGAAATC GTCACCACAG ATGTGCCTTT TGCCATCGAC AGAAATGGCA ACATCAGGAA 660  
 CACTGAGAAG CTGAGCTATG ACAAACAACA CCAGTATGAG ATCTGTGTGA CCGCCTACGA 720  
 CTGTGGACAG AAGCCCCGTG CTCAGGACAC CCTGGTGACG GTGGATGTGA AGCCAGTTTG 780  
 CAAGCCTGGC TGGCAAGACT GGACCAAGAG GATTGAGTAC CAGCCTGGCT CCGGGAGCAT 840  
 GCCCTGTTC CCCAGCATCC ACCTGGAGAC GTGCGATGGA GCCGTGTCTT CCCTCCAGAT 900  
 CGTCACAGAG CTGCAGACTA ATTACATTGG GAAGGGTTGT GACCGGGAGA CCTACTCTGA 960  
 GAAATCCCTT CAGAAGTTAT GTGGAGCCTC CTCTGGCATC ATTGACCTCT TGGCATCCCC 1020  
 TAGCGCTGCC ACCAACTGGA CTGCAGGACT GCTGGTGAGC AGCAGTGAGA TGATCTTCAA 1080  
 GTTTGACCGG AGGCAGGGTG CCAAAATCCC CGATGGGATT GTGCCAAGA ACCTGACCGA 1140  
 TCAGTTCACC ATCACCATGT GGATGAAACA CGGCCCCAGC CCTGGTGTGA GAGCCGAGAA 1200  
 GGAARACATC CTCTGCAACT CAGACAAAAC CGAAATGAAC CGGCATCACT ATGCCCTGTA 1260  
 TGTGACAAAC TGCCCGCTCG TCTTTCTCTT GCGGAAGGAC TTCGACCAGG CTGACACCTT 1320  
 TCGCCCCGGG GAGTTCACCT GGAAGCTGGA TCAGATTTGT GACAAGAGT GGCCTACTA 1380  
 TGTCTCAAT GTGGAGTTTC CTGTGGTAAC CTTATACATG GATGGAGCAA CATATGAACC 1440  
 ATACCTGGTG ACCAACGACT GGCCCATTTCA TCCATCTCAC ATAGCCATGC AACTCACAGT 1500  
 CGGCGCTTGT TGGCAAGGAG GAGAAGTCAC CAAACCACAG TTTGCTCAGT TCTTTTCATG 1560  
 AAGCCTGGCC AGTCTCACCA TCCGCCCTGG CAAAATGGAA AGCCAGAAGG TGATCTCCTG 1620  
 CCTGCAGGCC TGCAAGGAAG GGCTGGACAT TAATTCCTTG GAAAGCCTTG GCCAAGGAAT 1680  
 AAAGTATCAC TTCAACCCCT CGCAGTCCAT CTGTGTGATG GAAGGTGACG ACATTGGGAA 1740  
 CATTAAACGT GCTCTCCAGA AAGTCTCCTA CATCAACTCC AGGCAGTTCC CAACGGCGGG 1800  
 TGTGCGGCCG CTCAAAGTAT CTCTCAAAGT CCAGTGCTTT GGGGAAGACG TATGCATCAG 1860  
 TATCCCTGAG GTAGATGCTT ATGTGATGGT CCTCCAGGCC ATCGAGCCCC GGATCACCTT 1920  
 CCGGGGCACA GACCACTTCT GGAGACCTGC TGCCCACTTT GAAAGTGCCA GGGGAGTGAC 1980  
 CCTCTCCCTT GATATCAAGA TTGTGAGCAC CTTCGCCAAA ACCGAAGCCC CCGGGGACGT 2040  
 GAAAACCAAC GACCCCAAGT CAGAAGTCTT AGAGGAAATG TTTCATAACT TAGATTTCTG 2100  
 TGACATTTTG GTGATCGGAG GGGACTTGA CCAAGGCAG GAGTGTCTTG AGCTCAACCA 2160  
 CAGTGAGCTC CACCAACGAC ACCTGGATGC CACTAATTCT ACTGCAGGCT ACTCCATCTA 2220  
 CGGTGTGGGC TCCATGAGCC GCTATGAGCA GGTGCTACAT CACATCCGCT ACCGCAACTG 2280  
 GCGTCCGGCT TCCTTTGAGG CCCGGCGTTT CCGGATTAAG TGCTCAGAAC TCAATGGGCG 2340  
 CTACACTAGC AATGAGTTCA ACTTGAAGT CAGCATCCTT CATGAAGACC AAGTCTCAGA 2400  
 TAAGGAGCAT GTCAATCATC TGATTGTGCA GCCTCCCTTC CTCCAGTCTG TCCATCATCC 2460  
 TGAGTCCCCG AGTAGCATCC AGCACAGTTC AGTGGTCCCA AGCATTGCCA CAGTGGTCAT 2520  
 CATCATCTCC GTGTGATGCG TTTGTTTTGT CGTGGCCATG GGTGTGTACC GGGTCCGGAT 2580  
 CGCCCAACAG CACTTCATCC AGGAGACTGA GGCTGCCAAG GAATCTGAGA TGGACTGGGA 2640  
 CGATTCTGCG CTGACTATCA CAGTCAACCC CATGGAGAAA CATGAAGGAC CAGGGCATGG 2700  
 GGAAGATGAG ACTGAGGGAG AAGAGGAGGA AGAAGCCGAG GAAGAATAGA GCTCCAGCAG 2760  
 TGGCTCTGAC GACAGCGAAG AGGAGGAGGA GGAGGAAGGG ATGGGCAGAG GCAGACATGG 2820  
 CGAAGATGGA CCGAGGCAAG CCCAGCTGGA GTGGGATGAC TCCACCTCC CACTACTAGT 2880  
 CCCAGGGGTC TGCTGCCTGG CCCACATGTC CTTTTTGTAA ACCCTGACCC AGTGTATGCC 2940  
 CATGTCTATC ATACCTCAC TCTGATGTCT GTGACATGTC TGGGAAGGCC TTCTCCAGT 3000  
 TCCTGGAGCC CACCTTTTAA GCCTTGGGCA CTCCTGTGT TTTATCCATG GGGAAAGTTCC 3060  
 AAGAAGCCCA GCATGGCCAT CAGTGAGGAC TTCAGGGTAG ACTTTGTCTT GTAGCCTCCA 3120  
 CTCTGCCCCC AAGTTCCTCA GCATCCTGAC TACCTGTCTG CAGAGTTTGC CTTTGTTTT 3180  
 TCCTGCAAGG AAGAAGGCC ACCTTTGTGT CACTCACCTC CCCAGGCTCA GAGTCCCCAA 3240  
 GGCCTGGGGT TTTCAACTCA CTGTGCGTCT CCTCCACACA GACCAGTAGG TTCTCCTATG 3300  
 CTGACTCCAG GTTGCTTCAT ACAAGGAGGG TGGTTGAAC TCAACACCGT AAGGTCTTAG 3360  
 TGCTTAACAG TTTAAAGGAA AGTCTTGTG GAGGCAGAAC TAAGTTTACA GGGAAAGGTA 3420  
 CACACATTCT CTCTCTCTCT CTCTCTCTGT CTATCTAGTT CCCAGCTTG GAGAGCCTTT 3480  
 CCCCTTGCTT CTTTCTGAGG CCAATAAAGC TTATAAGAAA AGTCCCAAAC CAAGAATAGG 3540  
 TCCTTGGCCA CAAGCAGGGT CTGATCCCCC ATCAGAGCTA TCTGAGCTG CCTGTCTGGG 3600  
 CACCTGTGTC AACCATGCAG CTACCCTGCC AGGGGCACTC AGCAAACAGA ACCACAGGGC 3660  
 CCAGGAGGCA TTCCACACAG GCACTGCCCC AGGACAACAC AACCAAGGACA GTCACAACAA 3720  
 GGACAACAAG GACACAACAC AACACACAAC AAGGACAGTC ACAACAAGCC TAGAGCCAGA 3780  
 AAGCAGATGG AAATGCTAAT GAGGTCAAAC GTAGGCTTCA TGGTGGGTGG AGTGGGGGTG 3840  
 GCTGGGCTCC CCCAGGACAG AGGGGACCTT GAGGTTGGCA AGGCTCTCAC CACTCAGCCT 3900  
 TATGGTCCCT TATCTCCTAT CTTCCCTCTT GAGAAAATAC ACGTTTCTG CATGTATTAG 3960  
 AAACGCACGA GCTCCACCAA GTCTACAATG AAAGTTTGAA ATTTAACTGC AAGGAATTAG 4020  
 AAGCATATTT GCAATCATTG CAGCTTCTTC TTTCTTCTGC TCATAAAGG AGGAACACTT 4080  
 TAGATAGAGG GCAATATAT CTGAAAACCT AATTCTTTC TTTTGTGAT AAGGAAATCT 4140  
 TTTCCATCTC CATCTAACA TGACAACCT GTGAAGAGAA TTGTTTCTAT AGTAACTGGT 4200  
 CTGTGATCTT TTGTGGCCAA GAGAATAGCA GGCAAGAAAT AGGGCCTTGA CAGAATTTC 4260  
 ACGAAGCTCT GAGAACAATG TTGTTTCGAA TGTCTGATTC CTCTTTGTCA TCAATGTGTA 4320  
 TGCTCTGTCC CCATCCTTCA CTCCTCCTCA AGCTCACACC AATTGGTTTG GCACAGGCAC 4380  
 AGAGCTGGTC CCTAGTTAAG TGGCATTAT GTTAAAAAA A

Seq ID NO: 76 Protein sequence  
 Protein Accession #: NP\_071414

80  
 1 11 21 31 41 51  
 MLPGRLCWVP LLLALGVGSG SGGGGDSRQR RLLAAKVNKH KPWIIETSYHG VITENNDTVI 60  
 LDPPLVALDK DAPVPFAGEI CAFKIHQDEL PFEAVVLNKT SGEGLRLAKS PIDCELQKEY 120  
 TPIIQAYDCG ACPHPTAWIK SHKAVVHIQV KDVNEFAPTF KEPAYKAVVT EKKIYDSILQ 180  
 VEAIDEDCSF QYSQICNYEI VTDDVPFAID RNGNIRNTEK LSYDKQHQVE ILVTAYDCQG 240  
 KPAAQDTLVQ VDVKPVCKPG WQDWTKRIEY QPGSGSMPLF PSIHLETCDG AVSSLIQIVTE 300

LQTNVIGKGC DRETYSEKSL QKLCGASSGI IDLLPSPSAA TNWTAGLLVD SSEMIFKFDG 360  
 RQGAIPDGI VPKNLTDQFT ITMMMKHGPS PGVRAEKETI LCNSDKTEMN RHHYALYVHN 420  
 CRLVFLLRKD FDQADTFRPA EFHWKLDQIC DKEWHYYVIN VEFPPVVTLYM DGATYEPYLV 480  
 TNDWPIHPSH IAMQLTVGAC WQGGSEVTKPQ FAQFFHGSLSA SLTIRPGKME SQKVISCLOA 540  
 CKEGLDINSL ESLGGGIKYH FNPSQSILVM EGDDIGNINR ALQKVSYSINS RQFPTAGVRR 600  
 LKVSVKQVCF GEDVCISDPE VDAYVMVLQA IEPRTILRGT DHFWRPAAQF ESARGVTFLFP 660  
 DIKIVSTFAK TEAPGDVKTG DPKSEVLEEM LHNLDLDFCDIL VIGGDLDPDQ ECLELNHSEL 720  
 HQRHLDATNS TAGYSIYGVG SMSRYEQVLH HIRYRNWRPA SLEARRFRK CSELNGRYTS 780  
 NEFNLEVSIL HEDQVSDKEH VNHLIVQPPF LQSVHHPESR SSIQHSVVVP SIATVVIIIS 840  
 VCMLVFVVM GYVRVRIAQ HFIQETEAR ESEMDWDDSA LTITVNPMEK HEGPGHGEDE 900  
 TEGEEEEEEAE EEMSSSSGSD DSEEEEEEEG MGRGRHGQNG ARQAQLEWDD STLPY

Seq ID NO: 77 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 482..3007

1 11 21 31 41 51  
 AACTGAGCTA ACAAGAAATA CTAGAAAAGG AGGAAGGAGA ACATTGCTGC AGCTTGGATC 60  
 TACAACCTAA GAAAGCAAGA GTGATCAATC TCAGCTCTGT TAAACATCTT GTTTACTTAC 120  
 TGCATTCAGC AGCTTGCAAA TGGTTAACTA TATGCAAAAA AGTCAGCATA GCTGTGAAGT 180  
 ATGCCGTGAA TTTTAAATTGA GGGAAAAAGG GACAATTGCT TCAGGATGCT CTAGTATGCA 240  
 CTCTGCTTGA AATATTTTCA ATGAAATGCT CAGTATTCTA TCTTTGACCA GAGGTTTTAA 300  
 CTTTATGAAG CTATGGGACT TGACAAAAAG TGATATTTGA GAAGAAAGTA CGCAGTGGTT 360  
 GGTGTTTTCT TTTTTTAAAT AAAGGAATTG AATTACTTTG AACACCTCTT CCAGCTGTGC 420  
 ATTACAGATA ACGTCAGGAA GAGTCTCTGC TTACAGAAT CGGATTTCAT CACATGACAA 480  
 CATGAAGCTG TGGATTCATC TCTTTTATTC ATCTCTCCTT GCCTGTATAT CTTTACACTC 540  
 CCAAACTCCA GTGCTCTCAT CCAGAGGCTC TGTGTATTCT CTTTGCAATT GTGAGGAAAA 600  
 AGATGGCACA ATGCTAATAA ATTGTGAAGC AAAAGGTATC AAGATGGTAT CTGAAATAAG 660  
 TGTGCCACCA TCACGACCTT TCCAACCTAG CTATATAAAT AACGGCTTGA CGATGCTTCA 720  
 CACAAATGAC TTTTCTGGGC TTACCAATGC TATTCAATA CACCTTGGAT TTAACAATAT 780  
 TGCAGATATT GAGATAGGTG CATTAAATGG CCTTGGCCTC CTGAAACAAC TTCATATCAA 840  
 TCACAATTCT TTAGAAATTC TTAAGAGAGG TACTTTCCAT GGACTGGAAA ACCTGGAATT 900  
 CCTGCAAGCA GATCAACAAT TTATCAGAGT GATTGAACCA AGTGCCTTTA GCAAGCTCAA 960  
 CAGACTCAAA GTGTAAATTT TAAATGACAA TGCTATTGAG AGTCTTCCTC CAAACATCTT 1020  
 CCGATTTGTT CCTTTAACCC ATCTAGATCT TCGTGGAAAT CAATTACAAA CATTGCCTTA 1080  
 TGTGTGTTTT TCGCAACACA TTGGCCGAAT ATTGGATCTT CAGTTGGAGG ACAACAAATG 1140  
 GGCTGCAATT TGTGACTTAT TGCAGTTAAA AACTTGGTTG GAGAACATGC CTCCACAGTC 1200  
 TATAATTGGT GATGTTGTCT GCAACAGCCC TCCATTTTTT AAAGGAAGTA TACTCAGTAG 1260  
 ACTAAAGAAG GAATCTATTT GCCCTACTCC ACCAGTGTAT GAAGAACATG AGGATCCTTC 1320  
 AGGATCATTAT CATCTGGCAG CAACACTCTC AATAAATGAT AGTCGCATGT CAACTAAGAC 1380  
 CACGTCCATT CTAAAACAT CCACCAAGC ACCAGGTTTG ATACCTTATA TTACAAAGCC 1440  
 ATCCACTCAA CTCCAGGAC CTACTGCCC TATTCCTTGT AACTGCAAAG TCCTATCCCC 1500  
 ATCAGGACTT CTAATACATT GTCAGGAGCG CAACATTGAA AGCTTATCAG ATCTGAGACC 1560  
 TCCTCCGCAA AATCCTAGAA AGCTCATCTT AGCGGGAAT ATATTACACA GTTTAATGAA 1620  
 GTCTGATCTA GTGGAATATT TCACTTTGGA AATGCTTCAC TTGGGAAACA ATCGTATTGA 1680  
 AGTCTTGAA GAAGGATCGT TTATGAACCT AACGAGATTA CAAAACTCT ATCTAATATG 1740  
 TAACCACTG ACCAAATTAA GTAAAGGCAT GTTCTTGGT CTCCATAATC TTGAATACTT 1800  
 ATATCTTGAA TACAATGCCA TTAAGGAAAT ACTGCCAGGA ACCTTTAATC CAATGCCTAA 1860  
 ACTTAAAGCT CTGTATTATA ATAACAACCT CCTCCAAGTT TTACCACCA ATATTTTTTC 1920  
 AGGGGTTCTT CTAACCTAAG TAAATCTTAA AACAAACCAG TTTACCCATC TACCTGTAAG 1980  
 TAATATTTTG GATGATCTTG ATTTACTAAC CCAGATTGAC CTTGAGGATA ACCCTGGGA 2040  
 CTGCTCCTGT GACTGCTGTT GACTGCAGCA ATGGATACAA AAGTTAAGCA AGAACACAGT 2100  
 GACAGATGAC ATCCTCTGCA CTTCCTCCCG GCATCTCGAC AAAAAGGAAT TGAAGGCCCT 2160  
 AAATAGTGAA ATTCTCTGTC CAGGTTTAGT AAATAACCCA TCCATGCCAA CACAGACTAG 2220  
 TTACCTTATG GTCACCACTC CTGCAACAAC AACAAATACG GCTGATACTA TTTTACGATC 2280  
 TCTTACGGAG GCTGTGCCAC TGTCTGTTCT AATATTGGGA CTCTGATTA TGTTCATCAC 2340  
 TATGTTTTTC TGTGCTGCAG GGATAGTGGT TCTTGTCTT CACCGCAGGA GAAGATACAA 2400  
 AAAGAAACAA GTAGATGAGC AAATGAGAGA CAACAGTCCT GTGCATCTTC AGTACAGCAT 2460  
 GTATGGCCAT AAAACCACTC ATCACACTAC TGAAGAGCCC TCTGCCTCAC TCTATGAACA 2520  
 GCACATGGTG AGCCCCATGG TTCATGTCTA TAGAAGTCCA TCCTTTGGTC CAAAGCATCT 2580  
 GGAAGAGGAA GAAGAGAGGA ATGAGAAAGA AGGAAGTGAT GCAAAACATC TCCAAAGAAG 2640  
 TCTTTTGGAA CAGGAAATAT ATTCAACACT CACAGGGTCA AATATGAAAT ACAAACCCAC 2700  
 GAACCAATCA ACAGAAATTT TATCCTTCCA AGATGCCAGC TCATTGTACA GAAACATTTT 2760  
 AGAAAAAGAA AGGGAACCTC AGCAACTGGG AATCACAGAA TACCTAAGGA AAAACATTGC 2820  
 TCAGCTCCAG CCTGATATGG AGGCACATTA TCCTGGAGCC CACGAAGAGC TGAAGTTAAT 2880  
 GGAACATTA ATGTAATCAC GTCCAAGGAA GGTATTAGTG GAACAGACAA AAAATGAGTA 2940  
 TTTTGAACCT AAAGCTAATT TACATGCTGA ACCTGACTAT TTAGAAGTCC TGGAGCAGCA 3000  
 AACATAGATG GAGAGTTTGA GGGCTTTGCG AGAAATGCTG TGATTCTGTT TTAAGTCCAT 3060  
 ACCTTGTAAT TAAAGTGCCT ACCTGAGTGT GTCATCAATC AGAACCTAAG CACAGCAGTA 3120  
 AACATATGGG AAAAAAAG AAGAAGAAA GAAACTCAGG GATCACTGGG AGAAGCCATG 3180  
 GCATTATCTT CAGGCAATTT AGTCTGTCCC AAATAAAATC AATCTTGCA TGTAATC

Seq ID NO: 78 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MKLWIHLFYS SLLACISLHS QTPVLSSRGS CDSLNCNEEK DGTMLINCEA KGIKMWSEIS 60  
 VPPSPFQLS LLNNGLTMLH TNDFSGLTNA ISIHGFFNNI ADIEIGAFNG LGLLKQLHIN 120  
 HNSLEILKED TFHGLENFLE LQADNNFITV IEPSAFSKLN RLKVLILNDN AIESLPPNIF 180  
 RFPVPLTHLD RGNQLQTLFY VGFLEHIGRI LDQLLEDNKW ACNCDLLQLK TWLENNPPQS 240  
 IIGDVVCNSP PFFKGSILSR LKKEISICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT 300  
 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP 360

PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGSFMNL TRLOKLYLNG 420  
 NHLTKLSKGM FLGLHNLEVL YLEYNAIKEI LFGTFNPMPEK LKVLVLNNNL LQVLPPIHFS 480  
 GVPLTKVNLK TNQFTHLPVS NILDDLDTLT QIDLEDNPWD CSCDLVGLQQ WIKLSKNTV 540  
 TDDILCTSPG HLDKKEKAL NSEILCPGLV NNPSMPTQTS YLMVTTPATT TNTADTILRS 600  
 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM 660  
 YGHKTTHHTT ERPSASLYEQ HNVSPMVHVY RSPSFGPKHL EEEEEERNEKE GSDAKHLQRS 720  
 LLEQENHSPL TGSNMKYKTT NQSTEFLSFQ DASSLYRNIL EKERELQQLG ITEYLKKNIA 780  
 QLQPDMEAHY PGAHEELKLM ETLMYSRPRK VIVEQTKNEY FELKANLHAE PDYLEVLEQQ 840  
 T

Seq ID NO: 79 DNA sequence

Nucleic Acid Accession #: NM\_016640.2

Coding sequence: 39..1358

1 11 21 31 41 51  
 | | | | |  
 GCTTAAGTTG ACCTCTGGGT CCGGAATCGC GGGCAAAGAT GGCGGCGGCC AGGTGTTGGA 60  
 GGCCCTTTGCT AGCGCGTCCG AGGCTTTCAT TGCACACCGC GGCTAATGCC GCCGCCACGG 120  
 CTACAGAAAC GACCTCCCAA GACGTCGCGG CGACCCCGCT CGCGCGGTAC CCGCCGATTG 180  
 TGGCCTCCAT GACAGCCGAC AGCAAAGCTG CACGGCTGCG GCGGATCGAG CGCTGGCAGG 240  
 CGACGGTGCA CCGTCGGGAG TCGGTAGACG AGAAGCTGCG AATCCTCACC AAGATGCAGT 300  
 TTATGAAGTA CATGTTTAC CCGCAGACCT TCGCGCTGAA TGCCGACCGC TGGTACCAGT 360  
 ACTTCACCAA GACCGTGTTC CTGTCGGGTC TGCCGCGGCC CCCAGCGGAG CCCGAGCCCG 420  
 AGCCCGAACC CGAACCTGAA CCTGCGCTGG ACCTCGCGCG GCTGCGTGGC GTCGCTGCG 480  
 ACTGCCTGCT GCAGGAGCAC TTCTACCTGC GCGCGCAGCG GCGCGTGCAC CGTTACGAGG 540  
 AGAGCGAGGT CATATCTTTG CCTTCTCTGG ATCAGCTGGT GTCAACCCCT GTGGGCCTCC 600  
 TCAGCCACA CAACCCGCGC CTGCGCGCTG CCGCCCTCGA TTATAGATGC CCAATTTCAT 660  
 TTTACTGGGT GCGTGGTGAA GAAATTATTC CTCGTGGTCA TCGAAGAGGT CGAATTGATG 720  
 ACTTGGGATA CAGATAGAT GATAAACCAA ACAACAGAT TCGAATATCC AAGCAACTCG 780  
 CAGAGTTTGT GCCATTGGAT TATCTGTTC CTATAGAAAT CCCCATAATA AAATGTAAAC 840  
 CAGACAAACT TCATTATTC AAACGGCAGT ATGAAAACCA CATATTGTT GGCTCAAAAA 900  
 CTGCAGATCC TTGCTGTTAC GGTACACCCC AGTTTCATCT GTTACCTGAC AAATTAAGAA 960  
 GGGAAAGGCT TTTGAGACAA AACTGTGCTG ATCAGATAGA AGTTGTTTTT AGAGCTAATG 1020  
 CTATTGCAAG CCTTTTGTCT TGGACTGGAG CACAAGCTAT GTATCAAGGA TTCTGGAGTG 1080  
 AAGCAGATGT TACTCGACCT TTTGTCTCCC AGGCTGTGAT CACAGATGGA AAATACTTTT 1140  
 CCTTTTCTG CTACACGATA AATACTTTGG CACTGACTAC ACAAGCTGAT CAAAATAACC 1200  
 CTCGTAAAAA TATATGTTGG GGTACACAAA GTAAGCCTCT TTATGAAACA ATTGAGGATA 1260  
 ATGATGTGAA AGGTTTAAAT GATGATGTTT TACTTCAGAT AGTTCACTTT CTACTGAATA 1320  
 GACCAAAAGA AGAAAAATCA CAGCTGTTGG AAAACTGAAA AAGCATATTT GATTGAGAAC 1380  
 TGTGGGAATA TTTAAATTTT ACTGAAGGAA CAATAATGAT GAGATTGTA ACTGTCAACT 1440  
 ATTAATAACA TTGATTTTGG AGACAAAAAA AAAAAAAAAA AA

Seq ID NO: 80 Protein sequence

Protein Accession #: NP\_057724.1

1 11 21 31 41 51  
 | | | | |  
 MAAARCWRPL LRGPRLSLHT AANAATATE TTSQDVAATP VARYPPIVAS MTADSKAARL 60  
 RRIRWQATV HAESVDEKL RILTKMQFMK YMVYPQTFAL NADRWYQYFT KTVFLSGLPP 120  
 PPAEPEPEPE PEPFPAIDLA ALRAVACDCL LQEHFYLRRL RRVRHYESEE VISLPFLDQL 180  
 VSTLVGLLSP HNPALAAAL DYRCPVHFWY VRGEEIIPRG HRRGRIDDLR YQIDDKPNNO 240  
 IRISKQLAEF VPLDYSVPIE IPTIKCKPDK LPLPKRQYEN HIFVGSKTAD PCCYGHQTQPH 300  
 LLPDKLRRER LLRQNCADQI EVVFRANAIA SLFAWTGAQA MYQGFWSHAD VTRPFVSAV 360  
 ITDGKYFSFF CYQLNTLALT TQADQNNPRK NICWGTQSKP LYETIEDNDV KGFNDVLLQ 420  
 IVHFLNRPK EEKSQLLEN

Seq ID NO: 81 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..2070

1 11 21 31 41 51  
 | | | | |  
 ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCCGAC CCCGGGCTCT 60  
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCTC TGAGGCCGCA GAGCCCGCAG 120  
 CTCAGGCAGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180  
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAAAG CTCATGAGG AGATCGAGCA TCTGAAGCGG 240  
 GAAAAACAAG GTGAGCCGGC GCGGGGCCCT AGGCCGCGCC TGCCCTCCCA GGCACACTCA 300  
 ACATGCGCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCGGGCTCA 360  
 GGGGAACAC AGGACGGGGA GCCCTCCAG ACTGTCCTTG CCCACCTGGC TGCAGTGGCC 420  
 CCTGTATGCC AACCCAGTGG GTACAGGTTC TGGGGGACCT GGCAGATGCG CGTACTCTCT 480  
 AGCGTGGCT GGCAGATGTT ATGCAGCCAA GCACAGCAGG TGCTGCTCTC GGGGAGCCCA 540  
 GGGCTGAGG TCATTGCAAG GCGGCGAGTG GCCACAGGCT GCTCCCAAGA CCTCCCTCCT 600  
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG 660  
 CCTCAGATG CTGCTGTGGC CAGGCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720  
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
 GCAGCAACA TGGGACAAA GGGAGGAAGC AGAGTCTGT TCCCTTGCCA CTTGTCCAAG 840  
 GCACTTCCCC ATCTGACAG CGGCCCCAC CCAGCCAGG ATCCTGGGCT GTGGTCTCAA 900  
 GCTCACTTCC CATTATCTTT GGGGCTGGG CTGACATCAG GAGGACATCT GACTGGTGGG 960  
 TGGAGCCAGC CTGGGAACAT GCAGCTGGG GCAGTGCCTA GGGCTCTCCC TCCAGGGA 1020  
 GACATGGAGA AGGGGGTTGA GGGAGGGCCC TCCCTAGCC GCTGTGGCAA CTCCAGTGAG 1080  
 CTGTTCTGGG CAAAGTGTGG CCAAGTCGG CAGCCCCAGC CTGCGAGTGC TGGGGACGCT 1140  
 GACAGGACG GGAAGAGAGC CATGCTTCC CTGGGACCT GCTGTTCCAT GTGTCCCAAG 1200  
 CCTCCTGCT TCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGCGCTC TGCTCCCTTG 1260  
 GCGCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320

AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGCG 1380  
 GGCGGTAGCG CCGACACTGT GCGCTCTCCT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440  
 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500  
 TCCTTCAACA AGCAAGATTTC AAAAGCTGAC GTCTCCCGA AGGCGGACCT GGAAGAGGAG 1560  
 CCCTTACTTC ACAACAGCAA GCTGGACAAA GTTCCTGGGG TACAAGGGCA GGCCAGAAAG 1620  
 GAGAAAGCAG AGGCTCTTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACCAGGGC 1680  
 AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCCTGC CCTTCCCCCT GCGAAAGCCC 1740  
 ACCACACTTA GGCAGTGCAG AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCTGCAG 1800  
 ACCCAGAGC TCGCGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860  
 CCGGAGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCCAA GTCTCCACC 1920  
 AAGAGCCTCT CCAAGAAATC CCTGAGCCCA CTGTGGCGG AGCGTGCCAT CCTGCCCGCA 1980  
 CTGAAGCAGA CCCCAGAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040  
 AAACGGCGCC TGCATCGCTC AGTGCTTTGA

Seq ID NO: 82 Protein sequence  
 Protein Accession #: FGENSEH predicted

1 11 21 31 41 51  
 MSGAGVAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60  
 QQQHSEMLAK LHEEIEHLKR ENKGEPARGP RPALPPQAH S TLPLPQHRNT AINSSTRLGS 120  
 GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180  
 GPEVIAGRQV ATGCSPLDLP PSRAEMGRNP WDSFPCPARSL PQIAAVARPR ISSPMALSPH 240  
 MLGAQGIWTH SIQGSFLAIW AATMGTKGGS RVLFPCHLSK ALPHPDSEPH PAQDPGLWSQ 300  
 AHFPLSLGLG LTSGGHLTGG WSPQGNIAAG AVPRALPSQG DMEKGVGGP FPSRCGNSSE 360  
 LFWAKCGPSR QPQPCASGDA DRTREBAMLS LGTCCSMCPK PSCFPDGP SG NHLSRASAPL 420  
 GARWVCINGV WVEFPGPSPA RLKEGSSRTH RPPGKRGRLA GGSADTVRSP ADSLSMSSFQ 480  
 SVKSIANSAN SQKARQPQG SFNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQGGARK 540  
 EKAESANAGA ACMGNSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600  
 TQELRHLKSL LEGSQRPQAA PEEASFPRDQ BATHFPKVST KSLSKKCLSP PVAERAILPA 660  
 LKQTPKNNFA ERQKRLQAMQ KRLHRSVL

Seq ID NO: 83 DNA sequence  
 Nucleic Acid Accession #: NM\_005264.1  
 Coding sequence: 557..1954

1 11 21 31 41 51  
 GAATTCGGGC CAGAAGAAAT CTGGCCTCGG AACACGCCAT TCTCCGCGCC GCTTCCAATA 60  
 ACCACTAACA TCCCTAACGA GCATCCGAGC CGAGGGCTCT GCTCGGAAAT CGTCTGGCC 120  
 CAACTCGGCC CTTCGAGCTC TCGAAGATTA CCGCATCTAT TTTTCTTTTC TTTTCTTTCT 180  
 TTTCTAGCGC CAGATAAAGT GAGCCCGGAA AGGGAAGGAG GGGGCGGGGA CACCATTGCC 240  
 CTGAAGAAT AAATAAGTAA ATAAACAAAC TGGCTCCTCG CCGCAGCTGG ACCCGGTCGG 300  
 TTGATCCAG GTTGGGTGGG ACCTGAACCC CTAAAGCGG AACCGCTCC CGCCCTCGCC 360  
 ATCCCGGAGC TGAGTCGCGA GCGGCGGTGG CTGCTGCCAG ACCCGAGTT TCCTCTTTCA 420  
 CTGGATGGAG CTGAACCTTG GCGGCCAGA GCAGCACAGC TGTCCGGGGA TCGCTGCACG 480  
 CTGAGCTCCC TCGCAAGAC CCAGCGGCGG CTCGGGATT TTTTGGGGG GCGGGGACCA 540  
 GCGCCGCGCC GGCACCATGT TCCTGGCGAC CCTGTACTTC GCGCTGCGCG TCTTGACTTT 600  
 GCTCCTGTGC GCCGAAGTGA GCGGCGGAGA CCGCTGGAT TGCCTGAAAG CCAGTGATCA 660  
 GTGCCTGAAG GAGCAGAGCT GCAGCACCAA GTACCGCAGC CTAAGGCAGT GCGTGGCGGG 720  
 CAAGGAGACC AACTTCAGCC TGGCATCCGG CCTGGAGGCC AAGGATGAGT GCCGCAGCGC 780  
 CATGGAGGCC CTGAAGCAGA AGTCGCTCTA CAACTGCCGC TGCAAGCGGG GTATGAAGAA 840  
 GGAGAAGAAC TGCCCTGCGCA TTTACTGGAG CATGTACCAG AGCCTGCAGG GAAATGATCT 900  
 GCTGGAGGAT TCCCCATATG AACCAATTAA CAGCAGATTG TCAGATATAT TCCGGGTGGT 960  
 CCCATTCTATA TCAGATGTTT TTCAGCAAGT GGAGCACATT CCCAAAGGGA ACAACTGCCT 1020  
 GGATGCAGCG AAGGCTTGCA ACCTCGACGA CATTGTCAAG AAGTACAGGT CGGCGTACAT 1080  
 CACCCCGTGC ACCACGACG TGTCCAACGA TGTCTGCAAC CGCCGCAAGT GCCACAAGGC 1140  
 CCTCCGGGAC TCTTTTGACA AGGTCCCGGC CAAGCACAGC TACGGAATGC TCTTCTGCTC 1200  
 CTGCCGGGAC ATCGCTTGCA CAGAGCGGAG GCGACAGACC ATCGTGCCTG TGTGCTCCTA 1260  
 TGAAGAGAGG GAGAAGCCCA ACTGTTTGAA TTTGCAAGG TCCTGCAAGA CGAATTACAT 1320  
 CTGCAGATCT CGCCTTGCGG ATTTTCTTAC CAACTGCCAG CCAGAGTCAA GGTCTGTGAG 1380  
 CAGCTGTCTA AAGGAAACTC ACGCTGACTG CCTCTCGCC TACTCGGGGC TTATTGGCAC 1440  
 AGTCATGACC CCCAACTACA TAGACTCCAG TAGCCTCAGT GTGGCCCCAT GGTGTGACTG 1500  
 CAGCAACAGT GGAACGAGC TAGAAGAGTG CTGAAATTT TTGAATTTCT TCAAGGACAA 1560  
 TACATGTCTT AAAAATGCAA TTCAAGCCTT TGGCAATGGC TCCGATGTGA CCGTGTGGCA 1620  
 GCCAGCCTTC CCAGTACAGA CCACCACTGC CACTACCACC ACTGCCCTCC GGGTTAAGAA 1680  
 CAAGCCCTCG GGGCCAGCAG GGTCTGAGAA TGAATTTCCC ACTCATGTTT TGCCACCGTG 1740  
 TGCAAAATTA CAGGCACAGA AGCTGAAATC CAATGTGTGC GGCAATACAC ACCTCTGTAT 1800  
 TTCCAATGTT AATTATGAAA AAGAAGGTCT CGGTGCTTCC AGCCACATAA CCACAAAATC 1860  
 AATGGCTGCT CTCTCAAGCT GTGGTCTGAG CCCACTGCTG GTCCCTGGTG TAACCGCTCT 1920  
 GTCCACCTTA TTATCTTTAA CAGAAACATC ATAGCTGCAT TAAAAAATA CAATATGGAC 1980  
 ATGTAAAAAG ACAAAAACCA AGTTATCTGT TTCCTGTTCT CTGTATAGC TGAAATTTCA 2040  
 GTTTAGGAGC TCAGTTGAGA AACAGTTCCA TTCAACTGGA ACATTTTTTT TTTTCTTTT 2100  
 AAGAAAGCTT CTGTGTGATC TCGGGGCTT CTGTGAAAAA CTGATGCAG TGCTCCATTC 2160  
 AAACCTAGAA GGCCTTGGGA TATGCTGTAT TTAAAGGGA CAGTTTGTAA CTGGGCTGT 2220  
 AAAGCAAATC GGGCTGTGT TTCGATGAT GATGATCATC ATGATCATGA TGATTTTAA 2280  
 AGTTTACTT CTGGCCTTTC CTAGCTAGAG AAGGAGTTAA TATTTCTAAG GTAACCTCCA 2340  
 TATCTCTTTT AATGACATG ATTTCTAATG ATATAAATTT CAGCCTACAT TGATGCCAAG 2400  
 CTCTTTTGCC ACAAAAGAGA TTCTTACCAA GAGTGGGCTT TGTGGAAACA GCTGGTACTG 2460  
 ATGTTCACTT TTATATATGT ACTAGCATTT TCCACGCTGA TGTTTATGTA CTGTAAACAG 2520  
 TTCTGCACCT TTGTACAAAA GAAAAACCA CCGGAATTC

Seq ID NO: 84 Protein sequence  
 Protein Accession #: NM\_005264.1

```

1      11      21      31      41      51
5  MFLATLYFAL PLLDLLLSAE VSGGDRLCDV KASDQCLKEQ SCSTKYRTLr QCVAGKETNF 60
    SLASGLEAKD ECRSAMEALK QKSLYNCRCK RGMKKEKNCL RIYWSMYQSL QGNDLLEDSP 120
    YEPVNSRLSD IFRVVPFISD VFQQVEHIPK GNNCLDAAKA CNLDDICKKY RSAYITPCTT 180
    SVSNDVCRNR KCHKALRQFF DKVPAKHSYG MLFCSRDIA CTERRRQTIV PVCSEEREK 240
    PNCLNLQDSC KTNVICRSRL ADFFTNCPQE SRSVSSCLKE NYADCLLAYS GLIGVTMPFN 300
    YIDSSSLVA PWDCSNSGN DLEELCKFLN FFKDNTCLKN AIQAPNGSD VTVWQPAFPV 360
10 QTTTATTTTA LRVKNKPLGP AGSENEIPTH VLPPCANLQA QKLKSNVSGN THLCISNGNY 420
    EKEGLGASSH ITTKSMAAPP SCGLSPLLVL VVTALSTLLS LTETS

```

Seq ID NO: 85 DNA sequence

Nucleic Acid Accession #: XM\_027172.1

Coding sequence: 143..1405

```

1      11      21      31      41      51
20 GGTGGAGACA CCGCCTCAGG GCTCGGTGCA CAGTGGACAT TTGGGGAGCG TTGTGGGTGA 60
    CCCCCACACA GGCACCTGGGA ATGCAGGGGA GAGGGGGCCA AGGGGGAAAG GGGCCAGAGT 120
    GTTGGCTTTG GATTACGAGG GGATGGATTG CAGTCTTAGC TTGCCACTTA TTAGGACTCC 180
    TGAGAGCAGC CTCCATGAGG CCTCGGACCA GTGCATGACC GCCCTGGACC TCTTCCTCAC 240
    CAACCAAGTTC TCAGAAGSCA TCAGCTACCT CAAGCCGAGA ACCAAGGAAA GCATGTACCA 300
    CTCACGTACA TATGCCACCA TCCTGGAGAT GCAGGCCATG ATGACCTTTG ACCCTCAGGA 360
    CATCCTGCTT GCCCGCAACA TGATGAAGGA GGCACAGATG CTGTGTGAGA GGCACCGGAG 420
    GAAGTCTTCT GTAACAGATT CCTTCAGCAG CCTGGTGAAC CGCCCCACGC TGGGCCAATT 480
    CACTGAAGAG GAAATCCACG CTGAGGTCTG CTATGCAGAG TGCTTCTGTC AGCGAGCAGC 540
    CCTGACCTTC CTGCAGGGTT CCTCACACGG AGGGGCAGTC AGGCCCAGAG CCTTGCATGA 600
    TCCTCTCTAC GCCTGCAGCT GCCACCTGG GCCAGGCCGT CAGCATCTTT TCCTCCTGCA 660
    GGACGAGAAC ATGGTGAGCT TCATCAAAGG CGGCATCAAA GTTCGAAACA GCTACCAGAC 720
    CTACAAGGAG CTGGACAGCC TTGTTCACTC CTCACAATAC TGCAAGGGTG AGAACCACCC 780
    GCACTTTGAA GGAGGAGTGA AGCTTGGTGT AGGGGCCCTT AACCTGACAC TGTCCATGCT 840
    TCCTACTAGG ATCCTGAGGC TGTGGAGTT TGTGGGGTTT TCAGGAAACA AGGACTATGG 900
    GCTGCTGAGG CTGAGGAGG GAGCGTCAGG GCACAGCTTC CGCTCTGTGC TCTGTGTCT 960
    GCTCCTGCTG TGTACACACA CCTCCTCAC CTTGCTGCTC GGTACTGGGA ACGTCAACAT 1020
    CGAGGAGGCC GAGAAGCTCT TGAAGCCCTA CCTGAACCGG TACCCTAAGG GTGCCATCTT 1080
    CCTGTTCTTT GCAGGGAGGA TTGAAGTCAT TAAAGGCAAC ATTGATGCAG TGAGTGATGG 1140
    GGGTCCGGGC CGGGGCTGGG GATCCCTCGG GGTCTCCAG ACCAGCAGGA AGTCAGGCAC 1200
    ATGTGACATA CTCAGGGACA GGATAGACTG GGGGCGGGGG GGGGGCCAG AGAGAACCAA 1260
    CCAGAGAGCA GGGGCAGGAG AGGCCCTTCT GGCAGAGCAG CCTGGGAAGA CAAGGGAGGA 1320
    GGAGGCATTG GTGGTGCTGT GGATTTTGAC TGGGAGATAT AGGACTGCAG CATTGCACTG 1380
    GAGGAGGTG GAGGAGGTG CTTGAGGGAG GCAGAGGTTA GGAAGGCCA TCTGTTTAGG 1440
    GCATGACGAT TAGGCTGGAG TCTGGTACCT CCCCTCCATT ATAGCTCTCT CCTGCTCTTT 1500
    CATTTTGTGA CTAAAAACCA GAGTCCTAGG CGGGGGCTGT ATTTGAGCCC AACGTCATGT 1560
    AAGACTTAGG AGGTAAACAC AGGACTGGAG GCCAGATCTC CTGGCTCTGT GGGCCCCACC 1620
    TGAGCCTAGC ACAGGGCTGG ACCACTATGC CCTGGAGGAG TCCCGGTCTG CTGTGGTGT 1680
    GGGAGGTTCT GAGGATGCA AGGGGTTGGG GCTGGGTGGG CACCCGTCAG GCTGACCAGA 1740
    AGGTGCTGTC AGGCCATCCG GCGTTTCGAG GAGTGCTGTG AGGCCAGCA GCACTGGAAG 1800
    CAGTTCACAC ACTGTGTCTA CTGGGAGCTG ATGTGGTGTCT ACCTTACAA GGGCCAGTGT 1860
    AAGATGTCTT ACATTACGCA CGAAGCTGCT AGCAAGGAGA ACTGCTGGTC CAAGGTGGG 1920
    TGATGCCACG TGTTAGGGGC ATTGGGTGAC CAGGCTGAC TGTGTGCTC CAGACCACGG 1980
    GCCAATCCC TAAGTGAACA CAGATGTCTC AGCTGGAATC TAAACATAAC CTTAAATTCT 2040
    AATAGGACTC AGGCTTGGA GGAACATAAG ACCACAAGAG AAACCTTCTG ACCACAATGT 2100
    GTCACAAAGA GATTCTAGT CACAAAGGAC AGAAACATGG CTCCTCTGT CAGTAGAAC 2160
    TGTCTCTGTG GTAGAAATGT TCTACTTATG CACTGCCCAA ATATGTTAGT CACAGCCAC 2220
    ATGTGCACAA TGAGCACATG AAATGTGCTT AGTGCACTG GGAACACTGAT TGTTTTCAGT 2280
    TTTATTTAAT TTTAATTAA TAAATGTTAA ATTTAAATAG CCATGTAGGG CTTGTGGCCA 2340
    CTATATTGGA CTATGCAAGT CCAAAACACA AAAGGCTCAT ATAAGTGAAC ATTCTTGGCA 2400
    CATCCGACTT CAGGTAGGGC TGGATCCAGG AATTCAAATG ATGTGCTGTG GCTTGGTCTT 2460
    TCCATTGTGT GCTGTGCTCT CTCCTATGAC ATCTTTGTTT CTGCTGCATC TTTGCAGGAA 2520
    GGTTCCTCTC ATGTGACAGG CAAGGTGGCC ACGGGCTGCT TCTACTCATA TCCTCCCTTT 2580
    GGTTCACACC AGAGTCCAC AGTTTGAGCC TCACTGGTCT GACTTGTGAC CTGCCAATGC 2640
    CTGGAACAGA GGGGTGGGAA GATTCTCAT GGGCTGAGAG TAGGAGAGGG GTGGTTCCAC 2700
    AGAAGAAAAT GATGCACCCA GAAATAGTGG AGGGATTAAC AAGATGCCAT ACAGGCAAAA 2760
    CAAAGCCAAA CAGATGCCCG CCTACCAAAG ATGAAATTTA TCATGGTAAG TATTGAAATA 2820
    AGTGTAGCT TGTACCATCA TAGTAATGAT AGTGCAGAAA TTGGAACCAA GAGTCTTACA 2880
    ACCACCTAGC TCAGCAACAG TCTAATCTGT TATTTGTAAA TACACAGGAC ATGTGTCTTC 2940
    ATGGCTTCAT CCCCTGCCA TAGCAGACAT TGCTAATCAA TCCTCTGCCA TGAGCCTAGC 3000
    TGTGACCTTA GATACCTTCC CTGCAAGCT CCAGGAGGCC GTTAGAATG ACCCAATG 3060
    GCACCTGTTA GGAGACCTGT CATCTGCATC TGGTCCCTCC CCCTCCTCTG CATGGAGGTC 3120
    TCTTCCGTAG CCCTGCCTGG GGACCAAGCT GAAGGGGAAT TCTCTGGGTC TGGGGCAGGT 3180
    GGGGCTGGGG AAGGAGCAG GCTTCTACTG AGCTCTCAAC ATGTCTGGCA CCTGTCTGT 3240
    CCTCCACACC ACACCCAGT AGGAGAAGTT ATTATCTCCA TTGGGCACAT TGGGCCACT 3300
    GATGCTAAGC GAGGACTGTG ACTTTCCAC CCACATGGCT GTTGGTGACA GACACCGGAT 3360
    TTGAGGACAG TCCTGTGTGA CTCAGAGGCC TGTGCTTCT TCTTGTCTCT AGAGTCTCTC 3420
    TGAGGAGTGG GGGCTTGCCC TGAGCCACCC CTGCTGTTGA AGGTGCTTCC TCAGGCCAG 3480
    CTCCCATGGC CCCCACACCC CCTCCTCATC ACCTCCTACT CCCAAAAAG ACAAAGCCTC 3540
    AGGGAACCTT TTTTCTTTT TTAGAGACAG GGTCTTGCTA TGTGGTCTAG GCTAGTCTTG 3600
    AACTCCTGGG CCCAAGCAAT CTCCACCT CTGCTCCTA AAGTGTCTGG ATTCTGGGCC 3660
    TTAGGGAACC TTTTGAAGT GAAAGTGAAT CTCGAAGCCT TCCTGTAGAG TGAGGTGGGT 3720
    GGCTGGGGCT AACCATATGG GGAAGGAGAG ACCTGGTGGG GGCACACAGC TGCTATATAG 3780
    AGGAACAGAA GGTGGGCCAG GCCTCCACG TGTGAGGAAA TCTGGCTCAG TCCCCAGACC 3840
    GCTGTGTGGC TTTGGGGTGG CAGTCCCTC TCTCTTGCA ACACCTCTCT CATGAGGACT 3900
    TCTGTAAAAA ATGGGGGTGG TAACCTCTG AGTTCTGGGG CCCACCCAT TTTAATCTC 3960

```

CAGAACTTGG CCACCACAGA CTCACCAAC TTCTAGTCCT GGGGCCTGGG CCTCTGGCCA 4020  
 TTGCCATAGG CACCACCTGC TCTGTGCAGG CAGCGCCCCC CTCTGCCAGG ATCCTCCGAG 4080  
 GTCAGCTGCT GGGTCTGACC CGCAGACCCCT GGCTGAGCGA CGGATGAACG GAGTATGCGAG 4140  
 ACACAGGCTT GCCTGTGACG AGATGGGGGA CCCTGCCCAG AGTCAGCAGC GGGCCCCATA 4200  
 AGCCTGCCAC GCTTGCAATT ATTTAGTACA GATGTAATGA CAAAGGCCCTA AAGCAAATC 4260  
 CATTGTGGG TAATTAACAT TGTGCCCCC CCAGAAAGAG CAGTCCCTCCG CATGATGATT 4320  
 AAAGGCCAGG TTCCGAGGCC TAAGTAAACC AACTTATCTA GATCAATTC CTTACTTCTT 4380  
 GTTATCTACT CTGAGAGAAT TCAGCTGCCT TCAGCCAAAT CCTTTCCCGA AGCTTTTGCA 4440  
 AAACCTCCGA GCCTTCCAAG GTTGTCTTCT TTCTGTAATT TTCTCACCAC CCTGACCTTA 4500  
 TCTCTGCGAG TCAGCCCTGT GGAGGCCCTT GTGTTTCCCC CAGTGCTGGC AGCCTAGAGG 4560  
 CTGAGATGGC CAGAAACAAG TGGTGACAG TGGCGTGCTC AGGCTTGGG AAACCCAAGG 4620  
 AGCTAAAGGC ATGCCAGGC AACCAAAGAG GACAGGAAGG CTCTGAGGA GAGACCTCTG 4680  
 AGGTGGGTCT TGGAGAGGAA GGACTTAGGG AGGCAGAGTG GAGGAAGTGA GAGGACACCC 4740  
 CAAGCCAAGA GGGCGGCAGG ACCAAAGGCT CAGAAGCCAG GGGCTGCGAG AGGGGCTGTG 4800  
 TGCCACAGGG TGAAGAGTTT GTGTGGCAGA AGGGCAGGGG GCTTGCATCA GGGGTGACAG 4860  
 CTGCTCTTTT GTCCAGCAT AGCCCTGTGA CATCCCTGGA GAGCTGGGGC GTCCACAAC 4920  
 CTAAGTCACA GCCCCATCC TAACCTCTGT GGTGCACTGA GGGTGAGCTG TCTGTGGGCA 4980  
 GGAGGAAGA CTCTTGGAGA TGAGCCTGGT GAAGGGATAA TGGCATCCCG GGGCAGGAG 5040  
 CAGCACAGGC AGAGGCTTGG GGAGAGTTTA AGGAGTGTAG GGGAGGAAAT GGCAGAAGAT 5100  
 GAGCCAGAAA AAGAAAGGTT AGGGCAGGTC CTGGAGGACA TGAGTGGCTG TTTGGGCTTT 5160  
 ATCCAGCAGT GGGGGAGCCT TGGCAGGCTT GTGGCTTAGA TAGGTGCTTT AGAAAGCCCA 5220  
 CCAGCAGTTG CTGGGCCACC CCGCTGGCTG GGTCTGTCTC TAAGGCAGGA AATACAAGCA 5280  
 TGAGCAGGAA AAGACCCCTT CAGGCTCAC GTCTAGTGG GGAGACAGA AACACAGATG 5340  
 GGCAATATAA CACGATGTCT GGTTCAGTA AGTGCACTGA AGAACAAGCG AGGCTGGATG 5400  
 CAGGAGTGA TGGGAGGGG TTTGTAAAGG GAGGTGCGGG GAAGCCTGTC TCAGAGGACA 5460  
 CCAGAAATGA GCGCAGGAG AGCACGTGGC AGTCACATGG CAGGCCGTTA GGGCAGAGGG 5520  
 AGCTGGGCG GGCACAGCAG GGCAGGAGTG TGTTTGATGT GTCTGGGAA CCGCCTGAG 5580  
 GCGCTCGTGT GGCTGGAGTG CTGCAGGTGT CAAGGAAATT GTAGGAGATG TCTCCTGAGT 5640  
 GTGATGGAAT ATAAACAGAT TTCCAGAAGG AACTGACATG ATCTGACTTA AAAAGGTCAG 5700  
 TGTGCGAAT GGCTTGCAGG GGACAGGAGT GGGAGCAGGG AGATAGGAGA CAATGTGTAC 5760  
 CAGGACAGCA GAAAGACATC CCGGGTAGCC TGGAAACAGG AGACGGTGTG GAGATGGTGG 5820  
 CAGTCCGATA ATGAGAGCCG TAGGGCAAGG CCAGCAGGAT CCTAGAGTGA GACGGGAGGT 5880  
 AAAGTCACCG GGACTTGGTG TCTCCACGTC AGGGGCAGGG GAAAGGGAGA GGACAAGGGT 5940  
 GACCCGGGAG GTTAAAGATG GGACCGGGG CAGACGCACT GGCTCATGCC TGTAATCCTA 6000  
 GCACTTTGGG AGGCTGAGGC GGGCGGATAG CTTGAGGTCA GGAGTTTGA ACCAGCCTGG 6060  
 CCAACATGGT GAAACCCCTT CTCTACTAAA ATATACAAA ATTAGCCTGG CGTGGTGGTG 6120  
 CATGCTGCA GTCCAGCTA TTCAGGAGGC TGAGGCAACA AGAATCGCTT GAACCTGGGA 6180  
 GGCGGAGGTT GCAGTGAGCC GAGATCGCGC CATAGCACTC CAGCCTTAGC CTGGGCGACA 6240  
 GAGCGAGACC ACATC

Seq ID NO: 86 Protein sequence  
 Protein Accession #: XP\_027172.1

1 11 21 31 41 51  
 | | | | |  
 MDSSPSLPLI RTPESSLIHEA LDQCM TALDL FLTNQFSEAL SYLKPRTKES MYHSLTYATI 60  
 LEMQAMMTFD PQDILLAGN MKEAQM LQCR HRRKSSVTD FSSLVNRPTL GQFTREEIHA 120  
 EVCYAECLLQ RAALTFLQGS SHGGA VRPRA LHPD SHACSC PPGPGRQHLF LQDENMVVSF 180  
 IKGGIKVRNS YQYKELDSL VQSSQYCKGE NHPHFEGGVK LGVGFNLTL SMLPTRLRL 240  
 LEFVGFSGNK GTTAAAGATG ASGHSFRSVL CVM LLLCYHT FLTFLVLTGN VNIEAEKLL 300  
 KPYLNRYPKG AIFLFPAGRI EVIKGNIDAV SDGGPGRGWG SLGVSQTSRK SGTCDILRDR 360  
 IDWGRGGGQE RTNQRAGAGE ALLAEQPKT REEEAFVVP G ILTGRYRTAA LQWREVEGGA

Seq ID NO: 87 DNA sequence  
 Nucleic Acid Accession #: AB007921  
 Coding sequence: 143..1363

1 11 21 31 41 51  
 | | | | |  
 GGTGGAGACA CCGCTCAGG GCTCGGTGCA CAGTGGACAT TTGGGGAGCG TTGTGGGTGA 60  
 CCCCCACACA GGCCTGCGG ATGCAGGGGA GAGGGGGCCA AGGGGGAAAG GGGCCAGAGT 120  
 GTTGGCTTTG GATTCAGGAG GGATGGATTC CAGTCCTAGC TTGCCACTTA TTAGGACTCC 180  
 TGAGAGCAGC CTCCATGAG CCCTGGACCA GTGCATGACC GCCCTGGACC TCTTCCTCAC 240  
 CAACCAAGTTC TCAGAAGCAC TCAGCTACCT CAAGCCCAAGA ACCAAGGAAA GCATGTACCA 300  
 CTCACTGACA TATGCCACCA TCCTGGAGAT GCAGGCCATG ATGACCTTTG ACCCTCAGGA 360  
 CATCTGTCTT GCCGGCAACA TGATGAAGGA GGCACAGATG CTGTGTCAGA GGCACCGGAG 420  
 GAAGTCTTCT GTAACAGATT CCTTCAGCAG CCGGTGTAAC CGCCCCACGC TGGGCCAATT 480  
 CACTGAAGAG GAAATCCACG CTGAGGTCTG CTATGCAGAG TGCCTGCTGC AGCGAGCAGC 540  
 CCTGACCTTC CTGCGAGGTT CCTCACACGG AGGGGCAGTC AGGCCCAGAG CCTTGCATGA 600  
 TCCCTCTCAC GCCTGCAGCT GCCCACTTGG GCCAGGCCGT CAGCATCTTT TCTCCTGCA 660  
 GGACGAGAAC ATGGGTGAGT TCATCAAAGG CGGCATCAAA GTTCGAAACA GCTACCGAGC 720  
 CTACAAGGAG CTGACAGGCC TTGTTCAATC CTCACAATAC TGCAAGGGTG AGAACCAACC 780  
 GCACCTTGAA GGAGGAGTGA AGCTTGGTGT AGGGGCCCTT AACCTGACAC TGTCCATGCT 840  
 TCCTACTAGG ATCCTGAGGC TGTGGAGTT TGTGGGGTTT TCAGGAAACA AGGACTATGG 900  
 GCTGCTGAGC CTGAGGAGG GAGCGTCAGG GCACAGCTTC CGCTCTGTGC TCTGTGTCAT 960  
 GCTCTGCTG TGCTACCACA CCTTCCTCAC CTTCGTGCTC GGTACTGGGA ACGTCAACAT 1020  
 CGAGGAGGCC GAGAAGCTCT TGAAGCCCTA CCTGAACCGG TACCCTAAGG GTGCCATCTT 1080  
 CCTGTTCTTT GCAGGGAGGA TTGAAGTCAT TAAAGGCAAC ATTGATGCAG TGAGTGATGG 1140  
 GGGTCCGGGC CGGGGCTGGG GATCCCTCGG GGTCTCCAG ACCAGCAGGA AGTCAGGCAC 1200  
 ATGTGACATA CTCAGGGAGA GGATAGACTG GGGGCGGGGG GGGGGGCCAA GAGAGAACCA 1260  
 ACCAGAGAGC AGGGGCGACA GAGGCCCTTC TGGCAGAGCA GCCTGGGAAG ACAAGGGAGG 1320  
 AGGAGGCATT TGTGGTGCCT GGGATTTTGA CTGGGAGATA TAGGACTGCA GCATTGCAGT 1380  
 GGAGGAGAGT GGAGGAGAGT GCTTGAGGGA GGCAGAGGTT AGGAAAGCCC ATCTGTTTAG 1440  
 GGCATGACGA TTAGGCTGGA GTCTGGTACC TCCCCTCCAT TATAGCTCTC TCCTGCTCTT 1500

5 TCATTTTGT ACTAAAAACC AGAGTCCTAG GCGGGGGCTG TATTTGAGCC CAACGTCATG 1560  
 TAAGACTTAG GAGGTAAC CAGGACTGGA GGCCAGATCT CCTGGCTCCT GGGGCCCCAC 1620  
 CTGAGCCTAG CACAGGGCTG GACCACTATG CCTGGAGGA GTCCCGGTCT GCTGTGGTGT 1680  
 TGGGAGGTTT GGAGGATGCA GAGGGGTG GGTGGGTGG GCACCCGTC GGTGTACCAG 1740  
 AAGGTGCTG CAGGCCATCC GGGTTTCGA GGAGTGCTGT GAGGCCAGC AGCACTGGAA 1800  
 GCAGTTCCAC CACATGTGCT ACTGGGAGCT GATGTGGTGC TTCACCTACA AGGCCAGTG 1860  
 GAAGATGTCC TACTTCTACG CCGACCTGCT CAGCAAGGAG AACTGCTGGT CCAAGGTGGG 1920  
 CTGATGCCAC GTGTTAGGGG CATTGGGTGA CCAGGGCTGA CTGTGTGCTT CCAGACCACG 1980  
 10 GGCCAAATCC CTAATGAA ACAGATGTCT CAGCTGGAAT CTAACATAA CCTTAAATTC 2040  
 TAATAGGACT CAGGCTTGGA AGGAACTAAA GACCACAAGA GAACTTCTG AACCACAATG 2100  
 TGTACAAAG AGATTTCTAG TCACAAAGGA CAGAAACATG GCTCCCTCTG TCCAGTAGAA 2160  
 CTGTTTCTGT GGTAGAATG TTTCTACTAT GCACTGCCCA AATATGGTAG TCACCAGCCA 2220  
 CATGTGCACA CTGAGCACAT GAAATGTGCC TAGTGCAACT GGGAACTGA TTGTTTTCAG 2280  
 15 TTTTATTTAA TTTTAATTA CTAATGTATA AATTTAAATA GCATGTAGG GCTTGTGGCC 2340  
 ACTATATTTG ACTATGACG TCCAAAACAC AAAAGGCTCA TATAACTGAA CATTCTTGCC 2400  
 ACATCCGACT TCAGGTAGG CTGGATCCAG GAATTCAAAT GATGTGCTCT GGCTTGTCT 2460  
 TTCCATTGT GGTGTGCTC TCTCTATGA CATCTTTGTT TCTGTGCTAT CTTTGCAGGA 2520  
 AGGTTCTCTC CATGTGACAG GCAAGGTGGC CACGGGCTGC TTCTACTCAT ATCTCTCCCT 2580  
 20 TGGTTTCAAC CAGAGTCCCA CAGTTTGAGC CTCACTGGTC TGACTTGTCA CCTGCCAATG 2640  
 CCTGGAACAG AGGGGTGGGA AGATTCTCCA TGGGCTGAGA GTAGGAGAGG GGTGGTTCCA 2700  
 CAGAAGAAAA TGATGCACCC AGAAATAGTG GAGGGATTAA CAAGATGCCA TACAGGCAAA 2760  
 ACAAAGCCAA ACAGATGCCC GCCTACCAA GATGAAATTT ATCATGTGTA GTATTGAAAT 2820  
 AAGTGTAGC TTTGACCATC ATAGTAATGA TAGTGAGGAA ATTGGAACCA AGAGTCTTAC 2880  
 25 AACCACTAG CTCAGCAAAC GTCTAATCTG TTATTTGTAA ATACACAGGA CATGTGCTCT 2940  
 CATGGCTTCA TCCCTGCCC ATGGCAGACA TTGCTAATCA ATCTCTGCTC ATGAGCCTAG 3000  
 CTGTGACCTT AGATACCTTC CCTGCAAGC TCCAGGCAGC CGTTAGAACT GACCCACATT 3060  
 GGCACCTGTT AGGAGACCTG TCATCTGCAT CTGGTCCCTC CCCCCTCTCT GCATGGAGGT 3120  
 CTCTTCCGTA GCCCTGCTG GGGACCAAGC TGAAGGGGAA TTCTCTGGGT CTGGGGCAGG 3180  
 30 TGGGGCTGGG GAAGGGAGCA GGCCTTCTACT GAGCTCTCAA CATGTCTGGC ACCTGTCTAT 3240  
 TCCTCCACAC CACACCCAGT GAGGAGAAGT TATTATCTCC ATTGGGCACA TGAGGGCCAC 3300  
 TTGTGCTAAG CGAGGACTGT GACTTTCCCA CCCACATGGC TGTGTGTGAC AGACACCGGA 3360  
 TTTGAGGACA GTCCTGTGTG ACTCAGAGGC CTCCTGCTCT CTCTGTGCTC TAGAGTCTCT 3420  
 CTGAGAGTGC GGGGCTGGCC CTGAGCCAC CCTGCTGTG AAGGTGCTTC CTCAGGCCCA 3480  
 35 GCTCCCATGG CCCCACACC CCCTCTCAT CACCTCTAC TCCCAAAAG GACAAAGCCT 3540  
 CAGGGAACCT TTTTCTTTT TTTAGAGACG GGGTCTTGCT ATGTTGGTCA GGCTGGTCTT 3600  
 GAACCTCTGG GCCCAGGCAA TCTTCCCGCC TCTGCTCTCT AAAGTGCTGG GATTCTGGGG 3660  
 CTTAGGGAAC CTTTTGAAC TGAAAGTGAC GCTCGAAGCC TTCCTGTAGA GTGAGGTGGG 3720  
 TGGCTGGGGC TAAACATATG GGAAGGAGA GACCTGGTGG GGGCACACAG CTGCTATATA 3780  
 40 GAGGAACAGA AGGTGGGCCA GGCCTCCCAG CTGTGAGGAA ATCTGGCTCA GTCCCAGAC 3840  
 CGCTGTGTGG CTTTGGGGTG GCCAGTCCCT CTCTCTCTGC AACACTCTCC TCATGAGGAC 3900  
 TTTCTGTGAA AATGGGGTGT GTAACCCCTCT GAGTTCTGGG GCCCCACCCA TTTCTAATCT 3960  
 CCAAGAACTG GCCACACAG ACTCCACCA CTCTAGTCC TGGGGCCTGG GCCTCTGGCC 4020  
 ATTGCCATAG GCACCACTG CTCTGTGACG GCAGCGCCCC CCTCTGCCAG GATCCTCCGA 4080  
 45 GGTGAGCTGC TGGGCTGAC CCGCAGACCC TGGCTGAGCG ACGGATGAAC GGAGTATGCA 4140  
 GACACAGGCT TGCTTGTGAC CAGATGGGGG ACCCTGGCCA GAGTCAGCAG CGGCCCCAT 4200  
 AAGCCTGCCA CGCTTGCAAT TATTTAGTAC AGATGTAATG ACAAAGGCCT AAAGCAAAC 4260  
 CCATTTGTGG GTAATTAACA TTGTCGCCCC CCCAGAAAGA GCAGTCTCTC GCATGATGAT 4320  
 50 TAAAGGCCAG GTTCCGAGGC CTAAGTAAAC CAACCTATCT AGATCAATTC CCTTACTTCT 4380  
 TGTATCTAC TCTGAGAGAA TTCAGCTGCC TTCAGCCAAA TCCTTTCCCG AAGCTTTTGC 4440  
 AAAACCTCCG AGCCTTCCAA GGTTTGCTTC TTTCTGTAAT TTTTCTCACC ACCCTGAGCT 4500  
 ATCTCTGCA GTCAGCCCTG TGGAGGCCCT TGTGTTTCCC CAGTGTCTGG CAGCCTAGAG 4560  
 GCTGAGATGG CCAGAAACAA GGTGGTGACA GTGGCGTGCT CAGGGCTTGG GAAACCCAAG 4620  
 55 GAGCTAAAGG CATGCCCAGG CAACCAAAGA GGACAGGAAG GCTTCTGAGG AGAGACCTCT 4680  
 GAGGTGGGTC TTGGAGAGGA AGGACTTAGG GAGGCAGAGT GGAGGAAGTG AGAGGACACC 4740  
 CCAAGCCAAG AGGGCGGCAG GACCAAAGGC TCAGAAAGCA GGGCGCTGCA GAGGGGCTGT 4800  
 GTGCCACAGG GTGAAGAGTT TGTGTGGCAG AAGGGCAGGG GGCTTGCATC AGGGGTGACA 4860  
 GCTGCTCTTT TGTCCACGCA TAGCCCTGT ACATCCCTGG AGAGCTGGGG CGTCCACAAC 4920  
 60 TCTAAGTAC AGCCCTCATC CTAACCTGG TGGTGACATG AGGGTGAGCT GTCTGTGGGC 4980  
 AGGAGGGAAG ACTTCTGGAG ATGAGCCTGG TGAAGGGATA ATGGCATCCC GGGCCGAGGA 5040  
 GCAGCAGAGG CAGAGGCTG GGGAGAGTTT AAGGAGTGTA GGGGAGGAAA TGGCAGAAGA 5100  
 TGAGCCAGAA AAAGAAAGGT TAGGGCAGGT CCTGGAGGAC ATGAGTGGCT GTTTGGGCTT 5160  
 TATCCAGCAG TGGGGGAGCC TTGGCAGGCT TGTGGCTTAG ATAGGTGCTT TAGAAAGCCC 5220  
 ACCAGCAGTT GCTGGGCCAC CCGCTGGCT GGGTCTGTT CTAAGGCAGG AAATACAAGA 5280  
 65 ATGAGCAGGA AAAGACCCCT TCAAGGCTCA CGTCTAGTG GGGAGACAAG AAACACAGAT 5340  
 GGGCAATATA ACACGATGTC TGGTTCAGT AAGTGCAGTG AAGAACAGC GAGGCTGGAT 5400  
 GCAGGGAGTG ATGGGAGGGG CTTTGTAAAG GGAGGTGCGG GGAAGCCTGT CTCAGAGGAC 5460  
 ACCAGAAATG AGCGCAGGAG CAGCACGTGG CAGTCACATG GCAGGCCGTT AGGGCAGAGG 5520  
 GAGCTGGGCA GGGCACAGCA GGGCAGGAGT GTGTTTGATG TGTCTGGGA ACCGCCCTGA 5580  
 70 GGCCGTCGTG TGGCTGGAGT GCTGCAGGTG TCAAGGAAAT TGTAGGAGAT GTCTCTGAG 5640  
 TGTGATGGA TATAACAGCA TTTCCAGAAG GAACTGACAT GATCTGACTT AAAAAGGTCA 5700  
 GTGTGCGAAA TGGCTTGACG GGAAGCAGG TGGGAGCAGG GAGATAGGAG ACAATGTGTA 5760  
 CCAGGACAGC AGAAAGACAT CCCGGGTAGC CTGGAACAGG GAGACGCTGT GGAGATGGTG 5820  
 GCAGTCCGAT AATGAGAGCC GTAGGGCAAG GCCAGCAGGA TCCTAGAGTG AGACGGGAGG 5880  
 75 TAAAGTACC GGGACTTGGT GTCTCCACGT CAGGGGCGAG GGAAGGGAG AGGACAAGGG 5940  
 TGACCCGGGA GGTAAAGAT GGGACCGGGG CCAGACGAG TGGCTCATGC CTGTAATCCT 6000  
 AGCACTTTGG GAGGCTGAGG CGGGCGGATG GCTTGAGGTC AGGAGTTTGA AACCGGCTG 6060  
 GCCAACATGG TGAACCCCG TCTCTACTAA AATATACAAA AATTAGCCTG CGGTGGTGGT 6120  
 GCATGCCTGC AGTCCAGCT ATTACAGAGG CTGAGGCGAC AAGATCGCT TGAACCTGGG 6180  
 80 AGGCGGAGT TGCAGTGAGC CGAGATCGCG CCATAGCACT CCAGCCTTAG CCTGGGCGAC 6240  
 AGAGCGAGAC CACATC

Seq ID NO: 88 Protein sequence  
 Protein Accession #: BAA32297.1



	1	11	21	31	41	51	
5	VETPPQGSVH	SGHLGSVVGD	PHTGTGNAGE	RGPRGKGARV	LALDSGGMDS	SPSLPLIRTP	60
	ESSLHEALDQ	CMTALDLFLT	NQFSEALSYL	KPRTKESMYH	SLTYATILEM	QAMMTDFDQD	120
	ILLAGNMKME	AQMLCQRHRR	KSSVTDSESS	LVNRPTLGQF	TEEBIHAEVC	YAECLLQRAA	180
	LTFLLQSSSHG	GAVRPRALHD	PSHACSCPPG	PGRQHLFLQ	DENMVSFIKG	GKVRNSYQT	240
	YKELDSLVSQ	SQYCKGENHP	HFEGGVKLG	GAFNLTLML	PTRILRLLEF	VGFSGNKDYG	300
10	LLQLEEGASG	HSFRSVLCVM	LLLCYHTFLT	FVLGTGNVNI	EBAEKLKPY	LNRYPKGAIF	360
	LEFFAGRIEVI	KGNIDAVSDG	GPGRGWGSLG	VSQTSRKSQT	CDILRDRIDW	GRGGGPRENQ	420
	PESRGRRGPS	GRAAWEDKGG	GGICGAWDFD	WEI			

Seq ID NO: 89 DNA sequence  
 Nucleic Acid Accession #: AF007170  
 Coding sequence: 73..1725

	1	11	21	31	41	51	
20	AAGGAGGCGG	CCTCCGGGAA	AAGCGACCGC	AGGACTCCTG	AGAGCAGCCT	CCATGAGGCC	60
	CTGGACCACT	GCATGACCGC	CCTGGACCTC	TTCTCACCAC	ACCAGTTCTC	AGAAGCACTC	120
	AGCTACCTCA	AGCCAGAAAC	CAAGGAAAGC	ATGTACCACT	CACTGACATA	TGCCACCATC	180
	CTGGAGATGC	AGGCCATGAT	GACCTTTGAC	CCTCAGGACA	TCCTGCTTGC	CGGCACCATG	240
	ATGAAGGAGG	CACAGATGCT	GTGTCAAGG	CACCGGAGGA	AGTCTTCTGT	AACAGATTCC	300
25	TTGAGCAGCC	TGGTGAACCG	CCCCACGCTG	GGCCAATTCA	CTGAAGAAGA	AATCCACGCT	360
	GAGGTCTGCT	ATGCAGAGTG	CCTGCTGCAG	CGAGCAGCCC	TGACCTTCCT	GCAGGACGAG	420
	AACATGGTGA	GCTTCATCAA	AGGCGGCATC	AAAGTTCGAA	ACAGCTACCA	GACCTACAAG	480
	GAGCTGGACA	GCCTTGTTCA	GTCTCACA	TACTGCAAGG	GTGAGAACCA	CCCGCACTTT	540
	GAAGGAGGAG	TGAAGCTTGG	TGTAGGGGCC	TTCAACCTGA	CACTGTCCAT	GCTTCCTACT	600
	AGGATCCTGA	GGCTGTTGGA	GTTTGTGGGG	TTTTTCAGGA	ACAAGGACTA	TGGGCTGCTG	660
30	CAGCTGGAGG	AGGGAGCGTG	AGGGCACAGC	TTCCGCTCTG	TGCTCTGTGT	CATGCTCCTG	720
	CTGTGCTACC	ACACCTTCCT	CACCTTCGTG	CTCGGTACTG	GGAACGTCAA	CATCGAGGAG	780
	GCCGAGAAGC	TCTTGAAGCC	CTACCTGAAC	CGGTACCCTA	AGGGTGCCAT	CTTCCTGTTC	840
	TTTGACAGGA	GGATTGAAGT	CATTAAAGGC	AACATTGATG	CAGCCATCCG	GCCTTCGAG	900
35	GAGTGTCTGT	AGGCCAGCA	GCACTGGAAG	CAGTTTCACC	ACATGTGCTA	CTGGGAGCTG	960
	ATGTGTGTCT	TCACCTACAA	GGGCCAGTGG	AAGATGTCCT	ACTTCTACGC	CGACCTGCTC	1020
	AGCAAGGAGA	ACTGCTGGTC	CAAGGCCACC	TACATTTACA	TGAAGGCCGC	CTACCTCAGC	1080
	ATGTTTGGGA	AGGAGGACCA	CAAGCCGCTC	GGGGACGACG	AAGTGGAAAT	ATTTTCGAGT	1140
	GTGCCAGGCG	TGAAGCTCAA	GATTGCTGGG	AAATCTCTAC	CCACAGAGAA	GTTTGCCTATC	1200
40	CGGAAGTCCC	GGCGCTACTT	CTCTCCCAAC	CCTATCTCGC	TGCCAGTGCC	TGCTCTGGAA	1260
	ATGATGTACA	TCGTGAACGG	CTACGCCGTG	ATTGGGAAGC	AGCCGAAACT	CACGGATGGG	1320
	ATACTTGAGA	TTATCACTAA	GGCTGAAGAG	ATGCTGGAGA	AAGGCCCAGA	GAACGAGTAC	1380
	TCAGTGGATG	ACGAGTGCTT	GGTGAATTG	TTGAAAGGCC	TGTGTCTGAA	ATACCTGGGC	1440
	CGTGTCCAGG	AGGCCGAGGA	GAATTTTAGG	AGCATCTCTG	CCAATGAAAA	GAAGATTAAA	1500
45	TATGACCACT	ACTTGATCCC	AAACGCCCTG	CTGGAGCTGG	CCCTGCTGCT	TATGGAGCAA	1560
	GACAGAAACG	AAGAGGCCAT	CAAACTTTTG	GAATCTGCCA	AGCAAAACTA	CAAGAATTAC	1620
	TCCATGGAGT	CAAGGACACA	CTTTGCAATC	CAGGCAGCCA	CACTCCAAGC	CAAGTCTTCC	1680
	CTAGAGAACCA	GCAGGACATC	CATGGTCTCA	TCAGTGTCTT	TGTAGCTTTG	TGCAGCAGTT	1740
	CCGGGCTGGA	AGACAGAGAC	AGCTGGACAG	AGCTCCTGAA	AACATTTCAA	AATACCCCTT	1800
50	CCCCCTGCCC	TGCCCTGCCT	TTGGGGTCCA	CCGGCACTCC	AGTTGGATGG	CACAACATAG	1860
	TGTATCCGCT	CAGAAGCCGA	GCTGGCATT	TCACCACTGT	AGCCAAGGGC	CTTTGCCAAG	1920
	GGCAGAGCAG	GTGGAGCCCT	CTGCCTGCCC	TATCACACAT	ACGGGTACTT	GCTTTTCACT	1980
	GTGATGTTTA	AGAGAAATGA	TGAACAGTTT	ACATTTTCCT	TAGAAATACA	TTGATGGGAT	2040
	CACAGTTGGC	TTTAAAAAAC	AACAACAATC	AACCACTGT	AAGTCTTTGT	CTTCACCTAT	2100
55	TATCATCTGG	AGGTAATCT	CTTTATATGA	TGATGCCAAA	GGGCAAAATG	CTTTTCAAAT	2160
	TCAGCAAGTT	CTCAGCTTGT	GTGACGGAAG	GTCTCTCAGA	GGACCTGAGG	AATGCCTGGG	2220
	AGAGGCTAAG	CCTCAGGCTT	CAATGCTTCT	GGGGTTGGGC	ATGAGGATGT	ACACAGACAC	2280
	CCACTACCTT	ACTACTCACA	CTTCATTTC	CTCCTTTTGT	AAATTTCCAA	TTTAAAAATC	2340
	AAGCAGCTGT	TTTGTAGTGA	ATAAAATCTG	AGCTCTTCTG	TAGAAAAATC	AATCTCTACC	2400
60	AGTAGAAAA	GCAGGGGCTT	GATGGAAGAG	CTGTGTAGCC	CTTTCTATGC	CAAAGCCAGG	2460
	AAATTTGGGG	GGCAGGAGGA	GGTTCTCAGA	ATCCAGTCTG	TATCTTTGCT	GTATGCCAAA	2520
	CTGAAACCAC	TGGGAATAAT	TTATGAAACA	TAAAAATCTT	CTGTACTTCA	CTCCAAGGTA	2580
	CATTGTCTTA	CTGACAGCAT	TTTTGTAAAA	ACTGTTATTC	TTGAAAAAAA	AAAAAATAAA	2640
	AA						

Seq ID NO: 90 Protein sequence  
 Protein Accession #: AAC39582.1

	1	11	21	31	41	51	
70	KRAASGKSDR	RTPESSLHEA	LDQCMALDL	FLTNQFSEAL	SYLKPRTKES	MYHSLTYATI	60
	LEMQAMMTFD	PQDILLAGNM	MKEAQMCLQR	HRRKSSVTD	FSSLVNRPTL	GQFTFEEIHA	120
	EVCYAECLLQ	RAALFQLQDE	NMVSFIKGGI	KVRNSYQTYK	ELDSLVSQSS	YCKGENHPHF	180
	EGGVKLGFGA	FNLTLMLPT	RILRLLEFVG	FSGNKDYGIL	QLEEGASGHS	FRSVLCVMLL	240
75	LCYHTFLFTV	LGTGNVNIEE	AEKLLKPYLN	RYPKGAILFL	FAGRIEVIKG	NIDAAIRFE	300
	ECCEAQQHWK	QPHMCMYWE	MWCFTYKQW	KMSYFYADLL	SKENCWSKAT	YIYKMAAYLS	360
	MFGKEDHKPF	GDDEVLEFRA	VPGLKLKIAG	KSLPTEKFAI	RKSRRYFSSN	PISLVPVPALE	420
	MMYIWNQYAV	IGKQPKLTDG	ILEIITKABE	MLEKGPENEY	SVDDECLVKL	LKGLCLKYLG	480
80	RVQEAENFR	SISANEKKIK	YDHYLIPNAL	LELALLLMEQ	DRNEEAIKLL	ESAKQNYKNY	540
	SMESRTHFRI	QAATLQAKSS	LENSRSMVMS	SVSL			

Seq ID NO: 91 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 31..906

	1	11	21	31	41	51	
	CGGGTCGACC	CACGCGTCCG	GGGAGAAAGG	ATGGCCGGCC	TGGCGGCGCG	GTGGTCTCTG	60
5	CTAGCTGGGG	CAGCGGCGCT	GGCGAGCGGC	TCCCAGGGCG	ACCGTGAGCC	GGTGTACCGC	120
	GACTGCGTAC	TGCAGTGC	AGAGCAGAAC	TGCTCTGGGG	GCGCTCTGAA	TCACCTCCGC	180
	TCCCGCCAGC	CAATCTACAT	GAGTCTAGCA	GGCTGGACCT	GTCGGGACGA	CTGTAAGTAT	240
	GAGTGTATGT	GGGTACCCGT	TGGGCTCTAC	CTCCAGGAAG	GTACACAAAGT	GCCTCAGTTC	300
	CATGGCAAGT	GGCCCTTCTC	CCGGTTCTGT	TTCTTTCAAG	AGCCGCGCATC	GGCCGTGGCC	360
10	TCGTTTCTCA	ATGGCCTGGC	CAGCCTGGTG	ATGCTCTGCC	GCTACCGCAC	CTTCGTGCCA	420
	GCCTCTCC	CCATGTACCA	CACCTGTGTG	GCCTTCGCC	GGGTGTCCCT	CAATGCATGG	480
	TTCTGGTCCA	CAGTYTTCCA	CACCAGGGAC	ACTGACCTCA	CAGAGAAAAA	GGACTACTTC	540
	TGTGCCTCCA	CTGTCACTCT	ACACTCAATC	TACCTGTGCT	GCGTCAGCCT	CATCCGCTTC	600
	GACTATGGCT	ACAACCTGGT	GGCCAACGTG	GCTATTGGCC	TGGTCAACGT	GGTGTGGTGG	660
15	CTGGCCTGGT	GCCTGTGGAA	CCAGCGGCGG	CTGCCTCACG	TGCGCAAGTG	CGTGGTGGTG	720
	GTCTTGCTGC	TGCAGGGGCT	GTCCCTGCTC	GAGCTGCTTG	ACTTCCCA	GCTCTTCTGG	780
	GTCCCTGGATG	CCCATGCCAT	CTGGCACATC	AGCACCATCC	CTGTCCACGT	CCTCTTTTTC	840
	AGCTTTCTGG	AAGATGACAG	CCTGTACTCT	CTGAAGGAAT	CAGAGGACAA	GTTCAGCTG	900
20	GACTGAAGAC	CTTGGAGCGA	GTCTGCCCA	GTGGGGATCC	TGCCCCCGCC	CTGCTGGCCT	960
	CCCTTCTCCC	CTCAACCTTT	GAGATGATTT	TCTCTTTTCA	ACTTCTTGAA	CTTGGACATG	1020
	AAGGATGTGG	GCCCAGAATC	ATGTGGCCAG	CCCACCCCTT	GTGGGCCCTC	ACCAGCCTTG	1080
	GAGTCTGTTC	TAGGGAAGGC	CTCCAGCAT	CTGGGACTCG	AGAGTGGGCA	GCCCTCTAC	1140
	CTCTCTGGAGC	TGAAGTGGGG	TGGAAGTGG	TGTGCTCTTA	GCTCTACCGG	GAGGACAGCT	1200
	GCCTGTCTTC	TCCCATCAG	CCTCTCTCCC	ACATCCCCAG	CTGCCTGGCT	GGGTCTTGAA	1260
25	GCCCTCTGTC	TACCTGGGAG	ACCAGGGACC	ACAGGCCCTA	GGGATACAGG	GGGTCCCTTT	1320
	CTGTACAC	CCCCACCTT	CCTCCAGGAC	ACCACTAGGT	GGTGTCTGGT	GCTTGTCTCT	1380
	TGGCCAGCCA	AGGTTACCGG	CGATTCTCCC	CATGGGATCT	TGAGGGACCA	AGCTGCTGGG	1440
	ATTGGGAAGG	AGTTTACACC	TGACCTTGG	CCTAGCCAGG	TTCCCGAGAG	GCCTCACCAT	1500
30	ACTCCCTTTC	AGGGCCAGGG	CTCCAGCAAG	CCCAGGGCAA	GGATCCTGTG	CTGCTGTCTG	1560
	TTTGAGAGCC	TGCCACCGTG	TGTGCGGAGT	GTGGGCCAGG	CTGAGTGCAT	AGGTGACAGG	1620
	GCCGTGAGCA	TGGGCTGGG	TGTGTGTGAG	CTCAGGCACT	AGGTGCGCAG	TGTGGAGACG	1680
	GGTGTGTGCG	GGGAAGAGGT	GTGGCTTCAA	AGTGTGTGTG	GTGCAGGGGG	TKGGTGTGTT	1740
	AAGCGTGGGT	TAGGGAACG	TGTGTGCGCG	TGCTGGTGGG	CATGTGAGAT	GAGTGACTGC	1800
	CGGTGAATGT	GTCCACAGTT	GAGAGGTGG	AGCAGGATGA	GGGAATCCTG	TCACCATCAA	1860
35	TAATCACTTG	TGGAGCGCCA	CTTGGCCCAA	GACGCCACCT	GGGCGGACAG	CAGGAGCTCT	1920
	CCATGGCCAG	GCTGCTGTG	TGCACTGTCC	CTGTCTGGTG	CCCCCTTGCC	CGCCTCCTGC	1980
	AAACCTCACA	GGGTCCCCAC	ACAACAGTGC	CCTCCAGAAC	CAGCCCTCG	GAGGCAGAGG	2040
	AAGGAAATG	GGGATGGCTG	GGGCTCTCTC	CATCCTCTCT	TTCTCTTGC	CTTCGCATGG	2100
	CTGGCCTTCC	CCTCCAAAAC	CTCCATTCCC	CTGCTGCCAG	CCCCCTTGCC	ATAGCCTGAT	2160
40	TTTGGGGAGG	AGGAAGGGGC	GATTTGAGGG	AGAAGGGGAG	AAAGCTTATG	GCTGGGTCTG	2220
	GTTTCTTCCC	TTCCAGAGG	GTCTTACTGT	TCCAGGGTGG	CCCCAGGGCA	GGCAGGGGCC	2280
	ACACATATGCC	TGCGCCCTGG	TAAAGGTGAC	CCCTGCCATT	TACCAGCAGC	CCTGGCATGT	2340
	TCTTGCCCA	CAGGAATAGA	ATGGAGGGAG	CTCCAGAAAC	TTTCCATCCC	AAAGGCAGTC	2400
	TCCGTGGTTG	AAGCAGACTG	GATTTTGTCT	CTGCCCTGTA	CCCCCTGTCC	CTCTTTGAGG	2460
45	GAGGGGAGCT	ATGCTAGGAC	TCCAACCTCA	GGGACTCGGG	TGGCCTGCGC	TAGCTTCTTT	2520
	TGATACTGAA	AACCTTTAAG	GTGGGAGGGT	GGCAAGGGAT	GTGCTTAATA	AATCAATTCC	2580
	AAGCCTCAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAA			

Seq ID NO: 92 Protein sequence  
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
	MAGLAARLVL	LAGAAALASG	SQGDREPVYR	DCVLQCEEQN	CSGGALNHFR	SRQPIYMSLA	60
55	GWTCRDDCKY	ECMWVTVGLY	LQEGHKVPQF	HGKWPFSRFL	FFQEPASAVA	SFLNGLASLV	120
	MLCRYRTFVP	ASSPMYHTCV	AFANVSLNAW	FWSTVFHTRD	TDLTEKMDYF	CASTVILHSI	180
	YLCVVRVTVL	QHPAVVSFAFR	ALLLLMLTVH	VSYLSLIRFD	YGYNLVANVA	IGLVNVVWWL	240
	AWCLWNQRR	PHVRKCVVVV	LLLQGLSLLE	LLDFPPLFWV	LDAHAIWHIS	TIPVHVLFFS	300
	FLEDDSLYLL	KESEDKFKLD					

Seq ID NO: 93 DNA sequence  
Nucleic Acid Accession #: NM\_033419.1  
Coding sequence: 18..980

	1	11	21	31	41	51	
65	CGAGCCAGGG	AGAAAGGATG	GCCGGCCTGG	CGGCGCGGTT	GGTCTGCTA	GCTGGGGCAG	60
	CGGCGCTGGC	GAGCGGCTCC	CAGGGCGACC	GTGAGCCGGT	GTACCCGCGAC	TGCGTACTGC	120
	AGTGCGAAGA	GAGAACTG	TCTGGGGGCG	CTCTGAATCA	CTTCCGCTCC	CGCCAGCCAA	180
70	TCTACATGAG	TCTAGCAGGC	TGGACCTGTC	GGGACGACTG	TAAGTATGAG	TGTATGTGGG	240
	TCACCGTTGG	GCTCTACCTC	CAGGAAGGTC	ACAAAGTGCC	TCAGTTCCAT	GGCAAGTGGC	300
	CCTTCTCCCG	GTTCTGTGTT	TTTCAAGAGC	CGGCATCGGC	CGTGGCCTCG	TTTCTCAATG	360
	GCCTGGCCAG	CCTGGTGTATG	CTCTGCCGCT	ACCGCACCTT	CGTGCCAGCC	TCCTCCCCCA	420
	TGTACCACAC	CTGTGTGGCC	TTGCGCTGGG	TGTCCCTCAA	TGCATGGTTC	TGGTCCACAG	480
75	TTTTCACAC	CAGGGACACT	GACCTCACAG	AGAAAATGGA	CTACTTCTGT	GCCTCCACTG	540
	TCATCCTTGA	CTCAATCTAC	CTGTGCTGCG	TCAGGACCGT	GGGCTGCAG	CACCCAGCTG	600
	TGGTCAGTGC	CTTCCGGGCT	CTCTGCTGTC	TCATGCTGAC	CGTGCACGTC	TCCTACCTGA	660
	GCCTCATCCG	CTTCGACTAT	GGCTACAACC	TGGTGGCCAA	CGTGGCTATT	GGCCTGTGTC	720
	ACGTGGTGTG	GTGGCTGGCC	TGGTGCCTGT	GGAACACGCG	GCGGCTGCCT	CACGTGCGCA	780
80	AGTGCCTGGT	GGTGGTCTTG	CTGCTGCAGG	GGCTGTCCCT	GCTCGAGCTC	CTTGACTTCC	840
	CACGCTCTTT	CTGGGTCTCT	GATGCCCATG	CCATCTGGCA	CATCAGCACC	ATCCCTGTCC	900
	ACGTCTCTTT	TTTCACTTTT	CTGGAAGATG	ACAGCCTGTA	CCTGCTGAAG	GAATCAGAGG	960
	ACAAGTTCAA	GCTGGACTGA	AGACCTTGGG	GCGAGTCTGC	CCCAGTGGGG	ATCCTGCCCC	1020
	CGCCTGCTG	GCCTCCCTTC	TCCCCTCAAC	CCTTGAGATG	ATTTTCTCTT	TTCAACTTCT	1080
	TGAACCTGGA	CATGAAGGAT	GTGGGCCAGG	AATCATGTGG	CCAGCCCAAC	CCCTGTTGGC	1140

5  
10  
15  
20  
25

```

CCTCACCAGC CTGGAGTCT GTTCTAGGGA AGGCCTCCCA GCATCTGGGA CTCGAGAGTG 1200
GGCAGCCCTT CTACCTCCTG GAGCTGAAC TGGGTGGAAC TGAGTGTGCT CTTAGCTCTA 1260
CCGGGAGGAC AGCTGCCTGT TTCCTCCCA TCAGCCTCCT CCCACATCC CCAGCTGCCT 1320
GGCTGGGTCC TGAAGCCCTT TGTCTACCTG GGAGACCAGG GACCACAGGC CTTAGGGATA 1380
CAGGGGGTCC CCTTCTGTTA CCACCCCTCA CCTCCTCCA GGACACCACT AGGTGGTGTCT 1440
GGATGCTTGT TCTTTGGCCA GCCAAGGTTC ACGGCATTTC TCCCCATGGG ATCTTGAGGG 1500
ACCAAGCTGC TGGGATTGGG AAGGAGTTTC ACCCTGACCA TTGCCCTAGC CAGGTTCCCA 1560
GGAGGCTCTA CCATACTCCC TTTCAGGGCC AGGGCTCCAG CAAGCCCAGG GCAAGGATCC 1620
TGTGCTGTCT TCTGGTGTAG AGCCTGCCAC CGTGTGTGCG GAGTGTGGGC CAGGCTGAGT 1680
GCATAGGTGA CAGGGCCGTG AGCATGGGCC TGGGTGTGTG TGAGCTCAGG CTAAGGTGCG 1740
CAGTGTGGAG ACGGGTGTTC TCGGGGAAGA GTGTGTGCTT CAAAGTGTGT GTGTGCAGGG 1800
GGTGGGTGTG TTAGCTGGG TTAGGGGAAC GTGTGTGCGC GTGCTGGTGG GCATGTGAGA 1860
TGAGTGAAGT CCGGTGAATG TGTCCACAGT TGAGAGGTTG GAGCAGGATG AGGGAATCCT 1920
GTCAACATCA ATAATCACTT GTGGAGCGCC AGCTCTGCC CAGGCGCCAC CTGGGCGGAC 1980
AGCCAGGAGC TCTCCATGCG CAGGCTGCC TGTGTCATGT TCCCTGTCTG GTGCCCTTTT 2040
GCGCGCTCTC TGCAAACTTC ACAGGGTCCC CACACAACAG TGCCCTCCAG AAGCAGCCCC 2100
TCGGAGGACG AGGAAGGAAA ATGGGGATGG CTGGGGCTCT CTCCATCCTC CTTTTCTCCT 2160
TGCTTTCGCA TGCTTGGCTT TCCCTCCAA AACCTCCATT CCCCTGTGTC CAGCCCCCTT 2220
GCCATAGCCT GATTTTGGGG AGGAGGAAGG GCGGATTGGA GGGAGAAGGG GAGAAAGCTT 2280
ATGGCTGGGT CTGGTTCTT CCCTTCCAG AGGGTCTTAC TGTTCAGGG TGGCCCCAGG 2340
CGAGGCGAGG GCCACACTAT GCCTGCGCCC TGGTAAAGGT GACCCCTGCC ATTTACCAGC 2400
AGCCCTGGCA TGTCTCTGCC CCACAGGAAT AGAATGGAGG GAGCTCCAGA AACTTTCCAT 2460
CCCAAAGGCA GTCTCCGTGG TTGAAGCAGA CTGGATTTT GCTCTGCCCT TGACCCCTTG 2520
TCCCTCTTTG AGGGAGGGGA GCTATGCTAG GACTCCAACC TCAGGGACTC GGGTGGCCTG 2580
CGTAGCTTC TTTTGATACT GAAAACTTTT AAGGTGGGAG GGTGGCAAGG GATGTGCTTA 2640
ATAAATCAAT TCCAAGCCTC AAAAAA AAAA AAAA AA

```

Seq ID NO: 94 Protein sequence  
Protein Accession #: NP\_219487.1

30  
35

```

1      11      21      31      41      51
|      |      |      |      |      |
MKDVGPESCG QPTPCWPSPA LESVLGKASQ HLGLESGQPL YLLELNWGGT ECALSSTGRT 60
AACFLPISLL PTSPAAILGP EALCLPGRPG TTGLRDTGGP LLLPPPTLLQ DTTTRWCWMLV 120
LWPAKVHGDG PHGILRDQAA GIGKEFHDPD CPSQVPRRPH HTPFGQGSS KPRARILCCC 180
LVESLPPCVG SVGQAECIGD RAVSMGLGVC ELRPRCAVWR RVLSGKRCGF KVCVCRGWVC

```

Seq ID NO: 95 DNA sequence  
Nucleic Acid Accession #: XM\_090469  
Coding sequence:

40  
45  
50  
55  
60

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGGGTTTG GAGACCAGGG AACGGTGGAA GGGAGCCTAG GAACGTCGAA AGATAGCTCC 60
TGCCCGCTGC TGGACAGGAC GCAGGTGAAC AAGCCCTGCC TGCTGGAGGC TGCCAAGCAC 120
AGCCACACAC CCTTGCATGG ACAGTCGGTC AACAGCCACC CATCAGGTGC TCATCAGAAA 180
CCACCTGAAG TGAAAATGTT TGGAGCCAGT CAAGGTTTGC TGACAATGGA AACAAACCAG 240
TCCCTGGCAC AAGGCACAGG CTGCTCAGTG TGCTGGGAGG TGAACGGCCC AGGGTTGGAA 300
ATGTCTCTTC CTGGAGTGTCT CAGTGTCTGAT GCTGGCCAGG TGGAGCACAG AAGACAAATG 360
AACTCGCAG ATACTGACTG GGAACCTGAG GAGGAGCCAG GAAGTCTAGA TTTCGCCGTG 420
GCTGCCACAC AGGAAGACAT TTCTTTTTC AAAGACATCA AGCACACAAG TACGTTTCAGG 480
CAATCAGTTC AGCAGCAGAA TTGCAATTAC AGCCCCAGAG AAAAACCCCTG TGGGAATGTC 540
AGGGCACCTT GCGCGCCACC AAGGCAGAGG GCCCCGCTTG CCCTCAGCAG GCCCTGGCGG 600
CTCAGCCGCA GCCCGCGGCC GTCCCCACGT ACACCCATGG CGCCCTTCCC GACCTCTGAC 660
CGCGAGCTAG ACGCGCCAGG CCGGCCCTCC GGGCTGCGGA GCTCGGCAGC AGCCCTCAC 720
TGCTGCCCCG CGGCTCCAGA AGCCAGAAA CTCTTCTTCC TGCTGCCCTT TTATCCAGAT 780
GGCAGCCAC CACCTAAGGA CATCTTGAGC ACGCTCCAGC ACAAGGCACC TGGGAAGAGA 840
CTGCATCAAG AATCACCAGG TTCATTCCA ATAGGTTTAT GTAACAGAAC AGCTGAACCA 900
TGTATCAAAG GGGCTCTGGG TGTGGCTGCT GAAGCAGCAT TTCATTACA GTTTTCCAGT 960
GAATGA

```

Seq ID NO: 96 Protein sequence  
Protein Accession #: XP\_090469

65  
70  
75

```

1      11      21      31      41      51
|      |      |      |      |      |
MGFGDQGTVE GSLGTSKDSS CRVLDRTQVN KPCLLEAAKH SPHPLHGQSV NSHPSGAHQK 60
PPEVKMFGAS QGLLTMETNQ SLAQGTGCSV CWEVNGPGL MSLPGVLSAD AGQVEHRRQM 120
NSADTDWTE EPGSLDFAV AAHQEDTFFL KDIKHTSTFR QSVQQNCIY SPREKPCGNV 180
RAPCAPPRRE APLALSRPWR LSRSPAPSPR TPMAPPFTSD RELDAPGPPP GLRSSAAAPH 240
CLPAAPPAQK LFFLLPLYPD GSPPPKDILQ TLQHKAPGKR LHQESPSGFP IGLCNRTAEP 300
CIKALGVAA EAAFLHQLFSS E

```

Seq ID NO: 97 DNA sequence  
Nucleic Acid Accession #: NM\_003474.2  
Coding sequence: 37..3036

80

```

1      11      21      31      41      51
|      |      |      |      |      |
CACTAACGCT CTTCTAGTC CCCGGGCCAA CTCGGACAGT TTGCTCATTT ATTGCAACGG 60
TCAAGGCTGG CTTGTGCCAG AACGGCGCGC GCGCGACGCA CGCACACACA CGGGGGGAAA 120
CTTTTAAAAA AATGAAAGGC TAGAAGAGCT CAGCGGCGGC GCGGGCCGTG CGCGAGGGCT 180
CCGAGCTGA CTCGCCAGG CAGGAAATCC CTCGGTTCGC GACGCCCGGC CCCGCTCGGC 240
GCCCGCTGG GATGGTGAG CGCTCGCGCC CCGGCCCGAG AGCTGCTGCA CTGAAGGCCG 300

```

	GCGACGATGG	CAGCGCGCCC	GCTGCCCCGTG	TCCCCCGCCC	GCGCCCTCCT	GCTCGCCCTG	360
	GCCGGTGTCT	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420
	GCTGATGAAG	TTGTCACTGC	CTCTGTTCCG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
5	TTCGACTCCA	AGAATCATCC	AGAAGTGTCT	AATATTCGAC	TACAAACGGG	AAGCAAAGAA	540
	CTGATCATAA	ATCTGGAAAG	AAATGAAGGT	CTCATTTGCC	GCAGTTTCAC	GGAAACCCAC	600
	TATCTGCAAG	ACGGTACTGA	TGTCTCCCTC	GCTCGAAATT	ACACGGTAA	TCTGGGTGAC	660
	TGTTACTACC	ATGGACATGT	ACGGGGATAT	TCTGATTCAG	CAGTCAGTCT	CAGCACGTGT	720
	TCTGGTCTCA	GGGACTTAT	TGTGTTTGAA	AATGAAAGCT	ATGTCTTAGA	ACCAATGAAA	780
10	AGTGCAACCA	ACAGATACAA	ACTCTTCCCA	GCGAAGAAGC	TGAAAGCGT	CCGGGGATCA	840
	TGTGGATCAC	ATCACAACAC	ACCAAACCTC	GCTGCAAGA	ATGTGTTTCC	ACCACCTCT	900
	CAGACATGGG	CAAGAAGGCA	TAAAAGAGAG	ACCCTCAAGG	CAACTAAGTA	TGTGGAGCTG	960
	GTGATCGTGG	CAGACAACCG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020
	CAGCGATTAA	TAGAGATTGC	TAATCACGTT	GACAAGTTT	ACAGACCACT	GAACATTCGG	1080
	ATCGTGTGG	TAGGCGTGG	AGTGTGGAAT	GACATGGACA	AATGCTCTGT	AAGTCAGGAC	1140
15	CCATTACCA	GCCTCCATGA	ATTTCTGGAC	TGGAGGAAGA	TGAAGCTTCT	ACCTCGCAAA	1200
	TCCCATGACA	ATGCGCAGCT	TGTCAGTGGG	GTTTATTTCC	AAGGGACCAC	CATCGGCATG	1260
	GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATGTTCAT	GGACCATTCA	1320
	GACAAATCCC	TTGTGTGACG	CGTGACCCCTG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG	1380
20	AATCATGACA	CACTGGACAG	GGGCTGTAGC	TGTCAAATGG	CGGTTGAGAA	AGGAGGCTGC	1440
	ATCATGAACG	CTTCCACCGG	GTACCCATTT	CCCATGGTGT	TCAGCAGTTG	CAGCAGGAAG	1500
	GACTTGGAGA	CCAGCCTGGA	GAAAGGAATG	GGGGTGTGCC	TGTTTAACT	GCCGGAAGTC	1560
	AGGGAGTCTT	TCGGGGGCCA	GAAAGTGTGG	AACAGATTGT	TGGAAGAAGG	AGAGGAGTGT	1620
	GACTGTGGGG	AGCCAGAGGA	ATGTATGAAT	CGCTGCTGCA	ATGCCACCAC	CTGTACCCCTG	1680
25	AAGCCGAGCG	CTGTGTGCGC	ACATGGGCTG	TGCTGTGAAG	ACTGCCAGCT	GAAGCCTGCA	1740
	GGAAACAGCT	GCAGGAGACT	CAGCAACTCC	TGTGACCTCC	CAGAGTTCTG	CACAGGGGCC	1800
	AGCCCTCACT	GCCCAAGCCA	CGTGTACCTG	CACGATGGGC	ACTCATGTCA	GGATGTGGAC	1860
	GGCTACTGCT	ACAATGGCAT	CTGCCAGACT	CACGAGCAGC	AGTGTGTAC	ACTCTGGGGA	1920
	CCAGGTGCTA	AACCTGCCCC	TGGGATCTGC	TTTGAGAGAG	TCAATCTCTG	AGGTGATCCT	1980
30	TATGGCAACT	GTGGCAAACT	CTCGAAGAGT	TCTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
	AAATGTGGAA	AAATCCAGTG	TCAAGGAGGT	GCCAGCCGGC	CAGTCATTGG	TACCAATGCC	2100
	GTTTCCATAG	AAACAACACT	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
	CACGTGTACT	TGGGCGATGA	CATGCCGGAC	CCAGGGCTTG	TGCTTGCAGG	CACAAAGTGT	2220
	GCAGATGGAA	AAATCTGCCT	GAATCGTCAA	TGTCAAAATA	TTAGTGTCTT	TGGGGTTTCA	2280
35	GAGTGTGCAA	TGCAGTGCCA	CGGCAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340
	GAGGCCCACT	GGGCACCTCC	CTTCTGTGAC	AAGTTTGGCT	TTGGAGGAAG	CACAGACAGC	2400
	GGCCCCATCC	GGCAAGCAGA	TAACCAAGGT	TTAACCATAG	GAATCTGGT	GACCATCCTG	2460
	TGTCTTCTTG	CTGCCGATT	TGTGGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACTGCTG	2520
	TTTACAAATA	AGAAGACCAC	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
	CGTGGCTTCC	AACCTGTCTA	GGCTCACCTC	GGCCACCTTG	GAAAGGCCCT	GATGAGGAAG	2640
40	CCGCCAGATT	CCTACCCACC	GAAGGACAAT	CCCAGGAGAT	TGCTGCAGTG	TCAGAATGTT	2700
	GACATCAGCA	GACCCCTCAA	CGGCCGTGAAT	GTCCCTCAGC	CCCAGTCAAC	TCAGCGAGTG	2760
	CTTCTCTCCC	TCCACCGGGC	CCCAAGTGCA	CCTAGCGTCC	CTGCCAGACC	CCTGCCAGCC	2820
	AAGCCTGCAC	TTAGGCAGGC	CCAGGGGACC	TGTAAGCCAA	ACCCCTCTCA	GAAGCCTCTG	2880
	CCTGCAGATC	CTCTGGCCAG	AACAACCTCG	CTCACTCATG	CCTTGGCCAG	GACCCAGGA	2940
45	CAATGGGAGA	CTGGGCTCCG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000
	GTGCCCAGAT	CCACCCACAC	CGCCTATATT	AAGTGAGAAG	CCGACACCTT	TTTTCACAG	3060
	TGAAGACAGA	AGTTTGCACT	ATCTTTCAGC	TCCAGTTGGA	GTTTTTTGTA	CCAACTTTAA	3120
	GGATTTTTTT	TAATGTTTAA	AACATCATT	CTATAAGAAC	TTTGAGCTAC	TGCCGTGAGT	3180
50	GCTGTGCTGT	GCTATGGTGC	TCTGTCTACT	TGCACAGGTA	CTTGTAATTT	ATTAATTTAT	3240
	GCAGAAATGT	GATTACAGTG	CAGTGCCTG	TAGTAGGCAT	TTTTACCATC	ACTGAGTTTT	3300
	CCATGGCAGG	AAGGCTTGT	GTGCTTTTAG	TATTTTAGTG	AACTTGAAT	ATCCTGCTTG	3360
	ATGGGATTCT	GGACAGATG	TGTTTGCTT	CTGATCAAGG	CCTTATTGGA	AAGCAGTCCC	3420
	CCAACTACCC	CCAGCTGTGC	TTATGGTACC	AGATGCAGCT	CAAGAGATCC	CAAGTAGAAT	3480
55	CTCAGTTGAT	TTTCTGGATT	CCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGG	3540
	TGTGTTTGGC	TTTCAGGGAG	GCCCTGTGCC	CCTTGACAAC	TGGCAGGACG	GCTCCAGGG	3600
	ACACTGGGA	GAAATCTGGC	TTCTGGCCAG	GAAGCTTTGG	TGAGAACCTG	GGTTGCAGAC	3660
	AGGAATCTTA	AGGTGTAGCC	ACACCAGGAT	AGAGACTGGA	ACACTAGACA	AGCCAGAACT	3720
	TGACCCTGAG	CTGACCGGCC	GTGAGCATGT	TTGGAAGGGG	TCTGTAGTGT	CACTCAAGGC	3780
60	GGTGCTTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTCGCTG	TCCTTTCTAG	AGCACTGCCA	3840
	CCAGTAGGTT	ATTTAGCTTG	GGAAAGGTGG	TGTTTCTGTA	AGAAACCTAC	TGCCAGGCA	3900
	CTGCAAAACG	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACTGTARTA	3960
	CAATGATCCT	GTATTTCAGAC	AGATGAGGAC	TTTCCATGGG	ACCACAATA	TTTTCAGATG	4020
	TGAACCATTA	ACCAGATCTA	GTCATCAAG	TCTGTTTACT	GCAAGGTTCA	ACTTATTAAC	4080
65	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTCATGGG	4140
	TATAGTTTAT	GTCTGCTATC	ATTATTCGTA	GATATTGGAC	AAAGAACCTT	CTCTATGGGG	4200
	CATCCTCTTT	TTCCAACCTG	GCTGCAGGAA	TCTTTAAAG	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTATTTCT	TAAACACTTG	CAACCTACCT	GTTGAGCATC	ACAGAATGTG	ATAAGGAAAT	4320
	CAACTTGCTT	ATCAACTTCC	TAAATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCTTGAA	4380
70	CTCTTCACTC	TTCAATGCCC	TGACTAGGGA	GCCATGTTTC	ACAAGGTCTT	TAAAGTGACT	4440
	AATGGCATGA	GAAATACAAA	AATACTCAGA	TAAGGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGACTGGT	TTTCACTTAA	GAAGACAATT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCCTTCTTT	TGGGGTCAAC	AGTTTTCCTA	TGCTTTGAAA	CAGAAAAATA	4620
	TGTACCAAGA	ATCTTGGTTT	GCCTTCCAGA	AAACAAAACT	GCATTTCACT	TTCCCGGTGT	4680
75	TCCCACTGT	ATCTAGGCAA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CACGTGACAC	4740
	AAACACACAC	AAAAGGGGAA	CCAGCTCTAA	TACATTCCAA	CTCGTATAGC	ATGCATCTGT	4800
	TATTCTATA	GTTATTAAAGT	TCTTTAAAA	GTAAGCCCAT	GCTGGAAAAT	AATACTGCTG	4860
	AGATACATAC	AGAATTACTG	TAACTGATTA	CACCTGGTAA	TTGTACTAAA	GCCAAACATA	4920
	TATATACTAT	TAAAAAGGTT	TACAGAATTT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTTT	4980
80	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCT	CCAATTATA	GAGGATATGA	5040
	ACCAAAAAAA	AAAAAAAAAA	AA				

Seq ID NO: 98 Protein sequence  
Protein Accession #: NP\_003465

1 11 21 31 41 51  
 MAARPLPVSP ARALLALAG ALLAPCEARG VSLWNEGRAD EVVSASVRSR DLWIPVKSFD 60  
 SKNHPEVLNI RLQRESKELI INLERNEGLI ASSFTETHYL QDGTDVSLAR NYTVILGHCI 120  
 YHGHRVGYSD SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYKLFPK KLSVVRGSCG 180  
 SHHNTFNLAA KNVFPPPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLKVKQR 240  
 LIEIANHVOK FYRPLNIRIV LVGVEVWMD DKCSVSQDFP TSLHEFLDWR KMKLLPRKSH 300  
 DNAQLVSGVY FQGTIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMNH 360  
 DTLDRGCSQ MAVEGGCGIM NASTGYFFPM VFSSCSRKDL ETSLEKGMGV CLFNLPEVRE 420  
 SFGGQKGNR FVEEGEEDC GEPEECMNR CNATTCTLKP DAVCAHGLCC EDCQLKPAGT 480  
 ACRDSSNSCD LPEFCTGASP HCPANVYLHD GHSCQDVG DY CYNGICQTHE QQCVTWGF 540  
 AKPAPGICFE RVNSAGDPY NCGKVSXSSF AKCEMRDAKC GKIQCQGGAS RPIVIGTNAV 600  
 IETNIPLOQG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKICLNRCQ NISVFGVHEC 660  
 AMQCHGRGVC NNRKNCHCEA HWAPPCDFK FGGGSTDGSP IRQADNQLT IGILVTILCL 720  
 LAAGFVVYLK RKTILRLFT NKKTIEKLR CVRPSRPRG FQPCQHLGH LGKGLMRKPP 780  
 DSYPPKDNPR RLLQCQNDI SRPLNGLNVP QPQSTQRVLP PLHRAPRAPS VPARPLPAKP 840  
 ALRQAQGTCK PNPPQKPLPA DPLARTTILT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900  
 RSTHTAYIK

Seq ID NO: 99 DNA sequence  
 Nucleic Acid Accession #: NM\_003714  
 Coding sequence: 135..1043

1 11 21 31 41 51  
 GAGGAGGAGG GAAAAGGCGA GCAAAAAGGA AGAGTGGGAG GAGGAGGGGA AGCGGCGAAG 60  
 GAGGAAGAGG AGGAGGAGGA AGAGGGGAGC ACAAGGATC CAGGTCTCCC GACGGGAGGT 120  
 TAATACCAAG AACCATGTGT GCCGAGCGGC TGGGCCAGTT CATGACCCTG GCTTTGTGT 180  
 TGGCCACCTT TGACCCGGCG CGGGGGACCG ACGCCACCAA CCCACCCGAG GGTCCCAAG 240  
 ACAGGAGCTC CCAGCAGAAA GGCCTGCTGT CCTGCGAGAA TACAGCGGAG ATCCAGCACT 300  
 GTTGTGTCAG CGCTGGCGAT GTGGGGTGTG GCCTGTGTTA ATGTTTCGAG AACAACTCTT 360  
 GTGAGATTCT GGGCTTACAT GGGATTGCA TGACTTTCT GCACAACGCT GGAATAATTG 420  
 ATGCCCAGGG CAAGTCATTC ATCAAAGACG CCTTGAATG TAAGGCCAC GCTCTGCGGC 480  
 ACAGGTTCGG CTCGATAAGC CGGAAGTGCC CGGCCATCAG GGAAATGGTG TCCAGTTGC 540  
 AGCGGGAATG CTACCTCAAG CACGACCTGT GCGCGGCTGC CCAGGAGAAC ACCCGGGTGA 600  
 TAGTGGAGAT GATCCATTTC AAGGACTTGC TGCTGCACGA ACCCTACGTG GACCTCGTGA 660  
 ACTTGTGCT GACCTGTGGG GAGGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTT 720  
 AGTGTGAGCA GAACCTGGGA AGCCTGTGCT CCATCTTGAG CTCTGCAACC TCGGCCATCC 780  
 AGAAGCCTCC CACGGCGCCC CCGAGCGGCC AGCCCCAGGT GGACAGAACC AAGCTCTCCA 840  
 GGGCCACCA CGGGGAAGCA GGACATCACC TCCAGAGCC CAGCAGTAGG GAGACTGGCC 900  
 GAGGTGCCAA GGTGAGCGA GGTAGCAAGA GCCACCCAAA CGCCCATGCC CGAGGCAGAG 960  
 TCGGGGCTCT TGGGGCTCAG GGACCTTCCG GAAGCAGCGA GTGGGAAGAC GAACAGTCTG 1020  
 AGTATTCTGA TATCCGAGG TGAATGAAA GGCCTGGCCA CGAAATCTTT CCTCCAGGCC 1080  
 GTCCATTTTC TATCTATGG ACATTTACCA TTAGAGAGGG GGGATGTAC 1140  
 ACGCAGGATT CTGTGGGGAC TGTGGACTTC ATCAGAGGTG GTGTTTCGCG AACGGACAGG 1200  
 TGAGATGGAG ACCCTGGGG CCGTGGGGTC TCAGGGGTGC CTGGTGAATT CTGCATTAC 1260  
 ACGTACTCAA ATCTCGAGG CCGCGTTATC CTCGTACCTT TGTCTTCTTT CCATCTGTG 1320  
 AGTCAGTGGG TGTGCGCGC TCTGTTGTG GGGAGGTGAA CCAGGGAGGG GCAGGGCAAG 1380  
 GCAGGGCCCC CAGAGCTGGG CCACACAGTG GGTGCTGGG CTCGCCCGCA AGCTTCTGGT 1440  
 GCAGCAGCCT CTGGTGCTGT CTCGCGGAA GTCAGGGCGG CTGGATTCCA GGACAGGAGT 1500  
 GAATGTAAAA ATAATATCG CTTAGAATGC AGGAGAAGGG TGGAGAGGAG GCAGGGGCCG 1560  
 AGGGGGTGT TGGTGCCAAA CTGAAATTCA GTTTCTTGTG TGGGGCCTTG CGGTTCAAG 1620  
 CTCTTGGCGA GGTGGAGGG AGGAGTGTC TTTCTATGT TAATTTCTGA GCCATTGTAC 1680  
 TGTCTGGGCT GGGGGGACA CTGTCCAAGG GAGTGGCCCC TATGAGTTTA TATTTAACC 1740  
 ACTGCTTCAA ATCTCGATTT CACTTTTTTT ATTTATCCAG TTATATCTAC ATATCTGTCA 1800  
 TCTAAATAAA TGGCTTCAA ACAAGCAAC TGGGTCATTA AAACCACTC AAAGGGGGTT 1860  
 TAAAAAATA AAAACAGCC CATCTTTGA GGTGATTTT TCTTTTCTT AAGTCTCTATT 1920  
 TAAAAAGCTA TCAACAGCG ACATAGCCAT ACATCTGACT GCCTGACATG GACTCTGTCC 1980  
 CACTTGGGGG AAACCTTATA CCCAGAGGAA AATACACACC TGGGGAGTAC ATTTGACAAA 2040  
 TTTCCCTTAG GATTTCGTTA TCTACCTTG ACCCTCAGCC AAGATTGGTA AAGCTGCGTC 2100  
 CTGCGCATTC CAGGAGACCC AGCTGGAAC CTGGCTTCTC CATGTAGGG GATGGGAAAG 2160  
 GAAAGAAGAG AATGAAGACT ACTTAGTAAT TCCATCAGG AAATGCTGAC CTTTACATA 2220  
 AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTGGAAA 2280  
 TTTAGCAATA AGGAGAGGAG TCCAAGGGGA CAAATAAAGG CAGAGAGAGA GAGAGAGAGA 2340  
 GGGAGAGGAA GAAAAGAGAG AGAGAAAAGA GCCTCGTGCC

Seq ID NO: 100 Protein sequence  
 Protein Accession #: NP\_003705

1 11 21 31 41 51  
 MCAERLGQFM TLALVLATFD PARGTDATNP PEGPQDRSSQ QKGRSLQNT AEIQHCLVNA 60  
 GDVCGVFEC FENNSCEIRG LHGICMTFLH NAGKFDQAGK SFIKDALCK AHALHRRFGC 120  
 ISRKCPAIRE MVSQQLRECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180  
 CGEEVKEAIT HSVQVQCEQN WGSLSILSF CTSATQKPPT APPERQPOVD RTKLSRAHHG 240  
 EAGHHLPEPS SRETGRGAKG ERGSKHPNA HARGRVGGLG AQGPSPGSEW EDEQSEYSDI 300  
 RR

Seq ID NO: 101 DNA sequence  
 Nucleic Acid Accession #: NM\_005940  
 Coding sequence: 23..1489

1 11 21 31 41 51

AAGCCCAGCA GCCCCGGGGC GGATGGCTCC GGCCGCTGG CTCCGACGCG CGGCCGCGCG 60  
 CGCCCTCCTG CCCCCGATGC TGCTGCTGCT GCTCCAGCCG CCGCCGCTGC TGGCCCGGGC 120  
 TCTGCGCCCG GACGTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CTTGGCATGC 180  
 5 AGCCCTGCCC AGTAGCCCGG CACCTGCCCC TGCCACGCAG GAAGCCCCC GGCTGCCAG 240  
 CAGCCTCAGG CTTCCCGCT GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCCGCAA 300  
 CCGACAGAAG AGGTTCTGTC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG 360  
 GATCCTTCGG TTCCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420  
 CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCACG AGGGCCGTGC 480  
 10 TGACATCATG ATCGACTTCG CCAGGTACTG GCATGGGGAC GACCTGCCGT TTGATGGGCC 540  
 TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600  
 CGACTATGAT GAGACCTTGA CTATCGGGGA TGACCAGGGC ACAGACCTGC TGCAGGTGGC 660  
 AGCCCATGAA TTTGGCCACG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720  
 GTCCGCTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGCGCT 780  
 15 TCAACACCTA TATGGCCAGC CCTGGCCAC TGTCACCTCC AGGACCCAG CCTTGGGCC 840  
 CCAGGCTGGG ATAGACACA ATGAGATTGC ACCGCTGGAG CCAGACGCC CGCCAGATGC 900  
 CTGTGAGGCC TCCTTTGACC CGGTCTCCAC CATCCGAGGC GAGCTCTTT TCTCAAAGC 960  
 GGGCTTTGTG TGGCGCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTGGCCTC 1020  
 20 TCGCCACTGG CAGGACTTGC CCAGCCCTGT GGACGCTGCC TTCGAGGATG CCCAGGGCCA 1080  
 CATTGTGTTT TTCCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAGC CAGTCTCTGG 1140  
 CCCCACCC CTCACCGAGC TGGGCTGGT GAGGTTCCCG GTCCATGCTG CCTTGGTCTG 1200  
 GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCACCC 1260  
 CAGCACCCGG CGTGTAGACA CTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC 1320  
 25 CTCTGAGATC GACGCTGCCT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGC CGCGGCCG 1380  
 CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCCGTCTCGT 1440  
 GGGTCTGAC TTCTTTGGCT GTGCCGAGCC TGCCAACTCT TCTCTGAC CATGGCTTGG 1500  
 ATGCCCTCAG GGGTCTGAC CCTGCCAGG CCACGAATAT CAGGCTAGAG AGCCATGGCC 1560  
 ATCTTTGTGG CTGTGGGAC CAGGCATGGG ACTGAGCCCA TGTCTCTGCG AGGGGATGG 1620  
 30 GGTGGGGTAC AACCACATG ACAACTGCCG GGAGGGCCAC GCAGGTCTGT GTCCACTGCC 1680  
 AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740  
 GGGACCCGCT ATGCAGGTCC TGGCAAACCT GGCTGCCCTG TCTCATCCCT GTCCCTCAGG 1800  
 GTAGACCAT GGCAGGACTG GGGGAAGTGG AGTGCTCTTG CTGTATCCCT GTTGTGAGGT 1860  
 TCCTTCCAGG GGCTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC 1920  
 35 TGAGCAACTG GGCTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCTGC 1980  
 ATCTGTCTGC CTCTGGCTG ACAATCTGG AAATCTGTT TCCAGAATCC AGGCCAAAAA 2040  
 GTTCACAGTC AAATGGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100  
 CAACATACCT CAATCTCTGC CAGGCCGGA TCCTCTGAA GCCCTTTTCG CAGCACTGCT 2160  
 ATCCTCAAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220  
 TTTTAAACT GAGGATTGTC ATTAAACACA GTTGTTTCT

Seq ID NO: 102 Protein sequence

Protein Accession #: NP\_005931

1 11 21 31 41 51  
 MAPAAWLRS AARALLPPL LLLLPPLP ARALPPDVH LHAERRGPQ WHAALPSSPA 60  
 PAPATQEA PR PASSLRPPR GVPDPDGLS ARNRQKRFVL SGGRWEKTDL TYRILRFPWQ 120  
 LVQEQVRQ TM AEALKWVSD TPLTFTEVHE GRADIMIDFA RYWHGDDLFP DPGGILAHA 180  
 FFPKTHREGD VHFDDYDETWT IGDDQGTDL QVAAHEFGHV LGLQHTTAAK ALMSAFYTFR 240  
 50 YPLSLSPDDC RGVQHYLQGP WPTVTSRTPA LGPQAGIDTN ETAPLEPDAP PDACEASFDA 300  
 VSTIRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEFA QGHIWFFQGA 360  
 QYVWYDGEKP VLGPAPLTEL GLVRFVPVHAA LVWGPEKNKI YFRGRDYWR FHPSTRRVD 420  
 PVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFD P VKVKALEGFP RLVGPDPFFGC 480  
 AEPANTFL

Seq ID NO: 103 DNA sequence

Nucleic Acid Accession #: NM\_033151.2

Coding sequence: 351..4499

1 11 21 31 41 51  
 ACTGGGATAA AGCAAGAAGA CTGATTTTAT GAGCAGGGGT TTGATACATC AAAGGAGATT 60  
 GCCCAGGATC AAGGGTGCGG TGTGGGGGT GGGTTGGGA GGGTGGTTAG AGAAGGTTTC 120  
 ACTAAGTGAT TTGGGCTGGA GGCTGAGAA GATGTTTAAA AAGAGGGATC AAGCACAGGC 180  
 65 TAAGGAGAGG AAAGAGCAGG CACCAAAC TCTGCATGGC CCAATATGC TCCTGCAGG 240  
 GTAGTGGCCC CTCTCTGGC TGCTCAAGGC GAGATCTAAG CTTCTCTAA CTCCTGCTGT 300  
 CTTTTCATAT TCTCTGATTC TGGGAAACGA AGAATTGGCA GGAAGTAAA ATGACTAGGA 360  
 AGAGGACATA CTGGGTGCC AACTCTTCTG GTGGCCTCGT GAATCGTGGC ATGCACATAG 420  
 GCGATGACAT GGTTCAGGA CTTATTTATA AAACCTATAC TCTCCAAGAT GGCCCTGGA 480  
 70 GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCCACCG TGGGGGAAGT 540  
 ATGATGCTGC CTTGAGAACC ATGATTCCCT TCCGTCCCAA GCCGAGGTTT CTGCCCCC 600  
 AGCCCTGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC ACCCGCTCA 660  
 TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCCTCCACTG TCAGTCCATG 720  
 ATGCCTCAGA CAAAAATGTC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA GTCTCAAGGC 780  
 75 GAGGGATTGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA ACAAGGTTGA 840  
 TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATTGCCAG TGTAAGTGGG CCAATATTGA 900  
 TTATACCAAA GATCCTGGAA TATTAGAAG AGCAGTTGGG GAATGTTGTC CATGGAGTGG 960  
 GACTCTGCTT TGCCCTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTTC TCCTCCAGTT 1020  
 GGATCATCAA CCAACGCACA GCCATCAGT TCCGAGCAGC TGTTCCTCC TTTGCTTTG 1080  
 80 AGAAGCTCAT CCAATTTAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC ATCAGCTTCT 1140  
 TCACCGGTGA TGTAAACTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA GTACTGATCA 1200  
 CCTGGGCATC CTGTGCTCAT TGCAGCATTT CTCCTACTT CATTATTGGA TACATGCAT 1260  
 TTATTGCCAT CTTATGCTAT CTCCTGGTTT TCCACTGGC GGTATTTCAT ACAAGAATGG 1320  
 CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGCGACCA GCGCATCCGT GTGACCAAGT 1380  
 AAGTTCTCAC TTGCATTAAG CTGATTAATA TGTACACATG GGAGAAACCA TTTGCAAAA 1440

TCATTGAAGA CCTAAGAAGG AAGGAAAGGA AACTATTGGA GAAGTGCGGG CTGTGCCAGA 1500  
 GCCTGACAAG TATAACCTTG TTCAATCATCC CCACAGTGGC CACAGCGGTC TGGGTTCTCA 1560  
 TCCACACATC CTAAAGCTG AACTCACAG CGTCAATGGC CTTCAGCATG CTGGCCCTCCT 1620  
 TGAATCTCCT TCGGCTGTCA GTGTTCTTTG TGCCCTATTG AGTCAAAGGT CTCACGAATT 1680  
 5 CCAAGTCTGC AGTGATGAGG TTCAAGAAGT TTTTCTCTCA GGAGAGCCCT GTTTTCTATG 1740  
 TCCAGACATT ACAAGACCCC AGCAAAGCTC TGGTCTTTGA GGAGGCCACC TTGTCTATGGC 1800  
 AACAGACCTT TCCCGGGATC GTCAATGGGG CACTGGAGCT GGAGAGGAAC GGGCATGCTT 1860  
 CTGAGGGGAT GACCAGGCCT AGAGATGCCC TCGGGCCAGA GGAAGAAGGG AACAGCCTGG 1920  
 10 GCCCAGAGTT GCACAAGATC AACTTGGTGG TGTCAGAGGG GATGATGTTA GGGGTCTGCG 1980  
 GCAACACGGG GAGTGGTAAG AGCAGCCTGT TGTGAGCCAT CCTGGAGGAG ATGCACTTGC 2040  
 TCCAGGGGCTC GGTGGGGGTG CAGGGAAGCC TGGCCTATGT CCCCAGCAG GCCTGGATCG 2100  
 TCAGCGGGAA CATCAGGGAG AACATCTCTA TGGGAGGCGC ATATGACAAG GCCCGATACC 2160  
 TCCAGGTGCT CCACTGCTGC TCCCTGAATC GGGACCTGGA ACTTCTGCCC TTGGGAGACA 2220  
 TGACAGAGAT TGGAGAGCGG GGCCTCAACC TCTCTGGGGG GCAGAAACAG AGGATCAGCC 2280  
 15 TGGCCCGCGC CGTCTATTCC GACCGTCAGA TCTACCTGCT GGACGACCCC CTGTCTGCTG 2340  
 TGGACGCCCA CGTGGGGAAG CACATTTTGT AGGAGTGCAT TAAGAAGACA CTCAGGGGGA 2400  
 AGACGGTCTG CCTGGTGACC CACAGCTGTC AGTACTTAGA ATTTTGTGGC CAGATCATT 2460  
 TGTGGGAAAA TGGGAAAATC TGTGAAAATG GAACCTCAGG TGAGTTAATG CAGAAAAAGG 2520  
 20 GGAATATGCG CCAACTTATC CAGAAGATGC ACAAGGAAGC CACTTCGGAC ATGTTGCAGG 2580  
 ACACAGCAAA GATAGCAGAG AAGCCAAAGG TAGAAAGTCA GGCTCTGGCC ACCTCCCTGG 2640  
 AAGAGTCTCT CAACGGAAAT GCTGTGCCGG AGCATCAGCT CACACAGGAG GAGGAGATGG 2700  
 AAGAAGGCTC CTGAGTTGG AGGGTCTACC ACCACTACAT CCAGGCAGCT GGAGGTTACA 2760  
 TGGTCTCTTG CATATTTTCT TCTCTGTTGG TGCTGATCGT CTTCTTAACG ATCTTCAGCT 2820  
 25 TCTGGTGGCT GAGCTACTGG TTGGAGCAGG GCTCGGGGAC CAATAGCAGC CGAGAGAGCA 2880  
 ATGGAACCAT GGCAGACCTG GGCACATTG CAGACAAATC TCAACTGTCC TTCTACCAGC 2940  
 TGGTGTACGG GCTCAACGCC CTGCTCCTCA TCTGTGTGGG GGTCTGTCTC TCAGGGATTT 3000  
 TCACCAAGT CACGAGGAAG GCATCCACGG CCCTGCACAA CAAGCTCTTC AACAAAGTTT 3060  
 TCCGCTGCCC CATGAGTTTC TTTGACACCA TCCCAATAGG CCGGCTTTTG AACTGCTTCG 3120  
 30 CAGGGGACTT GGAACAGCTG GACCAGCTCT TGCCCATCTT TTCAGAGCAG TTCCTGTTCC 3180  
 TGTCCTTAAT GGTGATCGCC GTCTCTGTGA TTGTGAGTGT GCTGTCTCCA TATATCCTGT 3240  
 TAATGGGAGC CATATCATG GTTATTTGCT TCATTATTA TATGATGTTT AAGAAGGCCA 3300  
 TCGGTGTGTT CAAGAGACTG GAGAACTATA GCCGCTCTCC TTTATTCTCC CACATCCTCA 3360  
 ATTTCTGCA AGGCCTGAGC TCCATCCATG TCTATGGAAG AACTGAAGAC TTCATCAGCC 3420  
 35 AGTTTAAAGAG GCTGACTGAT GCGCAGAATA ACTACCTGCT GTTGTCTCTA TCTTCCACAC 3480  
 GATGGATGGC ATTAGGGCTG GAGATCATGA CCAACCTTGT GACCTTGGCT GTTGCCCTGT 3540  
 TCGTGGCTTT TGGCATTTCC TCCACCCCTT ACTCCTTTAA AGTCATGGCT GTCAACATCG 3600  
 TGCTGCAGCT GGCCTCCAGC TTCCAGGCCA CTGCCCGGAT TGGCTTGGAG ACAGAGGCAC 3660  
 AGTTCAACGC TGTAGAGAGG ATACTGCAGT ACATGAAGAT GTGTGTCTCG GAAGCTCCTT 3720  
 40 TACACATGGA AGGCACAAGT TGTCCCCAGG GGTGGCCACA GCATGGGGAA ATCATATTTT 3780  
 AGGATTATCA CATGAATATC AGAGACAACA CACCACCGT GCTTCACGGC ATCAACCTGA 3840  
 CCATCCGCGG CCACGAAGTG GTGGGCATCG TGGGAAGGAC GGGCTCTGGG AAGTCTCTCT 3900  
 TGGGCATGCG TCTCTTCCGC CTGGTGGAGC CCATGGCAGG CCGGATTCTC ATTGACGGCG 3960  
 TGGACATTG CAGCATCGGC CTGGAGGACT TGCGGTCCAA GCTCTCAGTG ATCCCTCAAG 4020  
 45 ATCCAGTGCT GCTCTCAGGA ACCATCAGAT TCAACCTAGA TCCCTTTGAC CGTCACACTG 4080  
 ACCAGCAGAT CTGGGATGCC TTGGAGAGGA CATTCTGAC CAAGGCCATC TCAAGTTTCC 4140  
 CCAAAAAGCT GCATACAGAT GTGGTGGAAA ACGGTGGAAA CTTCTCTGTG GGGGAGAGGC 4200  
 AGCTGCTCTG CATTGCCAGG GCTGTGCTTC GCAACTCCAA GATCATCTT ATCGATGAAG 4260  
 CCACAGCCTC CATTGACATG GAGACAGACA CCTGATCCA GCGCACAATC CGTGAAGCCT 4320  
 50 TCCAGGGCTG CACCGTGCTC GTCATTGCCC ACCGTGTCAC CACTGTGCTG AACTGTGACC 4380  
 ACATCTCTGT TATGGCAAT GGAAGGTGGG TAGAATTTGA TCGGCCGGAG GTACTGCGGA 4440  
 AGAAGCCTGG GTCAATGTTT GCAGCCCTCA TGGCCACAGC CACTTCTTCA CTGAGATAAG 4500  
 GAGATGTGGA GACTTTCATG AGGCTGGCAG CTGAGCTCAG AGGTTACAC AGGTGCAGCT 4560  
 TCGAGGCCCA CAGTCTGCCA CCTTCTTGT TGGAGATGAG AACTTCTCCT GGAAGCAGG 4620  
 55 GTAAATGTAG GGGGGGTGGG GATTGCTGGA TGGAAACCTT GGAATAGGCT ACTTGATGGC 4680  
 TCTCAAGACG TTAGAACCCT AGAACCATCT AAGACATGGG ATTCAGTGAT CATGTGTTTC 4740  
 TCTTTTAAAC TTACATGCTG AATAATTTTA TAATAAGGTA AAAGCTTATA GTTTTCTGAT 4800  
 CTGTGTTAGA AGTGTGCAA ATGCTGTACT GACTTTGTAA AATATAAAC TAAGAAAAAC 4860  
 TC

Seq ID NO: 104 Protein sequence  
 Protein Accession #: NP\_149163.2

1 11 21 31 41 51  
 65 MTRKRTYVWP NSSGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQERNP EAPGRAAVPP 60  
 WKYDAALRT MIPFRPKPRF PAPQPLDNAG LFSYLTVSWL TPLMIQSLRS RLDENTIPPL 120  
 SVHDASDNV QRLHRLWEEE VSRRIEKAS VLLVMLRFQR TRLIIFDALLG ICFIASVLG 180  
 PILIPKILE YSEEQLGNVV HGVGLCFALF LSECVKLSLF SSSWIINQRT AIRFRAAVSS 240  
 70 FAFELIQLFK SVIHITSGEA ISFFTGDVNY LFEGVCYGPL VLITCASLVI CSISSYFIIG 300  
 YTAFIALLCY LLVFPPLAVFM TRMAVKAQHH TSEVSDQIR VTSEVLTCIK LIKMYTWEKP 360  
 FAKIEDLRK KERKLEKCG LVQSLTSITL FIIPTVATAV WVLHTSLKL KLTASMAFSM 420  
 LASNLRLRS VFFVPIAVKG LTNSKSAVMR FKKFFLQESP VFVVTQLQDP SKALVFEEAT 480  
 LSWQQTCPGI VNGALELERN GHASEGMTRP RDALGPBEEG NSLGPBLHKI NLVSVKGMML 540  
 75 GVCNGTSGSK SSLLSAILEE MHLLEGSVGV QGSLAYVPQ AWIVSGNIRE NILMGGAYDK 600  
 ARYLQVLHCC SLNRDLLELL PGDMTEIGER GLNLSGGQKQ RISLARAVYS DRQIYLLDDP 660  
 LSAVDHVGK HIFEECIKKT LRKTVVLVT HQLQYLEFCG QIILLENGKI CENGTHSELM 720  
 QKKGKYLQI QKMKKEATSD MLQDTAKIAE KPKVESQALA TSLEESLNGN AVPEHQLTQE 780  
 EEMEEGSLSW RVYHHYIQA GGYMVSCIIF FVVVLIVFLT IFSFWLSYV LEQSGSTNSS 840  
 80 RESNGTMADL GNIDNPQLS FYQLVYGLNA LLLICVGVCS SGIFTKVKRK ASTALHNKLF 900  
 NKVFRCPMSF FDTPIPIGRL NCFAGDLEQL DQLLPPIFSEQ FLVLSLMVIA VLLIVSVLSP 960  
 YILLMGALIM VICFIYMMF KKAIGVFKRL ENYSRSLPFS HILNSLQGLS SIHYVGKTED 1020  
 FISQPKRLTD AQNNYLLFL SSTRWMLRL EIMTNLVTLA VALFVAFGIS STPYSFVKVMA 1080  
 VNIVLQLASS FQATARIGLE TEAQTAVER ILQYMKMVS EAPLHMEGTS CPQGWPOHGE 1140  
 IIFQDYHMKY RDNTPTVLHG INLTIRGHEV VGIVGRTGSG KSSLGMALFR LVEPMAGRIL 1200

IDGVDICSIG LEDLRSLKLSV IPQDPVLLSG TIRFNLDPPD RHTDQQIWDA LERTFLTKAI 1260  
SKFPKLLHTD VVENGGNFSV GERQLLCIAR AVLRNSKIIL IDEATASIDM ETDLIQRTI 1320  
REAFQGCIVL VIAHRVTTVL NCDHILVMGN GKVVEFDRPE VLRKKPGSLF AALMATATSS 1380  
LR

Seq ID NO: 105 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..4043

1 11 21 31 41 51  
| | | | | |  
ATGACTAGGA AGAGGACATA CTGGGTGCCC AACTCTTCTG GTGGCCTCGT GAATCGTGGC 60  
ATCGACATAG GCGATGACAT GGTTCAGGA CTTATTATA AAACCTATAC TCTCCAAGAT 120  
GGCCCTCGGA GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCCACCG 180  
TGGGGGAAGT ATGATGTGCT CTTGAGAAC ATGATTCCTT TCCGTCCCAA GCCGAGGTTT 240  
CCTGCCCCCC AGCCCTCGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC 300  
ACCCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCCTCCACTG 360  
TCAGTCCATG ATGCCTCAGA CAAAATGTC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA 420  
GTCTCAAGGC GAGGATGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA 480  
ACAAGGTTGA TTTTCGATGC ACTTCTGGGC ATCTGCTTCT GCATTGCCAG TGTACTCGGG 540  
CCAATATTGA TTATACCAA GATCCTGGAA TATTCAGAAG AGCAGTTGGG GAATGTTGTC 600  
CATGGAGTGG GACTCTGCTT TGCCCTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTTC 660  
TCTCCAGTT GATCATCA CCAACGCACA GCCATCAGT TCCGAGCAGC TGTTCCTCC 720  
TTTGCTTTG AGAAGCTCAT CCAATTTAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC 780  
ATCAGCTTCT TCACCGGTGA TGTAAGTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA 840  
GTACTGATCA CTGCGCATC GCTGGTCATC TGCAGCATTT CTCTCACTT CATTATTGGA 900  
TACACTGCAT TTATTGCCAT CTTATGCTAT CTCTGGTTT TCCACTGGC GGTATTCATG 960  
ACAAGATGG CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGCGACCA GCGCATCCGT 1020  
GTGACCAAGT AAGTTCTCAC TTGCATTAAG CTGATTAATA TGTACACATG GGAGAAACCA 1080  
TTTGCAAAAA TCATTGAAGG TATGGAAGT CTGACTTTCT GCTCCAAACC TGGTGTATGGC 1140  
ATGGCCTTCA GCATGCTGGC CTCTTGAAT CTCTTCGGC TGTCACTGTT CTTTGTGCTT 1200  
ATTGCAGTCA AAGTCTCTAC GAATTCGAAG TCTGCAGTGA TGAGGTTCAA GAAGTTTTC 1260  
CTCCAGGAGA GCCTGTTTT CTATGTCCAG ACATTACAAG ACCCCAGCAA AGCTCTGGTC 1320  
TTTGAGGAGG CCACCTTGTG ATGGCAACAG ACCTGTCCCG GGATCGTCAA TGGGGCACTG 1380  
GAGCTGGAGA GGAACGGGCA TGCTTCTGAG GGGATGACCA GGCTAGAGA TGCCCTCGGG 1440  
CCAGAGGAAG AAGGGAACAG CCTGGGCCCA GAGTTGCACA AGATCAACCT GGTGGTGTCC 1500  
AAGGGGATGA TGTTAGGGGT CTGCGGCAAC ACGGGGAGTG GTAAGAGCAG CCTGTTGTCA 1560  
GCCATCTCGG AGGAGATGCA CTTGCTCGAG GGCTCGGTGG GGTGTCAGGG AAGCCTGGCC 1620  
TATGTCCCC AGCAGGCTG GATCGTCAGC GGAACATCA GGAAGAACAT CCTCATGGGA 1680  
GGCGCATATG ACAAGGCCCG ATACCTCCAG GTGCTCCACT GCTGCTCCCT GAATCGGGAC 1740  
CTGGAACCTC TGCCCTTTGG AGACATGACA GAGATTGGAG AGCGGGGCCT CAACCTCTCT 1800  
GGGGGGCAGA AACAGAGGAT CAGCCTGGCC CGCGCGTCT ATTCCGACCG TCAGATCTAC 1860  
CTGCTGGACG ACCCCTGTG TGCTGTGGAC GCCACGTGG GGAAGCACAT TTTTGAGGAG 1920  
TGCAATTAAG AGACACTCAG GGGGAAGACG TCGTCTCTGG TGACCCACCA GCTGCAGTAC 1980  
TTAGAAATTT GTGGCCAGAT CATTTTGTG GAAAATGGGA AAATCTGTGA AAATGGAAC 2040  
CACAGTGAAT TAATGCAGAA AAAGGGGAAA TATGCCCAAC TTATCCAGAA ATGACACAAG 2100  
GAAGCCACTT CGGACATGTT GCAGGACACA GCAAAGATAG CAGAGAAGCC AAAGGTAGAA 2160  
AGTCAGGCTC TGGCCACCTC CCTGGAAGAG TCTCTCAACG GAAATGCTGT GCCGGAGCAT 2220  
CAGCTCACAC AGGAGGAGGA GATGGAAGAA GGCTCCTTGA GTTGGAGGGT CTACCAACCAC 2280  
TACATCCAGG CAGCTGGAGG TTACATGGTC TCTTGCTATA TTTTCTTCTT CGTGGTGTCT 2340  
ATCGTCTTCT TAACGATCTT CAGCTTCTGG TGGCTGAGCT ACTGGTTGGA GCAGGGCTCG 2400  
GGGACCAATA CAGCCGAGA GAGCAATGGA ACCATGGCAG ACCTGGGCAA CATTGCAGAC 2460  
AATCCTCAAC TGTCCTTCTA CCAGCTGGTG TACGGGCTCA ACGCCTGCTT CCTCATCTGT 2520  
GTGGGGTCTT GCTCCTCAGG GATTTTCACC AAAGTCAACA GGAAGGCATC CACGGCCCTG 2580  
CACAAACAGC TCTTCAACAA GGTTTCCGCG TGCCCATGA GTTCTTTTGA CACCATCCCA 2640  
ATAGGCCGGC TTTTGAACAT CTTCGAGGG GACTTGAAC AGCTGGACCA GCTCTGCCCC 2700  
ATCTTTTCTG AGCAGTTCTT GGTCTGTGCC TTAATGGTGA TCGCCGTCTT GTTGATTGTC 2760  
AGTGTGCTGT CTCCATATAT CTTGTTAATG GGAGCCATAA TCATGGTTAT TTGCTTCATT 2820  
TATTATATGA TGTTCAGGAA GGCCATCGGT GTGTTCAAGA GACTGGAGAA CTATAGCCGG 2880  
TCTCCTTTAT TCTCCACAT CCTCAATTCT CTGCAAGGCC TGAGCTCCAT CCATGTCTAT 2940  
GGAAAACTG AAGACTTCAT CAGCCAGTTT AAGAGGCTGA CTGATGCGCA GAATAACTAC 3000  
CTGCTGTTGT TTCTATCTTC CACACGATGG ATGGCATTGA GGCTGGAGAT CATGACCAAC 3060  
CTTGTGACCT TGGCTGTTGC CTTGTTCTGT GCTTTTGGCA TTTCTCTCAC CCCCTACTCC 3120  
TTTAAAGTCA TGGCTGTCAA CATCGTGTG CAGCTGGCGT CCAGCTTCCA GGCCACTGCC 3180  
CGGATTGGCT TGGAGACAGA GGCACAGTTC ACGGCTGTAG AGAGGATACT GCAGTACATG 3240  
AAGATGTGTG TCTCGGAAGC TCCTTTACAC ATGGAAGGCA CAAGTTGTCC CCAGGGGTGG 3300  
CCACAGCATG GGGAAATCAT ATTTCAAGAT TATCACATGA AATACAGAGA CAACACACCC 3360  
ACCGTGCTTC ACGGCATCAA CCTGACCATC CGCGGCCACG AAGTGGTGGG CATCGTGGGA 3420  
AGGACGGGCT CTGGGAAGTC CTCTTGGGC ATGGCTCTCT TCCGCTGGT GGAGCCCATG 3480  
GCAGGCCGGA TTCTCATTGA CGGCGTGGAC ATTTGCAGCA TCGGCCTGGA GGAATTGCGG 3540  
TCCAAGCTCT CAGTGATCCC TCAAGATCCA GTGCTGCTCT CAGGAACCAT CAGATTCAAC 3600  
CTAGATCCCT TTGACCGTCA CACTGACCAG CAGATCTGGG ATGCCTTGA GAGGACATTC 3660  
CTGACCAAGG CCATCTCAAA GTTCCCAAAA AAGCTGCATA CAGATGTGGT GGAACACGGT 3720  
GGAAACTTCT CTGTGGGGGA GAGGCAGCTG CTCTGCATTG CCAGGGCTGT GCTTCGCAAC 3780  
TCCAAGATCA TCCTTATCGA TGAAGCCACA GCCTCCATTG ACATGGAGAC AGACACCCCTG 3840  
ATCCAGCGCA CAATCCGTG AGCCTTCAG GGTGACCCG TGCTGTCAT TGCCACCGT 3900  
GTCACCACTG TGCTGAACCTG TGACCATC CTGGTTATGG GCAATGGGAA GGTGTAGAA 3960  
TTGATCGGC CGGAGGTACT GCGGAAGAAG CCTGGGTCAT TGTTGCGAGC CCTCATGGCC 4020  
ACAGCCACTT CTTCACTGAG ATAA

Seq ID NO: 106 Protein sequence

Protein Accession #: Eos sequence



```

1      11      21      31      41      51
|      |      |      |      |      |
MTRKRTYVWP NSSGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQERNP EAPGRAAVPP 60
5  WGKYDAALRT MIPFRPKPRF PAPQPLDNAG LFSYLTVSWL TPLMIQSLRS RLDENTIPPL 120
SVHDASDNV QRLHRLWEEE VSRRGIEKAS VLLVMLRFQR TRLIFDALLG ICFCIASVLG 180
PILIIPKILE YSEBQLGNV HVGVLGCFALF LSECVKSLSF SSSWIINQRT AIRFRAAVSS 240
FAFEKLIQFK SVIHITSGEA ISFFTGDVNY LFEGVGCGPL VLITCASLVI CSISSYFIIG 300
YTAFAIALCY LLVFPLAVFM TRMAVKAQHH TSEVSDQRIK VTSEVLTCIK LIKMYTWEKP 360
FAKIEGMES LTPCSKPGDG MAFSMLASLN LLRLSVFFVP IAVKGLTNSK SAVMRFKKFF 420
10 LQESPVFVYQ TLQDPSKALV FEEATLSWQQ TCGIVNGAL ELERNGHASE GMTRPRDALG 480
PEEBEGLSGP BLHKINLVVS KGMMLGVCGN TGSGKSSLLS AILEEMHLE GSVGVQGSLSA 540
YVPQAWIVS GNIRENILMG GAYDKARYLQ VLHCCSLNRD LELLFGDMT EIGERGLNLS 600
GGQKQRISLA RAVYSDRQIY LLDDPLSAVD AHVGKHIFEE CIKKTLRGKT VVLVTHQLQY 660
15 LEFCQGIILL ENKICENGIT HSELMQKKGK YAQLIQMKHK EATSDMLQDT AKIAEKPVE 720
SQALATSLSE SLNGNAVPEH QLTQEEEMEE GSLSWRVYHH YIQAGGYMV SCIIFFVVL 780
IVFLTIFSW WLSYWLQGS GTNSSRESNG TMADLGNAD NPQLSFYQLV YGLNALLLIC 840
VGVCSGGIFT KVTIRKASTAL HNKLPNKVFR CPMSFFDTIP IGRLLNCFAG DLEQLDQLLP 900
IFSEQFLVLS LNVIAVLIV SVLSPIILM GAIMVICFI YMMFKAIG VFKRLENYSR 960
20 SPLFSHILNS LQGLSSIHYV GKTEDFISQF KRLTDAQNNY LLLFLSSTRW MALRLEIMTN 1020
LVTLAVALFV AFGISSTPYV PKVMAVNIIVL QLASSFQATA RIGLETEAQF TAVERILQYM 1080
KMCVSEAPLH MEGTSCPGQW PQHGEIIFQD YHMKYRDNTF TVLHGINTLI RGHEVVGIVG 1140
RTGSGKSSLG MALFRLVEPM AGRILIDGVD ICSIGLEDLR SKLSVIPQDP VLLSGTIRFN 1200
LDPFDRHTDQ QIWDALERTF LTKAISKFPK KLHTDVVENG GNFSVGERQL LCIAARAVLRN 1260
25 SKIILIDEAT ASIDMETDTL IQRTIREAFQ GCTVLVIAHR VTTVLNCDHI LVMGNGKVVE 1320
FDRPEVLRKK PGSFLAALMA TATSSLR

```

Seq ID NO: 107 DNA sequence  
Nucleic Acid Accession #: NM\_024022  
Coding sequence: 202..1563

```

1      11      21      31      41      51
|      |      |      |      |      |
ACCGGGCACC GGACGGCTCG GGTACTTTCG TTCTTAATTA GGTTCATGCC GTGTGAGCCA 60
35 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGGC CTACTATCTC TTCCGTGGTG 120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180
AGAGGTCCTG AATAGTCCAC CATGGGGGAA AATGATCCGC CTGCTGTGA AGCCCCCTTC 240
TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAATAA GTCTGTGTC ACCAGATGCA 300
GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360
40 ATTGGGATCA TGGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
GGAGTCTCGG ATTGCAAGA CGGGAGGAC GAGTACCGCT GTGTCCGGT GGTGTGTCAG 540
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
AAGGGTCACT ACACCAATGT TGCTGTGCC CAACTGGGT TCCCAAGCTA TGTGAGTTCA 660
45 GATAACCTCA GAGTGAAGTC GCTGGAGGG CAGTTCGGG AGGAGTTGT TCCATCGAT 720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
TGTGCTCTG GCCACGTGGT TACCTTGCG TGACAGCCT GTGGTCATAG AAGGGGCTAC 840
AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCG AGTGGCCCTG GCAGGCCAGC 900
CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960
50 ACTGCTGCAC ACTGTGTTA TGACTTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080
AGCAAGTACA AGCAAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCAGGCCCA 1140
CTCAGTTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC 1200
GATGGAAGAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGG TGACGCCCTC 1260
55 CCTGCTCTGA ACCACGCGGC CGTCCCTTTG ATTTCCAACA AGATCTGCAA CCACAGGGAC 1320
GTGTACGGTG GCATCATCTC CCCCTCCATG CTCTGCGCGG GCTACCTGAG GGTGCGGTG 1380
GACAGCTGCC AGGGGAGCAG CGGGGGGCCC CTGGTGTGTC AAGAGAGGAG GCTGTGGAAG 1440
TTAGTGGGAG GCACCAAGCT TGGCATCGGC TGGCAGAGG TGAACAAGCC TGGGGTGTAT 1500
ACCCGTGTCA CCTCTTCTCT GGAAGTGCAT CACGAGCAGA TGGAGAGAGA CCTAAAAACC 1560
60 TGAAGAGGAA GGGGACAAGT AGCCACCTGA GTTCTGAGG TGATGAAGAC AGCCCCATCC 1620
TCCCTGGAC TCCCGTGTAG GAACCTGCAC ACGAGCAGAC ACCCTTGGAG CTCTGAGTTC 1680
CGGCACCACT AGCAGGCCCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA 1740
GCTGCTTTT GTTTTTTGT TTTTGGAGT GGAGTCTCGC TCTGTGCCC AGGCTGGAGT 1800
GCAGTGGCGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAAGC GATTCTCTTG 1860
65 CCTCAGCTTC CCCAGTAGCT GGGACCAAG GTGCCGCCA CCACACCAA CTAATTTTGT 1920
TATTTTAGT AGAGACAGG TTTACCATG TTGGCCAGGC TGCTCTCAA CCCCTGACCT 1980
CAAATGATGT GCCTGCTTCA GCCTCCACA GTGCTGGGAT TACAGGCATG GGCCACCACG 2040
CCTAGCCTCA CGCTCCTTTC TGATCTTCA TAAGAACAAA AGAAGCAGCA ACTTGCAAGG 2100
GCGGCCTTTC CCACTGGTCC ATCTGTTTT CTCTCCAGG GTCTTGCAA ATCTCTGACG 2160
70 AGATAAGCAG TTATGTGACC TCACGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA 2220
CCAGCCAGAG AGTGCAGAAC TGCAGTCACT GCACGTTTT ATCTCTAGG ACCAGAACCA 2280
AACCACCTCT TTCTACTTCC AAGACTTATT TTCACATGTG GGGAGGTTAA TCTAGGAATG 2340
ACTCGTTTAA GGCCATTATT CATGATTTCT TGTAGCATT TGGTGCTTGA CGTATTATTG 2400
75 TCCTTTGATT CCAATAATA TGTTCCTTTC CCTCAAAAAA AAAAAAAA AAAAAAAA 2460
AAAAA

```

Seq ID NO: 108 Protein sequence  
Protein Accession #: NP\_076927

```

1      11      21      31      41      51
|      |      |      |      |      |
MGENDPPAVE APFSFRSLFG LDDLKISVPA PDADAVAAQI LSLLEPKFFP IIVIGIILI 60
80 LALAIGLGIH FDCSGKYRRC SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLQVF 120
TAASWKTMCs DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
VTALHHSVYV REGCASGHYV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQPGGYH 240

```

LCGGSVITPL WIITAACHVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGVKVCWT SGWGATEDGG DASPVLNHAA 360  
 VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF 420  
 GIGCAEVNKP GUYTRVTSFL DWIHEQMERE LKT

Seq ID NO: 109 DNA sequence  
 Nucleic Acid Accession #: NM\_000493.2  
 Coding sequence: 97..2139

1 11 21 31 41 51  
 | | | | |  
 CACCTTCTGC ACTGCTCATC TGGGCAGAGG AAGCTTCAGA AAGCTGCCAA GGCACCATCT 60  
 CCAGGAACCTC CCAGCACGCA GAATCCATCT GAGAATATGC TGCCACAAAT ACCCTTTTGT 120  
 CTGCTAGTAT CCTTGAACCT GGTTCATGGA GTGTTTACG CTGAACGATA CCAATGCCCC 180  
 ACAGGCATAA AAGGCCCACT ACCCAACACC AAGACACAGT TCTTCATTCC CTACACCATA 240  
 AAGAGTAAAG GTATAGCAGT AAGAGGAGAG CAAGGTACTC CTGGTCCACC AGGCCCTGCT 300  
 GGACCTCGAG GGCACCCAGG TCCTTCTGGA CCACCAGGAA AACCAGGCTA CGGAAGTCCT 360  
 GGACTCCAAAG GAGAGCCAGG GTTGCCAGGA CCACCGGGAC CATCAGCTGT AGGGAAACCA 420  
 GGTGTGCCAG GACTCCAGG AAAACCCAGGA GAGAGAGGAC CATATGGACC AAAAGGAGAT 480  
 GTTGGACCAG CTGGCTTACC AGGACCCCGG GGCCACCCAG GACCACCTGG AATCCCTGGA 540  
 CCGGCTGGAA TTTCTGTGCC AGGAAAACCT GGACAACAGG GACCCACAGG AGCCCCAGGA 600  
 CCCAGGGGCT TTCTTGAGGA AAAGGGTGCA CCAGGAGTCC CTGGTATGAA TGGACAGAAA 660  
 GGGGAAATGG CGGTATGGTG TCTGTGTCGT CCAGGTGAGA GGGGTCTTCC AGGCCCTCAG 720  
 GGTCCCACAG GACCATCTCG CCCTCCTGGA GTGGGAAAAA GAGGTGAAAA TGGGGTTCCA 780  
 GGACAGCCAG GCATCAAAGG TGATAGAGGT TTTCCGGGAG AAATGGGACC AATTGGCCCC 840  
 CCAGGTCCCC AAGGCCCTCC TGGGGAACGA GGGCCAGAAG GCATTGGAAA GCCAGGAGCT 900  
 GCTGGAGCCC CAGGCCAGCC AGGGATTCCA GGAACAAAAG GTCTCCCTGG GGCTCCAGGA 960  
 ATAGCTGGGC CCCAGGGGCC TCCTGGCTTT GGGAAACCAG GCTTGCCAGG CCTGAAGGGA 1020  
 GAAAGAGGAC CTGCTGGCCT TCCTGGGGGT CCAGGTGCCA AAGGGGAACA AGGGCCAGCA 1080  
 GGTCTTCTGT GGAAGCCAGG TCTGACTGGA CCCCTTGGGA ATATGGGACC CCAAGGACCA 1140  
 AAAGGCATCC CGGTATGCCA TGGTCTCCCA GGCCCTAAAG GTGAGACAGG GCCAGCTGGG 1200  
 CCTGCAGGAT ACCCTGGGGC TAAGGGTGAA AGGGGTTCCT CTGGGTGAGA TGGAAAACCA 1260  
 GGGTACCAGG GAAACCCAGG TCTCGATGGT CCTAAGGGTA ACCCAGGGTT ACCAGTCCA 1320  
 AAAGGTGATC CTGAGATTGG AGGACCTCCT GGTCTCCAGG GCCCTGTGGG CCCAGCAGGA 1380  
 GCAAGGGGAA TGCCCGGACA CAATGGAGAG GCTGGCCCAA GAGGTGCCCC TGGAAATACCA 1440  
 GGTACTAGAG GCCCTATTGG GCCACAGGCT ATTCCAGGAT TCCCTGGGTC TAAAGGGGAT 1500  
 CCAGGAAGTC CCGGTCTCTC TGGCCAGCT GGCATAGCAA CTAAGGGCCT CAATGGACCC 1560  
 ACCCGGCCAC CAGGGCCCTC AGGTCCAAGA GGCCACTCTG GAGAGCCTGG TCTTCCAGGG 1620  
 CCCCCTGGGC CTCAGGGCCC ACCAGGTCAA GCAGTCATGC CTGAGGGTTT TATAAAGGCA 1680  
 GGCCAAAGGC CCACTCTTTC TGGGACCCCT CTTGTTAGTG CCAACCCAGG GGTAAACAGGA 1740  
 ATGCTGTGTG CTGCTTTTAC TGTTATTCTC TCCAAGCTT ACCCAGCAAT AGGAACTCCC 1800  
 ATACCAATTG ATAAATTTT GTATAACAGG CAACAGCATT ATGACCCAAG GACTGGAATC 1860  
 TTTACTTGTG AGATACAGG AATATACTAT TTTTCATACC ACCTGCATGT GAAAGGGACT 1920  
 CATGTTTGGG TAGGCCTGTA TAAGAAATGGC ACCCTGTAA TGTACACCTA TGTGAATAC 1980  
 ACCAAAGGCT ACCTGGATCA GGCTTCAGGG AGTGCCATCA TCGATCTCAC AGAAATGAC 2040  
 CAGGTGTGCG TCCAGCTTCC CAATGCCGAG TCAAATGGCC TATACTCTCT TGAGTATGTC 2100  
 CACTCTCTT TCTCAGGATT CCTAGTGGCT CCAATGTGAG TACACCCAC AGAGCTAATC 2160  
 TAAATCTTGT GCTAGAAAAA GCATTCTCTA ACTCTACCCC ACCCTACAAA ATGCATATGG 2220  
 AGGTAGGCTG AAAAGAATGT AATTTTTATT TTCTGAAATA CAGATTGTAG CTATCAGACC 2280  
 AACAAACCTT CCCCCTGAAA AGTGAGCAGC AACGTAAAAA CGTATGTGAA GCCTCTCTTG 2340  
 AATTTCTAGT TAGCAATCTT AAGGCTCTTT AAGGTTTTCT CCAATATTAA AAAATATCAC 2400  
 CAAAGAGATC CTGCTATGTT AAAAAACAAAC AACAAAAAAC AAAGCAACAA AAAAAAAAT 2460  
 TAAAAAATA AACAGAAATA GAGCTCTAAG TTATGTGAAA TTTGATTGTA GAAACTCGGC 2520  
 ATTTCTTTT TAAAAAAGCC TGTTTCTAAC TATGAATATG AGAACTTCTA GGAAACATCC 2580  
 AGGAGGTATC ATATACTTT GTAGAACTTA AATACTTGAA TATTCAAATT TAAAAAGCAC 2640  
 TGTATCCCTT AAAATATTTT TGATGGTGCA CTACTCTGAG GCCTGTATGG CCCCTTTCAT 2700  
 CAATATCTAT TCAATATATC AGGTGCATAT ATACTTGTTA AAGCTCTTAT ATAAAAAAGC 2760  
 CCCAAATAT TGAAGTTCAT CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTTCAAAA 2820  
 CTTTCTATG ATTGCAGAGA AGCTTTTTAT ATACCAGCA TAACTTGGAA ACAGGTATCT 2880  
 GACCTATTCT TATTAGTATA ACACAAGTGT GATTAATTTG ATTTCTTTAA TTCTTATTG 2940  
 AATCTTATGT GATATGATTT TCTGGATTTA CAGAACATTA GCACATGTAC CTGTGCTCTC 3000  
 CCATTCAAGT GAAGTTATAA TTTACACTGA GGGTTTCAAA ATTCGACTAG AAGTGGAGAT 3060  
 ATATTATTTA TTTATGCACT GTACTGTATT TTTATATTGC TGTTTTAAAC TTTTAAGCTG 3120  
 TGCTCACTT ATTAAGACCA AAAATGTTTT ACCTACTCCT TATTTACGAC ACAATAAAAT 3180  
 AACATCAATA GATTTTTAGG CTGAATTAAT TTGAAAGCAG CAATTTGCTG TTCTCAACCA 3240  
 TTTCTTCAAG GCTTTTCATT CGACACAATA AAATAACATC AATAG

Seq ID NO: 110 Protein sequence  
 Protein Accession #: NP\_000484.2

1 11 21 31 41 51  
 | | | | |  
 MLPQIPFLLL VSLNLVHGVF YAERYQMPTG IKGPLENTKT QFFIPYTIKS KGI AVRGEQG 60  
 TPGPFGPAGP RHGPGPSGPP GKPGYGSFPL QGEPGLPGPP GPSAVGKPGV PGLPGKPER 120  
 GPYGPKGDVG PAGLPGPRGP PGPPGIPGPA GISVPGKPGQ QGTPGAPGPR GFPGEKGAPG 180  
 VPGMNGQKGE MGYGAPGRPG ERGLPGPQGP TGSPGPPGVG KRGENGVPGQ PGIKGDRGPF 240  
 GEMGPIGPPG PQGPPGERGP EGIKPGAAAG APGQPGIPGT KGLPGAPGIA GPPGPPGFGK 300  
 PGLPLKGER GPAGLPGGPG AKGEQGPAGL PGKPLGTGPP GNMGPQGPKG IPGSHGLPGP 360  
 KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPLDGPK GNPLPGPKG DPGVGGPPGL 420  
 PGVPGPAGAK GMPHNGEAG PRGAPGIPGT RGPFGPPGIP GPPGSKGDPG SPGPPGPAI 480  
 ATKGLNGPTG PPGPPGPPG SGEPGLPGPP GPPGPPGQAV MPEGFIKAGQ RPSLSGTPLV 540  
 SANQGVGTMP VSAFTVILSK AYPAGTPIP FDKILYNRQO HYDPTGTIFT CQIPGIYFYS 600  
 YHVHVKGTHV WFGLYKNPTP VMYTYDEYTK GYLDQASGSA IIDLTENDQV WLQLPNAESN 660  
 GLYSSEYVHS SFGSLVAPM

Seq ID NO: 111 DNA sequence  
Nucleic Acid Accession #: NM\_000949  
Coding sequence: 285..2153

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55

1	11	21	31	41	51	
GGAGGCTGAA	ATCCCCAGAC	GCCGGTTTTC	TGGGCTGGGC	TTTCTGCTTA	CTCACTCCTT	60
CTCCCTCTTT	CTGGATTTTA	CCGACCGTTC	GCGAAACAGC	TTTCCACACA	ATGGAGCTTC	120
ATGTCTCTCGT	GCAGGAAGTA	CTCATCGACT	GATGTGGCAG	ACTTTGCTCC	CTGACAAAAC	180
TAAAGAACTC	TCCTATTTCAT	GGAGGCGAAC	ACTGAGGATG	CTTTCCACAT	GAACCCGTGA	240
GTGAACCTCT	GATACATTTT	CTGCAGCAAG	AGAAGGCAGC	CAACATGAAG	GAAAATGTGG	300
CATCTGCAAC	CGTTTTCACT	CTGCTACTTT	TTCTCAACAC	CTGCCTTCTG	AATGGACAGT	360
TACCTCTCTGG	AAAACCTGAG	ATCTTTAAAT	GTCTTCTCC	CAATAAGGAA	ACATTCACTT	420
GCTGGTGGAG	GCCTGGGACA	GATGGAGGAC	TTCTACCAA	TTATTCCTG	ACTTACCACA	480
GGGAAGGAGA	GACACTCATG	CATGAATGTC	CAGACTACAT	AACCGGTGGC	CCCAACTCCT	540
GCCACTTTGG	CAAGCAGTAC	ACCTCCATGT	GGAGGACATA	CATCATGATG	GTCAATGCCA	600
CTAACAGAT	GGGAAGCAGT	TTCTCGGATG	AACTTTATGT	GGACGTGACT	TACATAGTTC	660
AGCCAGACCC	TCCTTTGGAG	CTGGCTGTGG	AAGTAAACA	GCCAGAAGAC	AGAAAACCCCT	720
ACCTGTGGAT	TAAATGGTCT	CCACCTACCC	TGATTGACTT	AAAACTGGT	TGGTTCACGC	780
TCCTGTATGA	AATTCGATTA	AAACCCGAGA	AAGCAGCTGA	GTGGGAGATC	CATTTTGTCTG	840
GGCAGCAAA	AGAGTTTAA	ATTCTCAGCC	TACATCCAGG	ACAGAAATAC	CTTGTCCAGG	900
TTCTGTGCAA	ACCAGACCAT	GGATACTGGA	GTGCATGGAG	TCCAGCGACC	TTCATTGAGA	960
TACCTAGTGA	CTTCACCATG	AATGATACAA	CCGTGTGGAT	CTCTGTGGCT	GTCTTTTCTG	1020
CTGTCTCTCG	TTTGATTAT	GTCTGGGCG	TGGCTTTGAA	GGGCTATAGC	ATGGTGACCT	1080
GCATCTTTCC	GCCAGTTCC	GGGCCAAAA	TAAAGGATT	TGATGCTCAT	CTGTGGGAGA	1140
AGGGCAAGTC	TGAAGAATA	CTGAGTGCTT	TGGGATGCCA	AGACTTTCTT	CCCCTTCTG	1200
ACTATGAGGA	CTTGCTGGTG	GAGTATTTAG	AAGTAGATGA	TAGTGAGGAC	CAGCATCTAA	1260
TGTCAAGTCCA	TTCAAAAGAA	CACCCAAGTC	AAGGTATGAA	ACCCACATAC	CTGGATCCTG	1320
ACACTGACTC	AGGCCGGGGG	AGCTGTGACA	GCCCTTCCCT	TTTGTCTGAA	AAGTGTGAGG	1380
AACCCAGGC	CAATCCCTCC	ACATTTCTATG	ATCCTGAGGT	CATTGAGAAG	CCAGAGAATC	1440
CTGAAACAAC	CCACACCTGG	GACCCCAAGT	GCATAAGCAT	GGAAGGCAAA	ATCCCTTATT	1500
TTCTATGCTGG	TGGATCCAAA	TGTTCAACAT	GGCCCTTACC	ACAGCCAGC	CAGCACAACC	1560
CCAGATCCTC	TTACCAACAT	ATTACTGATG	TGTGTGAGCT	GGCTGTGGGC	CCTGCAGGTG	1620
CACCGGCCAC	TCTGTGTAAT	GAAGCAGGTA	AAGATGCTTT	AAAACTCTCT	CAAAACCATTA	1680
AGTCTAGAGA	AGAGGGAAG	GCAACCCAGC	AGAGGGAGGT	AGAAAGCTTC	CATTCTGAGA	1740
CTGACCAGGA	TACGCCCTGG	CTGCTGCCCC	AGGAGAAAAC	CCCCTTTGGC	TCCGCTAAAC	1800
CCTTGGATTA	TGTGTGAGAT	CACAAGGTCA	ACAAAGATGG	TGCATTATCA	TTGCTACCAA	1860
AACAGAGAGA	GAACAGCGGC	AAGCCCAAGA	AGCCCGGGAC	TCCTGAGAAC	AATAAGGAGT	1920
ATGCCAAGGT	GTCCGGGGTC	ATGGATAACA	ACATCTGGT	GTGTGTGCCA	GATCCACATG	1980
CTAAAAACGT	GGCTTGCTTT	GAAGAATCAG	CCAAAGAGGC	CCCACCATCA	CTTGAACAGA	2040
ATCAAGCTGA	GAAAGCCCTG	GCCAACTTCA	CTGCAACATC	AAGCAAGTGC	AGGCTCCAGC	2100
TGGGTGGTTT	GGATTACCTG	GATCCCGCAT	GTTTTACACA	CTCCTTTCAC	TGATAGCTTG	2160
ACTAATGGA	TGATTGGTTA	AAATGTGATT	TTCTTCAGG	TAACACTACA	GAGTACGTGA	2220
AATGCTCAAG	AATGTAGTCA	GACTGACACT	ACTAAGCTC	CCAGCTCCTT	TCATGCTCCA	2280
TTTTTAACCA	CTTGCTCTTT	TCTCCAGCAG	CTGATTCCAG	AACAAATCAT	TATGTTTCCT	2340
AACGTGTAT	TGTAGATTTA	CTTTTGTCTG	TTAGTTATAA	AACTATGTGT	TCAATGAAAT	2400
AAAAGCACAC	TGCTTAGTAT	TCTTGAGGGA	CAATGCCAAT	AGGTATATCC	TCTGGAAGAA	2460
GCTTTCATGA	TTTGGCATGG	GACAGACGGA	AATGAAATTG	TCAAAATTGT	TTACCATAGA	2520
AAGATGACAA	AAGAAAATT	TCCACATAGG	AAAATGCCAT	GAAAATTGCT	TTTGAAAAAC	2580
AACTGCATAA	CCTTTACACT	CCTCGTCCAT	TTTATTAGGA	TTACCCAAAT	ATAACCATTT	2640
AAAGAAAGAA	TGCATTCCAG	AACAAATTGT	TTACATAAGT	TCCTATACCT	TACTGACACA	2700
TTGCTGATAT	GCAAGTAAGA	AAT				

Seq ID NO: 112 Protein sequence  
Protein Accession #: NP\_000940

60  
65  
70

1	11	21	31	41	51	
MKENVASATV	FTLLFLNLC	LLNGQLPPGK	PEIFKCRSPN	KETFTCWWRP	GTGGLPTNY	60
SLTYHREGET	LMHECPDYIT	GGPNSCHFVK	QYTSMWRTYI	MMVNATNQM	SSFSDELYVD	120
VTYIVQDPDP	LELAVEVKQP	EDRKPYLWIK	WSPPTLIDLK	TGWFTLLYEI	RLKPEKAAEW	180
EIHFAQQQTE	FKILSLHPGQ	KYLQVVRCKP	DHGYWSAWSP	ATFIQIPSD	TMNDTTVWIS	240
VAVLSAVICL	IIVWAVALKG	YSMTVICFPP	VPQPKIKGFD	AHLLEKKGSE	ELLSALGCQD	300
FPPTSDYEDL	LVEYLEVDDS	EDQHLMSVHS	KEHPSQGMKP	TYLDPDTS	RGSCDSPSLL	360
SEKCEEPQAN	PSTFYDPEVI	EKPENPETTH	TWDPQCISME	GKIPYFHAGG	SKCSTWPLPQ	420
PSQHNPRSSY	HNITDVCELA	VGPAGAPATL	LNEAGKDALK	SSQTIKSREE	GKATQQREVE	480
SFHSETDQDT	PWLLPQEKTP	FGSAKPLDYV	BIHKVNKDGA	LSLLPKQREN	SGKPKPKGTP	540
ENNKEYAKVS	GVMDDNIIVL	VPDPHAKNVA	CFEESAKEAP	PSLBQNAEK	ALANFTATSS	600
KCRLQLGGLD	YLDPACTH	FS				

Seq ID NO: 113 DNA sequence  
Nucleic Acid Accession #: XM\_062811  
Coding sequence: 1..888

75  
80

1	11	21	31	41	51	
ATGTGGGGCG	CTCGCCGCTC	GTCCGTCTCC	TCATCCTGGA	ACGCCGCTTC	GCTCCTGCAG	60
CTGCTGCTGG	CTGCGCTGCT	GGCGGCGGGG	GCGAGGGCCA	GCGGCGAGTA	CTGCCACGGC	120
TGGCTGGAGC	CGCAGGGCGT	CTGGCGCATC	GGCTTCCAGT	GTCCCGAGCG	CTTCGACGGC	180
GGCGACGCCA	CATCTGCTG	GCGCAGCTGC	GCGTTGCGCT	ACTGCTGCTC	CAGCGCCGAG	240
GCGCGCCTGG	ACCAGGGCGG	CTGCGACAAT	GACCGCCAGC	AGGGCGCTGG	CGAGCCTGGC	300
CGGGCGGACA	AAGACGGCCC	CGACGGCTCG	GCAGTGCCCA	TCTACGTGCC	GTTCTTCATT	360
GTTGGCTCCG	TGTTTGTGCG	CTTTATCATC	TTGGGGTCCC	TGGTGGCAGC	CTGTTGCTGC	420

AGATGTCTCC GGCCTAAGCA GGATCCCCAG CAGAGCCGAG CCCAGGGGG TAACCGCTTG 480  
 ATGGAGACCA TCCCCATGAT CCCCAGTGCC AGCACCTCCC GGGGGTCGTC CTCACGCCAG 540  
 TCCAGCACAG CTGCCAGTTC CAGCTCCAGC GCCAAGCTCAG GGGCCCCGGG GCCCCCAACA 600  
 AGGTACACAGA CCAACTGTTG CTTGCCGGA GGGACCATGA ACAACGTGTA TGTCAACATG 660  
 CCCACGAATT TCTCTGTGCT GAACTGTCAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720  
 CAGTATCTGC ATCCCCCATA CGTGGGGTAC ACQGTGCAGC ACGACTCTGT GCCCATGACA 780  
 GCTGTGCCAC CTTTCATGGA CGGCCTGCAG CTTGGCTACA GGCAGATTCA GTCCCCCTTC 840  
 CCTCACACCA ACAGTGAACA GAAGATGTAC CCAGCGGTGA CTGTATAA

Seq ID NO: 114 Protein sequence  
 Protein Accession #: XP\_062811

1 11 21 31 41 51  
 MWGARRSSVS SSWNAASLLQ LLLAALLAAG ARASGEYCHG WLDAQGVWRI GFQCPERFDG 60  
 GDATICCGSC ALRYCCSSAE ARLDQGGCDN DRQQGAGEPG RADKDGPDGS AVPIYVFLI 120  
 VGSVFVAFII LGSIVAACCC RCLRPKQDPQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ 180  
 SSTAASSSSS ANSGARAPPT RSQTNCLPE GTMNNVYVM PTNFSVLNCQ QATQIVPHQG 240  
 QYLHPPYVGY TVQHDSVPMT AVPEFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV

Seq ID NO: 115 DNA sequence  
 Nucleic Acid Accession #: NM\_013257  
 Coding sequence: 223..1512

1 11 21 31 41 51  
 GGTGTGCTCT TGAGGGGATTA AATGCAAAGA GATCACACCA TGGACTACAA GGAAAGCTGC 60  
 CCAAGTGTA GCAATCCAG CTCCGATGAA CACAGAGAGA AAAAGAAGAG GTTTACTGTT 120  
 TATAAAGTTC TGGTTTCAGT GGGAAAGAAGT GAATGGTTTG TCTTCAGGAG ATATGCAGAG 180  
 TTTGATAAAC TTTTATAACAC TTTAAAAAAA CAGTTTCCTGT CTATGGCCCT GAAGATTCTT 240  
 GCCAAGAGAA TAATTTGGTGA TAATTTTGTAT CCAGATTTTA TTAACAAAG ACGAGCAGGA 300  
 CTAAACGAAT TCATTTCAGAA CCTAGTTAGG TATCCAGAAC TTTATAACCA TCCAGATGTC 360  
 AGAGCATTC TTCAAAATGGA CAGTCCAAAA CACCACTCAG ATCCATCTGA AGATGAGGAT 420  
 GAAAGAAGTT CTCAGAAGCT ACACCTTACC TCACAGAACA TCAACCTGGG ACCGCTCGGA 480  
 AATCCTCATG CCAAACCAAC TGACTTTGAT TTCTTAAAG TTATTTGAAA AGGCAGCTTT 540  
 GGCAAGGTTT TTTCTGCAAA ACGGAAACTG GATGGAATAT TTTATGCTGT CAAAGTGTTA 600  
 CAGAAAAAAA TAGTTCTCAA CAGAAAAGAG CAAAACATA TTATGGCTGA ACGTAATGTG 660  
 CTCTTGAAAA ATGTGAAACA TCCGTTTTTG GTTGGATTGC ATTATTCCTT CCAAACAAC 720  
 GAAAAGCTTT ATTTTGTCT GGAATTTGTT AATGGAGGG AGCTTTTTTT CCACTTACAA 780  
 AGAGAACCGT CTTTCTCTGA GCACAGAGCT AGGTTTACG CTGCTGAAAT TGCTAGTGCA 840  
 TTGGGTTACT TACATTCCAT CAAAATAGTA TACAGAGACT TGAAACCAGA AAATATTCCT 900  
 TTGGATTACG TAGGACATGT TGTCTTAACA GATTTTGGGC TTTGTAAAGA AGGAATTGCT 960  
 ATTTCTGACA CCACCTACCAC ATTTTGTGGG ACACAGAGT ATCTTGCACC TGAAGTAATT 1020  
 AGAAAACAGC CCTATGACAA TACTGTAGAT TGGTGGTGCC TTGGGGCTGT TCTGTATGAA 1080  
 ATGCTGTATG GATTGCCTCC TTTTATTGTC CGAGATGTTG CTGAAATGTA TGACAATATC 1140  
 CTTCAACAAC CCCTAAGTTT GAGGCCAGGA GTGAGTCTTA CAGCCTGGTC CATTCTGGAA 1200  
 GAACCTCTAG AAAAAGACAG GCAAAATCGA CTTGGTGCCA AGGAAGACTT TCTTGAAATT 1260  
 CAGAAATATC CTTTTTTTGA ATCACTCAGC TGGGCTGACC TTGTACAAA GAAGATTCCA 1320  
 CCACCATTTA ATCCTAATGT GGCTGGACCA GATGATATCA GAAACTTTGA CACAGCATT 1380  
 ACAGAAGAAA CAGTTCCATA TTCTGTGTGT GTATCTCTG ACTATTCTAT AGTGAATGCC 1440  
 AGTGTATTGG AGGCAGATGA TGCATTCGTT GGTTTCTCTT ATGCACCTCC TTCAGAAGAC 1500  
 TTATTTTGTG GAGCAGTTTG CCATTAGAA ACCATTGAGC AAAATAAGTC TATAGATGGG 1560  
 ACTGAACTT CTATTGTGTG GAATATATTC AAATATGTAT AACTAGTGCC TCATTTTAT 1620  
 ATGTAATGAT GAAACTATG AAAAAATGTA TTTTCTCTA TGTGCAAGAA AAATAGGGCA 1680  
 TTTCAAAGAG CTGTTTGTAT TAAAATTTAT ATTCTGTGT AATAAGCTTA TTTTAAACA 1740  
 ATTTAAAGC TATTATCTT AGCATTAAAC TATTTTAAA GAAACCTTT TTGCTATTGA 1800  
 CTGTTTTTCT CTTCTAAGTT TACACTAACA TCTACCCAAG ATAGACTGTT TTTTAAAGT 1860  
 CAATTTTCAGT TCAGCTAACA TATATTAATA CCTTTGTAAC TCTTTGCTAT GGCTTTTGTT 1920  
 ATCACACCAA AACTATGCAA TTGGTACATG GTTGTTAAG AAGAAACCGT ATTTTCCAT 1980  
 GATAAATCAC TGTTTGAAAT ATTGTGTTCA TGGTATGATC GAAATGTAAA AGCATAATTA 2040  
 ACACATTGGC TGCTAGTTAA CAATTGGAAT AACTTTATTC TGCAATCAT TTAAGAAGTA 2100  
 ACAGGCCGGG CGCGGTGGCT CACGCTGTA ATCCCAGCAC TTTGGGAGGC TGAGGCGGGC 2160  
 AGATCACCTG AGGTACAGAG TTGGAGACCA GCCTGACCAA CATGGACAAA CCCCGTCTCT 2220  
 ACTAAAAATA CAAATTTGGC AGGGTGTGGT GGCACATGCC TATAATCCCA GCTACTTGGG 2280  
 AGGCTAAGGC AGGAGAATCG CTTGAACCCG GGAGGCGGAG GTTGCAGTGA GCGGAGATCG 2340  
 CACCATTGCA CTCCTGCCTG GGCAACAAGA GTGAACTCC ATCTCCAAAA A

Seq ID NO: 116 Protein sequence  
 Protein Accession #: NP\_037389

1 11 21 31 41 51  
 MALKIPAKRI FGDNFDPDFI KQRRAGLNEF IQNLVRYPEL YNHPDVRAFL QMDSPKHQSD 60  
 PSEDEDERSS QKLHSTQNI NLGPGSNPHA KPTDFDFLKV IGKGSFGKVL LAKRKLDGKF 120  
 YAVKVLQKKI VLNRKEQKHI MAERNVLLKN VKHPFLVLGLH YSFQTEKLY FVLDFVNGGE 180  
 LFPHLQRERS FPBHRARFYA AEIASALGYL HSIKIVYRDL KPENILLDSV GHVVLTFDGL 240  
 CKEGIAISDT TTTFCGTPEY LAPEVIRKQP YDNTVDWVCL GAVLYEMLYG LPPFYCRDVA 300  
 EMDYNILHHP LSLRPGVSLD AWSILELLE KDRQNRIGAK EDFLEIQNHP FFESLSWADL 360  
 VQKKIPPPFN PNVAGPDDIR NFDATFTEET VPYSVCVSSD YSIVNASVLE ADDAFVGFYSY 420  
 APPSEDLFL

Seq ID NO: 117 DNA sequence  
 Nucleic Acid Accession #: NM\_004004.1

Coding sequence: 1..681

```

1      11      21      31      41      51
5      |      |      |      |      |      |
      ATGGATTGGG GCACGCTGCA GACGATCCTG GGGGGTGTGA ACAAACACTC CACCAGCATT 60
      GGAAAGATCT GGCTCACCGT CCTCTTCATT TTTCGCATTA TGATCCTCGT TGTGGCTGCA 120
      AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTTGTCTGCA ACACCCCTGCA GCCAGGCTGC 180
      AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACCA TCCGGCTATG GGCCCTGCAG 240
      CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
      GAGAAGAAGA GGAAGTTCAT CAAGGGGAG ATAAAGAGTG AATTAAAGGA CATCGAGGAG 360
      ATCAAAACCC AGAAGGTCG CATCGAAGGC TCCCTGTGGT GGACCTACAC AAGCAGCATC 420
      TTCTTCCGGG TCATCTTCGA AGCCGCTTC ATGTACGCTC TCTATGTCAT GTACGACGGC 480
      TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
      TTTGTGTCCC GGCCACCGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA 600
      ATTTGCATCC TGCTGAATGT CACTGAATTG TGTATTGTC TAATTAGATA TTGTTCTGGG 660
      AAGTCAAAA AGCCAGTTTA A

```

Seq ID NO: 118 Protein sequence  
Protein Accession #: NP\_003995.1

```

1      11      21      31      41      51
25     |      |      |      |      |      |
      MDWGLTQIL GGVNKHSTSI GKIWLTVLFI FRIMILVVA KEVVGDEQAD FVCNTLQPGC 60
      KNVCYDHYFP ISHRLWALQ LIFVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEFKDIEE 120
      IKTKQVRIEG SLWWTYTSI FFRVIFEAAF MYVFVVMYDG FSMQRLVKCN AWPCPNTVDC 180
      FVSRPTEKTV FTFVMIASVG ICILNVTEL CYLLIRYCSG KSKKPV

```

Seq ID NO: 119 DNA sequence  
Nucleic Acid Accession #: XM\_061091.1  
Coding sequence: 1..2481

```

1      11      21      31      41      51
35     |      |      |      |      |      |
      ATGCCAAATA CTTACGGAAC AACCAGGATT GAAATTGGC TTCTCCAAGA GCCGCCCGGG 60
      CACCGAGCGC TGGTCGCCGC TCTCCTCCG GTGAGTCCCA GCCCCGAGTT GGCTCTGGCG 120
      CCCGGGTACC CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGCTCCCGAT GATTGGAGGT 180
      CAGATGCATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTAA 240
      GTTGGGAAGC TCCCTTTTGA GGCAACGAA GTCCATGTAA GCAAAGAAAC CATCGGAAG 300
      ATTTCAAGCTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTCTCTGTTA 360
      GATGGGTCTA ACACGCTCGG GAAAGGGAGC TTGAAAGGT CCAAGCACTT TGCCATCACA 420
      GTCTGTGACG GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT 480
      TCCACTCCTC ATCTGGAATT CCCTTGGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA 540
      AGAATCAAGA GGATGGTTTT CAAAGGAGGG CGCACGGAGA CGGAACCTGC TCTGAAATAC 600
      CTTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
      GTCACGTATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720
      GGTGTCACTG TGTTTGCTGT GGGGGTCAGG TTTCCAGGT GGGAGGAGCT GCATGCACTG 780
      GCCAGCGAGC CTAGAGGGCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
      GGCCTCTTCA GCACCTTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC 900
      CCGAGGCTTG TCTTCATGGA GCGGTTAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG 960
      CAGCCCTGCC AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCCCTC 1020
      TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
      GTCGACCTCC TCTTCCTGCT GGACAGCTCT GCGGGCACC CTCTGGACGG CTCTCTGCGG 1140
      GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG GCCGTGCTGA GCGAGGACTC TCGGGCCCGA 1200
      GTGGGTGTGG CCACATACAG CAGGGAGCTG CTGGTGGCGG TGCTGTGGGG GGAGTACCAG 1260
      GATGTGCTGG ACCTGGTCTG GAGCCTCGAT GGCATTCCCT TCCGTGGTGG CCCACCCCTG 1320
      ACGGGCAAGT CCTGCGGCGA GCGGCGAGAG CGTGGCTTCG GGAGCGCCAC CAGGACAGGC 1380
      CAGGACCGGC CACGTAGAGT GGTGGTTTTG CTCACTGAGT CACACTCCGA GGATGAGGTT 1440
      GCGGGCCCGC CGCGTCACGC AAGGGCGCGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG 1500
      GCCGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
      GATCCTCAGG ATCTGTTCAA CCAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG 1620
      CGGCCAGGGT GCCGACACA AGCCCTGGAC CTCGTCTTCA TGTGGACAC CTCTGCCTCA 1680
      GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
      GAGGTGAACC CTGACGTGAC ACAGGTCGGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT 1800
      GCCTTCGGGC TGGACACCAA ACCCACCAGG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
      CCCTACCTAG GTGGGGTGGG CTCAGCCGGC ACCGCCCTGC TGCACATCTA TGACAAAGTG 1920
      ATGACCGTCC AGAGGGGTGC CCGGCCTGGT GTCCCCAAG CTGTGGTGGT GCTCACAGGC 1980
      GGGAGAGGCG CAGAGGATGC AGCCGTTTCT GCCCAGAAGC TGAGGAACAA TGGCATCTCT 2040
      GTCTTGGTCG TGGGCGTGGG GCCTGTCTTA AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC 2100
      CGGGATTCCC TGATCCACGT GGCAGCTTAC GCCGACCTGC GGTACCACCA GGAGCTGCTC 2160
      ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCAGTCAACC TCTGCAAAAC CAGCCCGTGC 2220
      ATGAATGAGG GCAGCTGCGT CCTGCAGAAAT GGGAGCTACC GCTGCAAGTG TCGGGATGGC 2280
      TGGAGGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
      GGATGGATTG TTGAGACGCC CCTGAGGCAC ATGGCTCCCG TGCAGGAGGG CAGCAGCCGT 2400
      ACCCTCCCA GCAACTACAG AAGAGGCCTG GGCAGTGAAG TGGTGCTTAC CTTCTGGAAT 2460
      GTCTGTGCCC CAGGTCCCTTA G

```

Seq ID NO: 120 Protein sequence  
Protein Accession #: XP\_061091.1

```

1      11      21      31      41      51
80     |      |      |      |      |      |
      MPNTSGTTRI EIWLLQEPPE HRALVAALLP VSPSPALALA PGYPPVPAAD DRFTLPMIGG 60
      QMHGEKVDLW SLGVLQYEFL V GKPPFEANE VHVSKETIGK ISAASKMMWC SAAVDIMFL 120

```

DGSNSVKGKS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQQEVKA 180  
 RIKRMVFKGG RTETELALKY LLHRLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240  
 GVTVFAVGRV FPRWELHAL ASEPRGQHV LAEQVEDATN GLFSTLSSSA ICSSATPAGS 300  
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR 360  
 5 VDLLFLDSS AGTTLDGFLR AKVFKRFRV AVLSEDSRAR VGVATYSREL LVAVPVGEYQ 420  
 DVPDLVWSLD GIPFRGGPTL TGSALRQAAE RGFGSATRTG QDRPRRVVVL LTESHSEDEV 480  
 AGPARHARAR ELLLLGVGSE AVRAELEET GSPKHMVYS DPQDLFNQIP ELQGLKCSRQ 540  
 RPGCRTQALD LVFMLDTSAS VGPENFAQMQ SFVRSALQF EVNPDVTQVQ LVVYGSQVQT 600  
 10 AFGLDTKPTR AAMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660  
 GRGAEDAAVP AQKLRNNGIS VLVVGVPVL SEGLRRLAGP RDSLIHVAAY ADLRYHQDV 720  
 IEWLCEGEAKQ PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVQS 780  
 GWILETPLRH MAPVQEGSSR TTPSNYREGL GTEMVPTFWN VCAPGP

Seq ID NO: 121 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2424

1 11 21 31 41 51  
 | | | | | |  
 20 ATGCCCCCTT TCCTGTGTCT GGAGGCCGTC TGTGTTTCC TGTTTTCCAG AGTGCCCCCA 60  
 TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120  
 AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTAGTA TGGGTCTAAC 180  
 AGCGTCGGGA AAGGGAGCTT TGAAGAGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT 240  
 25 CTGGACATCA GCCCCGAGAG GGTGAGAGTG GGAGCATTC AGTTCAGTTC CACTCCTCAT 300  
 CTGGAATTCC CCTTGGATTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360  
 ATGGTTTTCA AAGGAGGCGC CACGGAGACG GAACCTTGCTC TGAATATACC TCTGCACAGA 420  
 GGGTTGCTGT GAGGCGAGAA TGCTTCTGTG CCCAGATGCC TCATCATCGT CACTGATGGG 480  
 AAGTCCAGG GGGATGTGAA ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG 540  
 30 TTTGCTGTGG GGGTCAGGTT TCCGAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600  
 AGAGGGCAGC ACCTGTCTGT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660  
 ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720  
 CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGGAGTTCG CTGGCAATGC CCCATGCTGG 780  
 AGAGGATCGC GGGCGACCTT TCGCGTGCTG GCTGCACACT GTCCTTTCTA CAGCTGGAAG 840  
 35 AGAGTGTTC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCCTGTGAC 900  
 TCGCAGCCCT GCCAGATGG AGGCACATGT GTTCCAGAA GACTGGACGG CTACCAGTGC 960  
 CTCTGCCCGC TGGCTTTTGG AGGGGAGGCT AACTGTGCC TGAAGCTGAG CCGTGAATGC 1020  
 AGGGTCGACC TCTCTTCTCT GCTGGACAGC TCTGCGGCA CCACTCTGGA CGGCTTCTCTG 1080  
 CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140  
 40 CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGTTGG CGTGCCCTGT GGGGGAGTAC 1200  
 CAGGATGTGC CTGACCTGGT CTGGAGCCTC GATGGCATTC CCTTCCGTGG TGGCCCCACC 1260  
 CTGACGGGCA GTGCCTTGC GACGCGGCA GAGCGTGCT TCGGGAGCGC CACCAGACA 1320  
 GGCCAGGACC GGCCACGTAG AGTGTGTTG TTGCTCACTG AGTCACACTC CGAGGATGAG 1380  
 GTTGCGGGCC CAGCGCGTCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440  
 GAGGCGGTGC GGGCAGAGGA GGAGGAGATC ACAGGAGACC CAAAGCATGT GATGCTCTAC 1500  
 45 TCGGATCCTC AGGATCTGTT CAACCAATC CCTGAGCTGC AGGGGAAGCT GTGCAAGCCG 1560  
 CAGCGGCCAG GGTGCCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620  
 TCAGTAGGCG CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680  
 TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGACG 1740  
 ACTGCTTTCG GGCTGGACAC CAAACCCACC CGGGCTGCCA TGCTGCGGGC CATTAGCCAG 1800  
 50 GCCCCTACCC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860  
 GTGATGACCG TCCAGAGGGG TGCCCGGCCCT GGTGTCCCA AAGCTGTGGT GGTGCTCACA 1920  
 GCGCGGAGAG GCGCAGAGGA TGCAGCGTCT CTGCCCCAGA AGCTGAGGAA CAATGGCATT 1980  
 TCTGTCTTGG TCGTGGGCGT GGGGCTGTCT CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040  
 CCCCAGGATT CCCTGATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG 2100  
 55 CTATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160  
 TGCAATGAAT AGGGCAGCTG CTTCTGTCAG AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220  
 GGCTGGGAGG GCCCCACTG CGAGAACCGT GAGTGGAGCT CTGTCTCTGT ATGTGTGAGC 2280  
 CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC 2340  
 60 CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG 2400  
 AATGTCTGTG CCCAGGTCC TTAG

Seq ID NO: 122 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | | |  
 65 MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60  
 SVKGGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120  
 70 MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180  
 FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240  
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPPYSWK RVFLTHPATC YRTTGPCGPD 300  
 SQPCQNGGTC VPBGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360  
 RAKVFKRFV RVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVFDLWVSL DGIPFRGGPT 420  
 75 LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS 480  
 EAVRAELEEI TGSFKHVMVY SDPQDLFNQI PELQGLKCSR QRPGCRTQAL DLVFMMLDTS 540  
 SVGPENFAQM QSFVRSALQ FEVNPDTQV GLVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 APYLGGVGS A TALLHIYDK VMTVQRGARP GVPKAVVVL GGRGAEDAAV PAQKLRNNGI 660  
 SVLVVGVPV LSEGLRRLAG PRDSLIHVA YADLRYHQDV LIEWLCEGEAK QPVNLCKPSP 720  
 80 CMNEGSCVLQ NGSYRCKCRD WEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780  
 RTPPSNYREG LGTEMVPTFW NVCAFGP

Seq ID NO: 123 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 89..2356

	1	11	21	31	41	51	
5	GCCCCCTGGC	CCGAGCCGCG	CCCGGGTCTG	TGAGTAGAGC	CGCCCCGGCA	CCGAGCGCTG	60
	GTGCGCGCTC	TCCCTCCGTT	ATATCAACAT	GCCCCCTTTC	CTGTTGCTGG	AAGCCGCTCTG	120
	TGTTTTCCCTG	TTTTCAGAG	TGCCCCCATC	TCTCCCTCTC	CAGGAAGTCC	ATGTAAGCAA	180
	AGAAACCATC	GGGAAGATTT	CAGCTGCCAG	CAAAATGATG	TGGTGCTCGG	CTGCAGTGGA	240
	CATCATGTTT	CTGTTAGATG	GGTCTAACAG	CGTCGGGAAA	GGGAGCTTTG	AAAGGTCCAA	300
10	GCACTTTGCC	ATCACAGTCT	GTGACGGTCT	GGACATCAGC	CCCGAGAGGG	TCAGAGTGGG	360
	AGCATTTCCAG	TTCAAGTTCCA	CTCCTCATCT	GGAATTCCTC	TTGGATTTCAT	TTTCAACCCA	420
	ACAGGAAGTG	AAGGCAAGAA	TCAAGAGGAT	GGTTTTTCAA	GAGGGGCGCA	CGGAGACGGA	480
	ACTTGCTCTG	AAATACCTTC	TGCACAGAGG	GTTCCTGGA	GGCAGAAATG	CTTCTGTGCC	540
	CCAGATCCCT	ATCATCGTCA	CTGATGGGAA	GTCCAGGGG	GATGTGGCAC	TGCCATCCAA	600
15	GCAGCTGAAG	GAAAGGGGTG	TCACTGTGTT	TGCTGTGGGG	GTCAAGTTTC	CCAGGTGGGA	660
	GGAGCTGCAT	GCACTGGCCA	GCGAGCCTAG	AGGGCAGCAC	GTGCTGTTGG	CTGAGCAGGT	720
	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TCGGCCATCT	GCTCCAGCGC	780
	CACGCCAGAG	TGCAGGGTCG	AGGCTCACCC	CTGTGAGCAC	AGGACGCTGG	AGATGGTCCG	840
	GGAGTTTCGCT	GGCAATGGCC	CATGCTGGAG	AGGATCGCGG	CGGACCTTGG	CGGTGCTGGC	900
20	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCTTG	CCACCTGCTA	960
	CAGGACCACC	TGCCCAGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAATGGAG	GCACATGTGT	1020
	TCCAGAAGGA	CTGGACGGCT	ACCAATGCCT	CTGCCGCTG	GCCTTTGGAG	GGGAGGCTAA	1080
	CTGTGCCCTC	AAGCTGAGCC	TGGAATGCAG	GGTCGACCTC	CTCTTCTGCT	TGGACAGCTC	1140
	TGCGGGCACC	ACTCTGGACG	GCTTCTGCG	GGCCAAAGTC	TTGCTGAAGC	GGTTTGTGCG	1200
25	GGCCGTGCTG	AGCGAGGACT	CTCGGGCCCG	AGTGGGTGTG	GCCACATACA	GCAGGGAGCT	1260
	GCTGGTGGCG	GTGCCGTGTT	GGGAGTACCA	GGATGTGCCT	GACCTGGTCT	GGAGCCTCGA	1320
	TGGCATTTCCC	TTCCGTGGTG	GCCCCACCTT	GACGGGCAGT	GCCTTGCGGC	AGGCGGCAGA	1380
	GCCTGGCTTC	GGGAGCGCCA	CCAGGACAGG	CCAGGACCGG	CCACGTAGAG	TGGTGGTTTT	1440
	GCTCACTGAG	TCACACTCCG	AGGATGAGGT	TGCGGGCCCA	GCGGCTCACG	CAAGGGCGCG	1500
30	AGAGCTGCTC	TGCTGGGTG	TAGGCAGTGA	GGCCGTGCGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGCAGCCCA	AAGCATGTGA	TGGTCTACTC	GGATCCTCAG	GATCTGTTCA	ACCAAATCCC	1620
	TGAGCTGCAG	GGGAAGCTGT	GCAGCCGGCA	GCGGCCAGGG	TGCCGGACAC	AAGCCCTGGA	1680
	CCTCGTCTTC	ATGTTGGAACA	CCTCTGCCTC	AGTAGGGCCC	GAGAAATTTG	CTCAGATGCA	1740
	GAGCTTTGTG	AGAAGCTGTG	CCCTCCAGTT	TGAGGTGAAC	CCTGACGTGA	CACAGGTCCG	1800
35	CCTGGTGGTG	TATGGCAGCC	AGGTGCAGAC	TGCCTTCGGG	CTGGACACCA	AACCCACCCG	1860
	GGCTGCGATG	CTGCGGGCCA	TTAGCCAGGC	CCCCTACCTA	GGTGGGGTGG	GCTCAGCCGG	1920
	CACCGCCCTG	CTGCACATCT	ATGACAAAGT	GATGACCGTC	CAGAGGGGTG	CCCGCCCTGG	1980
	TGTCCCCAAA	GCTGTGGTGG	TGCTCACAGG	CGGGAGAGGC	GCAGAGGATG	CAGCCGTTCC	2040
	TGCCCAGAAG	CTGAGGAACA	ATGGCATCTC	TGCTTGGTTC	TGCGGCGTGG	GGCCTGTCTC	2100
40	AAGTGAGGGT	CTGCGAGGCG	TTGCAGGTCC	CCGGGATTCC	CTGATCCACG	TGGCAGCTTA	2160
	CGCCGACCTG	CGGTACCAACC	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAGCA	2220
	GCCAGTCAAC	CTCTGCAAAC	CCAGCCCGTG	CATGAATGAG	GGCAGCTGCG	TCCTGCAGAA	2280
	TGGAGGCTAC	CGCTGCAAGT	GTCCGGATGG	CTGGGAGGGC	CCCCACTGCG	AGAACCAGATT	2340
	CTTGAGACGC	CCCTGAGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCCG	TACCCCTCCC	2400
45	AGCAACTACA	GAGAAGGCCT	GGGCACTGAA	ATGGTGCCCTA	CCTTCTGGAA	TGCTGTGCC	2460
	CCAGGTCTCT	AGAATGTCTG	CTTCCCGCCG	TGGCCAGGAC	CACATATCTC	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTCAACCCAC	2580
	AAACGATGTT	GTTGAAAAGT	TTTGATGTGT	AAGTAAATAC	CCACTTTCTG	TACCTGCTGT	2640
	GCCTTGTGTA	GGCTATGTCA	TCTGCCACCT	TTCCCTTGAG	GATAACAACG	GGGTCTTGAA	2700
50	GACTTAAATT	TAGCGGCCCTG	ACGTTCTCTT	GCACACAATC	AATGCTCGCC	AGAATGTTGT	2760
	TGACACAGTA	ATGCCACAGA	GAGGCCTTTA	CTAGAGCATC	CTTTGGACGG		

Seq ID NO: 124 Protein sequence  
Protein Accession #: Eos sequence

55	1	11	21	31	41	51	
	MPPFLLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVGKSGFERS	KHFAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPLDSFST	QQEVKARIKR	120
60	MVFKGGRRET	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
	FAVGVRFPFW	EELHALASEP	RQHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCFPGPD	300
	SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLLLS	SAGTTLDGFL	360
	RAKVVFVKRF	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPDLVWSL	DGIPFRGGPT	420
65	LTGSALRQAA	ERGFSGSATRT	GQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLVGVS	480
	EAVRAELEBI	TGSPKHVMVY	SDPQDLFNQI	PELQGLCSR	QRFPGCRTQAL	DLVFMLDTSA	540
	SVGPENFAQM	QSFVRSALCQ	FEVNPDTVQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
	APYLGGVGSA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVL	GGRGAEAAV	PAQKLNRNGI	660
	SVLVVGVGPF	LSEGLRRLAG	PRDSLHVAA	YADLRYHQDV	LIEWLCGEAK	QPVNLCKPSP	720
70	CMNEGSCVLQ	NGSYRCKCRD	GWEGPHCENR	FLRRP			

Seq ID NO: 125 DNA sequence  
Nucleic Acid Accession #: NM\_031942.1  
Coding sequence: 145..1260

75	1	11	21	31	41	51	
	CCCGAGCCCC	GCCCCCTCCG	GCCCCGGTCTG	GCGCGCCAG	CCTGCCAGCC	GCGCTGCTGC	60
	TGCTCTCTCT	GCTGTGGGAG	CGCTGACCGC	GCGGCTGCTC	CGCTCTCCCC	GCTCCAAGCG	120
80	CCGATCTGGG	CACCCGCCAC	CAGCATGGAC	GCTCGCCGCG	TGCCCGAGAA	AGATCTCAGA	180
	GTAAGAAGAA	ACTTAAAGAA	ATTGAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCTCTGTGAT	CAGTGTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAACAC	GAGGCTGCAG	300
	TCAGTTCCGG	AAGGCTGTAG	GACCCGCAGC	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360
	GCGATGAAGT	TTCCAGCGCG	GAGTACCAGG	GGAGCAACCA	ACAAAAAAGC	AGAGTCCCCG	420
	CAGCCCTCAG	AGAATTCTGT	GACTGATTCC	AATCCGATT	CAGAAGATGA	AAGTGAATG	480

5	AATTTTTTGG	AGAAAAGGGC	TTTAAATATA	AAGCAAAACA	AAGCAATGCT	TGCAAACTC	540
	ATGTCGAAT	TAGAAAGCTT	CCCTGGCTCG	TTCCGTGGAA	GACATCCCTT	CCCAGGCTCC	600
	GACTCACAA	CAAGGAGACC	GCGAAGGCGT	ACATTCCTCG	GTGTTGCTTC	CAGGAGAAAC	660
	CCTGAACGGA	GAGCTCGTCC	TCTTACCAGG	TCAAGGTCCC	GGATCCTCGG	GTCCTTGGAC	720
	GCTCTACCCA	TGGAGGAGGA	GGAGGAAGAG	GATAAGTACA	TGTTGGTGAG	AAAGAGGAAG	780
	ACCGTGGATG	GCTACATGAA	TGAAGATGAC	CTGCCCAGAA	GCCGTGCTC	CAGATCATCC	840
	GTGACCCTTC	CGCATATAAT	TCGCCCAGTG	GAAGAAATTA	CAGAGGAGGA	GTTGGAGAAC	900
	GTCTGCAGCA	ATTCTCGAGA	GAAGATATAT	AACCGTTCAC	TGGGCTCTAC	TTGTCACTAA	960
10	TGCCGTGAGA	AGACTATTGA	TACCAAAACA	AACCTGCAGAA	ACCCAGACTG	CTGGGGCGTT	1020
	CGAGGCCAGT	TCTGTGGCCC	CTGCCTTCGA	AACCGTTATG	GTGAAGAGGT	CAGGGATGCT	1080
	CTGCTGGATC	CGAACTGGCA	TTGCCCGCCT	TGTCGAGGAA	TCTGCAACTG	CAGTTTCTGC	1140
	CGGCAGCGAG	ATGGACGGTG	TGCGACTGGG	GTCTTGTGT	ATTTAGCCAA	ATATCATGGC	1200
	TTTGGGAATG	TGCATGCCTA	CTTGAAAAGC	CTGAAACAGG	AATTTGAAAT	GCAAGCATAA	1260
15	TATCTGGAAA	ATTGCTGCCC	TGCCTTCTAC	TTCTCAAATC	TTTCTTGTA	AAGTTTCCAA	1320
	TTTTTTCACT	GAAACCTGAG	TTAAAAATCT	TGATGATCAG	CCTGTTTCAT	AAGAACTCC	1380
	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGGTA	TATTGCTAGT	1440
	TACACTTTGC	CCCTCTTGCA	TTTCTTCTCT	GCTCCCAACC	CCCATCTCAT	AGCATCCCCC	1500
	TCTATTTTCCA	ATGCTCCTCT	CCAACCGCTT	AGTTTCTGAA	TTTCTTTTAA	ATTACAGTTT	1560
	TATGAAAAGCA	TATTTTATTT	ACTTGGTGTT	GAAATAGCCC	TCATAAAACC	TAAGCACTTG	1620
20	GAAACACAAT	AATAGTATTA	ACTAACTAGA	TCTATTGAAT	TTCAGAGAAG	AGCCTTCTAA	1680
	CTTGTTTACA	CAAAAACGAG	TATGATTAG	CACCTACTAT	AGTTGAAATT	TTTAATAGAA	1740
	TCAGGGCACA	AAAGTCTTAA	AACCATGTGG	AAAAATTAGG	TAATTATTGC	AGATTGATGT	1800
	CTCTCAATCC	CATGTATTGC	GCTTATGTTA	CAAGTTGTTG	TCACAGTTGA	GACTTAATTT	1860
25	CTCCTAATTT	CTTCTGCCCC	AAGGGTAAAGT	GGTGCCTCCA	GCTTACACGA	TCATAATTCA	1920
	AAGGTTGGTG	GGCAATGTAA	TACTTAATTA	AAATAATGAT	GGAAGAGCTA	TCTGGAGATT	1980
	ATGAGTAAGC	TGATTTGAAT	TTTCAGTATA	AACTTTAGT	ATAATTGTAG	TTTGCAAAGT	2040
	TTATTTCACT	TCACATGTAA	GGTATTGCAA	ATAAATCTT	GGACAATTTT	GTATGGAAAC	2100
	TTGATATTAA	AACTAGTCT	TGTTTCTTTT	GCAGTTTCTT	GTAATTTTAT	AAACCAAGCA	2160
30	CAAGGTTCAA	GTTTAGATTT	TAAGCACTTT	TATAACAATG	ATAAGTGCTT	TTTTGGAGAT	2220
	GTAACCTTTA	GCACTTTGTT	AACCTGACAT	CTCTGCCAGT	CTAGTTTCTG	GGCAGGTTTC	2280
	CTGTGTGAGT	ATTCCTCCCTC	CTCTTTGCAT	TAATCAAGGT	ATTGTTGAGA	GGTGGAAATCT	2340
	AAGTGTGTTG	ATGTCCAATT	TACTTGCATA	TGTAAACCAT	TGCTGTGCCA	TTCAATGTTT	2400
	GATGCATAAT	TGGACCTTGA	ATCGATAAGT	GTAATAACAG	CTTTGATCT	GTAATGCTTT	2460
35	TATACAAAAG	TTTATTTTAA	TAATAAAATG	TTTGTCTTAA	AAAAAATAAA		

Seq ID NO: 126 Protein sequence  
Protein Accession #: NP\_114148.1

40	1	11	21	31	41	51	
	MDARRVPQKD	LRVKNLKKF	RYVKLISMET	SSSSDDSCDS	FASDNFANTR	LQSVREGCRT	60
	RSQCRHSGPL	RVAMKFPARS	TRGATNKKA	SRQPSSENSVT	DSNSDSEDES	GMNFLEKRAL	120
	NIKQNKAMLA	KLMSELESFP	GSFRGRHPLP	GSDSQSRRPR	RRTFPGVASR	RNPERRARPL	180
45	TRSRSRILGS	LDALPMEEEE	EEDKYMLVRK	RKTVDGYMNE	DDLPRSRRSR	SSVTLPHIIR	240
	PVEITEEEL	ENVCSNSREK	IYNRSLGSTC	HQCRQKTIDT	KTNCRNPDCW	GVRGQFCGPC	300
	LRNRYGEEVR	DALLDPNWHC	PPCRGICNCS	FCRQRDGRCA	TGVLVYLAKY	HGFNVHAYL	360
	KSLKQEFEMQ	A					

Seq ID NO: 127 DNA sequence  
Nucleic Acid Accession #: AF305616.1  
Coding sequence: 1..863

55	1	11	21	31	41	51	
	ATGCACCGCT	TGATGGGGGT	CAACAGCACC	GCCGCCGCGG	CCGCCGGGCA	GCCCAATGTC	60
	TCCTGCACGT	GCAACTGCAA	ACGCTCTTTG	TTCCAGAGCA	TGGAGATCAC	GGAGCTGGAG	120
	TTTGTTCAGA	TCATCATCAT	CGTGGTGTTG	ATGATGGTGA	TGGTGGTGGT	GATCACGTGC	180
	CTGCTGAGCC	ACTACAGCT	GCTGTCACGG	TCCTTCATCA	GCCGGCACAG	CCAGGGGCGG	240
60	AGGAGAGAAG	ATGCCCTGTC	CTCAGAAGGA	TGCTGTGGC	CCTCGGAGAG	CACAGTGTCA	300
	GGCAACGGA	TCCCAGAGCC	GCAGGTCTAC	GCCCCGCCCT	GGCCACCGA	CCGCTGGCC	360
	GTGCCGCCCT	TCGCCAGCG	GGAGCGCTTC	CACCGCTTCC	AGCCCACTA	TCCGTACCTG	420
	CAGCACGAGA	TCGACCTGCC	ACCCACCATC	TCGCTGTGAG	ACGGGGAGGA	GCCCCACCC	480
	TACCAGGGCC	CCTGCACCTT	CCAGCTTCGG	GACCCGAGC	AGCAGCTGGA	ACTGAACCGG	540
	GAGTCGGTGC	GCGCACCCCC	AAACAGAACC	ATCTTCGACA	GTGACCTGAT	GGATAGTGCC	600
65	AGGCTGGGCG	GCCCTGCCCC	CCCCAGCAGT	AACTCGGGCA	TCAGCGCCAC	GTGCTACGGC	660
	AGCGGCGGGC	GCATGGAGGG	GCCGCCGCC	ACCTACAGCG	AGGTCATCGG	CCACTACCGG	720
	GGGTCTCTCT	TCCAGCACCA	GCAGAGCAGT	GGGCCGCCCT	CCTTGCTGGA	GGGGACCCGG	780
	CTCCACCACA	CACACATCGC	GCCCTTAGAG	AGCGCAGCCA	TCTGGAGCAA	AGAGAAGGAT	840
70	AAACAGAAAG	GACACCCTCT	CTAG				

Seq ID NO: 128 Protein sequence  
Protein Accession #: AAL09357.1

75	1	11	21	31	41	51	
	MHRLMGVNST	AAAAAGQPNV	SCTCNCKRSL	FQSMETETE	FVQIIIVVV	MMVMVVVITC	60
	LLSHYKLSAR	SFISRSQGR	RREDALSSEG	CLWPSESTVS	NGIPEPQVY	APPRPTDRLA	120
	VPPFAQRERF	HRFPQTPYPL	QHEIDLPTTI	SLSDGEEPPP	YQGPTLQLR	DPEQQLNLNR	180
80	ESVRAPPNRT	IFDSDLMDSA	RLGGPCPPSS	NSGISATCYG	SGGRMEGPPP	TYSEVIGHYP	240
	GSSFQHQSS	GPSSLLEGTR	LHHTHIAPLE	SAAIWSKEKD	KQKGHPL		

Seq ID NO: 129 DNA sequence  
Nucleic Acid Accession #: NM\_004952.1



Coding sequence: 1..718

5  
10  
15

1	11	21	31	41	51	
ATGGCGGCGG	CTCCGCTGCT	GCTGCTGCTG	CTGCTCGTGC	CCGTGCCGCT	GCTGCCGCTG	60
CTGGCCCAAG	GGCCCGGAGG	GGCGCTGGGA	AACCGGCATG	CGGTGTACTG	GAACAGCTCC	120
AACCAGCACC	TGCGGCGAGA	GGGCTACACC	GTGCAGGTGA	ACGTGAACGA	CTATCTGGAT	180
ATTACTGCC	CGCACTACAA	CAGCTCGGGG	GTGGGCCCCG	GGGCGGGACC	GGGGCCCGGA	240
GGCGGGGCG	AGCAGTACGT	GCTGTACATG	GTGAGCCGCA	ACGGCTACCG	CACCTGCAAC	300
GCCAGCCAGG	GCTTCAAGCG	CTGGGAGTGC	AACCGGCCGC	ACGCCCCGCA	CAGCCCCATC	360
AAGTTCTCGG	AGAAGTTCCA	GCGCTACAGC	GCCTTCTCTC	TGGGCTACGA	GTTCACAGCC	420
GGCCACGAGT	CTCCACGCCC	ACTCACAACC	TGCACTGGAA	GTGTCTGAGG		480
ATGAAGGTGT	TGCTCTGCTG	CGCTCCACCA	TGCACTCCG	GGGAGAAGCC	GGTCCCCACT	540
CTCCCCCAGT	TCACCATGGG	CCCCAATGTG	AAGATCAACG	TGCTGGAAGA	CTTTGAGGGA	600
GAGAACCCTC	AGGTGCCCAA	GCTTGAGAAG	AGCATCAGCG	GGACCAGCCC	CAAACGGGAA	660
CACCTGCCCC	TGCGCGTGGG	CATCGCCTTC	TTCTCATGA	CGTCTTGGC	CTCCTAG	

Seq ID NO: 130 Protein sequence  
Protein Accession #: NP\_004943.1

20  
25

1	11	21	31	41	51	
MAAAPLLLLL	LLVPVPLPL	LAQSPGGALG	NRHAVYWNSS	NQHLRREGYT	VQVNVNDYLD	60
IYCPHYNSSG	VGPAGGPGPG	GGAEQVLYM	VSRNGYRTCN	ASQGFKRWEC	NRPHAPHSPI	120
KFSEKFORYS	AFSLGYEFHA	GHEYIYSTP	THNLHWKCLR	MKVFFVCCAST	SHSKEKPVPT	180
LPQFTMGPNV	KINVLDFEFG	ENPQVPKLEK	SISGTSFKRE	HLPLAVGIAF	FLMTFLAS	

Seq ID NO: 131 DNA sequence  
Nucleic Acid Accession #: NM\_012445.1  
Coding sequence: 276..1271

30  
35  
40  
45  
50  
55  
60  
65

1	11	21	31	41	51	
GCACGAGGGA	AGAGGGTGAT	CCGACCCGGG	GAAGGTCGCT	GGGCAGGGCG	AGTTGGGAAA	60
CGGCGAGCCC	CGCCCGCCCC	CGCAGCCCTT	TCTCCTCCTT	TCTCCACAGT	CCTATCTGCC	120
TCTCGCTGGA	GGCCAGGCCG	TGCAGCATCG	AAGACAGGAG	GAACCTGGAG	CTCATTGGCC	180
GGCCCCGGGC	GCCCGGCTCG	GGCTTAAATA	GGAGCTCCCG	GCTCTGGCTG	GGACCCGACC	240
GCTGCCGGCC	GGCTCTCCCG	TGCTCTGCTG	GGGTGATGGA	AAACCCGAGC	CCGGCCGCGC	300
CCCTGGGCAA	GGCCCTCTGC	GCTCTCTCTC	TGGCCACTCT	CGGCGCCGCC	GGCCAGCCTC	360
TTGGGGGAGA	GTCCATCTGT	TCCGCCAGAG	CCCCGGCCAA	ATACAGCATC	ACCTTCACGG	420
GCAAGTGGAG	CCAGAGCGGC	TTCCCAAGC	AGTACCCCTT	GTTCGCCCCC	CCTGCGCAGT	480
GGTCTTCGCT	GCTGGGGGCC	CGGCATAGCT	CCGACTACAG	CATGTGGAGG	AAGAACCAGT	540
ACGTCAATAA	CGGGCTGCGC	GACTTTGCGG	AGCGCGGCGA	GGCCTGGGCG	CTGATGAAGG	600
AGATCGAGGC	GGCGGGGGAG	GCGCTGCAGA	GCGTGACCGC	GGTGTTCG	GGCGCCGCGC	660
TCCCCAGCGG	CACCGGGCAG	ACGTGGCGCG	AGCTGGAGGT	GCAGCGCAGG	CACTCGCTGG	720
TCTCGTTTGT	GGTGCGCATC	GTGCCAGGCC	CCGACTGGTT	CGTGGGCGTG	GACAGCCTGG	780
ACCTGTGCGA	CGGGGACCGT	TGGCGGGAAC	AGCGCGCGCT	GGACCTGTAC	CCCTACGACG	840
CCGGGACGGA	CAGCGGCTTC	ACCTTCTCCT	CCCCCAACTT	CGCCACCATC	CCGCAGGACA	900
CGGTGACCGA	GATAAGCTTC	TCCTCTCCCA	GCCACCCGGC	CAACTCCTTC	TACTACCCGC	960
GGCTGAAGGC	CCTGCCTCCC	ATCGCCAGGG	TGACACTGGT	GCGGCTGCGA	CAGAGCCCCA	1020
GGGCTTTCAT	CCCTCCCGCC	CCAGTCTCTG	CCAGCAGGGA	CAATGAGATT	GTAGACAGCG	1080
CCTCAGTTCC	AGAAACGCCG	CTGGACTGCG	AGGTCTCCCT	GTGGTCTGTC	TGGGGACTGT	1140
GCGGAGGCCA	CTGTGGGAGG	CTCGGGACCA	AGAGCAGGAC	TGCTACGTC	CGGGTCCAGC	1200
CCGCCAACA	CGGGAGCCCC	TGCCCGAGC	TGGAAGAAGA	GGCTGAGTGC	GTCCCTGATA	1260
ACTGCGTCTA	AGACCGAGAG	CCCGCAGCCC	CTGGGGCCCC	CGGAGCCATG	GGGTGTGCGG	1320
GGCTCCTGTG	CAGGCTCATG	CTGCAGGCGG	CCGAGGCACA	GGGGGTTTCG	CGCTGCTCCT	1380
GACCGCGGTG	AGGCCGCGCC	GACCATCTCT	GCACTGAAGG	GCCCTCTGGT	GGCCGCGCAG	1440
GGCATTGGGA	AACAGCTCTC	TCCTTTCCCA	ACCTTGCTTC	TTAGGGGCCC	CCGTGTCCCG	1500
TCTGCTCTCA	CCTCTCTCCT	CCTGCAGGAT	AAAGTCATCC	CCAAGGCTCC	AGCTACTCTA	1560
AATTATGGTC	TCCTTATAAG	TTATTGCTGC	TCCAGGAGAT	TGCTCTTCAT	CGTCCAGGGG	1620
CCTGGCTCCC	ACGTGGTTGC	AGATACCTCA	GACCTGGTGC	TCTAGGCTGT	GCTGAGCCCC	1680
CTCTCCCGAG	GGCGCATCCA	AGCGGGGGCC	ACTTGAGAAG	TGAATAAATG	GGGCGGTTTC	1740
GGAAGCGTCA	GTGTTTCCAT	GTATATGATC	TCTCTGCGTT	TGAATAAAGA	CTATCTCTGT	1800
TGCTCAC						

Seq ID NO: 132 Protein sequence  
Protein Accession #: NP\_036577.1

70  
75

1	11	21	31	41	51	
MENPSPAAL	GKALCALLLA	TLGAAGQPLG	GESICSARAP	AKYSITFTGK	WSQTAFFPKQY	60
PLFRPPAQWS	SLLGAHSSD	YSMWRKNQYV	SNGLRDFAE	GEAWALMKEI	EAAGEALQSV	120
HAVFSAPAVP	SGTGQTSDEL	EVQRRHSLVS	FVVRIVPSPD	WFGVDSLDDL	CDGDRWREQA	180
ALDLYPYDAG	TDSGFTFSSP	NFATIPQDTV	TEITSSSPSH	PANSFYYPRL	KALPPIARVT	240
LVRRLQSPRA	FIPPAVPLPS	RNEIIVDSAS	VPETPLDCEV	SLWSSWGCLG	GHCGRGLTKS	300
RTRYVRVQPA	NNGSPCELE	EBAECVFDNC	V			

Seq ID NO: 133 DNA sequence  
Nucleic Acid Accession #: NM\_019894  
Coding sequence: 1..1314

80

1	11	21	31	41	51	
ATGTTACAGG	ATCCTGACAG	TGATCAACCT	CTGAACAGCC	TCGATGTCAA	ACCCCTGCGC	60

5 AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120  
 CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCTCATCA AGGTGATTCT GGATAAATAC 180  
 TACTTCCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240  
 CTGGACTGTC CTTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300  
 GCAGTGGCAG TCCGCCTCTC CAAGGACCGA TCCCACTGTC AGGTGCTGGA CTCGGCCACA 360  
 GGGAACCTGGT TCTCTGCCTG TTTCGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420  
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480  
 GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGATGCG GAACTCAAGT 540  
 10 GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG 600  
 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660  
 AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720  
 CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780  
 GGCTCAGACA AACTGGGCAG CTTCCTCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840  
 15 TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900  
 ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960  
 GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020  
 GACATACTGC TGCAGGCGTC AGTCCAGTTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080  
 GCGTACCAGG GGAAGTCCAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140  
 20 GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200  
 TTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260  
 AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

Seq ID NO: 134 Protein sequence

Protein Accession #: NP\_063947.1

25 1 11 21 31 41 51  
 MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPILIAL LSLASIIIV VLIKVILDKY 60  
 30 YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT 120  
 GNWFSACFDN FEALAEATK RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180  
 GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWFPQV SIQYDKQHV GGSILDPHV 240  
 LTAHCFRKH TDVFNKVKRA GSKLGSFSP LAVAKIIIE FNPMPKND IALMKLQFPL 300  
 TFSGTVRPIC LPFDEBELT ATPLWIIWG FTKQNGKMS DILLQASVQV IDSTRCNADD 360  
 35 AYQGEVTEKM MCAGIPEGGV DTCQDSGGP LMYQSDQWHV VGIVSWGYGC GGPSTPGVYT 420

Seq ID NO: 135 DNA sequence

Nucleic Acid Accession #: NM\_003045

Coding sequence: 148..2037

40 1 11 21 31 41 51  
 CGATCCTGCC GGAGCCCGCG CGCCGCCGCG TTGGATTCTG AAACCTTCCT TGTATCCCTC 60  
 45 CTGAGACATC TTGTGCTCAA GATCGAGGCT GTCCTCTGGT GAGAAGGTGG TGAGGCTTCC 120  
 CGTCATATTC CAGCTCTGAA CAGCAACATG GGGTGCAAAG TCCTGCTCAA CATTGGGCAG 180  
 CAGATGCTGC GCGGGAAGGT GGTGACTGT AGCCGGGAGG AGACGCGGCT GTCTCGCTGC 240  
 CTGAACACTT TTGATCTGGT GGCCCTCGGG GTGGGCAGCA CACTGGGTGC TGGTGTCTAC 300  
 GTCTTGCTG GAGCTGTGGC CCGTGAGAAT GCAGGCCCTG CCATTGTCTAT CTCTTCTCTG 360  
 50 ATCGCTGCGC TGGCCTCAGT GCTGGCTGGC CTGTGCTATG GCGAGTTTGG TGCTCGGGTC 420  
 CCCAAGACGG GCTCAGCTTA CCTCTACAGC TATGTCACCG TTGGAGAGCT CTGGGCCCTC 480  
 ATCACCAGCT GGAAGTAAAT CCTCTCTTAC ATCATCGGTA CTTCAAGCGT AGCGAGGGCC 540  
 TGGAGCGCCA CCTTCAGAGA GCTGATAGGC AGACCCATCG GGGAGTTCTC ACGGACACAC 600  
 ATGACTCTGA AGCCCCCGG CGTGTCTGGT GAAAACCCCG ACATATTCGC AGTGATCATA 660  
 55 ATTTCTCATC TGACAGGACT TTAACTCTT GGTGTGAAAG AGTCGGCCAT GGTCAACAAA 720  
 ATATTCACTT GTATTAACTT CCTGGTCTCT GGCCTCATAA TGGTGTGAGG ATTTGTGAAA 780  
 GGATCGGTTA AAAAAGTGGC GCTCACGGAG GAGGATTTTG GGAACACATC AGGCCGTCTC 840  
 TGTTTGAACA ATGACACAAA AGAAGGGAAG CCCGGTGTG GTGGATTCTAT GCCCTTCGGG 900  
 TTCTCTGGTG TCCTGTGCGG GGCAGCGACT TGCTTCTATG CCTTCGTGGG CTTTGACTGC 960  
 60 ATCGCCACCA CAGGTGAAGA GGTGAAGAAC CCACAGAAGG CCATCCCCGT GGGGATCGTG 1020  
 GCGTCCCTCT TGATCTGCTT CATCGCCTAC TTTGGGGTGT CGGCTGCCCC CACGCTCATG 1080  
 ATGCCCTACT TCTGCCTGGA CAATAACAGC CCCCTGCCCG ACGCCCTTAA GCACGTGGGC 1140  
 TGGGAAGGTG CCAAGTAGC AGTGGCCGTG GGCTCCCTCT GCGCTCTTTC GCACAGTCTT 1200  
 CTAGGTCCCA TGTTCCTCAT GCCTCGGGTT ATCTATGCCA TGGCTGAGGA TGGACTGCTA 1260  
 65 TTTAAATCTT TAGCAACAGT CAATGATAGG ACCAAAACAC CAATAATCGC CACATTAGCC 1320  
 TCGGGTCCCG TTGCTGCTGT GATGGCCTTC CTCTTTGACC TGAAGGACTT GGTGGACCTC 1380  
 ATGTCCATTG GCACTCTCTT GGCTTACTCG TTGGTGGCTG CCTGTGTGTT GGTCTTACGG 1440  
 TACCAGCCAG AGCAGCCTAA CCTGGTATAC CAGATGGCCA GTACTTCCGA CGAGTTAGAT 1500  
 CCAGCAGACC AAAATGAATT GGCAAGCACC AATGATTCCC AGCTGGGGTT TTTACCAGAG 1560  
 70 GCAGAGATGT TCTCTTTGAA AACCACTCTC TCACCCAAAA ACATGGAGCC TTCCAAAATC 1620  
 TCTGGGCTAA TTGTGAACAT TTCAACCAGC CTTATAGCTG TTCTCATCAT CACCTTCTGC 1680  
 ATTGTGACCG TGCTTGAAG GGAGGCTCTC ACCAAAGGGG CGCTGTGGGC AGTCTTTCTG 1740  
 CTCGACGGGT CTGCCCTCCT CTGTGCCGTG GTCACGGGCG TCATCTGGAG GCAGCCCGAG 1800  
 AGCAAGACCA AGCTCTCATT TAAGGTTCCC TTCTGTCCAG TGCTCCCCAT CCGTGGACATC 1860  
 75 TTCGTGAACG TCTATCTCAT GATGCAGCTG GACCAGGGCA CCTGGGTCCG GTTTGCTGTG 1920  
 TGGATGCTGA TAGGCTTATC CATCTACTTT GGCTATGGCC TGTGGCACAG CGAGGAGGCG 1980  
 TCCCTGGATG CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCAAGT CAAGTGACGC 2040  
 ACAGCCCGCG CCCCCGAGG TGGCAGCAGC CCCGAGGGAC GCCCCAGAG GACCGGGAGG 2100  
 CACCCACACC TCCCAACAGG TGCAACAGAA ACCACCTGCG TCCACACCCT CACTGCA

Seq ID NO: 136 Protein sequence

Protein Accession #: NM\_003045

80 1 11 21 31 41 51

MGCKVLLNIG QQMLRRKVV D CSREETRLSR CLNTFDLVAL GVGSTLGAGV YVLGAVARE 60  
 NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELWA FITGWNILS 120  
 YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPGVL AENPDIFAVI IILILTGLLT 180  
 LGVKESAMVN KIFTCINVLV LGFIMVSGFV KGSVKNWQLT EEDFGNTSGR LCLNNDTKEG 240  
 KPGVGGFMPF GFSGLVSGAA TCFYAFVGF D CIATTGEEVK NPQKAIPVGI VASLLICFIA 300  
 YFGVSAALTL MPMYFCLDNN SPLPDAFKHV GWEGAKYAVA VGSLLCALSAS LLGSMFPMMPR 360  
 VIYAMAEDGL LFKFLANVND RTKTPIIATL ASGAVAAMVA FLFDLKDLDV LMSIGTLLEY 420  
 SLVAACVLVL RYQPEQPNLV YQMASTDEL DPADQNELAS TNDSQLGFLP EAEMFSLKTI 480  
 LSPKNMEPSK ISGLIVNIST SLIAVLIITF CIVTVLGRE A LTKGALWAVF LLAGSALLCA 540  
 VVTGVIWRQP ESKTKLSFKV PFLFVLPILS IFVNVYLMQ LDQGTWVRFA VWMIGFIITY 600  
 FGYGLWHSEE ASLDADQART PDGNLDQCK

Seq ID NO: 137 DNA sequence

Nucleic Acid Accession #: NM\_032044.1

Coding sequence: 182..658

1 11 21 31 41 51  
 AAGATATAAA AGCTCCAGAA ACGTTGACTG GGACCACTGG AGACACTGAA GAAGGCAGGG 60  
 GCCCTTAGAG TCTTGGTTGC CAAACAGATT TGCAGATCAA GGAGAACCCA GGAGTTTCAA 120  
 AGAAGCGCTA GTAAGGTCTC TGAGATCCTT GCACTAGCTA CATCCTCAGG GTAGGAGGAA 180  
 GATGGCTTCC AGAAGCATGC GGCTGCTCCT ATTGCTGAGC TGCCTGGCCA AAACAGGAGT 240  
 CCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCCTGGA TGGTTTACC ACAAGTCCAA 300  
 TTGCTATGGT TACTTCAGAA AGCTGAGGAA CTGGTCTGAT GCCGAGCTCG AGTGTCTAGT 360  
 TTACGGAAAC GGAGCCCACT TGGCATCTAT CCTGAGTTTA AAGGAAGCCA GCACCATAGC 420  
 AGAGTACATA AGTGGCTATC AGAGAAGCCA GCCGATATGG ATTGGCCTGC ACGACCCACA 480  
 GAAGAGGCAG CAGTGGCAGT GGATTGATGG GGCCATGTAT CTGTACAGAT CCTGGTCTGG 540  
 CAAGTCCATG GGTGGGAACA AGCACTGTGC TGAGATGAGC TCCAATAACA ACTTTTAAAC 600  
 TTGGAGCAGC AACGAATGCA ACAAGCGCCA ACACTTCTCTG TGAAGTACC GACCATAGAG 660  
 CAAGAATCAA GATTCTGCTA ACTCCTGCAC AGCCCCGTCC TCTTCTCTTC TGCTAGCCTG 720  
 GCTAAATCTG CTCAATATTT CAGAGGGGAA ACCTAGCAAA CTAAGAGTGA TAAGGGCCCT 780  
 ACTACACTGG CTTTTTATAG CTTAGAGACA GAAACTTTAG CATTTGGCCA GTAGTGGCTT 840  
 CTAGCTTAA ATGTTTGGCC CGCCATCCCT TTCCACAGTA TCCTTCTTCC CTCCTCCCT 900  
 GTCTCTGGCT GTCTCGAGCA GTCTAGAAGA GTGCATCTCC AGCCTATGAA ACAGCTGGGT 960  
 CTTTGGCCAT AAGAAGTAAA GATTGAAGA CAGAAGGAAG AAACCTCAGG GTAAGCTTCT 1020  
 AGACCCCTTC AGCTTCTACA CCCTTCTGCC CTCTCTCCAT TGCCCTGCACC CCACCCAGC 1080  
 CACTCAACTC CTGCTTGTTC TTCCCTTGGC CATAGGAAGG TTACACAGTA GAATCCTTGC 1140  
 TAGGTTGATG TGGGCATAC ATTCTTTAA TAAACCATTG TGTACATAAG AAAAAAAAAA

Seq ID NO: 138 Protein sequence

Protein Accession #: NP\_114433.1

1 11 21 31 41 51  
 MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWFYHKS N CYGYFRKL RN WSDAELEQCS 60  
 YNGNAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLRSWSG 120  
 KSMGKNKHCA EMSSNNNFLT WSSNECNKRO HFLCKYRP

Seq ID NO: 139 DNA sequence

Nucleic Acid Accession #: XM\_051860.2

Coding sequence: 52..3042

1 11 21 31 41 51  
 GCTCACCCAG GAAAAATATG CAATCGTCCC ATTGATATAC AGGCCACTAC AATGGATGGA 60  
 GTTAACCTCA GCACCGAGGT TGTCTACAAA AAAGGCCAGG ATTATAGGTT TGCTTGCTAC 120  
 GACCGGGGCA GAGCCTGCGG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180  
 CCCAAACTCA CAGTACCATT TGACACCAAT GTGAACAGCA CCATTCTGAA CTGGAGGAT 240  
 AATGTACAGT CATGGAAACC TGGAGATACC CTGGTCATTG CCAGTACTGA TTAATCCATG 300  
 TACCAGGCAG AAGAGTTCCA GGTGCTTCCC TGCAGATCCT GCGCCCCCAA CCAGGTCAAA 360  
 GTGGCAGGGA AACCATATGA CTGACATC GGGGAGGAGA TAGACGCGT GGACATGCGG 420  
 GCGGAGGTTG GGCTTCTGAG CCGGAACATC ATAGTGATGG GGGAGATGGA GGACAAATGC 480  
 TACCCCTACA GAAACCACAT CTGCAATTTT TTTGACTTCG ATACCTTTGG GGGCCACATC 540  
 AAGTTTGCTC TGGGATTTAA GGCAGCACAC TTGGAGGGCA CGGAGCTGAA GCATATGGGA 600  
 CAGCAGCTGG TGGGTCAATA CCCGATTAC TCCACCTGG CCGTGATGT AGACGAAAGG 660  
 GGAGGTTATG ACCCAACCCAT ATACATCAGG GACCTCTCCA TCCATCATAC ATTCTCTCGC 720  
 TGCGTCACAG TCCATGGCTT CAATGGCTTG TTGATCAAGG ACGTTGTGGG CTATAACTCT 780  
 TTGGGCCACT GCTTCTTAC GGAAGATGGG CCGGAGGAAC GCAACACTTT TGACCACTGT 840  
 CTGGCCCTCC TTGTCAAGTC TGGAAACCTC CTCCTCTCGG ACCGTGACAG CAAGATGTGC 900  
 AAGATGATCA CAGGAGACTC CTACCCAGGG TACATCCCCA AGCCCAAGCA AGACTGCAAT 960  
 GCTGTGTCCA CCTTCTGGAT GGCCCAATCCC AACAACAACC TCATCAACTG TGCCCTGTGA 1020  
 GGATCTGAGG AAACCTGATT TTGTTTATT TTTCAACAG TACCAACGGG CCCCTCCGTG 1080  
 GGAATGTACT CCCCAGGTTA TTCAGAGCAC ATTCCACTGG GAAAATTCTA TAACAACCGA 1140  
 GCACATTCCA ACTACCGGGC TGGCATGATC ATAGACAACG GAGTCAAAAC CACCGAGGCC 1200  
 TCTGCCAAGG ACAAGCGGCC GTTCTCTCA ATCATCTCTG CCAGATACAG CCCTCACCAG 1260  
 GACGCCGACC CGCTGAAGCC CCGGAGGCGG GCCATCATCA GACACTTCAT TGCCCTACAAG 1320  
 AACCAGGACC ACGGGGCGCT GCTGCGCGGC GGGGATGTGT GGCTGGACAG CTGCCGGTTT 1380  
 GCTGACAAAG GCATTGGCCT GACCTTGGCC AGTGGTGGA CCTTCCCGTA TGACGACGGC 1440  
 TCCAAGCAAG AGATAAAGAA CAGCTTGTTC GTTGGCGAGA GTGGCAACGT GGGGACGGAA 1500  
 ATGATGGAGA ATAGGATCTG GGGCCTGGCC GGCTTGGACC ATAGCGGAAG GACCTCCCT 1560  
 ATAGGCCAGA ATTTTCCAAT TAGAGGAATT CAGTTATATG ATGGCCCCAT CAACATCCAA 1620  
 AACTGCACTT TCCGAAAGTT TGTGGCCCTG GAGGGCCGGC ACACCAAGCG CCTGGCCTTC 1680  
 CGCTGAATA TGCTCTGGCA GAGCTGCCCC CATAACAACG TGACCGGCAT TGCCTTTGAG 1740  
 GACGTTCCGA TTACTTCCAG AGTGTCTTTC GGAGAGCCTG GCGCTTGGTT CAACCACTG 1800

GACATGGATG GGGATAAGAC ATCTGTGTTT CATGACGTCG ACGGCTCCGT GTCCGAGTAC 1860  
 CCTGGCTCCT ACCTCACGAA GAATGACAAAC TGGCTGGTCC GGCACCCAGA CTGCATCAAT 1920  
 GTTCCCGACT GGAGAGGGGC CATTTGCACT GGGTGTCTAT CACAGATGTA CATTTCAAGCC 1980  
 TACAGACCA GTAACTTGGC AATGAAGATC ATCAAGAATG ACTTCCCCAG CCACCTCTT 2040  
 TACCTGGAGG GGGCGCTCAC CAGGAGCACC CATTACCAGC AATACCAACC GGTGTGCACC 2100  
 CTGCGAAGG GCTACACCAT CCACTGGGAC CAGACGGCCC CCGCCGAACT CGCCATCTGG 2160  
 CTATCAACT TCAACAAGGG CGACTGGATC CGAGTGGGGC TCTGCTACCC GCGAGGCACC 2220  
 ACATTCTCCA TCCTCTCGGA TGTTCACAA CTGCTGTGTA AGCAAAACGTC CAAGACGGGC 2280  
 GTCTTCGTGA GGACCTTGCA GATGGACAAA GTGGAGCAGA GCTACCCTGG CAGGAGCCAC 2340  
 TACTACTGGG ACGAGGACTC AGGGCTGTTG TTCTGAAGC TGAAGACTCA GAACGAGAGA 2400  
 GAGAAGTTTG CTTTCTGCTC CATGAAAGGC TGTGAGAGGA TAAAGATTAA AGCTCTGATT 2460  
 CCAAAGAACG CAGGCGTCAG TGAATGCACA GCCACAGCTT ACCCCAAGTT CACCGAGAGG 2520  
 GCTGTCTGTA ACGTGCCTGAT GCCCAAGAAG CTCTTTGGTT CTCAGCTGAA AACAAAGGAC 2580  
 CATTTCTTGG AGGTGAAGAT GGAGAGTTCC AAGCAGCACT TCTTCCACCT CTGGAACGAC 2640  
 TTCTCTTACA TTGAAGTTGA TGGGAAGAAG TACCCAGTT CGGAGGATGG CATCCAGGTG 2700  
 GTGGTGATTG ACGGGAACCA AGGGCGCGTG GTGAGCCACA CGAGCTTCAG GAACCTCCATT 2760  
 CTGCAAGGCA TACCATTGGCA GCTTTTCAAC TATGTGGCGA CCATCCCTGA CAATTCCATA 2820  
 GTGCTTATGG CATCAAGGGG AAGATACGTC TCCAGAGGCC CATGGACCAG AGTGGTGGAA 2880  
 AAGCTTGGGG CAGACAGGGG TCTCAAGTTG AAAGAGCAAA TGGCATTCTG TGGCTTCAAA 2940  
 GGCAGCTTCC GGGCCATCTG GGTGACACTG GACACTGAGG ATCACAAGC CAAATCTTTC 3000  
 CAAGTTGTGC CCATCCCTGT GGTGAAGAAG AAGAAGTTGT GAGGACAGCT GCCGCCCGGT 3060  
 GCCACCTCGT GGTAGACTAT GACGGTACT CTGTGGCAGCA GACCAAGTGG GGTGGTCTGG 3120  
 GTCCCCCAGC CCTTGGCAGC AGCTGCCTGG GAAGGCCGTG TTTCAAGCCT GATGGGCCAA 3180  
 GGGAGGGCTA TCAGAGACCC TGGTGTCTGCC ACCTGCCCTT ACTCAAGTGT CTACCTGGAG 3240  
 CCCCTGGGGC GGTGCTGGCC AATGCTGGAA ACATTCACTT TCCTGCAGCC TCTTGGGTGC 3300  
 TTCTCTCTTA TCTGTGCTTC TTCAAGTGGG GTTTGGGGAC CATATCAGGA GACCTGGTTC 3360  
 GTGCTGACAG CAAAGATCCA CTTTGGCAGG AGCCCTGACC CAGCTAGGAG GTAGTCTGGA 3420  
 GGGCTGGTCA TTCACAGATC CCCATGGTCT TCAGCAGACA AGTGAGGGTG GTAAATGTAG 3480  
 GAGAAAGAGC CTTGGCTTAA AGGAAATCTT TACTCCTGTA AGCAAGAGCC AACCTCACAG 3540  
 GATTAGGAGC TGGGGTAGAA CTGGCTATCC TTGGGGAAGA GGCAGGCCCT GCCTCTGGCC 3600  
 GTGTCCACCT TTCAAGGAGC TTTGAGTGGC AGGTTTGGAC TTGGACTAGA TGACTCTCAA 3660  
 AGGCCCTTTT AGTTCTGAGA TTCCAGAAAT CTGCTGCATT TCACATGGTA CCTGGAACCC 3720  
 AACAGTTCAT GGATATCCAT TGATATCCAT GATGCTGGGT GCCCCAGCGC ACACGGGATG 3780  
 GAGAGGTGAG AACTAATGCC TAGCTTGAGG GGTCTGCAGT CCAGTAGGGC AGGCAGTCAG 3840  
 GTCCATGTGC ACTGCAATGC CAGGTGGAGA AATCACAGAG AGGTAAAATG GAGGCCAGTG 3900  
 CCATTTCAGA GGGGAGGCTC AGGAAGGCTT CTGTCTTACA GGAATGAAGG CTGGGGGATG 3960  
 TTTGTGCGGG GGAGATGAGG CAGCCTCTGG AATGGCTCAG GGATTACGCC CTCCTGCGG 4020  
 CTGCTGCTG AAGCTGGTGA CTACGGGGTC GCCCTTTGCT CACGTCTCTC TGGCCCACTC 4080  
 ATGATGGAGA AGTGTGGTCA GAGGGGAGCA ATGGGCTTGT CTGCTTATGA GCACAGAGGA 4140  
 ATTCAGTCCC CAGGCAGCCC TGCCCTGTAC TCCAAGAGGG TGAAGTCCAC AGAAGTGAGC 4200  
 TCCTGCCTTA GGGCTCTATT TGCTCTTCTT CCAGGGAATC GAGCACAGGG GGCCTCCAGG 4260  
 AGACCCTAGA TGTGCTCGTA CTCCTCTGGC CTGGGATTTC AGAGCTGGAA ATATAGAAAA 4320  
 TATCTAGCCC AAAGCCTTCA TTTTAACAGA TGGGGAAAGT GAGCCCCCAA GATGGGAAAG 4380  
 AACCAACAG CTAAGGGAGG GCCTGGGGAG CCCCACCTTA GCCCTGTCTG CCACACCACA 4440  
 TTGCTCTAAC AACCAGCCCC AGAGTGCCCC GGCACCTCTG AGGTAGCTTC TGGAAATGGG 4500  
 GACAAGTCCC CTCGAAGGAA AGGAAATGAC TAGAGTAGAA TGACAGCTAG CAGATCTCTT 4560  
 CCTCCTGCT CCCAGCGCAC ACAAACCCGC CCTCCCCTTG GTGTTGGCGG TCCCTGTGGC 4620  
 CTTCACTTTC TTCACTACCT GTCAAGCCAG CCTGGGTGCA CAGTAGCTGC AACTCCCCAT 4680  
 TGGTGCTACC TGGCTCTCCT GTCTCTGCAG CTCTACAGGT GAGGCCAGC AGAGGGAGTA 4740  
 GGGCTCGCCA TGTTTCTGGT GAGCCAATTT GGCTGATCTT GGGTGTCTGA ACAGCTATTG 4800  
 GGTCCACCCC AGTCCCTTTC AGCTGCTGCT TAATGCCCTG CTCTCTCCCT GGCCCACTT 4860  
 ATAGAGAGCC CAAAGAGCTC CTGTAAGAGG GAGAACTCTA TCTGTGGTTT ATAATCTTGC 4920  
 ACGAGGCACC AGAGTCTCCC TGGGTCTTGT GATGAACCTA ATTTATCCCC TTCTCTGCC 4980  
 CAACCACAAA CTCTTCTCTT CAAAGAGGGC CTGCTGGCT CCCTCCACCC AACTGCACCC 5040  
 ATGAGACTCG GTCCAAGAGT CCATTCCCCA GGTGGGAGCC AACTGTACAG GAGGTCTTTC 5100  
 CCACCAACAA TCTTTCAGCT GCTGGGAGGT GACCATAGGG CTCTGCTTTT AAAGATATGG 5160  
 TGCTTTCAA GGCAGAGTAC ACAGGAAGGA CTTCTTCCAG GGAGATTAGT GGTGATGGAG 5220  
 AGGAGAGTTA AATGACCTC ATGTCTCTCT TGTCCACGGT TTTGTGAGT TTTCACTCTT 5280  
 CTAATGCAAG GGTCTCACAC TGTGAACCAC TTAGGATGTG ATCACTTTCA GGTGGCCAGG 5340  
 AATGTTGAAT GCTCTTGGCT CAGTTCAATT AAAAAAGATA TCTATTGAA AGTTCTCAGA 5400  
 GTGTACATA TGTTCACAG TACAGGATCT GTACATAAAA GTTCTTTTCC TAAACCATTC 5460  
 ACCAAGAGCC AATATCTAGG CATTTTCTTG GTAGCACAAA TTTTCTTATT GCTTAGAAAA 5520  
 TTGCTCTCTT TGTATTATT GTTTGTAAGA CTTAAGTGAG TTAGGTCTTT AAGGAAAGCA 5580  
 ACGCTCTCTT GAAATGCTTG TCTTTTCTT GTTGCCGAAA TAGCTGGTCC TTTTTCGGGA 5640  
 GTTAGATGTA TAGAGTGTTC GTATGTAAAC ATTTCTTGTA GGCATCACA TGAACAAAGA 5700  
 TATATTTTCT ATTTATTTAT TATATGTGCA CTTCAAGAAG TCACTGTCAG AGAAATAAAG 5760  
 AATTGTCTTA AATGTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA

Seq ID NO: 140 Protein sequence  
 Protein Accession #: XP\_051860.2

1 11 21 31 41 51  
 | | | | |  
 75 MDGVNLSTEV VYKKGQDYRF ACYDRGRACR SYRVRFLCGK PVRPKLTVTI DTNVNSTILN 60  
 LEDNVQSWKP GDTLVLIAST YSMYQABEFQ VLPSCRSCAPN QVKVAGKPMY LHIGEIDGV 120  
 DMRAEVGLLS RNIIVMGEME DKCYPYRNHI CNFFDFDTFG GHIKFALGFK AAHLEGTELK 180  
 HMGQQLVQGQ PIHFHLAGDV DERGGVDPPT YIRDLSIHHT FSRCVTVHGS NGLLIKDVVG 240  
 80 YNSLGHCFFT EDGPEERNTF DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300  
 DCNAVSTFWM ANPNINNLINK AAAGSEETGF WFIHFHVPTG PSVGMSPGY SEHIPLGKPY 360  
 NNRAHSNYRA GMIIDNGVKT TEASAKDKRP FLSTISARYS PHQDADPLKP REPAIIRHFI 420  
 AYKNQDHGAW LRGGDVWLDS CRFADNGIGL TLAGSGTFFPY DDGSKQEIKN SLFVGESGNS 480  
 GTEMMDNRIV GPGGLDHSGR TLPICQNFPI RGILYDGPNI NIONCTFRKF VALEGRHTSA 540  
 LAFRLNNAWQ SCPHNNVTGI AFEDVPITSR VFFGEPGPWF NQLDMGDGKT SVFHDVDGVS 600

SEYPGSYLTK NDNWLVRHPD CINVPDWRGA ICSGQYQMY IQAYKTSNLR MKIIKNDFPS 660  
 HPLYLEGALT RSTHYQQYQP VVTLQKGYTI HWDQTAPAEI AIWLINFNKG DWIRVGLCYP 720  
 RGTTFSILSD VHNRLKQTS KTGVEFVRTIQ MDKVEQSYPG RSHYYWDEDS GLLFLKLKAQ 780  
 NEREKFAFCS MKGCERIKIK ALIPKNAGVS DCTATAYPKF TERAVVDVPM PKLLFGSQLK 840  
 TKDHFLEVKM ESSKQHFPHL WNDFAIEVD GKYPSSSEDG IQVVVIDGNQ GRVVSHTSFR 900  
 NSILQGIPIWQ LFNVVATIPD NSIVLMASKG RYVSRGPWTR VLEKLGADRG LKLKEQMAFV 960  
 GPKGSFRPIW VTLDTEDHKA KIFQVVPV VKKKKL

Seq ID NO: 141 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 261..2861

1	11	21	31	41	51	
GAGCTAGCGC	TCAAGCAGAG	CCCAGCGCGG	TGCTATCGGA	CAGAGCCTGG	CGAGCGCAAG	60
CGGCGCGGGG	AGCCAGCGGG	GCTGAGCGCG	GCCAGGGTCT	GAACCCAGAT	TTCCCAGACT	120
AGCTACCACT	CCGCTTGCCC	ACGCCCCGGG	AGCTCGCGGC	GCCTGGCGGT	CAGCGACCAG	180
ACGTCCGGGG	CCGCTCGGCT	CCTGGCCCGC	GAGGCGTGAC	ACTGTCTCGG	CTACAGACCC	240
AGAGGGAGCA	CATGCCAGG	ATGGGAGCTG	CTGGGAGGCA	GGACTTCTCT	TTCAAGGCCA	300
TGCTGACCAT	CAGCTGGCTC	ACTCTGACCT	GCTTCCCTGG	GGCCACATCC	ACAGTGGCTG	360
CTGGGTGCCC	TGACCAGAGC	CCTGAGTTGC	AACCCCTGGAA	CCCTGGCCAT	GACCAAGACC	420
ACCATGTGCA	TATCGGCCAG	GGCAAGACAC	TGCTGCTCAC	CTCTTCTGCC	ACGGTCTATT	480
CCATCCACAT	CTCAGAGGGA	GGCAAGCTGG	TCATTAAAGA	CCACGACGAG	CCGATTGTTT	540
TGCGAACCCT	GCACATCCTG	ATTGACAACG	GAGGAGAGCT	GCATGCTGGG	AGTGCCCTCT	600
GCCCTTTCCA	GGGCAATTTT	ACCATCATT	TGTATGGAA	GGCTGATGAA	GGTATTGAGC	660
CGGATCCCTA	CTATGGTCTG	AAGTACATTG	GGGTGTTGTA	AGGAGGCGCT	CTTGAGTTGC	720
ATGGACAGAA	AAAGCTCTCC	TGGACATTTC	TGAACAAGAC	CCTTCACCCA	GGTGGCATGG	780
CAGAAGGAGG	CTATTTTTTT	GAAAGGAGCT	GGGGCCACCG	TGGAGTTATT	GTTCATGTCA	840
TCGACCCCAA	ATCAGGCACA	GTCATCCATT	CTGACCCGTT	TGACACCTAT	AGATCCAAGA	900
AAGAGAGTGA	ACGCTCTGTC	CAGTATTGTA	ACGCGGTGCC	CGATGGCAGG	ATCCTTTCTG	960
TTGCAGTGAA	TGATGAAGGT	TCTCGAAATC	TGGATGACAT	GGCCAGGAAG	GCGATGACCA	1020
AATTGGGAAG	CAAAACCTTC	CTGCACCTTG	GATTTAGACA	CCCTTGGAGT	TTTCTAACTG	1080
TGAAAGGAAA	TCCATCATCT	TCAGTGGAA	ACCATATTGA	ATATCATGGA	CATCGAGGCT	1140
CTGCTGCTGC	CCGGGTATTC	AAATTGTTCC	AGACAGAGCA	TGGCGAATAT	TTCAATGTTT	1200
CTTTGTCCAG	TGAGTGGGTT	CAAGACGTGG	AGTGGACGGA	GTGGTTCGAT	CATGATAAAG	1260
TATCTCAGAC	TAAAGTGGG	GAGAAAATTT	CAGACCTCTG	GAAAGCTCAC	CCAGGAAAAA	1320
TATGCAATCG	TCCCATTGAT	ATACAGGCCA	CTACAATGGA	TGGAGTTAAC	CTCAGCACCG	1380
AGGTTGTCTA	CAAAAAGGC	CAGGATTATA	GGTTTGCTTG	CTACGACCGG	GGCAGAGCCT	1440
GCCGGAGCTA	CCGTGTACGG	TTCTCTGTG	GGAAGCCTGT	GAGGCCCAAA	CTCACAGTCA	1500
CCATTGACAC	CAATGTGAAC	AGCACCATT	TGAACCTGGA	GGATAATGTA	CAGTCAATGGA	1560
AACCTGGAGA	TACCTTGGTC	ATTGCCAGTA	CTGATTACTC	CATGTACCAG	GCAGAAAGAGT	1620
TCCAGGTGCT	TCCTCTGAGA	TCCTGCGCCC	CCAACCAAGT	CAAAGTGGCA	GGGAAACCAA	1680
TGTACCTGCA	CATCGGGGAG	GAGATAGACG	GCGTGGACAT	CGGGGCGGAG	GTGGGGCTTC	1740
TGAGCCGGAA	CATCATAGTG	ATGGGGGAGA	TGGAGGACAA	ATGCTACCCC	TACAGAAACC	1800
ACATCTGCAA	TTTCTTTGAC	TTGATACCT	TTGGGGGCCA	CATCAAGTTT	GCTCTGGGAT	1860
TTAAGGCAGC	ACACTTGGAG	GGCACGGAGC	TGAAGCATAT	GGGACAGCAG	CTGGTGGGTC	1920
AGTACCCGAT	TCACTTCCAC	CTGGCCGGTG	ATGTAGACGA	AAGGGGAGGT	TATGACCCAC	1980
CCACATACAT	CAGGGACCCT	TCCATCCATC	ATACATTCTC	TCGCTGCGTC	ACAGTCCATG	2040
GCTCCAATGG	CTTGTGTGAT	AAGGACGTTG	TGGGCTATAA	CTCTTTGGGC	CACGTCTTCT	2100
TCACGGAAGA	TGGGCCGGAG	GAAACGCAACA	CTTTTGACCA	CTGCTCTGGC	CTCCTTGTCA	2160
AGTCTGGAAC	CCTCTTCCCC	TCGGACCGTG	ACAGCAAGAT	GTGCAAGATG	ATCACAGAGG	2220
ACTCTTACCC	AGGGTACATC	CCCAAGCCCA	GGCAAGACTG	CAATGCTGTG	TCCACCTTCT	2280
GGATGGCCAA	TCCCAACAAC	AACTCATCA	ACTGTGCGCG	TGCAGGATCT	GAGGAAACTG	2340
GATTTTGGTT	TATTTTTTCA	CACGTACCAA	CGGGCCCCCT	CGTGGGAATG	TACTCCCCAG	2400
GTTATTGAGA	GCACATTCCA	CTGGGAAAAT	TCTATAACAA	CCGAGCACAT	TCCAACCTACC	2460
GGGCTGGCAT	GATCATAGAC	AACGGAGTCA	AAACCACCGA	GGCCTCTGCC	AAGGACAAGC	2520
GGCCGTTCCT	CTCAATCATC	TCTGCCAGAT	ACAGCCCTCA	CCAGGACGCC	GACCCGCTGA	2580
AGCCCCGGGA	GCCGGCCATC	ATCAGACACT	TCATTGCGCTA	CAAGAACCAG	GACCAACGGG	2640
CCTGGCTGCG	CGGCGGGGAT	GTGTGGCTGG	ACAGCTGCCA	TTTCAGAGGG	GAGGCTCAGG	2700
AAGGCTTCTT	GCTTACAGGA	ATGAAGGCTG	GGGGCATTTT	GCTGGGGGGA	GATGAGGCAG	2760
CCTCTGGAAT	GGCTCAGGGA	TTTCCGCTCT	CCTGCCGCTG	CCTGCTGAAG	CTGGTGACTA	2820
CGGGGTGCCC	CTTTGCTCAC	GTCTCTCTGG	CCCACTCATG	ATGGAGAAAT	GTGGTCAGAG	2880
GGGAGCAATG	GGCTTTGCTG	CTTATGAGCA	CAGAGGAATT	CAGTCCCCAG	GCAGCCCTGC	2940
CTCTGACTCC	AAGAGGGTGA	AGTCCACAGA	AGTGAGCTCC	TGCCTTAGGG	CCTCATTTGC	3000
TCTTCATCCA	GGGAACCTGAG	CACAGGGGGC	CTCCAGGAGA	CCCTAGATGT	GCTCGTACTC	3060
CCTCGGCTCT	GGATTTTCTA	GCTGGAAATA	TAGAAAATAT	CTAGCCCCAA	GCCTTCATTT	3120
TAACAGATGG	GGAAAGTGAG	CCCCAAGAT	GGGAAAGAAC	CACACAGCTA	AGGGAGGGCC	3180
TGGGGAGCCC	CACCCTAGCC	CTTGCTGCCA	CACCACATTG	CCTCAACAAC	CGGCCCCAGA	3240
GTGCCCAGGC	ACTCCTGAGG	TAGCTTCTGG	AAATGGGGAC	AAGTCCCTCT	GAAGGAAAGG	3300
AAATGACTAG	AGTAGAATGA	CAGCTAGCAG	ATCTCTTCCC	TCCTGCTCCC	AGCGCACACA	3360
AACCCGCCCT	CCCTTGGTGG	TTGGCGGTCC	CTGTGGCCTT	CACCTTTGTT	ACTACCTGTC	3420
AGCCAGCCTT	GGGTGCACAG	TAGCTGCAAC	TCCCATTTGG	TGCTACCTGG	CTCTCCTGTC	3480
TCTGCAGCTC	TACAGGTGAG	GCCCAGCAGA	GGGAGTAGGG	CTGCCATGTT	TTCTGGTGAG	3540
CCAATTTGGC	TGATCTTGGG	TGTCTGAACA	GCTATTGGGT	CCACCCAGAT	CCCTTTCAGC	3600
TGCTGCTTAA	TCTCCCTGGC	CCACCTTATA	GAGAGCCCAA	AGAGCTCCCT	GCTGCTGCTG	3660
TAAGAGGGAG	AACTCTATCT	GTGGTTTATA	ATCTTGACAG	AGGCACCAGA	GTCTCCCTGG	3720
GTCTTGTGAT	GAACATCAT	TATCCCTTTT	CCTGCCCCAA	CCACAAACTC	TTTCTCTCAA	3780
AGAGGGCCTG	CCTGGCTCCC	TCCACCCAAC	TGCACCCATG	AGACTCGGTC	CAAGAGTCCA	3840
TTCCCCAGGT	GGGAGCCAAC	TGTGAGGGAG	GTCTTTCCCA	CCAAACATCT	TTGAGTCTGT	3900
GGGAGGTGAC	CATAGGGCTC	TGCTTTTAAA	GATATTGGCT	CTTCAAGGTC	CAGAGTCACA	3960
GGAGGACTT	CTTCCAGGGA	GATTAGTGGT	GATGGAGAGG	AGAGTTAAAA	TGACCTCATG	4020
TCCTTCTTGT	CCACGGTTTT	GTTGAGTTTT	CACTCTTCTA	ATGCAGGGGT	CTCACACTGT	4080
GAACCACTTA	GGATGTGATC	ACTTTAGGTT	GGCCAGGAAT	GTGGAATGTC	TTTGGCTCAG	4140
TTCAATTTAAA	AAAGATATCT	ATTGAAAGT	TCTCAGAGTT	GTACATATGT	TTCACAGTAC	4200

AGGATCTGTA CATAAAAGTT TCTTTCCTAA ACCATTACACC AAGAGCCAAT ATCTAGGCAT 4260  
 TTTCTTGGTA GCACAAATTT TCTTATTGCT TAGAAAATTG TCCTCCTTGT TATTTCTGTT 4320  
 TGTAAGACTT AAGTGAGTTA GGTCTTTAAG GAAAGCAACG CTCTCTGTA ATGCTTGTCT 4380  
 TTTTCTGTT GCCGAAATAG CTGGTCCTTT TTCGGGAGTT AGATGTATAG AGTGTGTTGA 4440  
 TGTAACACATT TCTGTAGGC ATCACCATGA ACAAAGATAT ATTTTCTATT TATTTATTAT 4500  
 ATGTGCACTT CAAGAAGTCA CTGTGAGAGA AATAAAGAAT TGTCTTAAAT GTCATGATTG 4560  
 GAGATGTCCT TTGCATTGCT TGAAGGGGT GTACCTAGAG CCAAGGAAAT TGGCTCTGGT 4620  
 TTGGAAAAAT TTTGCTGTTA TTATAGTAAA CATACAAAGG ATGTCAAAAA AAAAAAATAA 4680  
 AAAAAAATAA AAAAAAATAA AA

Seq ID NO: 142 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MGAAGRQDFL FKAMLTISWL TLTCFFGATS TVAAGCPDQS PELQPWNPGH DQDHHVHIGQ 60  
 GKTLTLLTSSA TVYSIHISEG GKLVIKDHDE PIVLRTRHIL IDNGGELHAG SALCPFGQNF 120  
 TIILYGRADE GIQDPDYYGL KYIGVGKGGG LELHGGKGLS WTFLNKTLLHP GGMAEGGYFF 180  
 ERSWGHGRVI VHVDPKSGT VIHSDRFDY RSKKESERLV QYLNAPVDGR ILSVAVNDEG 240  
 SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLTVMGNPSS SVEDHIEYHG HRGSAARVF 300  
 KLFQTEHGEY FNVSLSSSEW QVWEWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID 360  
 IQATTTMDGVN LSTEYVYKKG QDYRFACYDR GRACRSYRVR FLCGKPVPRK LTVTIDTNVN 420  
 STILNLEDNV QSWKPGDTLV IASTDYSMYQ AEEFQVLPDR SCAPNQVKVA GKPMYLIHGE 480  
 EIDGVDMAE VGLLSRNII IV MGEMEDKCYR YRNHICNFFD FDTFGGHIKF ALGFKAAHLE 540  
 GTELKHMGGQ LVQYPIHFH LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI 600  
 KDVVGYNSLG HCFEFTEDGPE ERNTFDHCLG LLVKSQTLLP SDRDSKMCKM ITEDSYPGYI 660  
 PKPRQDCNAV STEWMANPN NLINCAAAGS EETGFWFIFH HVPTGPSVGM YSPGYSEHIP 720  
 LGKFYNNRAH SNYRAGMI ID NGVKTTEASA KDKRPFLSII SARYSHPQDA DPLKPREPAI 780  
 IRHFIAYKNQ DHGAWLRGGD VWLDSCHFRG EAQEGFLLTG MKAGGILLGG DEAAAGSMAQG 840  
 FSPFCRLLEK LVTITGSPFAH VSLAHS

Seq ID NO: 143 NM DNA sequence  
 Nucleic Acid Accession #: NM\_006017  
 Coding sequence: 38..2635

1 11 21 31 41 51  
 CCAAGTCTTA CCTCATGTTT GGAGGATCTT GCTAGCTATG GCCCTCGTAC TCGGCTCCCT 60  
 GTTGCTGCTG GGGCTGTGCG GGAACCTCCTT TTCAGGAGGG CAGCCTTCAT CCACAGATGC 120  
 TCCTAAGGCT TGGAATTATG AATTGCCTGC AACAAATTAT GAGACCCAAG ACTCCCATAA 180  
 AGCTGAGACC ATTTGGCATTCT TCTTTGAACCT AGTGCAATAT TTTCTCTATG TGGTACAGCC 240  
 CGCTGATTTC CCAGAAGATA CTTTGAGAAA ATTCTTACAG AAGGCATATG AATCCAAAAT 300  
 TGATTATGAC AAGCCAGAAA CTGTAATCTT AGGTCTAAAG ATTGTCTACT ATGAAGCAGG 360  
 GATTATTCTA TGCTGTGTCC TGGGGCTGCT GTTTATTATT CTGATGCCCT TGGTGGGGTA 420  
 TTTCTTTTGT ATGTGTGCTT GCTGTAAACAA ATGTGGTGGA GAAATGCACC AGCGACAGAA 480  
 GGAAAAATGG CCCTTCCTGA GGAAATGCTT TGCAATCTCC CTGTTGGTGA TTTGTATAAT 540  
 AATAAGCATT GGCATCTTCT ATGGTTTGTG GGCAATCAC CAGGTAAGAA CCCGGATCAA 600  
 AAGGAGTCGG AAATGGCAG ATAGCAATTT CAAGGACTTG CGAATCTCT TGAATGAAAC 660  
 TCCAGAGCAA ATCAAAATATA TATTGGCCCA GTACAACACT ACCAAGGACA AGGCGTTCAC 720  
 AGATCTGAAC AGTATCAATT CAGTGCTAGG AGGCGGAATT CTGACCGAC TGAGACCCAA 780  
 CATCATCCCT GTTCTTGATG AGATTAAGTC CATGGCAACA GCGATCAAGG AGACCAAAGA 840  
 GGGCTTGGAG AACATGAACA GCACCTTGAA GAGCTTGCAC CAACAAAGTA CACAGCTTAG 900  
 CAGCAGTCTG ACCAGCGTGA AAACCTAGCCT GCGGTCTACT CTCAATGACC CTCTGTGCTT 960  
 GGTGCATCCA TCAAGTGAAA CCTGCAACAG CATCAGATTG TCTCTAAGCC AGCTGAATAG 1020  
 CAACCCCTGAA CTGAGGCAGC TTCCACCCGT GGATGCAGAA CTTGACAACG TTAATAACGT 1080  
 TCTTAGGACA GATTTGATG GCCTGGTCCA ACAGGGCTAT CAATCCCTTA ATGATATACC 1140  
 TGACAGAGTA CAACGCCAAA CCACGACTGT CGTAGCAGGT ATCAAAAGGG TCTTGAATTC 1200  
 CATTTGGTCA GATATCGACA ATGTAACCTCA GCGTCTTCCT ATTCAAGATA TACTCTCAGC 1260  
 ATTCTCTGTT TATGTTAATA ACACTGAAAG TTACATCCAC AGAAATTTAC TCACATTGGA 1320  
 AGAGTATGAT TCATACTGGT GGCTGGGTGG CCTGGTCTAT TGCTCTCTGC TGACCCCTCAT 1380  
 CGTGATTTTT TACTACCTGG GCTTACTGTG TGGCGTGTGC GGCTATGACA GGCATGCCAC 1440  
 CCGGACCACC CGAGGCTGTG TCTCCAACAC CGGAGGCGTC TTCTCTATGG TTGGAGTTGG 1500  
 ATTAAGTTTC CTCTTTTGCT GGATATTGAT GATCATTGTG GTTCTTACCT TGTCTTTGG 1560  
 TGCAAAATGTG GAAAACTGA TCTGTGAACC TTACACGAGC AAGGAATTAT TCCGGGTTTT 1620  
 GGATACACCC TACTTACTAA ATGAAGACTG GGAATACTAT CTCTCTGGGA AGCTATTTAA 1680  
 TAAATCAAAA ATGAAGCTCA CTTTGAACA AGTTTACAGT GACTGCAAAA AAAATAGAGG 1740  
 CACTTACGGC ACTCTTCAAC TGCAGAACAG CTTCAATATC AGTGAACATC TCAACATTAA 1800  
 TGAGCATACT GGAAGCATAA GCAGTGAATT GGAAGTCTG AAGGTAATC TTAATATCTT 1860  
 TCTGTTGGGT GCAGCAGGAA GAAAAACCT TCAGGATTTT GCTGCTGTG GAATAGACAG 1920  
 AATGAATTAT GACAGCTACT TGGCTCAGAC TGGTAAATCC CCGCAGGAG TGAATCTTTT 1980  
 ATCATTTGCA TATGATCTAG AAGCAAAAGC AAACAGTTTG CCCCAGGAA ATTTGAGGAA 2040  
 CTCCTGAAA AGAGATGCAC AAACATTAA AACAAATCAC CAGCAACGAG TCCTTCCTAT 2100  
 AGAACAATCA CTGAGCACTC TATACCAAAG CGTCAAGATA CTTCAACGCA CAGGGAATGG 2160  
 ATTTGTTGGG AGAGTAACTA GGATCTAGC TTCTCTGGAT TTTGCTCAGA ACTTCATCAC 2220  
 AAACAATACT TCCTCTGTTA TTATTGAGGA AACTAAGAAG TATGGGAGAA CAATAATAGG 2280  
 ATATTTTGAA CATATCTGCG AGTGGATCGA GTTCTCTATC AGTGAGAAAG TGGCATCGTG 2340  
 CAAACCTGTG GCCACCGCTC TAGATACTGC TGTGTATGTC TTTCTGTGTA GCTACATTAT 2400  
 CGACCCCTTG AATTTGTTTT GGTGTCAT AGGAAAAGCT ACTGTATTTT TACTTCCGGC 2460  
 TCTAATTTTT CGCGTAAAAC TGGCTAAGTA CTATCGTCGA ATGGATTCCG AGGACGTGTA 2520  
 CGATGATGTT GAAACTATAC CATGAAAAA TATGGAATAT GGTAAATAAT GTTATCATAA 2580  
 AGATCATGTA TATGGTATTC ACAATCCTGT TATGACAAGC CCATCACAAC ATTGATAGCT 2640  
 GATGTTGAAA CTGCTTGAGC ATCAGGATAC TCAAGTGGA AAGGATCACA GATTTTGTGT 2700  
 AGTTTCTGGG TCTACAAGGA CTTTCAAAAT CCAGGAGCAA CGCCAGTGGC AACGTAGTGA 2760  
 CTCAGGCGGG CACCAAGGCA ACGGCACCAT TGGTCTCTGG GTAGTGCTTT AAGAATGAAC 2820

ACAATCACGT TATAGTCCAT GGTCCATCAC TATTCAAGGA TGA CTCCCTC CCTTCCTGTC 2880  
 TATTTTGTGT TTTTACTTTT TTACTACTGAG TTTCTATTTA GACTACTACAA CATATGGGGT 2940  
 GTTTGTTCCT ATTTGGATGCA TTTCTATCAA AACTCTATCA AATGTGATGG CTAGATTCTA 3000  
 ACATATTGCC ATGTGTGGAG TGTGCTGAAC ACACACCAGT TTACAGGAAA GATGCATTTT 3060  
 GTGTACAGTA AACGGTGTAT ATACCTTTTG TTACCACAGA GTTTTTTAAA CAAATGAGTA 3120  
 TTATAGGACT TTCTTCTAAA TGAGCTAAAT AAGTCACCAT TGACTTCTTG GTGCTGTTGA 3180  
 AAATAATCCA TTTTCACTAA AAGTGTGTGA AACCTACAGC ATATTCTTCA CGCAGAGATT 3240  
 TTCATCTATT ATACTTTATC AAAGATTGGC CATGTTCCAC TTGGAATGG CATGCAAAAG 3300  
 CCATCATAGA GAAACCTGCG TAACTCCATC TGACAAATTC AAAAGAGAGA GAGAGATCTT 3360  
 GAGAGAGAAA TGCTGTTTCG TCAAAAGTGG AGTGTGTTTA ACAGATGCCA ATTACGGTGT 3420  
 ACAGTTTAAAC AGAGTTTCTT GTTGCCATTAG GATAAACATT AATTGGAGTG CAGCTAACAT 3480  
 GAGTATCATC AGACTAGTAT CAAGTGTCTT AAAATGAAAT ATGAGAAGAT CCTGTACAAA 3540  
 TTCTTAGATC TGGTGTCCAG CATGGATGAA ACCTTTGAGT TTGGTCCCTA AATTTGCATG 3600  
 AAAGCACAAG GTAAATATTC ATTTGCTTCA GGAGTTTCAT GTTGGATCTG TCATTATCAA 3660  
 AAGTGATCAG CAATGAAGAA CTGGTCGGAC AAAATTTAAT GTTGATGTAA TGGAAATCCA 3720  
 GATGTAGGCA TTCCCCCAG GTCTTTTCAT GTGCAGATTG CAGTTCTGAT TCATTTGAAT 3780  
 AAAAAGGAAC TTGG

Seq ID NO: 144 NP Protein sequence  
 Protein Accession #: NP\_006008.1

1 11 21 31 41 51  
 | | | | |  
 MALVLGSLLL LGLCGNSFSG QPSSSTDAPK AWNYELPATN YETQDSHKAG PIGILFELVH 60  
 IFLYVQPRD FPEDTLRKFL QKAYESKIDY DKPETVILGL KIVYYEAGII LCCVLGLLFI 120  
 ILMPLVGYFF CMCRCCKKCG GEMHQROKEN GPFLRKCFAI SLLVICIIIS IGIFYGFVAN 180  
 HQVTRTRKRS RKLADSNFKD LRTLLNETPE QIKYILAQYN TTKDKAFDNL NSINSVLGGG 240  
 ILDRLRPNII PVLDEIKSMA TAIKETKEAL ENMNSTLKS LQQSTQLSSS LTSVKTSLSR 300  
 SLNDPLCLVH PSSETCMSIR LSLSQLNSNP ELRLQPPVDA ELDNVNVLRL TDLGLVQQG 360  
 YQSLNDIPDR VQRQTTTVVA GIKRVLSNSG SDIDNVQRL PIQDILSAPS VYVNNTESYI 420  
 HRNLPTLEEY DSWWLLGGLV ICSLLTLIVI FYLLGLLGGV CGYDRHATPT TRGCVSNTGG 480  
 VFLMVGVGLS FLPCWILMII VVLTFVFGAN VEKLICEPYT SKELFRVLDL PYLLNEDWEY 540  
 YLSGKLFNKS KMKLTFFQVY SDCKKNRGTY GTLHLQNSFN ISEHLNINEH TGSISSELES 600  
 LKVMNLNIFLL GAAGRKNLQD FAACGIDRMN YDSYLAQTGK SPAGVNLISF AYDLEAKANS 660  
 LPPGNLRNSL KRDAQTIKTI HQQRVLPLEQ SLSTLYQSVK ILQRTGNGLL ERVTRILASL 720  
 DPAQNFIITN TSSVIIIEETK KYGRITIGYF BHLQWIEFS ISEKVASCKP VATALDVAID 780  
 VFLCSYIIDP LNLFWFGIGK ATVFLLPALI FAVKLAKYYR RMDSEVDYDD VETIPMKNME 840  
 NGNNGYHKDH VYGIHNPVMT SPSQH

Seq ID NO: 145 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 38..2605

1 11 21 31 41 51  
 | | | | |  
 CCAAGTTCTA CCTCATGTTT GGAGGATCTT GCTAGCTATG GCCCTCGTAC TCGGCTCCCT 60  
 GTTGCTGCTG GGGCTGTGCG GGAACCTCCTT TTCAGGAGGG CAGCCTTCAT CCACAGATGC 120  
 TCCTAAGGCT TGGAAATTAT AATTGCCTGC AACAAATATG GAGACCCAAG ACTCCCATAA 180  
 AGCTGGACCC ATTGGCATTC TCTTTGAACT AGTGCAATAT TTTCTCTATG TGGTACAGCG 240  
 GCGTGATTTC CCAGAAAGATA CTTTGAGAAA ATTCTTACAG AAGGCATATG AATCCAAAAT 300  
 TGATTATGAC ATTGTCTACT ATGAAGCAGG GATTATTCTA TGCTGTGTCC TGGGGCTGCT 360  
 GTTTATTATT CTGATGCTCT TGGTGGGGTA TTTCTTTTGT ATGTGTGCTT GCTGTAACAA 420  
 ATGTGGTGGA GAAATGCACC AGCGACAGAA GGAATATGGG CCCTTCTGTA GGAATGCTT 480  
 TGCAATCTCC CTGTTGGTGA TTTGTATAAT AATAAGCATT GGCATCTTCT ATGGTTTTGT 540  
 GGCAATCAC CAGGTAAGAA CCCGGATCAA AAGGAGTCGG AAACCTGGCAG ATAGCAATTT 600  
 CAAGGACTTG CGAATCTCTT TGAATGAAAC TCCAGAGCAA ATCAAAATATA TATTGGCCCA 660  
 GTACAAACAT ACCAAGGACA AGGCGTTTAC AGATCTGAAC AGTATCAATT CAGTGTAGG 720  
 AGGCGGAATT CTTGACCGAC TGAGACCCAA CATCATCCCT GTTCTTGATG AGATTAAAGT 780  
 CATGGCAACA CGCATCAAGG AGACCAAGA GCGCTTGGAG AACATGAACA GCACCTTGAA 840  
 GAGCTTGACAC CAACAAAGTA CACAGCTTAG CAGCAGTCTG ACCAGCGTGA AAACCTAGCCT 900  
 GCGGTCTATC CTCAATGACC CTCTGTGCTT GGTGCATCCA TCAAGTGAAG CCTGCAACAG 960  
 CATCAGATTG TCTCTAAGCC AGCTGAATAG CAACCTGAA CTGAGGCAGC TTCCACCCGT 1020  
 GGATGCAGAA CTTGACAACG TTAATAACGT TCTTAGGACA GATTGTGATG GCCTGGTCCA 1080  
 ACAGGGCTAT CAATCCCTTA ATGATATACC TGACAGAGTA CAACGCCAAA CCACGACTGT 1140  
 CGTAGCAGGT ATCAAAAGGG TCTTGAATTC CATTGGTTCA GATATCGACA ATGTAACCTA 1200  
 GCGTCTTCTT ATTCAAGATA TACTCTCAGC ATCTCTGTGT TATGTTAATA AACTGAAAG 1260  
 TTACATCCAC AGAATTTTAC TCACATTGGA AGAGTATGAT TCATACTGGT GGCCTGGTGG 1320  
 CCTGGTCTAT TGCTCTCTGC TGACCCCTCAT CGTGATTTT TACTACCTGG GCTTACTGTG 1380  
 TGGCGTGTGC GGCTATGACA GGCATGCCAC CCCGACCACC CGAGGCTGTG TCTCCAACAC 1440  
 CGGAGGCGTC TTCTCATGG TTGGAGTTGG ATTAAGTTTC CTCTTTTGCT GGATATTGAT 1500  
 GATCATTGTG GTTCTTACCT TTGTCTTTGG TGCAATGTG GAAAACTGA TCTGTGAACC 1560  
 TTACACGAGC AAGGAATTAT TCCGGGTTTT GGATACACCC TACTTACTAA ATGAAGACTG 1620  
 GGAATACTAT CTCTCTGGGA AGCTATTTAA TAAATCAAAA ATGAAGCTCA CTTTGAACA 1680  
 AGTTTACAGT GACTGCAAAA AAAATAGAGG CACTTACGGC ACTCTTACC TGCAGAACAG 1740  
 CTTCAATATC AGTGAACATC TCAACATTAA TGAGCATACT GGAAGCATAA GCAGTGAATT 1800  
 GGAAAGTCTG AAGGTAATC TTAATATCTT TCTGTGGGT GCAGCAGGAA GAAAAACCT 1860  
 TCAGGATTTT GCTGCTTGTG GAATAGACAG AATGAATTAT GACAGCTACT TGGCTCAGAC 1920  
 TGGTAAATCC CCCGACGAG TGAATCTTTT ATCATTGCA TATGATCTAG AAGCAAAAGC 1980  
 AAACAGTTTG CCCCAGGAA ATTTGAGGAA CTCCCTGAAA AGAGATGCAC AAACATTAA 2040  
 AACAAATCAC CAGCAACGAG TCCTTCTCTAT AGAACAATCA CTGAGCACTC TATACCAAAG 2100  
 CGTCAAGATA CTCAACGCA CAGGGAATGG ATTGTTGGAG AGAGTAACCTA GGATCTAGC 2160  
 TTCTCTGATG TTTGCTCAGA ACTTCATCAC AAACAATACT TCCTCTGTTA TTATTGAGGA 2220  
 AACTAGAAG TATGGAGAA CAATAATAGG ATATTTTGA CATTATCTGC AGTGGATCGA 2280  
 GTTCTCTATC AGTGAGAAAG TGGCATCTGT CAAACCTGTG GCCACCGCTC TAGATACTGC 2340

TGTGTGATGTC TTTCTGTGTA GCTACATTAT CGACCCCTTG AATTTGTTTT GGTITGGCAT 2400  
 AGGAAAAGCT ACITGATTTTT TACTTCCGGC TCTAATTTTT GCGGTAAAAC TGGCTAAGTA 2460  
 CTATCGTCGA ATGGATTCCG AGGACGTGTA CGATGATGTT GAAACTATAC CCATGAAAAA 2520  
 TATGGAAAAAT GGTAAATAATG GTTATCATAA AGATCATGTA TATGGTATTC ACAATCCTGT 2580  
 TATGACAAGC CCATCACAAAC ATTGATAGCT GATGTTGAAA CTGCTTGAGC ATCAGGATAC 2640  
 TCAAAGTGGG AAGGATCACA GATTTTGGT AGTTTCTGGG TCTACAAGGA CTTTCCAAAT 2700  
 CCAGGAGCAA CGCCAGTGGC AACGTAGTGA CTCAGGCGGG CACCAAGGCA ACGGCACCAT 2760  
 TGGTCTCTGG GTAGTGTCTT AAGAAATGAAC ACAATCACGT TATAGTCCAT GGTCCATCAC 2820  
 TATTCAGGA TGACTCCCTC CCTTCTGTG TATTTTGTG TTTTACTTTT TTACACTGAG 2880  
 TTTCTATTTA GACACTACAA CATATGGGGT GTTGTGTTCC ATTGGATGCA TTTCTATCAA 2940  
 AACTCTATCA AATGTGATGG CTAGATTCTA ACATATTGCC ATGTGTGGAG TGTGCTGAAC 3000  
 ACACACCAGT TTACAGGAAA GATGCATTTT GTGTACAGTA AACGGTGTAT ATACCTTTTG 3060  
 TTACCACAGA GTTTTTTAAA CAAATGAGTA TTATAGGACT TTCTTCTAAA TGAGCTAAAT 3120  
 AAGTCACCAT TGACTTCTTG GTGCTGTTGA AAATAATCCA TTTTCACTAA AAGTGTGTGA 3180  
 AACCTACAGC ATATTCTTCA CGCAGAGATT TTCACTATT ATACTTTATC AAAGATTGGC 3240  
 CATGTTCCAC TTGGAATGAG CATGCAAAAG CCATCATAGA GAAACCTGCG TAACTCCATC 3300  
 TGACAAATTC AAAAGAGAGA GAGAGATCTT GAGAGAGAAA TGCTGTTCGT TCAAAAGTGG 3360  
 AGTGTGTTTA ACAGATGCCA ATTACGGTGT ACAGTTTAAC AGAGTTTCTT GTTGCAATTAG 3420  
 GATAAACATT AATGGAGTGC GACCTAACAT GAGTATCATC AGACTAGTAT CAAGTGTCTT 3480  
 AAAATGAAAT ATGAGAGAT CCTGTCAAA TTCTTAGATC TGGTGTCCAG CATGGATGAA 3540  
 ACCTTTGAGT TTGGTCCCTA AATTGTCATG AAAGCACAA GTAAATATTC ATTTGCTTCA 3600  
 GGAGTTTCAT GTTGGATCTG TCATTATCAA AAGTGATCAG CAATGAAGAA CTGGTCGGAC 3660  
 AAAATTTAAC GTTGATGTAA TGGAAATCCA GATGTAGGCA TTCCCCCAG GTCTTTTCAT 3720  
 GTGCAGATTG CAGTTCTGAT TCATTTGAAT AAAAAGGAAC TTGG

Seq ID NO: 146 Protein sequence  
 Protein Accession #:

1 11 21 31 41 51  
 MALVLGSLLL LGLCGNSFSG QPSSTDAPK AMNYELPATN YETQDSHKAG PIGILFELVH 60  
 IFLYVVQPRD FPEDTLRKFL QKAYESKIDY DIVVYEAGII LCCVLGLLFI ILMPLVGYYF 120  
 CMCRCCNKCG GEMHQKQKEN GPFLRKCFAT SLLVICIIIS IGIFYGFVAN HQVTRIKRS 180  
 RKLADSNFKD LRTLLNETPE QIKYILAQYN TTKDKAFDLD NSINSVLGGG ILDRLRPNII 240  
 PVLDEIKSMA TAIKETKEAL ENMNSTLKS L HQSTQLSSS LTSVKTSLSR SLNDPLCLVH 300  
 PSSETCNSIR LSLSQLNSNP ELRQLPPVDA ELDNVNNVLR TDLDGLVQQG YQSLNDIPDR 360  
 VQRQTTTVA GIKRVLSIG SDIDNVORL PIQDILSAFS VVYNNTESYI HRNLPLEEY 420  
 DSYWVLGGLV ICSLLTLIVI FYFLGLCGV CGYDRHATPT TRGCVSTNGG VFLMVGVLIS 480  
 FLFCWILMII VVLTFVFGAN VEKLICEPYT SKELFRVLDL PYLLNEDWEY YLSGKLFNKS 540  
 KMKLTFFQYV SDCKKNRGTY GTLHLQNSFN ISEHLNINEH TGSISSELES LKVNLIIFLL 600  
 GAAGRKNLQD FAACGIDRMN YDSYLAQTGK SPAGVNLISF AYDLEAKANS LPPGNLRNSL 660  
 KRDAQTIKTI HQQRVLPTEQ SLSTLYQSVK ILQRTGNGLL ERVTRILASL DFAQNFTINN 720  
 TSSVIIIBETK KYGRITIGYF EHYLQWIEFS ISEKVASCCK VATALDTAVD VFCLSYIIDP 780  
 LNLFWFVGIGK ATVFLLPALI FAVKLAKYYR RMDSEDVYDD VETIPMKNME NGNNGYHKDH 840  
 VYGHNPVMT SPSQH

Seq ID NO: 147 DNA sequence  
 Nucleic Acid Accession #: BC012089.1  
 Coding sequence: 236..2806

1 11 21 31 41 51  
 ATGCTCTCAG CTCTCCCGCC GCGGGATGGT GCCTTGAGTG AATGACCCCC TTGGAGAACA 60  
 TTCTTCCGCA TCCCTCGCCT CAAGCCAGCC TCAGACAGAA AACTGAAGAT TCAGCAGATC 120  
 CAGTGTCTCC TGCTCCTCTT CTGCCAGGA ACACGCTTGC CTTCCCCAAG GCTTCCAGAA 180  
 GCTCTGAGGC AGGAGGCCAC AAGTTCTACC TCATGTTTGG AGGATCTTGC TAGCTATGGC 240  
 CCTCGTACTC GGGCTCCTGT TGCTGTGGG GCTGTGCGGG AACTCTTTT CAGGAGGGCA 300  
 GCCTTCATCC ACAGATGCTC CTAAGGCTTG GAATTATGAA TTGCCTGCAA CAAATTATGA 360  
 GACCAAGAGC TCCATAAAG CTGGACCCAT TGGCATTCTC TTTGAAGTAG TGCATATCTT 420  
 TCTCTATGTG GTACAGCCGC GTGATTTCCT AGAAGATACT TTGAGAAAAA TCTTACAGAA 480  
 GGCATATGAA TCCAAAATTG ATTATGACAA GATTGTCTAC TATGAAGCAG GGATTATTCT 540  
 ATGCTGTGTC CTGGGGCTGC TGTATTAT TCTGATGCCT CTGGTGGGGT ATTTCTTTTG 600  
 TATGTGTCGT TGCTGTAAAC AATGTGTGAG AGAATATGCAC CAGCGACAGA AGGAAAATGG 660  
 GCCCTTCCTG AGGAAATGCT TTGCAATCTC CCTGTTGGTG ATTTGTATAA TAATAAGCAT 720  
 TGGCATCTTC TATGGTTTTG TGGCAATCA CCAGGTAAGA ACCCGGATCA AAAGGAGTCG 780  
 GAAACTGGCA GATAGCAATT TCAAGGACTT GCGAATCTCT TGAATGAAA CTCAGAGCAA 840  
 AATCAAAATAT ATATTGGCCC AGTACAACAC TACCAAGGAC AAGCGCTTCA CAGATCTGAA 900  
 CAGTATCAAT TCAGTGCTAG GAGCGGAAT TCTTGACCGA CTGAGACCCA ACATCATCCC 960  
 TGTCTTGTAT GAGATTAAAT CCAATGGCAAC AGCGATCAAG GAGACCAAG AGGCGTTGGA 1020  
 GAACATGAAC AGCACCTTGA AGAGCTTGCA CCAACAAAGT ACACAGCTTA GCAGCAGTCT 1080  
 GACCAGCGTG AAAACTAGCC TGCGGTCAAT TCTCAATGAC CCTCTGTGCT TGGTGCATCC 1140  
 ATCAAGTGAA ACTTGCAACA GCATCAGATT GTCTCTAAGC CAGCTGAATA GCAACCTGTA 1200  
 ACTGAGGCAG CTTCCACCCG TGGATGCAGA ACTTGACAAC GTTAATAACG TTCTTAGGAC 1260  
 AGATTTGATG GGCCTGTGTC AACAGGGCTA TCAATCCCTT AATGATATAC CTGACAGAGT 1320  
 ACAACGCCAA ACCACGACTG TCGTAGCAGG TATCAAAAGG CTCTTGAAAT CCATTGGTTC 1380  
 AGATATCGAC AATGTAATCT AGCGTCTTCC TATTGAGGAT ATACTCTCAG CATTCTCTGT 1440  
 TTATGTTAAT AACACTGAAA GTTACATCCA CAGAAATTTA CCTACATTGG AAGAGTATGA 1500  
 TTCTACTGG TGCTGTGGTG GCCTGGTCTG CTGCTCTCTG CTGACCTCTA TCGTGATTTT 1560  
 TTACTACCTG GGCTTACTGT GTGGCGTGTG CGGTATGAC AGGCATGCCA CCCCAGCCAC 1620  
 CCGAGGCTGT GTCTCCAACA CCGGAGGCGT CTTCCTCATG GTTGGAGTTG GATTAAGTTT 1680  
 CCTCTTTTGC TGGATATTGA TGCATATTGT GGTTCCTTACC TTTGTCTTTG GTGCAATGT 1740  
 GGAAAACTG ATCTGTGAAC CTTACACGAG CAAGGAATTA TTCCGGGTTT TGGATACACC 1800  
 CTACTTACTA ATGAAGACT GGGAACTACT TCTCTCTGGG AAGCTATTTA ATAAATCAAA 1860  
 AATGAAGCTC ACTTTTGAAC AAGTTTACAG TGACTGCAAA AAAAATAGAG GCACCTACGG 1920



	CACCTCTTCAC	CTGCAGAAC	GCTTCAATAT	CAGTGAACAT	CTCAACATTA	ATGAGCATAC	1980
	TGGAAGCATA	AGCAGTGAAT	TGGAAAGTCT	GAAGGTAAAT	CTTAATATCT	TTCTGTTGGG	2040
	TGCAGCAGGA	AGAAATAACC	TTCAAGGATTT	TGCTGCTTGT	GGAATAGACA	GAATGAATTA	2100
5	TGACAGCTAC	TTGGCTCAGA	CTGGTAATC	CCCCGAGGA	GTGAATCTTT	TATCATTGTC	2160
	ATATGATCTA	GAAGCAAAAG	CAAAACAGTTT	GCCCCAGGA	AATTTGAGGA	ACTCCCTGAA	2220
	AAGAGATGCA	CAAACTATTA	AAACAATTCA	CCAGCAACGA	GTCCTTCTTA	TAGAACCAATC	2280
	ACTGAGCACT	CTATACCAAA	GCGTCAAGAT	ACTTCAACGC	ACAGGGAATG	GATTGTTGGA	2340
	GAGAGTAACT	AGGATTCTAG	CTTCTCTGGA	TTTGTCTCAG	AACTTCATCA	CAAAACAATAC	2400
10	TTCTCTGTTT	ATTATTGAGG	AAACTAAGAA	GTATGGGAGA	ACAATAATAG	GATATTTTGA	2460
	ACATTATCTG	CAGTGGATCG	AGTTCTCTAT	CAGTGAGAAA	GTGGCATCGT	GCAAAACCTGT	2520
	GGCCACCGCT	CTAGATACTG	CTGTTGATGT	CTTTCTGTGT	AGCTACATTA	TCCAGCCCTT	2580
	GAATTTGTTT	TGGTTTGGCA	TAGGAAAAGC	TACTGTATTT	TTACTTCCGG	CTCTAATTTT	2640
	TGCGGTAAAA	CTGGCTAAGT	ACTATCGTCG	AATGGATTCT	GAGGACGTGT	ACGATGATGT	2700
15	TGAAACTATA	CCCATGAAAA	ATATGGAAAA	TGGTAATAAT	GGTTATCATA	AAGATCATGT	2760
	ATATGGTATT	CACAATCCTG	TTATGACAA	CCCATCACAA	CATTGATAGC	TGATGTTGAA	2820
	ACTGCTTGG	CATCAGGATA	CTCAAAGTGG	AAAGGATCAC	AGATTTTGTG	TAGTTTCTGG	2880
	GTCTACAAGG	ACTTTCCAAA	TCCAGGAGCA	ACGCCAGTGG	CAACGTAGTG	ACTCAGGCGG	2940
	GCACCAAGGC	AACCGCACCA	TTGGTCTCTG	GGTAGTGTCT	TAAGAAATGAA	CACAATCACG	3000
20	TTATAGTCCA	TGGTCCATCA	CTATTCAAGG	ATGACTCCCT	CCCTTCTCTG	CTATTTTGTG	3060
	TTTTTACTTT	TTTACACTGA	GTTTCTATTT	AGACACTACA	ACATATGGGG	TGTTTGTTC	3120
	CATTGGATGC	ATTTCATCA	AAACTCTATC	AAATGTGATG	GCTAGATTCT	AACATATTGC	3180
	CATGTGTGGA	GTGTGCTGAA	CACACACCAG	TTTACAGGAA	AGATGCATTT	TGTGTACAGT	3240
	AAACGGTGTA	TATACCTTTT	GTTACACAG	AGTTTTTTAA	ACAAATGAGT	ATTATAGGAG	3300
25	TTTCTCTTAA	ATGAGCTAAA	TAAAGTCACA	TTGACTTCTT	GGTGCTGTG	AAAATAATCC	3360
	ATTTTCACTA	AAAGTGTGTG	AAACCTACAG	CATATCTTTC	ACGCAGAGAT	TTTCTATCTA	3420
	TATACCTTAT	CAAAGATTGG	CCATGTTCCA	CTTGGAAATG	GCATGCAAAA	GCCATCATAG	3480
	AGAAACCTGC	GTAACCTCAT	CTGACAAATT	CAAAAGAGAG	AGAGAGATCT	TGAGAGAGAA	3540
	ATGCTGTTGC	TTCAAAAGTG	GAGTTGTTT	AACAGATGCC	AATTACGGTG	TACAGTTTAA	3600
30	CAGAGTTTTC	TGTTGCATTA	GGATAAACAT	TAATTGGAGT	GCAGCTAACA	TGAGTATCAT	3660
	CAGACTAGTA	TCAAGTGTTC	TAAATGAAAA	TATGAGAAGA	TCCTGTACCA	ATTCTTAGAT	3720
	CTGGTGTCCA	GCATGGATGA	AACCTTTGAG	TTTGGTCCCT	AAATTTGCAT	GAAGACACAA	3780
	GGTAAATATT	CATTGCTTTC	AGGAGTTTCA	TGTTGGATCT	GTCATTATCA	AAAGTGATCA	3840
	GCAATGAAGA	ACTGCTCGGA	CAAAATTTAA	CGTTGATGTA	ATGGAATTCC	AGATGTAGGC	3900
35	ATTCCCCCCA	GGTCTTTTCA	TGTGCAGATT	GCAGTTCCTG	TTCATTTGAA	TAAAAAGGAA	3960
	CTTGAAAAAA	AAAAAAAATA	AAA				

Seq ID NO: 148 Protein sequence

Protein Accession #: AAH12089.1

40	1	11	21	31	41	51	
	MALVLGSLLL	LGICGNSFSG	GQPSSTDAPK	AWNYELPATN	YETQDSHKAG	PIGILFELVH	60
	IFLYVVQPRD	FPEDTLRKL	QKAYESKIDY	DKIVYYEAGI	ILCCVLGLLF	IILMPLVGYF	120
	FCMCRCCNKC	GGEMHQROKE	NGPFLLKCF	ISLLVICIII	SIGIFYGFVA	NHQVRTRIKR	180
45	SRKLADSNEF	DLRTLLNETP	EQIKYILAQY	NTTKDKAFTD	LNSINSVLGG	GILDRLRPNI	240
	IPVLDEIKSM	ATAIKETKEA	LENMNSTLKS	LHQSTQLSS	SLTSVKTSRL	SSLNDPLCLV	300
	HPSSETCNIS	RLSLQLNSN	PELRQLPPVD	ABLDNVNVL	RTDLGLVQQ	GYQLNDIPD	360
	RVQRQTTTVV	AGIKRVLSNI	GSDIDNVQTR	LPIQDILSAF	SVYVNNTESY	IHRNLPTELE	420
50	YDSYNWLGGL	VICSLTLIV	IFYLGLLCLG	VCGYDRHATP	TRRGCVSNTG	GVFLMVGVL	480
	SPLFCWILMI	IVVLTFVFGA	NVEKLICEPY	TSKELFRVLD	TPYLLNEDWE	YYLSGKLFNK	540
	SKMKLTFEQV	YSDCKKNRGT	YGTLLHLQNSF	NISEHLNINE	HTGSISSELE	SLKVNLIIFL	600
	LGAAGRKNLQ	DFAACGIDRM	NYDSYLAQTG	KSPAGVNLIS	FAYDLEAKAN	SLPPGNLRNS	660
	LKRDAQTIKT	IQQRVLPTE	QSLSTLYQSV	KILQRTGNGL	LERVTRILAS	LDFAQNFTTN	720
55	NTSSVIIIEG	KKYGRITIGY	FEHYLQWIEF	SISEKVASCK	PVATALDTAV	DVFLCSYIID	780
	PLNLFWFGIG	KATVFLLPAL	IFAVKLAKY	RMDSSEVDYD	DVETIPMKNM	ENGNNGYHKD	840
	HVYGIHNPVM	TSPSQH					

Seq ID NO: 149 DNA sequence

Nucleic Acid Accession #: NM\_033049.1

Coding sequence: 28..1566

60	1	11	21	31	41	51	
	CCACGCGTCC	GAGCAAGAAC	AGCTAAAAATG	AAAGCCATCA	TCATCTTTAC	TCTTCTTGCT	60
65	CTCCTTTCTG	TAAACACAGC	CACCAACCAA	GGCAACTCAG	CTGATGCTGT	AACAACCACA	120
	GAAACTGCGA	CTAGTGGTCC	TACAGTAGCT	GCAGCTGATA	CCACTGAAAC	TAATTTCCCT	180
	GAAACTGCTA	GCACCACAGC	AAATACACCT	TCTTTCCCAA	CAGCTACTTC	ACCTGCTCCC	240
	CCATAATTA	GTACACATAG	TTCTCCACA	ATTCCTACAC	CTGCTCCCCC	CATAATTAGT	300
70	ACACATAGTT	CCTCCACAAT	TCTTATACCT	ACTGCTGCAG	ACAGTGAGTC	AACCACAAAT	360
	GTAAATTCAT	TAGCTACCTC	TGACATAATC	ACCGCTTCAT	CTCCAATGTA	TGGATTAATC	420
	ACAATGGTTC	CTTCTGAAAC	ACAAAGTAAC	AATGAAATGT	CCCCCACCAC	AGAAGACAAT	480
	CAATCATCAG	GGCCTCCCCA	TGGCACCCTG	TTATTGGAGA	CCAGCACCCT	AAACAGCACA	540
	GGTCCAGCA	ATCCTTGCCA	AGATGATCCC	TGTGCAGATA	ATTCTGTTATG	TGTTAAGCTG	600
75	CATAATACAA	GTTTTTGCCCT	GTGTTTGAGAA	GGGTATTACT	ACAACTCTTC	TACATGTAAG	660
	AAAGGAAAGG	TATTCCTCTGG	GAGAGATTTC	GTGACAGTAT	CAGAAACATT	TGACCCAGAA	720
	GAGAAACATT	CCATGGCCTA	TCAAGACTTG	CATAGTGAAA	TTACTAGCTT	GTTTAAAGAT	780
	GTATTTGGCA	CATCTGTTTA	TGGCAGAGCT	GTAATTCCTA	CTGTAAGCAC	ATCTCTGTCA	840
	CCAAGATCTG	AAATGCGTGC	TGATGACAA	TTGTTAATG	TAACAATAGT	AACAATTTTG	900
80	GCAGAAACCA	CAAGTGACAA	TGAGAAGACT	GTGACTGAGA	AAATTAATAA	AGCAATTAGA	960
	AGTAGCTCAA	GCAACTTTCT	AAACTATGAT	TTGACCCCTC	GGTGTGATTA	TTATGGCTGT	1020
	AACCGAGCTG	CCGATGCTGC	CCTCAATGGT	TTAGCATGCG	ATTGCAAAATC	TGACCTGCAA	1080
	AGGCCTAACC	CACAGAGCCC	TTTCTGCGTT	GCTTCCAGTC	TCAAGTGTCC	TGATGCGTGC	1140
	AACGCACAGC	ACAAGCAATG	CTTAATAAAG	AAGAGTGGTG	GGGCCCTGTA	GTGTGCGTGC	1200
	GTGCCCGGCT	ACCAGGAAGA	TGCTAATGGG	AACCTGCCAA	AGTGTGCATT	TGGCTACAGT	1260

GGACTCGACT GTAAGGACAA ATTTACAGTG ATCCTCACTA TTGTGGGCAC CATCGCTGGC 1320  
 ATTGTCAATC TCAGCATGAT AATTGCATTG ATTGTCACAG CAAGATCAAA TAACAAAACG 1380  
 AAGCATATTG AAGAAGAGAA CTTGATTGAC GAAGACTTTC AAAATCTAAA ACTGCGGTGCG 1440  
 ACAGGCTTCA CCAATCTTGG AGCAGAAGGG AGCGTCTTTC CTAAGGTCAG GATAACGGCC 1500  
 TCCAGAGACA GCCAGATGCA AAATCCCTAT TCAAGACACA GCAGCATGCC CCGCCCTGAC 1560  
 TATTAGAATC ATAAGAATGT GGAACCCGCC ATGGCCCCCA ACCAATGTAC AAGCTATTAT 1620  
 TTAGAGTGT TAGAAAGACT GATGGAGAAG TGAGCACCAG TAAAGATCTG GCCTCCGGGG 1680  
 TTTTCTCTCC ATCTGACATC TGCCAGCCTC TCTGAATGGA AGTTGTGAAT GTTTGCAACG 1740  
 AATCCAGCTC ACTTGCTAAA TAAGAATCTA TGACATTAAA TGATAGATG GCTATTAGCG 1800  
 CTGTGCAGAG AGGTGGTTTT CTTCATCAG TACAAAAGTAC TGAGACAATG GTTAGGGTTG 1860  
 TTTTCTTAAT TCTTTTCTCG GTAGGGCAAC AAGAACCAT TCCAATCTAG AGGAAAGCTC 1920  
 CCCAGCATTG CTGTCTCTCG GGCAACATT GCTCTTGAGT TAAGTGACCT AATTCCTCTG 1980  
 GGAGACATAC GCATCAACTG TGGAGGTCCG AGGGGATGAG AAGGGATACC CACCACCTTT 2040  
 CAAGGGTCAC AAGCTCACTC TCTGACAAGT CAGAATAGGG ACACCTGCTC TATCCCTCCA 2100  
 ATGGAGAGAT TCTGGCAACC TTTGAACAGC CCAGAGCTTG CAACCTAGCC TCACCCAAGA 2160  
 AGACTGGAAA GAGACATATC TCTCAGCTTT TTCAAGAGGC GTGCCTGGGA ATCCAGGAAC 2220  
 TTTTGTATGC TAATTGTAAG GCCTGGACTA AAAATGTCCA CTATGGGGTG CACTCTACAG 2280  
 TTTTGAATG GCTAGGAGGC AGAAGGGGCA GAGAGTAAAA AACATGACCT GGTAGAAGGA 2340  
 AGAGAGGCA AGGAAACTGG GTGGGGAGGA TCAATTAGAG AGGAGGCACC TGGGATCCAC 2400  
 CTCTCTCTCT AGTCTCCCTC CTCCATCAGC AAAGGAGCAC TTCTCTAATC ATGCCCTCCC 2460  
 GAAGACTGGC TGGGAGAAGG TTTAAAAACA AAAAATCCAG GAGTAAGAGC CTTAGGTCAG 2520  
 TTTGAATGG GAGACAAACT GTCTGGCAAA GGGTGGCAGA GGGAGCTTGT GCTCAGGAGT 2580  
 CCAGCCGTCC AGCCTCGGGG TGTAGGTTTC TGAGGTGTGC CATTTGGGGC TCAGCCTTCT 2640  
 CTGGTGACAG AGGCTCAGCT GTGGCCACCA ACACACAACC ACACACACAC AACCACACAC 2700  
 ACAAAATGGG GCAACCAAG CCAATCAAG CTTTACAAA TGTATTAGT GTCTTTTCTT 2760  
 ATTTCTAATG CCTGTCTCTC TTTAAAGTTA TTTTATTGT TATTATTATT TGTCTCTGAC 2820  
 TGTAAATTGT GAATGGTAAT GCAATAAAGT GCCTTTGTGA GATGGTGAAA AAAAAAATAA 2880  
 AAAAAA

Seq ID NO: 150 Protein sequence  
 Protein Accession #: NP\_149038.1

1 11 21 31 41 51  
 | | | | |  
 MKAIHLTL ALLSVNTATN QGNSADAVTT TETATSGPTV AAADTTETNF PETASTTANT 60  
 PSFPTATSPA PPIISTHSSS TIPTAPPPII STHSSSTIPI PTAADSESTT NVNLSLSDI 120  
 ITASSPNLGL ITMVPSTGCT NNEMSPPTED NQSSGPPTGT ALLETSTLNS TGPSPNQCDD 180  
 PCADNSLCVK LHNTSLFLCL EGYIYNSSSTC KKGKVFPGKI SVTVSETFDP EEKHSMAYPD 240  
 LHSEITSLFK DVFGTSVYQG TVILTVSTSL SPRSEMRADD KFNVTIVITI LAETTSDEK 300  
 TVTEKINKAI RSSSSNLFNY DLTLRCDYVG CNQTADDCLN GLACDCKSDL QRPNPQSPFC 360  
 VASSLKCPDA CNAQHKQLI KKSOGAPECA CVPGYQEDAN GNCQKCAFY SGLDCKDKFQ 420  
 LILITIVGTIA GIVILSMIIA LIVTARSNNK TKHIEENLI DEDFQNLKLR STGFTNLGAE 480  
 GSVFPKVRIT ASRDSQMNP YSRHSSMPRP DY

Seq ID NO: 151 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 87..914

1 11 21 31 41 51  
 | | | | |  
 AGTACGCGGG GCCGCGTTTT GCCTCCGCAG CAGCTCTGGG CTCTTCTCAG CTGCGCGAGC 60  
 AGCTGCTCCA ATGCCCCGGA GTGGCCATGG GCGCCCCGCA CTGGTGGGAC CAGCTGCAGG 120  
 CTGGTAGCTC GGAGGTGGAC TGGTGGCAGG ACAACTACAC CATCGTGCCCT GCTATCGCCG 180  
 AGTTCTACAA CAGCATCAGC AATGTCTTAT TTTTCAATTT ACCGCCCATC TGCATGTGCT 240  
 TGTTCGTGCA GTATGCAACA TGCTTCAACA GTGGCATCTA CTTAATCTGG ACTCTTTTGG 300  
 TTGTAGTGGG AATTGGATCC GTCTACTTCC ATGCAACCCCT TAGTTTCTTG GGTGAGATGC 360  
 TTGATGAATC CAGATCTCTT TGGGTTCTGA TGTGTGCTTT GGCCATGTGG TTCCCCAGAA 420  
 GGTATCTACC AAAGATCTTT CGGAATGACC GGGGTAGGTT CAAGGTGGTG GTCAGTGTCC 480  
 TGTCTGCGGT TACGACGTGC CTGGCATTGG TCAAGCCTGC CATCAACAAC ATCTCTCTGA 540  
 TGACCCCTGG AGTTCCCTTG ACTGCATGCG CTATCGCAGA GCTAAAGAGG TGTGACAACA 600  
 TGCCTGTGTT TAAGCTGGGC CTCTTCTCGG GCCTCTGGTG GACCTTGGCC CTGTTCTGCT 660  
 GGATCAGTGA CCGAGCTTTC TGCGAGCTGC TGTCTATCCT CAACTTCCCC TACCTGCACT 720  
 GCATGTGGCA CATCTCATC TGCCTTGCTG CCTACCTGGG CTGTGTATGC TTTGCCTACT 780  
 TTGATGCTGC CTCAGAGATT CCTGAGCAAG GCCCTGTCTC CAAGTTCTTG CCCAATGAGA 840  
 AATGGGCCCT CATTTGGTGT CCCTATGTGT CCCTCCTGTG TGCCAACAAG AAATCATCAG 900  
 TCAAGATCAC GTGATGGCAA GATGGTGGCT GGCTTCTCTG CTTATCGCCC CTCATGCAGT 960  
 GGGCTTCTCT TGCTAGGAAG ACAGCCAAGG GAGTTCGAAT AGTTGGGGTG TGGGCTATCT 1020  
 TTTCAAAAAT CTATTGCTG GGGCTCTTAA TTTCTTTAGT GTTCTTTGTA TGTAGGGATT 1080  
 TAAACTTTGT CATATGGTAC AAATATTCCC TGCCCCCTCG CAGTTTCCCA TTTGTCTTTC 1140  
 AGTATGTTAA TATTTTGTGT CCATACTGGT TTTAACTTT CATGTTGTCA CATCTGTTAA 1200  
 TCTTTCTTCT AGGATTTCTG GATTTTGTGT AATTTTAA AAGTCCCCT CCTCTCCCT 1260  
 AATGTGTCTG TGGACCACCT GGATTCCACT GTACAAGGGG AAAAGTGTCT ATTCCTTTCC 1320  
 CAAAGATGGA AAATGGAGGG CTTAGGGACA CTAGATGCAT CTTTCTCAGC ATCATCTCCA 1380  
 GATGCAGTGA CTTGTGGGCG TGCGTCTCTA ATGGCCATGG CAGAGCAGTC CCTTGGGGGA 1440  
 TCCAGCCCTG TACAATGCAT CTCTCTCTGG AGAAAGCTGG CCTGCTCCAG ACCCCACCAT 1500  
 TCCCAGGCGC CCTTGGAGTG GACTCTACTG ATGACAGACA GACCTCTGA GAGACAAGAC 1560  
 CCTCTGACTC TGTGATGGA GATGCCAGAG ATTTTCTCTT GGGTAATTG TCCTTAAACA 1620  
 AAACCAACAC ATGGAACAC ACACAGGACT TGTGGCTAAA AAGGCTAGTT TTTCACTTGC 1680  
 ATTTCTCAAC TAACCCAGGT TTTACATGCA TCTGTGAATC CTTTACTTAC TACCTCTGTG 1740  
 GAGAGATGGA GAGACTTCAG ATAACCTGTA AGCTAATGAG TAAACCTCTC TCTGCCAAA 1800  
 CCTCACCTGC ACTTTAGGCC CTCTTGAAG ATGAGCACA TTTTAAATA CTGAGCACA 1860  
 TTTTAAATA CTGACATCAC TTCTCTTCC CCCTCCACC CCAGCTCAGC AGCCTCAAAT 1920  
 CTACAGAGAA GAAGAATTAT GGCATGAACA TTCCACAGA CCCACCATCT TTAAGACTTG 1980  
 ACCTCTGTAA GTTTACAAA GGGCTCTCA CAATTGTGGT GGGGGTCTG GTTCAAAATT 2040

5 TGGAGCAAAAC ATGAAGTTTT TGGAAACGTT TTCTCATTTG AAGCCTCCAG TATGCTGTAC 2100  
 TATTCGTGGAA ATTACCTTCA AGAGTCTCAC TTCTTGTTTC TGTGTGTTT TCTGTGGGCA 2160  
 TCACTGTTCTT CACGCTTGCA GTAGAAGGTG CTTCTCGGT TTCCACAGAT ATCCAACGGC 2220  
 TCACCTTTCT CAAGTCTGGG CAGTAGCTAT GCACTCACGG GCTGGTTTGG GTCGCTGGTG 2280  
 CAGCAGCGCA AATCTGTTGC CTTCTGAATT TTCTCACCT AATGTGACAC TGGCTACAAT 2340  
 GAATCTTCTC TTCATCGGGC TGAATGAAAG ATTCAAGAAC CATCTTCAAG GTGCATGGTG 2400  
 GGAATTATCA ACCTCAGGGA TACTCATTTT AACTCAGGCG TGTCTGCTT TGTAACATT 2460  
 CATTTGTTGGG AGAGGGCAGG ACAGGTGTGT TCTTCTGTGG GCAGGAGTCA TGCTACTGTC 2520  
 10 GTACATATGT AAGAGTTGGG AAGGTGACGA TTTTGTACAC ATCCAGGAAC TCTTACTCTA 2580  
 GTTAGAATTT GTACCGATC CAAGGTGAAA ACCCCAATAA GCAACTGAAT TTAGAGTTTA 2640  
 AAAATGAATG ACTTTATGCT ACATCTGTGG TTATCAAATT ATATAGTTTG TTGAGAAGCA 2700  
 GAACGCTGTT TGTAGTAAGA AATCTTTGTG GAACCCAGT GTGTGAAGTA AATTGTATGT 2760  
 TATTAATTTT ATTTAAGTTT AAATTTATGG CATTACTTA ATAATATATG AGGTGGTGAA 2820  
 AATGCAAATT AACAAATGG TAATTTCCAA GGTAGAAAAA TTAGGTGTTG AATGAATGTA 2880  
 15 TATGTTGGTT TATTATAGTT TTATATATAT ATAGAGAGAG TGTTTTGT TTGAGTCAGG 2940  
 GTCTTGCTCT ATTACCCAGG CTGGAGTGCA GTGGTGCACT CATGACTCAC TGAGCCTCT 3000  
 GTCTCCAGG CTCAAGTGAT CCTCTCACCT CAGCCTCCCC AGGAGCTGGG AGTACTGGTG 3060  
 CGTGCCTCCA CTCCCAGCTA ATTTTGTAT TTTTTCATAG AGATGGGGTT TCACCATTTT 3120  
 GCCCAGGCTG GTCTCAAAC TCTGGGCTCA AGAGATTGCG CCGCCTCGGC CTCCCAAAGT 3180  
 20 GCTGGGAATA GGCATGAGCC GTCCGCGCTG GCCTAAAAAA TATTTTAAAT ATGATCTTTG 3240  
 AATTAATAT TCGTAGAATT TCTAATGTAT CTCTTTGAGA CCTAGGAGGT TGATGGGAACA 3300  
 GAACGTCTGT TAAGTCTTTT GGGTTTCAAG TCTAGAATTT TTTAAAGGCA AATATCAGCT 3360  
 CATCTTATT TTAGATGAC CTTATCAGGC ATGGATTCTG GTCTCATCTA CTTTATGGTA 3420  
 TAAATGCTCC AAGGTAGGGG GTTTGGTATA TATTTTAAGC CCGGCTTTTT TTTTTTTTTT 3480  
 25 TTTTTTTTTT TTTTAAATGT GAGAAGCAGA ATGTGCTTCT AGAACTGGT TTTAAAGAGA 3540  
 TGAGCTGAGA AAGAAATGTG GAATGGAGTA TATTGAGGA GGACAAAACA TAACCTCACT 3600  
 TTTGAACAGA AATCACTCTA GCTTGCCAGC ATGGGATGTA AACCAGAGA GTAGAAATAT 3660  
 ACCCATCTTA TTTTAAGTTG GGTTTATGGC ATCGCTCATA TATGTAAAG CACTACAAAC 3720  
 TCTTTAAAGA AAATTTGGGA ACTACAGAGA AGTCAAAGAA AAAAAAAGT AACCCATATT 3780  
 30 TCTATTGCC AGGTATAATC CTTGTTAATA TTTTGGTTTG GTCTCCTCTT TTTTCCCCC 3840  
 AATATAGTTG TAAATAATG ATGCTTTTCA GAGTTGACAT TTATCCTGTA GCTTGAATGG 3900  
 CATGTAATG CCAAGTTGTAT ATTTTTCAT GAAGTGTAGG TTTGGAATAC ACTAGAGTTA 3960  
 GCTATATGCT TGAATGCTGA TCACCTGGAT CTGAGACTGA CTAAGTATG TACCTTTTTA 4020  
 ATCAAGCCTA ACATGAATGG GCTCCAAAAA GTAATGAATG TAATGTACT TTTTGTATG 4080  
 35 CCTCTGCACT TGGCTGTGTG AGTCATCATA AATAGCTGTT AAATATGTGA CTTTACAGAT 4140  
 TTTGATATGT TCAGATTGTA AAAAATGAAT AGTTTATTTT ATTAATTGAT GGCAGTCAA 4200  
 GAATCTCCCT CC

Seq ID NO: 152 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 45 MGAPHWWDQL QAGSSEVDWC EDNYTIVPAI AEFYNTISNV LFFILPPICM CLFRQYATCF 60  
 NSGIYLIWTL LVVVIGISVY PHATLSFLGQ MLDELAVLWV LMCALAMWFP RRYLPKIFRN 120  
 DRGRFKVVVS VLSAVTTCLA FVKPAINNIS LMTLGVPTA LLIAELKRCN NMRVFKLGLF 180  
 SGLWNTLALF CWISDRAFC LSSFNFPYL HCMWHILICL AAYLGVCVFA YFDAASEIPE 240  
 QGPVIKFWPN EKWAFIGVPY VSLLCANKKS SVKIT

Seq ID NO: 153 DNA sequence  
 Nucleic Acid Accession #: NM\_001432.1  
 Coding sequence: 167..676

55 1 11 21 31 41 51  
 TCACTTGCCT GATATTCCCA GTGTCAGAGG GACACAGCCA ACGTGGGGTC CCTTCTAGGC 60  
 TGACAGCCCG TCTCCAGCCA CTGCCGCGAG CCGTCTGCT CCCGCCCTGC CCGTGCACTC 120  
 TCCGACCGCG CCTCCGCGCA AGCCCGAGCG CCGCTCCCA TCGCCGATGA CCGCGGGGAG 180  
 GAGGATGGAG ATGCTCTGTG CCGGAGGGT CCTGCGCTG CTGCTCTGCC TGGGTTTCCA 240  
 60 TCTTCTACAG GCATCCCTCA GTACAACGTG GATTCCATCA TGTATCCAG GAGAGTCCAG 300  
 TGATAACTGC ACAGCTTTAG TTCAGACAGA AGACAATCCA CGTGTGCTC AAGTGTCAAT 360  
 AACAAAGTGT AGCTCTGACA TGAATGGCTA TTGTTTGCAT GGACAGTGCA TCTATCTGGT 420  
 GGACATGAGT CAAAACACT GCAGGTGTGA AGTGGGTTAT ACTGGTGTCC GATGTGAACA 480  
 CTTCTTTTAA ACCGTCCACC AACCTTAAAG CAAAGAGTAT GTGGCTTTGA CCGTGATTCT 540  
 65 TATTATTTTG TTTCTTATCA CAGTCGTCGG TTCCACATAT TATTCTGCA GATGGTACAG 600  
 AAATCGAAAA AGTAAAGAAC CAAAGAAGGA ATATGAGAGA GTTACCTCAG GGGATCCAGA 660  
 GTTGCCGCAA GTCTGAATGG CGCCATCAAA CTTATGGGCA GGGATAACAG TGTGCCTGGT 720  
 TAATATTAAT ATTCATTTT ATTAATAATA TTTATGTTGG GTCAAGTGT AGGTCAATAA 780  
 CACTGTATTT TAAATGACTT GAAAAATGTT TTTATTTTGT TTTATTTT GACAGACTAT 840  
 70 TTGCTAATGT ATAATGTGCA GAAATATTTT AATATCAAAA GAAAATTGAT ATTTTATATC 900  
 AAGTAATTTT CTGAGCTTAA TGCTTCATTG AAAGCTTCAA AGTTTATATG CCTGGTGCAC 960  
 AGTGCTTAGA AGTAAGCAAT TCCAGGTGTA TAGCTCAAGA ATTGTTAGCA AATGACAGAT 1020  
 TTCTGTAGC CTATATATAT AGTCAATCG ATTTAGTAAG TATGTTTTT ATGTTCTCTCA 1080  
 75 AATCAGTGAT AATTTGGTTG ACTGTACCAT GGTGTTGATAT GTAGTTGGCA CCATGGTATC 1140  
 ATATATTAATA AATAATATG AATTAGAATT TGGGAGAAGC AAATATAGGT CCTGTGTTAA 1200  
 ACACACACCA TTTGAAACAA GCTAACCTG GGGAGTCTAT GGTCTCTTCA CTCAGGTCTC 1260  
 AGCTATAATT CTGTTATATG AGGGGCGATG GACAGTTCCT TATGCCAAT CACGACTCCT 1320  
 ACAGGTACTA GTCACTCATC TACCAGATTC TGCCTATGTA AAATGAATTG AAAACAATT 1380  
 80 TTCTGTAATC TTTTATTTAA GTAGTGGGCA TTTATAGCT TCACAATGTT CCTTTTGT 1440  
 ATATTACAACT ATTATGTGTA GGTAAATTAT GCTCAACAGA CAATTAGAAA AAAGTCCACA 1500  
 CTTGAAGCCT AAATTTGTGC TTTTAAAGAA TATTTTGA CTATTTCTTT TTATAGGGGC 1560  
 TTTGCTGAAT TCAACATTA AATCAGGCC CAAAATTTGA TGGACTAATT ATTATTTTAA 1620  
 AATATATGAA GACAATAATT CTACATGTTG TCTTAAGATG GAAATACAGT TATTTATCT 1680  
 TTTATTCAGG GAGTTTTAA CTTTAATACA GCTCAGTAAA TGGCTTCTTC TAGAATGTAA 1740

AGTTATGTAT TTAAGGTTGT ATCTTGACAC AGGAAATGGG AAAAAACTTA AAAATTAAATA 1800  
 TGGTGTATTT TTCCAAATGA AAAATCTCAA TTGAAAGCTT TTAATAATGA GAAACTTAAA 1860  
 CACACCTTCC TGTGGAGGCT GAGATGAAAA CTAGGGCTCA TTTTCTGAC ATTTGTTTAT 1920  
 TTTTGGGAAG AGACAAAGAT TTCTTCTGCA CTCTGAGCCC ATAGGTTCTCA GAGAGTTAAT 1980  
 AGGAGTATTT TTGGGCTATT GCATAAGGAG CCACTGCTGC CACCACITTTT GGATTTTATG 2040  
 GGAGGCTCCT TCATCGAATG CTAAACCTTT GAGTAGAGTC TCCTTGGATC ACATACCAGG 2100  
 TCAGGGAGGA TCTGTTCTTC CTCTACGTTT ATCCTGGCAT GTGCTAGGGT AAACGAAGGC 2160  
 ATAATAAGCC ATGGCTGACC TCTGGAGCAC CAGGTGCCAG GACTTGTCTC CATGTGTATC 2220  
 CATGCATTAT ATACCTTGGT GCAATCACAC GACTGTCTATC TAAAGTCCTG GCCCTGGCCC 2280  
 TTACTATTAG GAAAAATAAC AGACAAAAAC AAGTAAATAT ATATGGTCCT ATACATATTG 2340  
 TATATATATT CATATACAAA CATGTATGTA TACATGACCT TAATGGATCA TAGAATTGCA 2400  
 GTCAATTTGGT GCTCTGCTAA CCATTTATAT AAAACTTAAA AACAAGAGAA AAGAAAAATC 2460  
 AATTAGATCT AAACAGTTAT TTCTGTTTCC TATTTAATAT AGCTGAAGTC AAAATATGTA 2520  
 AGAACACATT TTAATACTC TACTTACAGT TGGCCCTCTG TGGTTAGTTC CACATCTGTG 2580  
 GATTCAACCA ACCAAGGACG GAAAAATGCTT AAAAAATAAT ACAACAACAA CAAAAAATAC 2640  
 ATTATAACAA CTATTTACTT TTTTTTTTTT CTTTTTGAGA TGGAGTCTCG CTCTGTGGCC 2700  
 CAGGTTGGAG TGCAGTGGCA CGATCTCGGC TCACTGCAAC CTCACCTCCC GGGTTCAAGA 2760  
 GATCCTCCTG CCTCAGCCTC CTGAGCAGCT GGGACTACAG GCGCATGCCA CCATGCCAG 2820  
 CTAATTTTGT TATTTTTAGT AGAGCGGGG TTTCAACCATG TTGGCCAGGA TGGTCTCAAT 2880  
 CTCTAACCTT TGAGATCCAC CCTCCACAGC CTCCCAACT GCTGGGATTA CAGGCGTGAG 2940  
 CCACCCGACG TAGCATTTAC ATTAGGTATT ACAAGTAATG TAAAGATGAT TTAAGTATAC 3000  
 AGGAGGATGT GAATAGGTTA TATGCAAGCA CTATGCCCTT TTATATAAGT GACTTGAAAC 3060  
 TCTGTGCCCG ATTTTAGTAT GTGCAGGGGG GCGACTCTGG AATCAGTCCC CTGTGGATAC 3120  
 CRAAGTACAA CTGTATTTAT TAACGCTTAC TAGATGTGAG GAGAGTCTGA ATATTTTCAG 3180  
 TGATCTTGGC TGTTCACAAA AAATCTATTG ACTTTTCAAT AAATCAGCTG CAATCCATTT 3240  
 ATTTCAATTA CAAAAGATTT ATTGTAAGCC TCTCAATCTT GGTTTTTCAG TTGATCTTAA 3300  
 GCATGTCAAT TCATAAAAAA AAGTCATTTT TGTATTTTTC ATCTTTAAGA ATGCTTAAAA 3360  
 AAGCTAATCC CTAAAAAGT TAGATCTTTG TAAATGCATA TTAATAATAA AAGTATGACC 3420  
 CACATTAATT TTTATGGGTG AAAATAAGAC AAAAAATAA GTTTTAGTGA GGATGGTGCT 3480  
 GAGTAAACAT AAAAATCATG TTGCTCTCAG CTGATGTGTC CTGTACACAG TGGGAAGATT 3540  
 TTAGTTACAA CTAGTCTCAA CTCCTCCATT TTACAGATTT CTCACATAT ATATTTCTAG 3600  
 AAGGGGCTAT GCATATTCAA TGTATTGAGA ACCAAAGCAA CCACAATGC ATAAATGCAT 3660  
 AATTTATGGT CTTCAACCAA GGCCACATA TAACCCAGTT AACTTACTCT TTAACACGGA 3720  
 ATATTAAGTT CTATACTAG TACTCAAGGT TTAACCTTAA AATTAAGATT TCCTTAACCT 3780  
 TAACCTTAAA ATTGATATTA TATTAACAT ACATAATACA ATGTAACCTC ACTGTTCTCC 3840  
 TGAATATTTT TTGCTCTAAT CTCTCTGCCG AAAGTCAAAAG TGATGGGAGA ATTTGGTATAC 3900  
 TGGTATGACT ACCTCTTAAG TCAGATTTT ATTATGAGT CTTTGAGACT AAATTCATC 3960  
 ACCACAGGT ATCAAAATCAA CTTTTATGCA GCAAAATATAT GATTCTAGTG TCTGACTTTT 4020  
 GTTAAATTCG ATAAATGATG TTTTAAAAAC CTGTATCTGA CCCACTTTGT AATTTTGTCT 4080  
 CCAATATCCA TTTCTGTAGC TTTTGAAAAA AAAGTTTTTA ATTTGATGCC CAATATATTC 4140  
 TGACCGTTAA AAAATTCTTG TTCATATGGG AGAAGGGGGA GTAATGACT GTACAAACAG 4200  
 TATTCTGGT GTATATTTTA ATGTTTTTAA AAAGAGTAAT TTCATTTAAA TATCTGTTAT 4260  
 TCAAAATTGA TGATGTTAAA TGTAAATATA TGTATTTTCT TTTTATTTTG CACTCTGTAA 4320  
 TTGCACTTTT TAAGTTTGAA GAGCCATTTT GGTAAACGGT TTTTATTTAA GATGCTATGG 4380  
 AACATAAAGT TGTATTGCAT GCAATTTAAA GTAACCTATT TGACTATGAA TATTATCGGA 4440  
 TTAATGAATT GTATCAATTG GTTTGTGTTT AATATCAGCT TTGATAATTG TGTACCTTAA 4500  
 GATATTGAAG GAGAAAAATG ATAAATTACA AGATATTATT AATTTTATT TATTTTCTT 4560  
 GGGAAATTGA AAAAAATTGA ATAAATAAAA ATGCATTGAA CATCTTGCAT TCAAAATCTT 4620  
 CACTGAC

Seq ID NO: 154 Protein sequence  
 Protein Accession #: NP\_001423.1

1 11 21 31 41 51  
 | | | | |  
 MTAGRRMEML CAGRVPALLL CLGFHLLQAV LSTTVIPSCI PGESSDNCTA LVQTEDNPRV 60  
 AQSITKCSS DMNGYCLHGQ CIYLVDSQON YCRCEVGYTG VRCEHFFLTV HQPLSKEYVA 120  
 LTVILILFL ITVVGSTYYF CRWYRNRKSK EPKKEYERV TSGDFELPQV

Seq ID NO: 155 DNA sequence  
 Nucleic Acid Accession #: NM\_013282.2  
 Coding sequence: 85..2466

1 11 21 31 41 51  
 | | | | |  
 CGACTCCTTA GAGCATGGCA TGGCTCAGAG GTGCTGGTAA AACTGATGGG GGTTTTGTCT 60  
 GTCCCTCCCC TCAGCGCCGA CACCATGTGG ATCCAGGTTT GGACCATGGA CGGGAGGCAG 120  
 ACCCACACGG TGGACTCGCT GTCCAGGCTG ACCAAGGTGG AGGAGCTGAG GCGGAAGATC 180  
 CAGGAGCTGT TCCACGTGGA GCCAGGCTG CAGAGGCTGT TCTACAGGGG CAAACAGATG 240  
 GAGGACGGCC ATACCTCTCT GACTACGAG GTCCGCTGTA ATGACACCAT CCAGCTCTCTG 300  
 GTCCGCCAGA GCCTCGTGCT CCCCCACAGC ACCAAGGAGC GGGACTCCGA GCTCTCCGAC 360  
 ACCGACTCCG GCTGCTGCCT GGGCCAGAGT GAGTCAGACA AGTCTCCAC CCACGGCGAG 420  
 GCGGCCGCCG AGACTGACAG CAGGCCAGCC GATGAGGACA TGTGGGATGA GACGGAATTG 480  
 GGGCTGTACA AGGTCAATGA GTACGTCGAT GCTCGGGACA CGAACATGGG GCGGTGGTTT 540  
 GAGGCGCAGG TGGTCAGGGT GACGCGGAAG GCCCCTCTCC GGGACGAGCC CTGCAGCTCC 600  
 ACGTCCAGGC CGGCGCTGGA GGAGGACGTC ATTTACCACG TGAATAACGA CGACTACCCG 660  
 GAGAACGGCG TGGTCCAGAT GAACTCCAGG GACGTCCGAG CGCGCGCCCG CACCATCATC 720  
 AAGTGGCAGG AACTGGAGGT GGGCCAGGTG GTCATGCTCA ACTACAACCC CGACAACCCC 780  
 AAGGAGCGGG CTTCTTGTTA CGACGCGGAG ATCTCCAGGA AGCGCGAGAC CAGGACGGCG 840  
 CGGGAACCTCT ACGCCAACGT GGTGCTGGGG GATGATTCTC TGAACGACTG TCGGATCATC 900  
 TTCGTGGACG AAGTCTTCAA GATTGAGCGG CCGGGTGAAG GGAGCCCCAT GGTTGACAAC 960  
 CCCATGAGAC GGAAGAGCGG GCCGTCTGTC AAGCACTGCA AGGACGACGT GAACAGACTC 1020  
 TGCAGGTCTT GCGCTGCGCA CCTGTGCGGG GGCCGCGCAG ACCCGACACA GCAGCTCATG 1080  
 TGCATGAGT GCGACATGGC CTTCCACATC TACTGCCTGG ACCCGCCCTT CAGCAGTGTT 1140

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45

```

CCCAGCGAGG ACGAGTGGTA CTGCCCTGAG TGCCGGAATG ATGCCACGGA GGTGGTACTG 1200
GCGGGAGAGC GGCTGAGAGA GAGCAAGAAG AAGGCGAAGA TGGCCTCGGC CACATCGTCC 1260
TCACAGCGGG ACTGGGGCAA GGGCATGGCC TGTGTGGGCC GCACCAAGGA ATGTACCATC 1320
GTCCCGTCCA ACCATACCGG ACCCATCCCG GGGATCCCGG TGGGCACCAT GTGGCGGTTC 1380
CGAGTCCAGG TCACGCGAGT GGGTGTCCAT CGGCCCCACG TGGCTGGCAT ACACGGCCCG 1440
AGCAACGAGC GAGCGTACTC CCTAGTCCCT GCGGGGGGCT ATGAGGATGA CGTGGACCAT 1500
GGGAATTTTT TCACATACAC GGGTAGTGGT GGTGAGATC TTCCGGCAA CAAGAGGACC 1560
GCGGAACAGT CTTGTGATCA GAAACTCACC AACACCAACA GGGCGCTGGC TCTCAACTGC 1620
TTTGCTCCCA TCAATGACCA AGAAGGGGCC GAGGCCAAGG ACTGGCGGTC GGGGAAGCCG 1680
GTCAGGGTGG TGCCCAATGT CAAGGGTGGC AAGAATAGCA AGTACGCCCC CGCTGAGGGC 1740
AACCCTACG ATGGCATCTA CAAGGTGTG AAATACTGGC CCGAGAAGGG GAAGTCCGGG 1800
TTTCTCGTGT GCGCTACCT TCTGCGGAGG GACGATGATG AGCCTGGCCC TTGGACGAAG 1860
GAGGGGAAGG ACCGGATCAA GAAGCTGGGG CTGACCATGC AGTATCCAGA AGGCTACCTG 1920
GAAGCCCTGG CCAACCGAGA GCGAGAGAAG GAGAACAGCA AGAGGAGGA GGAGGAGCAG 1980
CAGGAGGGGG GCTTCGCTG CCCAGGACG GGCAAGGGCA AGTGAAGCG GAAGTCGGCA 2040
GGAGGTGGCC CGAGCAGGGC CGGGTCCCCG CGCCGACAT CCAAGAAAAC CAAGGTGGAG 2100
CCCTACAGTC TCACGCCCCA GCAGAGCAGC CTCATCAGAG AGGACAAGAG CAACGCCAAG 2160
CTGTGGAATG AGGTCCCTGC GTCACTCAAG GACCGGCGCG CGAGCGGCAG CCCGTTCCAG 2220
TTGTTCTGTA GTAAAGTGGG GGAGACGTTT CAGTGTATCT GCTGTGAGGA GCTGGTGTTC 2280
CGGCCCATCA CGACCGTGTG CCAGCAAC GTGTGCAAGG ACTGCCTGGA CAGATCCTTT 2340
CGGGCACAGG TGTTCACTG CCCTGCCTGC CGCTACGACC TGGGCCGCG CTAATGCCATG 2400
CAGGTGAACC AGCCTCTGCA GACCGTCTCT AACCAGCTCT TCCCCGGCTA CGGCAATGGC 2460
CGGTGATCTC CAAGCACTTC TCGACAGGCG TTTTGCTGAA AACGTGTCGG AGGGCTCGTT 2520
CATCGGCACT GATTTTGTTC TTAGTGGGCT TAACCTAAAC AGGTAGTGT TCTCCGTTT 2580
CCTAAAGAGG TTTGTCTTCT TTTTATTTT TTTTATTTT TCAAATCTAT ACATTTTCAG 2640
GAATTTATGT ATTCTGCTTA AAGTTGGAC TTCTCAGTAT TGTGTTTAGT TCTTTGAAAA 2700
CATAAAGGCC TGCAATTTCT CGACAAACA ACACAAGATT TTTTAAAGAT GGAATCAGAA 2760
ACTACGTGGT GTGGAGCTTC TTGATGTTTC TGGTGTCAAG TTCTCAGAAG TTGCTGCCAC 2820
CAACTCTTTA AGAAGGCGAC AGGATCAGTC CTCTCTAGG GTTCTGGCCC CCAAGTCCAG 2880
AGCAAGCATC TTCCTGACAG CATTTTGTCA TCTAAAGTCC AGTGACATGG TTCCCGTGG 2940
TGGCCCGTGG CAGCCCGTGG CATGGCGTGG CTCAGCTGTC TGTGTAAGTT GTTGCAAGGA 3000
AAAGAGGAAA CATCTCGGGC CTAGTTCAAA CCTTGCCTC AAAGCCATCC CCCACCAGAC 3060
TGCTTAGCGT CTGAGATCCG CGTGAAAGT CCTCTGCCA CGAGAGCAGG GAGTTGGGGC 3120
CACGCAGAAA TGGCCTCAAG GGGACTCTGC TCCACGTGGG GCCAGGCGTG TGACTGACGC 3180
TGTCGACAGA AGGCGGCCAC GGACGGACGC CAGCACACGA AGTCACGTGC AAGTGCCTTT 3240
GATTCGTTC TTTCTTTTAA AGACGACAGT CTTTGTGTT AGCACTGAAT TATTGAAAAT 3300
GTCAACCAGA TTTAGAAAC TGCGGTCTAT CAGTCTTCC TGACACCGGA TGGGTGCTTG 3360
GGAACCGTTT GAGCCTTATA GATCATTTAC ATTCATTTT TTTAACTCAG CAAGTGAGAA 3420
CTTACAGAG GGTTTTTTTT TAATTTTTT TTCTCTTAAT GAACACATT TCTAAATGAA 3480
TTTTTTTGT AGTTACTGTA TATGTACCAA GAAAGATATA ACCTTAGGGT TTGGTTGTTT 3540
TTGTTTTGT ATTTTCTTTC TTTGAAAGG GTTTGTTAAT TTTCTAATT TTACCAAAGT 3600
TTGCAGCTTA TACCTCAATA AAACAGGGAT ATTTTAAATC ACATACCTGC AGACAACTG 3660
GAGCAATGTT ATTTTAAAG GGTTTTTTTC ACCTCCTTAT TCTTAGATTA TTAATGTATT 3720
AGGGAAGAA AGACAATTT TGTGTAGGCT TTTTCTAAAG TCCAGTACTT TGTCAGATT 3780
TTAGATTCTC AGAATAAATG TTTTTCACAG ATTGAAAAA AAAAAAAA
  
```

Seq ID NO: 156 Protein sequence  
 Protein Accession #: NP\_037414.2

50  
 55  
 60  
 65

```

1 11 21 31 41 51
| | | | |
MWIQVRTMDG RQHTVDSLS RLTKEVELRR KIQLFHVPEP GLQLFYRGK QMEDGHTLFD 60
YEVRNDTIQ LLVRQSLVLP HSTKERDSEL SDTDSGCCLG QSESDKSSTH GEAAAEETDSR 120
PAEDMWDNET ELGLYKNEY VDARDTNMGA WFEAQVVRVT RKAPSRLDEPC SSTSRPALEE 180
DVIYHVKYDD YPENGVMQMN SRDVRARART IIKWQDLEVG QVVMNLNPNP NPKERGFWDY 240
AEISRKRRETR TARELYANVH LGDDSLNDCR IIFVDEVFKI ERPEGSEPMV DNPMMRKS GP 300
SKHKCKDDVN RLRCVVCACH CGGRQDPDKQ LMCDECDMAF HIYCLDPPLS SVPSDEWYVC 360
PECRNDASEV VLAGERLRES KKKAKMASAT SSSQRDWKGG MACVGRTEKEC TIVPSNHYGP 420
IPGIPVGTMMW RFRVQVSESG VHRPHVAGIH GRSNDGAYSL VLAGGYEDDV DHGNFFTYTG 480
SGGRDLSGNK RTAEQSCDQK LTNTRALAL NCFAPINDQE GAEAKDWRSG KPVVRVVRNVK 540
GGKNSKYAPA EGNRYDGIYK VVKYWPEKGK SGFLVWRYLL RRDDDEPGPW TKEGKDRIKK 600
LGLTMQYPEG YLEALANRER EKENSKEEEE EQQEGGFASP RTGKGKWKRK SAGGGPSRAG 660
SPRRTSKKTK VEPYSLTAQQ SSLIREDKSN AKLWNEVLAS LKDRPASGSP FQLFLSKVEE 720
TFQCICQQL VFRPITTVQC HNVCKDCLDR SFRAQVFSFP ACRYDLGRSY AMQVNPQLQT
  
```

Seq ID NO: 157 DNA sequence  
 Nucleic Acid Accession #: NM\_000756.1  
 Coding sequence: 186..776

70  
 75  
 80

```

1 11 21 31 41 51
| | | | |
AGAAACTCAG AGACCAAGTC CATTGAGAGA CTGAGGGGAA AGAGAGGAGA GAAAGAAAAA 60
GAGAGTGGGA ACAGTAAAGA GAAAGGAAGA CAACCTCCAG AGAAAGCCCC CGGAGACGTC 120
TCTCTGCAGA GAGGCGGCAG CACCCGGCTC ACCTGCGAAG CGCCTGGGAA GCGAGTGCCT 180
CTAACATGCG GCTGCGCGCTG CTTGTGTCCG CGGGAGTCCT GCTGGTGGCT CTCCTGCCCT 240
GCCCGCCATG CAGGCGGCTC CTGAGCCGCG GCGCGGTCCC GGGAGCTCGG CAGGCGCCGC 300
AGCACCCCTA GCCCTTGGAT TTCTTCCAGC CGCCGCGGCA GTCCGAGCAG CCCAGCAGC 360
CGCAGGCTCG GCCGTCTCTG CTCCGATGG GAGAGGAGTA CTCTCTCCG CTGGGGAACC 420
TCAACAAGAG CCCGCGCGCT CCCCTTTCGC CCGCCTCCTC GCTCCTCGCC GGAGGCAGCG 480
GCAGCCGCCC TTCGCGGGA CAGGCGACCG CCAACTTTT CCGCGTGTG CTGACGACG 540
TGCTGCTGCG TCGGCGCTCG CTCGACAGCC CCGCGGCTCT CGCGGAGCGC GGCGCTAGGA 600
ATGCCCTCGG CGGCCACCG GAGGCACCGG AGAGAGAAAG GCGGTCCGAG GAGCCTCCCA 660
TCTCCCTGGA TCTCACCTTC CACCTCCTCC GGAAGTCTT GGAATGGCC AGGGCCGAGC 720
AGTTAGCACA GCAAGCTCAC AGCAACAGGA AACTCATGGA GATTATTGGG AAATAAAACG 780
  
```

GTGCGTTTGG CCAAAAAGAA TCTGCATTGA GCACAAAAAA AATTAAAAAA AATACAGTAT 840  
 TCTGTACCAT AGCGCTGCTC TTATGCCATT TGTTATTTT TATATAGCTT GAAACATAGA 900  
 GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTTAGCATGC ACAAAGTGTA TTCACGTGCA 960  
 GCAGCAACAC AATGTTATTC GTTTTGCTA CGTTTAGTTT CCGTTTCCAG GTGTTTATAG 1020  
 TGGTGTTTTA AAGAGAATGT AGACCTGTGA GAAAACGTTT TGTGTGAAAA AGCAGACAGA 1080  
 AGTCACTCAA TTGTTTTTGT TGTGGTCTGA GCCAAAGAGA ATGCCATTCT CTTGGGTGGG 1140  
 TAAGACTAAA TCTGTAAGCT CTTTGAAACA ACTTCTCTT GTAAACGTTT CAGTAATAAA 1200  
 ACATCTTTCC AGTCCTTGGT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT 1260  
 TAATAAAGT TGCAAAGGT

Seq ID NO: 158 Protein sequence  
 Protein Accession #: NP\_000747.1

1 11 21 31 41 51  
 | | | | |  
 MRLPLLVSAG VLLVALLPCP PCRALLSRGP VPGARQAPQH PQPLDFFQPP PQSEQPQQPQ 60  
 ARPVLLRMGE EYFLRLGNLN KSPAAPLSPA SLLLAGSGS RPSPEQATAN FFRVLLQQLL 120  
 LPRRLDSPA ALAERGARNA LGGHQEAPER ERRSEEPPI SLDLTFHLLRE VLEMARAEQL 180  
 AQAHSNRKL MEIIGK

Seq ID NO: 159 DNA sequence  
 Nucleic Acid Accession #: NM\_001200.1  
 Coding sequence: 325..1514

1 11 21 31 41 51  
 | | | | |  
 GGGGACTTCT TGAAGTTCAG GGGAGAATAA CTTGCGCACC CCACTTTGCG CCGGTGCCTT 60  
 TGCCCCAGCG GAGCCTGCTT CGCCATCTCC GAGCCCCACC GCCCTCCAC TCCTCGGCCT 120  
 TGCCCCGACAC TGAGACGCTG TTCCCAGCGT GAAAAGAGAG ACTGCGCGGC CGGCACCCGG 180  
 GAGAAGGAGG AGGCAAGAGG AAGGAACGGA CATTGCTCC TTGCGCCAGG TCCTTTGACC 240  
 AGAGTTTTC CATGTGGACG CTCTTTCAAT GGACGTGTCC CCGCGTGCTT CTTAGACGGA 300  
 CTGCGGTCTC CTAAGGTGCG ACCATGGTGG CCGGGACCCG CTGTCTTCTA GCGTTGCTGC 360  
 TTCCCCAGGT CCTCCTGGGC GCGCGGCTG GCCTCGTTCC GGAGCTGGGC CGCAGGAAGT 420  
 TCGCGGCGGC GTCGTGCGGC CGCCCCCTCAT CCCAGCCCTC TGACGAGGTC CTGAGCGAGT 480  
 TCGAGTTGCG GCTGCTCAGC ATGTTGCGCC TGAACACAG ACCCACCCCC AGCAGGGACG 540  
 CCGTGGTGCC CCCTACATG CTAGACCTGT ATCGCAGGCA CTCAGGTCAG CCGGGCTCAC 600  
 CCGCCCCAGA CCACCGGTTG GAGAGGGCAG CCAGCCGAGC CAACACTGTG CGCAGCTTCC 660  
 ACCATGAAGA ATCTTTTGAA GAATACCCAG AAACGAGTGG GAAAACAACC CGGAGATTCT 720  
 TCTTTAATTT AAGTTCATC CCCACGGAGG AGTTTATCAC CTCAGCAGAG CTTAGGTTT 780  
 TCCGAGAACA GATGCAAGAT GCTTTAGGAA ACAATAGCAG TTTCCATCAC CGAATTAATA 840  
 TTTATGAAAT CATAAACCT GCAACAGCCA ACTCGAAATT CCCCCTGACC AGACTTTTG 900  
 ACACAGGTT GGTGAATCAG AATGCAAGCA GGTGGGAAAG TTTTGATGTC ACCCCGCTG 960  
 TGATGCGGTG GACTGCACAG GGACACGCCA ACCATGGATT CGTGGTGGAA GTGGCCCACT 1020  
 TGGAGGAGAA ACAAGGTGTC TCCAAGAGAC ATGTTAGGAT AAGCAGGTCT TTGCACCAAG 1080  
 ATGAACACAG CTGGTCACAG ATAAGGCCAT TGCTAGTAAC TTTTGCCCAT GATGGAAAAG 1140  
 GGCATCCTCT CCACAAAAGA GAAAACGTC AAGCCAAACA CAACACGCGG AAACGCCTTA 1200  
 AGTCCAGCTG TAAGAGACAC CCTTTGTACG TGGACTTCAG TGACGTGGGG TGGAAATGACT 1260  
 GGATTGTGGC TCCCCCGGGG TATCACGCCCT TTTACTGCCA CGGAGAATGC CCTTTTCTC 1320  
 TGGCTGATCA TCTGAAGTCC ACTAATCATG CCATTGTTCA GACGTTGGTC AACTCTGTGA 1380  
 ACTCTAAGAT TCCTAAGGCA TGCTGTGTCC CGACAGAACT CAGTGTCTAT TCATGCTGT 1440  
 ACCTTGACGA GAATGAAAAG GTTGATTAAG AGAATATCA GGACATGGTT GTGGAGGGTT 1500  
 GTGGGTGTCG CTAGTACAGC AAAATTAAAT ACATAAATAT ATATATA

Seq ID NO: 160 Protein sequence  
 Protein Accession #: NP\_001191.1

1 11 21 31 41 51  
 | | | | |  
 MVAGTRCLLA LLLPQVLLGG AAGLVPGLGR RKFAAASSGR PSSQPSDEVL SEFELRLLSM 60  
 FGLKQRPPTS RDAVVPYML DLYRRHSGQP GSPAPDHRLE RAASRANTVR SPFHHEESLEE 120  
 LPETSGKTR RFFFNLSIP TEEFITSDEL QVFREQMQDA LGNNSSFHHR INIYELIKPA 180  
 TANSKFPVTR LLDT

Seq ID NO: 161 DNA sequence  
 Nucleic Acid Accession #: NM\_001999.2  
 Coding sequence: 1..8736

1 11 21 31 41 51  
 | | | | |  
 ATGGGGAGAA GACGGAGGCT GTGTCTCCAG CTCTACTTCC TGTGGCTGGG CTGTGTGGTG 60  
 CTCTGGGCGC AGGGCACGGC CGGCCAGCCT CAGCCTCCTC CGCCCAAGCC GCCCCGGCCC 120  
 CAGCCGCCGC CGCAACAGGT TCGGTCCGCT ACAGCAGGCT CTGAAGGCGG GTTCTAGCG 180  
 CCGAGTATC GCGAGGAGGG TGCCGCAATG GCCAGCCGCG TCCGCCGGCG AGGACAGCAG 240  
 GACGTGCTCC GAGGGCCCAA CGTGTGCGGC TCAGATTCC ACTCCTACTG CTGCCCTGGA 300  
 TGGAGAGACG TCCTTGAGG AAACAGGTGC ATGTGCTCCG TTTGTAGAAA TAGTTGTGGA 360  
 GATGGATTTT GTTCCCGTCC TAACATGTGT ACTTGTCCA GTGGGCAAAT ATCATCAACC 420  
 TGTGGATCAA AATCAATTCA GCAGTGCAGT GTGAGATGCA TGAATGGTGG GACCTGTGCA 480  
 GATGACCACT GCCAGTGCCA GAAAGGATAT ATTGGAACCT ATTGTGGACA ACCTGTCTGT 540  
 GAAAATGGAT GTCAGAAATG TGGACGTTGC ATCGCCCAAC CGTGTGCTTG TGTATATGG 600  
 TTCACTGGTC CACAGTGTGA AAGAGATTAC AGGACAGGCC CGTGTTCAC TCAGGTCAAC 660  
 AACCAGATGT GCCAAGGGCA GCTGACAGGC ATGTGCTGCA CGAAGACTCT GTGCTGTGCC 720  
 ACCACTGGAC GGGCGTGGGG CCATCCCTGT GAGATGTGTC CAGCCAGGCC TCAGCCCTGC 780  
 CGACGGGGTT TCATCCCCCA CATCCGCACT GGAGCTTGCC AAGATGTTGA TGAATGCCAG 840  
 GCTATCCAG GGATATGCCA AGGAGGAAAC TGTATCAATA CAGTGGGCTC TTTTGAATGC 900

	AGATGCCCTG	CTGGTCACAA	ACAGAGTGAA	ACTACTCAGA	AATGTGAAGA	CATTGATGAG	960
	TGCAGCATCA	TTCCTGGGAT	ATGTGAAACT	GGTGAATGTT	CCAACACCGT	GGGAAGCTAT	1020
	TTTTGTGTTT	GTCCACGTGG	ATATGTAAAC	TCAACAGATG	GCTCTCGATG	CATCGATCAG	1080
5	AGAACAGGCA	TGTGTTTCTC	GGGCGCTGGT	AATGGCCGCT	GTGCACAAGA	GCTCCCGGGG	1140
	AGAATGACGA	AAATGCAGTG	CTGCTGTGAG	CCTGGCCGCT	GCTGGGGCAT	CGGAACCAAT	1200
	CCTGAAGCCT	GTCCCTGTGAG	AGGTTCCTGAG	GAATATCGCA	GACTTTGCAT	GGATGGACTT	1260
	CCAATGGGAG	GAATCCAGG	GAGTGTGGT	TCCAGACCTG	GAGGCACCTG	GGGAAATGGC	1320
	TTTGCCCCAA	GTGGCAATGG	CAATGGCTAT	GGCCAGGAG	GGACAGGCTT	CATCCCCATC	1380
	CCTGGAGGCA	ATGGCTTTTC	TCTTGGCGTT	GGGGGAGCCG	GTGTGGGGGC	CGGGGGACAG	1440
10	GGACCTATCA	TCACCTGGAC	AACAATTCTG	AACCAGACAA	TAGATATCTG	TAAGCATCAT	1500
	GCTAACCTTT	GTTTAAATGG	ACGCTGTATA	CCAACCTGCT	CAAGCTACCG	ATGTGAATGC	1560
	AACATGGGTT	ATAAGCAGGA	TGCAAAATGA	GATTGTATAG	ATGTTGATGA	ATGCACATCA	1620
	AATCCCTGCA	CTAATGGAGA	TTGTGTTAAC	ACACCTGGTT	CCTATTATTG	TAAATGTCAT	1680
	GCTGGATTCC	AGAGGACTCC	TACCAAGCAA	GCATGCATTG	ATATTGATGA	GTGCATCCAG	1740
15	AATGGGGTTT	TTGTGAAAA	CGGTGATGC	GTGAACTCAG	ATGGAAGTTT	CCAGTGCATT	1800
	TGCAATGCCG	GCTTTGAATT	AACACAGAT	GGAAAAAACT	GTGTTGATCA	TGATGAATGT	1860
	ACAACTACCA	ACATGTGTTT	GAATGGAATG	TGCATCAATG	AAGATGGCAG	CTTCAAGTGC	1920
	ATCTGCAAA	CAGGATTTGT	CTTGGCTCCA	AATGGGCGTT	ACTGTACTGA	TGTTGATGAA	1980
	TGCCAGACCC	CAGGATCTG	CATGAATGGG	CACCTGCATCA	ACAGTGAAGG	GTCCCTCCGC	2040
20	TGTGACTGTC	CGCCAGGCTT	GGCTGTGGGC	ATGGATGGAC	GTGTGTGTGT	TGATACTCAC	2100
	ATGCGCAGTA	CCTGCTATGG	AGGAATCAAG	AAAGGAGTGT	GTGTGCGTCC	TTTCCCGGCT	2160
	GCAGTGACCA	AGTCCGAATG	CTGCTGTGCC	AATCCAGACT	ATGGTTTGTG	AGAACCCCTG	2220
	CAGCCATGCC	CTGCAAAAA	TTCACTGAA	TTCCACGGCC	TTTGTAGTAG	TGGAGTAGGT	2280
	ATCACTGTGG	ATGGAAGAGA	TATCAATGAA	TGTGCTTTGG	ATCCTGATAT	ATGTGCCAAT	2340
25	GGGATTTTGT	AAAACCTTAC	TGGTAGTTAC	CGTTGTAATT	GCAACAGTGG	CTATGAACCA	2400
	GATGCTCTGT	GAAGAACTG	TATTGACATT	GATGAATGTT	TAGTAAACAG	ACTGCTTTGT	2460
	GATAACGGAT	TGTGCCGAAA	CACGCCAGGA	AGTTACAGCT	GTACGTGCCC	ACCAGGGTAT	2520
	GTGTTACAGG	CTGAGACAGA	GACCTGTGAA	GATATAAATG	AATGTGAAAG	CAACCCATGT	2580
30	GTCAATGGGG	CCTGCAGAAA	CAACCTTGA	TCTTTCAATT	GTGAATGTTT	GCCCGGCAGC	2640
	AAACTCAGCT	CCACAGGATT	GATCTGTATT	GACAGCCTGA	AGGGGACCTG	TTGGCTCAAC	2700
	ATCCAGGACA	CCGCTGTGTA	GGTGAATATT	AATGGAGCCA	CTCTGAAATC	TGAATGCTGT	2760
	GCCACCTCTG	GAGCCGCTG	GGGGAGCCCC	TGTGAGCGGT	GTGAACCTAGA	TACAGCTTGC	2820
	CCAAGAGGGC	TTGCCAGGAT	TAAAGGTGTT	ACGTGTGAAG	ATGTTAATGA	GTGTGAGGTG	2880
35	TTCCCTGGCG	TTTGTCCAAA	TGGACGCTGT	GTCAACAGTA	AGGGATCTTT	TCATTGCGAG	2940
	TGCCCTGAAG	GCCTTACGTT	GGATGGGACT	GGCCGTGTAT	GTTTGGATAT	TCGCATGGAG	3000
	CAGTGTACT	TGAAGTGGGA	TGAAGATGAA	TGCATCCACC	CCGTTCTGGG	AAAGTTCCCG	3060
	ATGGATGCCT	GCTGCTGTGC	TGTCGGGCGC	GCTTGGGGCA	CCGAGTGTGA	GGAGTGCCCC	3120
	AAACCTGGCA	CCAAGGAATA	CGAGACACTG	TGCCCCCGCG	GGGCTGGCTT	TGCTAACCGA	3180
40	GGGGATGTTT	TTACTTGGCG	GCCATTTTAC	AAAGACATCA	ATGAATGCAA	AGCATTTCCT	3240
	GGGATGTGCA	CTTATGGGAA	GTGCAGAAAT	ACAATCGGAA	GCTTCAAATG	CCGTTGCAAT	3300
	AGTGGCTTTG	CTCTAGACAT	GGAGGAAAGA	AACCTGACCG	ACATCGACGA	GTGCAGGATT	3360
	TCTCTGACC	TCTGTGGCAG	TGGAATCTGC	GTCAATACAC	CGGGCAGCTT	TGAGTGCAG	3420
	TGCTTCGAAG	GCTATGAAAG	TGGCTTCATG	ATGATGAAGA	ACTGCATGGA	CATTGACGGA	3480
	TTGGAACGTA	ACCTCTCTCT	TTGTAGGGGT	GGCAGCTGTG	TGAACACTGA	GGGCAGCTTT	3540
45	CAGTGTGACT	GGCCACTGGG	ACACGAGCTG	TCACCATCCC	GTGAGGACTG	TGTGGATATT	3600
	AATGAATGCT	CCCTGAGTGA	CAATCTCTGC	AGAAATGGAA	AATGTGTGAA	CATGATTGGA	3660
	ACCTATCAGT	GCTCTTGCAA	TCCTGGATAT	CAGGCTACGC	CAGACCCGCA	GGGCTGTACA	3720
	GATATTGATG	AATGTATGAT	AATGAACGGA	GGCTGTGACA	CCCACTGCAC	AAATTACAGAG	3780
	GGAAAGCTAC	AATGCAGCTG	CAGTGAAGGT	TATGCCCTGA	TGCCAGATGG	GAGATCGTGT	3840
50	GCAGACATTG	ATGAATGTGA	AAACAATCCT	GATATCTGTG	ATGGCGGCCA	GTGTACCAAC	3900
	ATTCTGGAG	AGTATCGCTG	CCTCTGCTAT	GATGGCTTCA	TGGCTTCCAT	GGACATGAAA	3960
	ACATGCAATT	ATGTCAATGA	ATGTGACCTA	AATTCAAATA	TCTGCATGTT	TGGGGAATGT	4020
	GAGAACACAA	AGGGATCTCT	CATTTGCCAC	TGTCAGCTGG	GTTACTCAGT	GAAGAAGGGG	4080
	ACCACAGGAT	GTACAGATGT	GGATGAGTGT	GAATTTGGTG	CTCATAACTG	CGACATGCAT	4140
55	GCCTCATGTC	TGAATATCCC	AGGAAGCTTC	AAGTGTAGCT	GCAGAGAAGG	CTGGATTGGA	4200
	AACGGCATCA	AGTGTATTGA	TCTGGACGAA	TGTTCTAATG	GAACCCACCA	GTGTAGCATC	4260
	AATGCTCAGT	GTGTAAATAC	CCCGGCTCA	TACCGCTGTG	CCTGCTCCGA	AGGTTTCACT	4320
	GGTGATGGCT	TTACCTGCTC	AGATGTTGAT	GAGTGTGCAG	AAAACATAAA	CCTCTGTGAG	4380
	AACGGACAGT	GCCTTAATGT	CCCGGCTGCA	TATCGCTGCG	AGTGTGAGAT	GGGCTTCACT	4440
60	CCAGCCTCAG	ACACGAGATC	CTGCCAAGAT	ATTGATGAAT	GCTCCTTCCA	AAACATTTGT	4500
	GTCTCTGGAA	CATGTAATAA	CCTGCCTGGA	ATGTTTCATT	GCATCTGCGA	TGATGGTTAT	4560
	GAATTGGACA	GAACAGGAGG	GAACGTGTACA	GATATTGATG	AGTGTGCAGA	TCCTATAAAC	4620
	TGTGTCAATG	GCCTATGTGT	CAACACGCCT	GGTGCCTATG	AGTGTAACTG	CCCACCCGAT	4680
65	TTTCAGTTGA	ACCCAACTGG	TGTGGGTTGT	GTTGACAAAC	GTGTGGGCAA	CTGCTACCTG	4740
	AAGTTTGGAC	CTCGAGGAGA	TGGGAGTCTG	TCTTGCAACA	CCGAGATCGG	GGTGGGCGTC	4800
	AGTGCCTCTT	CATGCTGCTG	CTCTCTGGGA	AAGGCCTGGG	GAAACCCCTG	TGAGACATGC	4860
	CCCCCTGTCA	ATAGCACTGA	ATATTACACC	CTGTGTCCCG	GAGGTGAAGG	CTTCAGACCT	4920
	AACCCCATCA	CAATCATTTT	AGAAGACATT	GACGAATGCC	AGGAGTTACC	AGGTCTCTGC	4980
	CAGGGTGGAA	ACTGCATCAA	CACTTTGGGG	AGCTTCCAGT	GTGAGTGCCC	ACAAGGCTAC	5040
70	TACCTCAGCG	AGGATACCCG	CATCTGTGAG	GATATTGATG	AGTGTTTTGC	ACATCTCTGT	5100
	GTGTGTGGGC	CTGGGACCTG	CTATAACACC	CTGGGAAATT	ACACCTGCAT	TTGCCACCTT	5160
	GAGTACATGC	AGGTCAATGG	AGGCCACAA	TGCATGGACA	TGAGAAAAAG	CTTTTGCTAC	5220
	CGAAGCTATA	ATGGAACCA	TTGTGAGAA	GAGTTGCCCT	TCAATGTGAC	AAAAAGGATG	5280
75	TGCTGCTGCA	CATATAATGT	GGGCAAGCT	GGGAACAAAC	CTTGTGAACC	ATGCCCAACT	5340
	CCAGGAACAG	CTGACTTTAA	AACCATATGT	GGAAATATTC	CTGGATTAC	CTTTGACATT	5400
	CACACAGGAA	AAGCTGTTGA	CATTGATGAA	TGTAAAGAGA	TTCCAGGCAT	TTGTGCAAT	5460
	GGTGTGTGCA	TTAACAGCAT	TGGCAGTTTC	CGCTGTGAAT	GCCCTACAGG	ATTCAAGTAC	5520
	AATGACCTGC	TGTTGGTTTG	TGAAGATATA	GATGAGTGCA	GCAATGGTGA	TAATCTCTGC	5580
	CAGCGGAATG	CAGACTGCAT	CAATAGTCTT	GGTAGTTACC	GCTGTGAATG	TGCCGCGGGT	5640
80	TTCAAACTTT	ATCCCAATGG	GGCCTGTGTA	GATCGCAATG	AATGTTTAGA	AATTCCTAAC	5700
	GTGTGCACTG	CAGCTGTGTC	TGTTGATGTC	CAAGGAAGTT	ACCAGTGCAT	CTGCCACAAT	5760
	GGCTTTAAGG	CTTCTCAGGA	CCAGACCATG	TGCATGGATG	TTGATGAGTG	CGAGCGGCAC	5820
	CCATGTGGAA	ATGGAACCTG	TAAAAACACC	GTGGATCCCT	ATAACTGTCT	GTGCTACCCA	5880
	GGGTTTGAAC	TCATCATATA	TAATGATTGC	CTGGACATAG	ATGAGTGCAG	TTCTTTT	5940

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

GGTCAGGTGT GCAGAAATGG ACGTTGTTTT AATGAAATTG GTTCTTTCAA GTGTCTATGT 6000  
AACGAAGGTT ATGAACTTAC CCCAGATGGC AAAAAGCTGA TAGACACTAA TGAGTGTGTC 6060  
GCCCTTCCCG GCTCTTGCTC TCCTGGTACC TGTGAGAAAT TGGAGGGATC CTTGAGATGC 6120  
ATCTGTCCCC CAGGGTATGA AGTAAAGAGC GAGAACTGCA TTGATATAAA TGAATGTGAT 6180  
GAAGATCCCA ACATTTGTCT TTTTGGTTCC TGTACTAATA CTCCAGGGGG CTTCCAGTGC 6240  
CTCTGCCCCC CTGGCTTTGT ACTATCTGAT AATGGACGGA GATGCTTTGA TACTCGCCAG 6300  
AGCTTCTGCT TCACAAATTT TGAAAATGGA AAGTGTCTG TACCCAAAGC TTTCAACACC 6360  
ACAAAGACAA AATGCTGCTG TAGTAAGATG CCAGGAGAGG GCTGGGGGGA CCCCTGTGAG 6420  
CTGTGCCCCA AAGACGATGA AGTTGCATTT CAGGATTTGT GTCCATATGG CCATGGAAT 6480  
GTCCCTAGTC TTCATGATAC ACGTGAAGAT GTCAATGAGT GTCTTGAGAG CCCAGGCATT 6540  
TGTTCAAAATG GTCAATGTAT CAACACCCGAC GGATCTTTTC GCTGTGAATG TCCAATGGGC 6600  
TACAACCTTG ACTACACTGG AGTACGCTGT GTGGATACTG ATGAGTGTTC AATCGGCAAT 6660  
CCGTGTGGAA ATGGTACATG CACCAATGTT ATTGGGAGTT TTGAATGCAA TTGCAATGAA 6720  
GGCTTTGAGC CAGGGCCCAT GATGAATTTGT GAAGATATCA ACGAATGTGC CCAGAACCCA 6780  
CTGCTGTGTG CTTTACGCTG CATGAACACT TTTGGGTCTC ATGAATGCAC GTGCCCGATT 6840  
GGCTATGCCC TCAGGGAAGA TCAAAAGATG TGCAAGATC TGGATGAATG TGCTGAAGGG 6900  
TTACACGACT GTGAATCTAG GGCATGATG TGTAAGAATC TAATCGGCAC CTTTATGTGC 6960  
ATCTGCCCTC GTGGAATGGC CCGAAGGGCC GATGGAGAAG GCTGTGTAGA TGAAAATGAA 7020  
TGCAGGACCA AGCCAGGAAT CTGTGAAAAT GGACGTTGTG TTAACATTAT TGGAAAGCTAT 7080  
AGATGTGAGT GTAATGAAGG ATTCCAGTCA AGTTCTTCAG GCACTGAATG CCTTGACAAT 7140  
CGACAGGGTC TCTGCTTTGC AGAGGTACTG CAGACAATAT GTCAAATGGC ATCCAGTAGT 7200  
CGCAATCTCG TCACTAAGTC AGAATGCTGC TGTGATGGTG GCGCAGGCTG GGGCCACCAG 7260  
TGCGAGCTTT GCCCACTTCC TGGAACTGCC CAGTACAAAA AGATATGTCC TCATGGCCCA 7320  
GGATATACAA CTGATGGAAG AGATATTGAT GAATGTAAGG TAATGCCAAA CCTCTGCACC 7380  
AATGGTCAGT GCATCAATAC CATGGGCTCA TTCCGATGCT TCTGCAAGT TGGCTACACC 7440  
ACAGACATCA GTGGAACCTC TTTGATAGAC CTTGATGAAT GCTCCAGTC CCCGAAACCA 7500  
TGCAACTACA TCTGCAAGAA CACTGAGGGG AGTTATCAGT GTTCATGTCC GAGGGGGTAT 7560  
GTCCCTGCAAG AGGATGGAAG GACATGCAAA GACCTTGATG AATGTCAAAC AAAGCAGCAT 7620  
AAGTGCACAG TCTCTGTGTG CAACACCCCTG GGGGGGTTTA CCTGTAAATG TCCACCTGGT 7680  
TTTACACAGC ATCACACTGC TTTGATCGAC AACAACGAAT GTGGGTCTCA ACCTTTGCTT 7740  
TGTGGAGGAA AGGGAATCTG TCAAAACACT CCAGGCAGTT TCAGCTGTGA ATGCCAAAGA 7800  
GGGTCTCTCT TTTGATGCCAC CGGACTGAAC TGTGAAGATG TTGATGAATG TGATGGGAAC 7860  
CACAGGTGCC AACACGGCTG CCAGAATATC CTGGGTGGCT ACAGATGTGG CTGCCCCCAA 7920  
GGTACATACC AGCACTACCA GTGGAATCAG TGTGTGATG AGAATGAATG CTCCAATCCC 7980  
AATGCTCTGT GCTCTGCTTC CTGCTACAAC ACCCTGGGGA GTTACAAGTG CGCCTGCCCC 8040  
TCCGGGTCTC GTTCTGACCA GTTCTCCAGT GCCTGCCACG ACGTGAATGA GTGCTCGTCC 8100  
TCCAAGAACC CTTGCAATTA CGGCTGCTCT AACACGGAGG GGGGCTACCT CTGTGGCTGC 8160  
CCCCCTGGGT ATTACAGAGT GGGACAAGGC CACTGTGCTC CAGGAATGGG ATTTAACAAG 8220  
GGGCAGTACC TGTCACTGGA TACAGAGGTC GATGAGGAAA ATGCTCTGTC CCCAGAAGCA 8280  
TGTCTACGAGT GCAAAATCAA CGGCTATCCT AAGAAAGACA GCAGGCAGAA GAGAAGTATT 8340  
CATGAACCTG ATCCCACTGC TGTGAAACAG ATCAGCCTAG AGAGTGTGCA CATGGACAGC 8400  
CCCCGTCACA TGAAGTTCAA CCTCTCCAC CTTGGCTCTA AGGAGCACAT CTGGAACCTA 8460  
AGGCCCCGCA TCCAGCCCCC CAACAACCCAC ATCCGTTATG TCATCTCTCA AGGGAACGAT 8520  
GACAGCGTCT TCCGATCCCA CCAAGGAAT GGGCTCAGCT ACTTGACAC GGCACAAGAG 8580  
AAGCTCATGC CCGGCACATA CCACTGGAA ATCACTAGCA TCCTCTCTA CAAGAAGAAG 8640  
GAGCTTAAGA AACTGGAAGA GAGCAATGAG GATGACTACC TCCTAGGGA GCTTGGGAG 8700  
GCTCTCAGAA TGAGGCTGCA GATTGAGTCT TATTAACCGT TCACAGACTT GGGCCAGGC 8760  
TCAATCCCTA GCACAGCCAG TCTGCAGAAG CATTTGAAAA GTCAAGGACT AATTTTAAAG 8820  
AGGAAAAATA ATAATACTC TTGTTTCTTT CCTCCCTGTC TTAGACTTTG AATGTTGACC 8880  
CTCACAGGGA GGGATAATTT AGACTCTGGT ATGGCCAAAG ATTTGAGCTC AAAGGCCAAC 8940  
GTGGTTACTG TATTTTATAT ATAATTTCAT TTTAAAAAT ATTTAAAGAA ACCTAAATGT 9000  
TCAAGATATC AGCATATGCG ACTAAATGCA CAAAAATAAT GTGAGCTTTT TTTTTTTTTT 9060  
CCTGTTAGCA GTCTGTAAAC CTTTGGGTAT TTTGCTATAG TTGCTAATTA AAAAAATATA 9120  
GATTGTTTAT TATTTTAAAT GCAGTAATAT ATGGAGAAAT GAACAAACTA TGTAAACAAA 9180  
AAGGGAACCT CACTGTGTTT TCTTTAGATT TATAAATTG AGCTATTTTT TTTAGAGGTG 9240  
CTTTTTAAAA ATCCAATAGA TACAAGAGAT GTTTCCTTTG GTTTTCTGCC AGTCATCCAG 9300  
CTGATACACA CCTGATCGAT TTTAAAGAAA GCCACACAGA GCTGAATCGG GCGATGCTAA 9360  
TCAATAATTT AAAAGACATG AATGTCATTA GATCCTTTAT AACGTAGATC GAAGCCAAAG 9420  
CAGCTCATTT GTGACAACAT TTCATATCAC CAGACACACC AGGCAACAGA AGTTGAAGCA 9480  
CAACCACTGT AGCAAAATAC CTTGACTGCT TGTGAGACCA TTAGCATGTC AGGCCAAACC 9540  
GTACTGTATT TCCTTCTCAT AACCTCAAGG AACCATATGT GCTACCCACA ACACCTCATT 9600  
CTTACCCAGG GTGCGCTGCG TCCTCATGGT ACTGTAGGCA GCTGAAGAAC CGCCGTTCCC 9660  
TTGAAAGGGA ACACCTGGCA TTCTGTGGTG TTTCTGTGCTG TCTTAAATAA TGGTGCATTT 9720  
ATTATGTTCA AGTTATTTCA GGATTGCCAT ATGTGCAAAAC AAATCATGCA ATGCAGCCAA 9780  
GGAATATATG TGTGTGTTGT TGTTTTAAAC CCATTTTTTT TTTAGAATTT TCATTAATAC 9840  
TGTAAGTTATA CACCATATGC CTCATTTTAT CATAGCCTAT TGTGTATGAA AGATGTTTGT 9900  
ACAATGAATT GATGTTTATG TTGCTTTAGT CATTTAAAAA GATATTGTAC CAGGATGTGC 9960  
TATTAAGAGC ACGTATCCAT TATTCTTCTC AACCCAAAGAA CCTGTTTCCCT GGACCAAGTA 10020  
CCAAACCTCA TATGTGAATG GGCCAAAGCA CATGCAGGCT CCTGGTTGTT CCTCTCAAAC 10080  
CTGTGCTGAC CAAAGATTAG TAACCAGTTA TACCCAGTAT TTTGAGGTTT TATTGTTTTT 10140  
TTAATAACTA AAAAAAACT CGTGCC

Seq ID NO: 162 Protein sequence  
Protein Accession #: NP\_001990.1

1 11 21 31 41 51  
MGRRRRLCLQ LYFLWLGCVV LWAQGTAGQP QPPPPKPPRP QPPPPQVRSR TAGSEGGFLA 60  
PEYREBGAIV ASRVRRRGQQ DVLRGPNVCG SRFHSYCCPG WKTLPNGNQ IVPICRNSG 120  
DGFCSRPNMC TCSSGQISST CGSKSIQCCS VRCMNGGTCA DDHCQCQKGY IGTGCGPVC 180  
ENGCONGGRC IQAPCAVVG FTGPQCERDY RTGPGCFQVN NQMCQQLTG IVCTKTLCCA 240  
TTGRANGHPC EMCPAQPQPC RRGFIPIRIT GACQDVDECQ AIPGICQGGN CINTVGSFEC 300  
RCFAGHKQSE TTQKEDIDE CSIIPIGICET GECSNTVGSY FCVCPRGVYT STDGSRCIDQ 360  
RTGMCFSGLV NGRCAQELPG RMTKMQCCCE PGRCWIGITI PEACPVRSGE BYRRCLMDGL 420



PMGGIPGSAG SRPGGTGGNG FAPSGNGNGY GPGGTGFIP I PGGNGFSPGV GGAGVGAGGQ 480  
 GPIITGLTIL NQTIDICKHH ANLCLNGRCI PTVSSYRCEC NMGYKQDANG DCIDVDECTS 540  
 NPCTNGDCVN TPGSYCKCH AGFQRTPTKQ ACIDIDEIQ NGVLCKNGRC VNSDGSFQCI 600  
 5 CNAGFELTID GKNCDVHDDEC TTTNMCLNGM CINEDGSFKC ICKPGFVLAP NGRYCTDVDE 660  
 CQTPGICMNG HCINSEGSFR CDCPPGLAVG MDGRVCVDTH MRSTCYGGIK KGVCVRPFPG 720  
 AVTKSECCCA NPDYGFGEPC QPCPAKNSAE FHGLCSSGVG ITVDGRDINE CALDPDICAN 780  
 GICENLRGSY RCNCSNGYEP DASGRNCIDI DECLVNRLLC DNGLCRNTPG SYSTCPCPGY 840  
 VFRTEETCE DINECESNPC VNGACRNNLG SFNCECSPGS KLSSTGLICI DSLKGTCLWN 900  
 10 IQDSRCEVNI NGATLKSECC ATLGAAWSP CERCELDTAC PRGLARIKGV TCEDVNECEV 960  
 FPGVCPNGRC VNSKGSFHCE CPEGLTLDTG GRVCLDIRME QCYLKWDEDE CIHPVPGKFR 1020  
 MDACCAVGA AWGTBCEBPC KPGTKEYETL CPRGAGFANR GDVLTRGPFI KDINECKAFP 1080  
 GMCTYGKCRN TIGSFKRCRN SGFALDMEER NCTDIDECRI SPDLCSGIC VNTPGSFECE 1140  
 CFEYGESGFM MMKNMCDIDG CERNPLLCRG GTCVNTGSGF QCDCPLGHEL SPSREDCVDI 1200  
 15 NECSLSDNLC RNGKCVNMIG TYQCSNPGY QATPDRQGT DIDECEMIMG GCDTQCTNSE 1260  
 GSYECSCSEG YALMPDGRSC ADIDECENN DDCDGGQCTN IPGEYRCLCY DGFMASSMDMK 1320  
 TCIDVNECDL NSNICMFGEC ENTKGFSICH CQLGYSVKKG TTGCTDVDEC EIGAHCMDMH 1380  
 ASCLNIPGSF KCSREGWIG NGIKCIDLDE CSNGTHQCSI NAQCVNTPGS YRACSESGFT 1440  
 GDGFTCSVD ECAENILCE NGQCLNVGA YRCECEMGFT PASDSRSCQD IDECSFNIC 1500  
 20 VSGTCNNLPG MFHCICDDGY ELDRTGGNCT DIDEADPIN CVNGLCVNTP GRYECNCPFD 1560  
 FQLNPTGVGC VDNRVGNCYL KFGPRGDGSL SCNTEIGVGV SRSSCCCSLG KAWGNPCETC 1620  
 PPNVSTEYIT LCPGGEGFRP NPITILEDI DECQELPGLC QGGNCINTFG SFQCECPQGY 1680  
 YLSEDRICE DIDECAHFG VCGPGTCYNT LGNYTCICPP EYMQVNGGHN CMDMRKSPCY 1740  
 RSYNGTTCEN ELPPFNVTIRM CCCTYNVGA GNKPCEPCPT PGTADEFKIC GNIPGFTFDI 1800  
 25 HTGKAVDIDE CKEIPGICAN GVCINQIGSF RCECPTGFSY NDLLLVCEDI DECSNGDNL 1860  
 QRNADCINSP GSYRCEAAG FKLSPNGACV DRNECLEIPN VCSHGLCVDL QGSYQICHN 1920  
 GFKASQDQTM CMDVDECERH PCGNGTCKNT VGSYNCLCYP GFELTHNDC LDIDECSFF 1980  
 GQVCRNGRCF NEIBSGFKLC NEGYELTPDG KNCIDTNECV ALPGSCSPGT CQNLEGSFRC 2040  
 ICPPGYEVKS ENCIDINECD EDPNICLFSG CTNTPGGFQC LCPPGFVLS NGRRCFDTQ 2100  
 30 SFCFTNFENG KCSVPKAFNT TKAKCCSKM PGEWGDPCE LCPKDEVAF QDLCPYGHGT 2160  
 VPSLHDTRED VNECLESPI CSNGQCINTD GSFRCECPMG YNLDTYGVRC VDTDECSIGN 2220  
 PCNGTCTNV IGSFECNCNE GFEPGPMNC EDINECAQNP LICALRCMNT FGSYECTCPI 2280  
 GYALREDQKM CKDLDECARG LHDCESTRGM CKNLIGTFMC ICPPGMARRP DGEVGDENE 2340  
 CRTKPGICEN GRCVNIIGSY RCECNEGFQS SSSGTECLDN RQGLCFEVL QTICQMASS 2400  
 35 RNLVTKSECC CDGGRGWGHQ CELCPLPATA QYKKICPHGP GYTTDGRDID ECKVMPNLCT 2460  
 NQQCINTMGS FRFCCKVGYT TDISGTSCID LDECSQSPKP CNYICNTG SYQCSCPRGY 2520  
 VLQDEGKTK CKDLDECQKH NCQFLCVNTL GGFTCKCPG FTQHTTACID NNECSQPL 2580  
 CGGKICQNT PGSFSCCQR GFLSDATGLN CEDVDECDGN HRCQHGQNI LGGYRCGCPQ 2640  
 GYIHYQWQ CVDENECNP NACGSASCYN TLGSYKCAP SGFSFDQFSS ACHDVNECSS 2700  
 40 SKNPNYNGCS NTEGYLCGC PPGYRVGQG HCVSGMGFNK GQYLSLDTVE DEENALSPEA 2760  
 CYECKINGYP KDSRQKRSI HEPDPTAVEQ ISLESVDMS PVMKFNLSH LGSKEHILEL 2820  
 RPAIQPLNNH IRYVISQND DSVFRIHQRN GLSYLHTAKK KLMPGYTLE ITSIPLYKKK 2880  
 ELKKLEESNE DDYLLGELGE ALRMRLQIQL Y

Seq ID NO: 163 DNA sequence

Nucleic Acid Accession #: NM\_013372.1

Coding sequence: 63..617

1 11 21 31 41 51  
 50 GCGGCCGCAC TCAGCGCCAC GCGTCGAAAG CGCAGGCCCC GAGGACCCGC CGCACTGACA 60  
 GTATGAGCCG CACAGCCTAC ACGGTGGGAG CCCTGCTTCT CCTCTGGGG ACCCTGCTCC 120  
 CGGCTGCTGA AGGGAAGGAG AAGGGTCCC AAGGTCCCAT CCCCAGGCA GACAAGGCC 180  
 AGCACAATGA CTGAGAGCAG ACTCAGTCGC CCCAGCAGCC TGGCTCCAGG AACCGGGGGC 240  
 55 GGGGCCAAGG CGGGGCACT GCCATGCCCG GGGAGGAGGT GCTGGAGTCC AGCCAAGAGG 300  
 CCCTGCTATG GACGGAGCGC AAATACCTGA AGCAGAGACT GTGCAAAACC CAGCCGCTTA 360  
 AGCAGACCAT CCACGAGGAA GGCTGCAACA GTCCGACCAT CATCAACCCG TCTCTGTACG 420  
 GCGAGTGCAA CTCTTTCTAC ATCCCGAGG ACATCCGGA GAGGAGGAGT TCCTTTTCAGT 480  
 CCTGCTCCTT CTGCAAGCCC AAGAAATTCA CTACCATGAT GGTCAACTC AACTGCCCTG 540  
 60 AACTACAGCC ACCTACCAAG AAGAAGAGAG TCACACGTGT GAAGCAGTGT CGTTGCATAT 600  
 CCATCGATTG GGATTAAGCC AAATCCAGGT GCACCCAGCA TGCTTAGGA ATGCAGCCCC 660  
 AGGAAGTCCC AGACCTAAAA CAACCAAGATT CTTACTTGGC TTAACCTAG AGGCCAGAAG 720  
 AACCCTCAGC TGCTCTCTGG CAGGAGCCTG CTTGTGCGTA GTTCGTGTGC ATGAGTGTGG 780  
 ATGGGTGCTT GTGGGTGTTT TTAGACACCA GAGAAACAC AGTCTCTGCT AGAGAGCACT 840  
 65 CCTATTTTG TAAACATATC TGCTTTAATG GGGATGTACC AGAAACCCAC CTACCCCGG 900  
 CTACATCTA TAAAGGCGGG GCGGTGGTCT GGTCTGACT TTGTGTTTT GTGCCCTCT 960  
 GGGGACAGA ATCTCCTTTC GGAATGAATG TTCATGGAAG AGGCTCCTCT GAGGGCAAGA 1020  
 GACCTGTTTT AGTCTGCTAT TCGACATGGA AAGTCTCTT TAACCTGTGC TTGCATCTC 1080  
 CTTTCTCTCT CCTCTCACA ATCCATCTCT TCTTAAGTTG ATAGTGACTA TGTCAGTCTA 1140  
 70 ATCTCTTGTG TGCCAAGGTT CCTAAATTA TCACTTAAC CATGATGCAA ATGTTTTTCA 1200  
 TTTTGTGAAG ACCCTCCAGA CTCTGGGAGA GGCTGGTGTG GGCAAGGACA AGCAGGATAG 1260  
 TGGAGTGAGA AAGGGAGGCT GGAGGGTGAG GCCAAATCAG GTCCAGCAA AGTCAGTAGG 1320  
 GACATTGCAG AAGCTTGAAA GGCCAATACC AGAACACAGG CTGATGCTTC TGAGAAAGTC 1380  
 TTTTCTTAGT ATTAAACAGA ACCCAAGTGA ACAGAGGAGA AATGAGATTG CCAGAAAGTC 1440  
 75 ATTAACCTTG GCGTGTCAA TCTGCTCAA CCTAACCCA AACTGAAAC ATAAATACTG 1500  
 ACCACTCCTA TGTTCCGACC CAAGCAAGTT AGCTAAACCA AACCACTCC TCTGCTTTGT 1560  
 CCTCAGGTG GAAAAGAGAG GTAGTTTAGA ACTCTCTGCA TAGGGGTGGG AATAATCAA 1620  
 AAACCKCAGA GGCTGAAATT CCTAATACCT TTCCTTTATC GTGGTTATAG TCAGCTCATT 1680  
 TCCATTCCAC TATTTCCCAT AATGCTTCTG AGAGCCACTA ACTTGATTGA TAAAGATCCT 1740  
 80 GCCTCTGCTG AGTGTACTCT ACAGTAAGTC TAAAGATGAR AGAGTTTAGG GACTACTCTG 1800  
 TTTTAGCAAG ARATATTKTG GGGGTCTTTT TGTTTTAACT ATTGTGAGGA GATTGGGCTA 1860  
 RAGAGAAGAC GACGAGAGTA AGGAAATAAA GGGGATTGCC TCTGGCTAGA GAGTAAGTTA 1920  
 GGTGTTAATA CCTGGTAGAA ATGTAAGGGA TATGACCTCC CTTTCTTTAT GTGCTCACTG 1980  
 AGGATCTGAG GGGACCTCTG TAGGAGACA TAGCATCATG ATGTATTAGT TGTTCATCTG 2040  
 CTACTGGTTG GATGGACATA ACTATTGTAA CTATTCAGTA TTTACTGTGA GGCAGTCTCC 2100

TCTGATTAAA CTTGGCCTAC TGGCAATGGC TACTTAGGAT TGATCTAAGG GCCAAAGTGC 2160  
 AGGGTGGGTG AACTTTATTG TACTTTGGAT TTGGTTAACC TGTTTTCTTC AAGCTGAGG 2220  
 TTTTATATAC AAACCTCCCTG AATACTCTTT TTGCCTTGTA TCTTCTCAGC CTCCTAGCCA 2280  
 AGTCCTATGT AATATGGAAA ACAAACTG CAGACTTGAG ATTCAGTTGC CGATCAAGGC 2340  
 TCTGGCATTC AGAGAACCCT TGCAACTCGA GAAGCTGTTT TTATTTCGTT TTTGTTTTGA 2400  
 TCCAGTGTCT TCCCATCTAA CAACTAAACA GGAGCCATT CAAGCGGGA GATATTTTAA 2460  
 ACACCCAAAA TGTGGGTCT GATTTTCAAA CTTTAAACT CACTACTGAT GATTCTCAG 2520  
 CTAGGCGAAT TTGTCCAAAC ACATAGTGTG TGTGTTTTGT ATACACTGTA TGACCCCAAC 2580  
 CCAATCTTT GTATTGTCCA CATTCTCCAA CAATAAAGCA CAGAGTGGAT TTAATTAAGC 2640  
 ACACAAATGC TAAGGCAGAA TTTTGAGGGT GGGAGAGAAG AAAAGGGAAA GAAGCTGAAA 2700  
 ATGTAAAACC ACACCAGGA GAAAAATGA CATTCAAGAC CAGCAACAC TGAATTTCTC 2760  
 TTGTTGTTTT AACTCTGCCA CAAGAATGCA ATTCGTTAA TGGAGATGAC TTAAGTTGGC 2820  
 AGCAGTAATC TTCTTTTAGG AGCTTGTACC ACAGTCTTGC ACATAAGTGC AGATTGGCT 2880  
 CAAGTAAAGA GAATTCCTC AACACTAACT TCACTGGGAT AATCAGCAGC GTAACCTACC 2940  
 TAAAAGCATA TCACTAGCCA AAGAGGAAA TATCTGTTCT TCTTACTGTG CCTATATTAA 3000  
 GACTAGTACA AATGTGGTGT GTCTTCCAAC TTTCAATTGAA AATGCCATAT CTATACCATA 3060  
 TTTTATTGTA GTCACTGATG ATGTAATGAT ATATTTTTTC ATTATTATAG TAGAATATTT 3120  
 TTATGGCAAG ATATTGTGG TCTTGATCAT ACCTATTAAA ATAATGCCAA ACACCAATA 3180  
 TGAATTTTAT GATGTACACT TTGTGCTTGG CATTAAAAGA AAAAACAACA CATCTGGAA 3240  
 GTCTGTAAGT TGTTTTTTGT TACTGTAGGT CTTCAAAGTT AAGAGTGTAA GTGAAAAATC 3300  
 TGGAGGAGAG GATAATTTCC ACTGTGTGGA ATGTAATAG TTAATGAAA AGTTATGGTT 3360  
 ATTTAATGTA ATTATTACT CAAATCCTTT GGTCACTGTG ATTTCAAGCA TGTTTTCTTT 3420  
 TTCTCCTTTA TATGACTTTC TCTGAGTTGG GCAAAGAAGA AGCTGACACA CCGTATGTTG 3480  
 TTAGAGTCTT TTATCTGTGC AGGGGAAAACA AAATCTTGAC CCAGCTGAAC ATGTCTTCTC 3540  
 GAGTCAGTGC CTGAATCTTT ATTTTTTAAA TTGAATGTTC CTTAAAGGTT AACATTTCTA 3600  
 AAGCAATATT AAGAAAGACT TTAATGTITA TTTTGAAGA CTTACGATGC ATGTATACAA 3660  
 ACGAATAGCA GATAATGATG ACTAGTTCAC ACATAAAGTC CTTTAAAGGA GAAAACTAA 3720  
 AATGAAAAGT GGATAACAG AACATTTTATA AGTGATCAGT TAATGCCATA GAGTGAAAGT 3780  
 AGTTCTATTG ACATTCCTCA AGATATTTAA TATCAACTGC ATTATGTATT ATGTCTGCTT 3840  
 AAATCATTTA AAAACGGCAA AGAATATAT AGACTATGAG GTACCTTGCT GTGTAGGAGG 3900  
 ATGAAAGGGG AGTTGATAGT CTCATAAAC TAATTTGGCT TCAAGTTTCA TGAATCTGTA 3960  
 ACTAGAATTT AATTTTACC CCAATAATGT TCTATATAGC CTTTGCTAAA GAGCAACTAA 4020  
 TAAATTAAC CTATTCTTT AAAAAAAA

Seq ID NO: 164 Protein sequence  
 Protein Accession #: NP\_037504.1

1 11 21 31 41 51  
 MSRTAYTVGA LLLLLGLTLP AAEGKKKGSQ GAIPPPDKAQ HNDSEQTQSP QPGSRNRGR 60  
 GQGRGTAMPG BEVLSSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFYCG 120  
 QCNSFYIPRH IRKEGFSQS CSFCKPKKFT TMMVTLNCP E LQPPTKKRV TRVKQCRICIS 180  
 IDLD

Seq ID NO: 165 DNA sequence  
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51  
 GAATTGCATC GGACAGAGCT TCGCCATGGC CGAGTTGCGC GTGGTTGTGG CACTAACACT 60  
 GCTACGTTTC CGCTTGAGCG TGGACCGAAC GCGCAAGGTG CGGCGAAGC CGGAGCTCAT 120  
 ACTGCGCAGC GAGAACGGGC TCTGGCTCAA G

Seq ID NO: 166 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..1650

1 11 21 31 41 51  
 ATGCCACCTC TGCCATCCAG AATGTCTCGG GGGCCCTCCT TGGTGACAGG CAGGATGCTG 60  
 CCCATCACAG ACCGCCTGCT GCACCTCCTG GGGCTGGAGA AGACGGCGTT CCGCATATAC 120  
 GCGGTGTCCA CCCTTCTCCT CTCTCTGCTC TTCTTCTGT TCCGCTGCT GCTGCGGTTC 180  
 CTGAGGCTCT GCAGGAGCTT CTACATCACC TGCCGCGGCG TGCGCTGCTT CCCCAGCCT 240  
 CCCCAGCCTC ACTGGCTGCT GGGCCACCTG GGCATGTACC TTCCAAATGA GCGGGGCTT 300  
 CAAGATGAGA AGAAGGTACT GGACAACATG CACCATGTAC TCTTGGTATG GATGGGACCT 360  
 GTCCTGCCGC TGTGTGTTCT GGTGACCCCT GATTACATCA AACCCTTTT GGGAGCCTCA 420  
 GCTGCCATCG CCCCAGGA TGACCTCTT TATGGCTTCC TAAAACCTTG GCTAGGGGAT 480  
 GGGCTGCTGCT TCAGCAAAGG TGACAAGTGG AGCCGGCACC GTCGCTGCT GACACCCGCC 540  
 TTCCACTTTG ACATCTTGAA GCCTTACATG AAGATCTTCA ACCAGAGCGC TGACATTATG 600  
 CATGTAAAT GCGCGCATCT GGCAGAGGGC TCAGCGGTCT CCCTTGATAT GTTTGAGCAT 660  
 ATCAGCCTTA TGACCTGGA CAGTCTTCAG AAATGTGTCT TCAGCTACAA CAGCAACTGC 720  
 CAAGAGAAGA TGAGTGATTA TATCTCCGCT ATCATTGAAC TGAGCGCTCT GTCTGTCCGG 780  
 CGCCAGTATC GCTTGACCA CTACCTCGAC TTCATTACT ACCGCTCGGC GGATGGGCGG 840  
 AGGTTCCGGC AGGCCGTGTA CATGGTGCAC CACTTACCA CTGAAGTCAT CCAGGAACGG 900  
 CGGCGGCGAC TGCCTCAGCA GGGGGCCGAG GCCTGGCTTA AGGCCAAGCA GGGGAAGACC 960  
 TTGGACTTTA TTGATGTGCT GCTCTGGCC AGGGATGAAG ATGGAAGGA ACTGTGAGAC 1020  
 GAGGATATCC GAGCCGAAGC AGACACCTTC ATGTTTGAGG GTCACGACAC AACATCCAGT 1080  
 GGGATCTCTT GGATGCTGTT CAATTGGCA AAGTATCCGG AATACCAGGA GAAATGCCGA 1140  
 GAGAGATTTC AGAAGTTCAT GAAAGGCCGG GAGCTGGAGG AGCTGGAGTG GGACGATCTG 1200  
 ACTCAGCTGC CCTTTACAAC TATGTGCATT AAGGAGAGCC TGCGCCAGTA CCCACCTGTC 1260  
 ACTCTGTCT CTCGCCAATG CACGGAGGAC ATCAAGCTCC CAGATGGGCG CATCATCCCC 1320  
 AAAGGAATCA TCTGCTTGT CAGCATCTAT GGAACCCACC ACAACCCAC AGTGTGGCCT 1380  
 GACTCCAAGG GTTACAACCC CTACCGCTTT GACCCGACA ACCCAGACA GCGCTCTCCA 1440

CTGGCCTATG TGCCCTTCTC TGCAGGACCC AGGAATTGCA TCGGACAGAG CTTGCGCATG 1500  
 GCCGAGTTGC GCGTGGTGT GGCCTAACA CTGCTACGTT TCCGCTGAG CGTGGACCGA 1560  
 ACGCGCAAGG TCGGCGGAA GCCGGAGCTC ATACTGCGCA CGGAGAACGG GCTCTGGCTC 1620  
 AAGGTGGAGC CGTGCCCTCC GCGGGCTGA

Seq ID NO: 167 Protein sequence  
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
 | | | | |  
 MPPLPSRMSR GPSLVTGRML PITDRLLHLL GLEKTAFRY AVSTLLLFLL FFLFRLLLR 60  
 LRLCRSFYIT CRRLRCPFP PRRNWLGLH GMYLPNEAGL QDEKKVLDNM HHVLLVWMP 120  
 VLPPLVLVHP DYIKPLLGS AAIAPKDDLF YGFLKPWLG LLLSKGDKW SRHRLRLTPA 180  
 FHFDILKPYM KIFNQSDIM HAKWRHLAEG SAVSLDMFEH ISLMTLDSLQ KCVFSYNSNC 240  
 15 QEKMSDYISA IIELSALSVR RQYRLHHYLD FIYRSADGR RFRQACDMVH HFTTEVIQER 300  
 RRALRQQGAE AWLKAKQKGT LDFIDVLLLA RDEGKELSD EDIRAEADTF MFEHDTTSS 360  
 GISWMLFNLA KYPYQEKGR EEELEWDDL TQLPFTTMC KESLRQYPPV 420  
 TLVSRQCTED IKLPDGRIP KGIICLVSIY GTHHNPTVWP DSKVYNPYRF DPNPQQRSP 480  
 20 LAVVPFSAGP RNCIGQSFAM AELRVVVALT LLRFRLSVDR TRKVRKPEL ILRTENGLWL 540  
 KVEPLPPRA

Seq ID NO: 168 DNA sequence  
 Nucleic Acid Accession #: AK058088.1  
 Coding sequence: 252..1772

1 11 21 31 41 51  
 | | | | |  
 AGGAAACCAA GGCAAGCTCC CCTGTCAAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA 60  
 30 GCCCCAGATG TGATGAGCGC TTCCAGGCTT CAGGCTCAGA AGGCGCCCC AGCTCTCCTG 120  
 TAACCTCAGAG GCCAGTGTGA TGGGAGTTCC TCCACTCAGC ACACCTCCCC TGTAAACACG 180  
 CCTGTGGTGG GCAAAAGGGC TTTGGAACGG TTGCTGTCT TTTCTCTCCT GCGTAATTTT 240  
 CACTTTCATT CATGATAATG TCGAACACGC ACAAAGCTCG GCTGGAACGC CGGGTCACTG 300  
 GCTCAACCAA CCGGTGCGGT TTGCCCAAAC AGCCTTTCTC TGGGGACCTG CTCTCACTTT 360  
 35 CCCAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT 420  
 TATGCAATTC ACAAATCCAG AAGTTTTTCT TTGAGAATTT CAAGAACAAG GACATCCAAA 480  
 GTGGGGAAGC AGATGTGATT CTCGAGTGCC TGGGCTTCAA ATGGGAGCTC CATCAGCCCC 540  
 GGCTTTTTC A GTCTGAGACC TTGGCCAAGC TCTACCTGAA AGCCCTGGCG CAGGGCACCA 600  
 CACACCCCTC GAGGGAGCTT GAGGAGCTTC TCGGAGCTCA ATCACCTAAG AAGACCAAAG 660  
 40 AAAAATCCCC TGCAAAGAGG ATCATCATTT CCTTGAAGAT CAATGACCCA CTGGTCACTA 720  
 AAGTCGCTT CGCCACGGCC CTGAAGAACC TCTACATGAG TGAGGTGGAG ATTAACCTGG 780  
 AAGACCTACT GGGAGTGTG GCTTCCGCCC ACATCCTCCA GTTCAGTGGC CTGTTTCAAA 840  
 GGTGCGTGG A TGATGATA GCCAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG 900  
 CCGGCTGCAA GTACAAGAA GAGCAGCTCA CCACCGGCTG CGAGAAGTGG CTGGAATAGA 960  
 45 ACTTGGTTCC TCTAGGGGGG ACGCAGATCC ACCTCCACAA AATCCACAG GACCTGCTCC 1020  
 ACAAGTGTG GAAGTCCCCC AGGTTATTTA CCTTAGTGA ATTCCATCTT CTGAAACAA 1080  
 TGCTTTTGT GGTCTTCTG CAACTGAACT ACAAGATTC GGAATTCG ACTTATGAAA 1140  
 CCGTGATGAC ATTTTTTAAG AGCTTCTCTG AGAACTGTTG CTTCTGAGC CGGGACATAG 1200  
 GACGGAGCTT GAGGCGCTC TTCTCTGCT TGGCTCTGCA CGGCATCACC AAAGGCAAGG 1260  
 50 ATCTGGAGGT GCTGCGGCAC CTTAACTTCT TCCAGAGTCA ATGGCTCGAC CAGGTTACAG 1320  
 TCAACCATTA CCACGCACTG GAGAATGGGG GCGACATGGT CCACCTGAAA GATCTTAACA 1380  
 CCGAGGCTGT GAGATTGGG CTGCTCTTTA ACCAGGAGAA TACAATTAT TCGAAAACGA 1440  
 TTGCTCTATA TGGAATCTTC TTTAAGATAA AGGGACTCAA ACATGATACT ACCTCTTATA 1500  
 GTTTTACAT GCAGAGAATA AAGCACACAG ACCTGGAATC TCCCTCTGCG GTCTACGAGC 1560  
 55 ACAACACAGT CAGCCTGCGA GCGGCACGCC TGGTGAAGTA TGAGATCAGA GCAGAGGCC 1620  
 TGTTGACGG CAAGTGGCAG GAGTTCAGGA CAAACAGAT CAAGCAGAAG TTTGGGTGA 1680  
 CCACGTCATC CTGCAAAAGC CATACCTTGA AAATCCAAAC TGTGGGCATC CCAATCTATG 1740  
 TAAGTTTTCG ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGAATCT ATGGGATTTT 1800  
 CCCCCACTG GTCTGCATAA AAGAAAATAA AATGACATAA AAGGGAGC

Seq ID NO: 169 Protein sequence  
 Protein Accession #: BAB71658.1

1 11 21 31 41 51  
 | | | | |  
 MIMSNTHKAR LERRVTGSTN RWRLPKQFFS GDLLSLSQMC KALSIDFEEA LRNPDRLCIS 60  
 65 QIQKFFENF KNKDIQSGEA DVILECLGFK WELHQPRLFQ SETLAKLYLK ALAQGTTHPL 120  
 RELEELLRAQ SPKKTKEKSP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDLL 180  
 GVLASAHILQ FSGLFQRCVD VMARLKPST IKKFYEAGCK YKEEQLTGCE EKWLENNLVP 240  
 70 LGGTQIHLHK IPQDLLHKVL KSPRLTFPSE FHLLKTMLLW VFLQLNYKIQ AIPTYETVMT 300  
 FFKSFPENCC FLDRDIGRSL RPLFLCLRLH GITKGKDLV LRHLNFPES WLDQVTNNHY 360  
 HALENGGDMV HLKDLNTQAV RFGLLFNQEN TTYSKTIALY GFFFKIKGLK HDTSYSFYM 420  
 QRIKHTDLES PSAVYEHNVH SLRAARLVKY EIRAEALVDG KWQEFRTNQI KQKFLGTTSS 480  
 CKSHTLKIQT VGPIYVSFA FIFPAS

Seq ID NO: 170 DNA sequence  
 Nucleic Acid Accession #: NM\_007000.1  
 Coding sequence: 1...777

1 11 21 31 41 51  
 | | | | |  
 ATGGCGTCTG CGGCAGCAGC GGAGGCCGAG AAGGGATCTC CAGTTGTGGT GGGCCTGCTA 60  
 80 GTTGTGGGCA ATATCATATT TCTGCTGTCA GGCCTGTCCC TGTCTGCTGA GACCATATGG 120  
 GTGACAGCCG ACCAGTACCG TGTATACCCA CTGATGGGAG TCTCAGGCAA GGATGACGTC 180  
 TTCGCTGGTG CCTGGATTGC CATCTTCTGC GGCTTCTCCT TCTTCATGGT AGCCAGTTTT 240

5 GGTGTGGGTG CCGCACTCTG CCGCCGCCGG TCCATGGTCC TCACGTACCT GGTGCTCATG 300  
 CTCATCGTCT ACATCTTCTGA GTGCGCCTCC TGCATCACGT CCTACACCCA CCGTGACTAC 360  
 ATGGTGTCCA ACCATCCCTT GATCACCAAG CAGATGCTGA CCTTCTACAG CGCGGACACC 420  
 GACCAGGGCC AGGAGCTGAC CCGCCTCTGG GACCGCGTCA TGATTGAGCA AGAATGCTGT 480  
 GGCACATCTG GTCCCATGGA CTGGGTGAAC TTCACGTGAG CCTTCCGGGC GGCCACTCCG 540  
 GAGGTGGTGT TCCCTTGCC CCACTGTGTC TGTGCGCGGA CGGAAACTT CATCCCCTC 600  
 AACGAGGAGG GCTGCCGCTT GGGGCACATG GACTACCTGT TCACCAAGGG CTGCTTCGAA 660  
 CACATCGGCC ACGCCATCGA CAGCTACACG TGGGTATCT CGTGGTTTGG GTTGGCCATC 720  
 10 CTGATGTGGA CGCTCCCGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGA

Seq ID NO: 171 Protein sequence  
 Protein Accession #: NP\_008931.1

15 1 11 21 31 41 51  
 MASAAAAEAE KGSPVVVGLL VVGNIIILLS GLSLFAETIW VTADQYRVYP LMGVSGKDDV 60  
 FAGAWIAIFC GFSPFMVASF GVGAALCRRR SMVLTLYLVM LIVYIFECAS CITSYTHRDY 120  
 MVSNPSLITK QMLFFYSADT DQGQELTRLW DRVMIQECC GTSGPMDVWN FTSAFRAATP 180  
 20 EVVFPWPPLC CRRGNFPL NEEGCRLGHM DYLFKGCFFE HIGHAIDSYT WGISWFGFAI 240  
 LMWTLFVMLI AMYFYTML

Seq ID NO: 172 DNA sequence  
 Nucleic Acid Accession #: NM\_006760.1  
 Coding sequence: 39..593

25 1 11 21 31 41 51  
 GAAAGCCTGC CAGCACCTAT TCCACCTCCC AGCCACGAT GGCACCCCTG CTGCCCATCC 60  
 30 GGACCTTGCC CTTGATCCTG ATTCTGCTGG CTCTGCTGTC CCCAGGGGCT GCAGACTTCA 120  
 ACATCTCAAG CCTCTCTGGT CTGCTGTCCC CGGCGCTAAC GGAGAGCCTG CTGGTTGCTT 180  
 TGCCCCCTG TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGAGGA GCCAATGACA 240  
 GCAAAGTGGT GACGTCCAGC TTTGTGGTGC CTCGCTGCCG TGGGCGCAGG GAACTGGTGA 300  
 GTGTGGTGGG CAGTGGTGCT GGCTTCACAG TCACTCGGCT CAGTGCATAC CAGGTGACAA 360  
 35 ACCTCGTGCC AGGAACCAAA TTCTACATTT CCTACCTAGT GAAGAAGGGG ACAGCCACTG 420  
 AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGGAA TCCATTGGGC 480  
 TGGGTATGGC CCGCACAGGG GGCATGGTGG TCATCACGGT GCTGCTCTCT GTGCCATGT 540  
 TCCTGCTGGT GCTGGGCTTC ATCATTGCCC TGGCACTGGG CTCCCGCAAG TAAGGAGGTC 600  
 TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGGCACCA TCCAGCTCCC CAGCCACCT 660  
 40 GCTCCAGGC CCCAGGCTG TGGCTCCCTT GGTGCCCTCG CCTCTCTC CTGCCCTCCT 720  
 CTCCCTAGA GCCCTCTCTT CCTCTGTCC CTCCTCTTGC CCCAGTGCC TCACCTTCCA 780  
 AACTCTCATT ATTCCTCTCA CCCACTCCT GTCCAGATTG ACTTCTCTCC CATTTTACCA 840  
 CTTTAAACAC CCCATAACA ATCCCCCAT CCTTCAGTGA ACTAAGTCCC TATAATAAAG 900  
 GCTGAGGCTG CATCTGCCAA AAAAAAAAAA AA

Seq ID NO: 173 Protein sequence  
 Protein Accession #: NP\_006751.1

50 1 11 21 31 41 51  
 MAPLLPIRTL PLILILLALL SPGAADFNIS SLSGLLSPAL TESLLVALPP CHLTGGNATL 60  
 MVRRANDSKV VTSSFVPPC RGRRELVSUV DSGAGFTVTR LSAVQVTLNV PGTKFYISYL 120  
 VKKGTATESS REIPMSTLPR RNMESIGLGM ARTGGMVVIT VLLSVAMFLV VLGFIIALAL 180  
 GSRK

Seq ID NO: 174 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..2733

60 1 11 21 31 41 51  
 ATGAAAGTTG GAGTGCTGTG GCTCATTCTT TTCTTCACCT TCACTGACGG CCACGGTGGC 60  
 TTCCTGGGGA AAAATGATGG CATCAAAACA AAAAAAGAAC TCATTGTGAA TAAGAAAAAA 120  
 CATCTAGGCC CAGTCGAAGA ATATCAGCTG CTGCTTCAGG TGACCTATAG AGATTCCAAG 180  
 65 GAGAAAAGAG ATTTGAGAAA TTTTCTGAAG CTCTGAAGC CTCCATTATT ATGGTCACAT 240  
 GGGCTAATTA GAATTATCAG AGCAAAGGCT ACCACAGACT GCAACAGCCT GAATGGAGTC 300  
 CTGCAGTGTA CCTGTGAAGA CAGCTACACC TGGTTTCTCT CCTCATGCCT TGATCCCCAG 360  
 AACTGCTACC TTCACACGGC TGGAGCACTC CCAAGCTGTG AATGTCTCT CAACAACCTC 420  
 AGCCAGAGTG TCAATTCTGT TGAGAGAACA AAGATTGGGG GCACTTTCAA AATTAATGAA 480  
 70 AGGTTTACAA ATGACCTTTT GAATTCATCT TCTGCTATAT ACTCCAAATA TGCAATGGA 540  
 ATTGAAATTC AACTTAAAAA AGCATATGAA AGAATTCAAG GTTTTGAGTC GGTTCAGGTC 600  
 ACCCAATTTC GAAATGGAAG CATCGTTGCT GGGTATGAAG TTGTTGGCTC CAGCAGTGCA 660  
 TCTGAACCTG TGTCAACCAT TGAACATGTT GCCGAGAAGG CTAAGACAGC CCTTCACAAG 720  
 CTGTTTCCAT TAGAAGACGG CTCTTTCAGA GTGTTTCGAA AAGCCAGTGT TAATGACATT 780  
 75 GTCTTTGGAT TTGGGTCCAA GGATGATGAA TATACCTTGC CCTGCAGCAG TGGCTACAGG 840  
 GGAACATCA CAGCCAAAGT TGAGTCTCTT GGGTGGCAGG TCATCAGGGA GACTTGTGTG 900  
 CTCTCTCTGC TTGAAGAACT GAACAAGAAT TTCAGTATGA TTGTAGGCAA TGCCACTGAG 960  
 GCAGCTGTGT CATCCTCTGT GCAAAATCTT TCTGTCATCA TTGGGCAAAA CCCATCAACC 1020  
 ACAGTGGGGA ATCTGGCTTC GGTGGTGTCT ATTCTGAGCA ATATTTTCAT TCTGTCACTG 1080  
 80 GCCAGCCATT TCAGGGTGTG CAATTCAACA ATGGAGGATG TCATCAGTAT AGCTGACAAAT 1140  
 ATCCTTAATT CAGCCTCAGT AACCAACTGG ACAGTCTTAC TGCGGGAAGA AAAGTATGCC 1200  
 AGCTCACGGT TACTAGAGAC ATTAGAAAAC ATCAGCACTC TGGTGCCTCC GACAGCTCTT 1260  
 CCTCTGAATT TTTCTCGGAA ATTCATTGAC TGGAAAGGGA TTCCAGTGAA CAAAAGCCAA 1320  
 CTCAAAAGGG GTTACAGTAA TCAGATTAAA ATGTGTCCTC AAAATACATC TATTCCTATC 1380  
 AGAGGCCGTG TGTTAATTGG GTCAGACCAA TTCAGAGAT CCCTTCCAGA AACTATTATC 1440

AGCATGGCCT CGTGGACTCT GGGGAACATT CTACCCGTTT CCAAAAAATGG AAATGCTCAG 1500  
 GTCAATGGAC CTGTGATATC CACGGTTATT CAAAACCTATT CCATAAATGA AGTTTTCTTA 1560  
 TTTTTCCTCA AGATAGAGTC AAACCTGAGC CAGCCTCATT GTGTGTTTTG GGAATTCAGT 1620  
 CATTGTCAGT GGAACGATGC AGGCTGCCAC CTAGTGAATG AAACCTCAAGA CATCGTGACG 1680  
 TGCCAATGTA CTCACCTTAC CTCCTTCTCC ATATTGATGT CACCTTTTGT CCCCTCTACA 1740  
 ATCTTCCCGG TTGTAAAATG GATCACCTAT GTGGGACTGG GTATCTCCAT TGGAGTCTC 1800  
 ATTTTATGCC TGATCATCGA GGCTTTGTTT TGGAGCAGA TTAATAAAG CCAACCTCT 1860  
 CACACACGTC GTATTGTCAT GGTGAACATA GCCCTGTCCC TCTTGATGTC TGATGCTGG 1920  
 TTTATTGTTG GTGCCACAGT GGACACCACG GTGAACCCTT CTGGAGTCTG CACAGCTGCT 1980  
 GTGTCTTTTA CACACTTCTT CTACCTCTCT TTGTCTTCTT GGATGCTCAT GCTTGGCATC 2040  
 CTGCTGGCTT ACCGGATCAT CCTCGTGTTC CATCACATGG CCCAGCATTT GATGATGGCT 2100  
 GTTGGATTTT GCCTGGGTTA TGGGTGCCCT CTCATTATAT CTGTCATTAC CATGCTGTC 2160  
 ACGCAACCTA GCAATACCTA CAAAGGAAA GATGTGTGTT GGCCTAACTG GTCCAATGGA 2220  
 AGCAAAACCAC TCCTGGCTTT TGTGTCCCT GCACTGGCTA TTGTGGCTGT GAACCTCGTT 2280  
 GTGGTGCTGC TAGTCTCTAC AAAGCTCTGG AGGCCGACTG TTGGGGAAG ACTGAGTCGG 2340  
 GATGACAAGG CCACCATCAT CCGCGTGGGG AAGAGCCTCC TCATTCTGAC CCCTCTGCTA 2400  
 GGGCTCACCT GGGCTTTTGG AATAGGAACA ATAGTGACA GCCAGAATCT GGCTTGGCAT 2460  
 GTTATTTTGT CTTTACTCAA TGCATTCCAG GGATTTTATA TCTTATGCTT TGAATACTC 2520  
 TTGGACAGTA AGCTGCGACA ACTTCTGTTT AACAGTTGT CTGCCTTAAG TTCTTGAAG 2580  
 CAAACAGAAA AGCAAAACTC ATCAGATTTA TCTGCCAAAC CCAAAATCTC AAAGCCTTTC 2640  
 AACCCACTGC AAAACAAGG CCATTATGCA TTTTCTCATA CTGGAGATTC CTCGACAAAC 2700  
 ATCATGCTAA TCAGTTTGT CTCAATGAA TAA

Seq ID NO: 175 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MKVGVWLWIS FFFTFDGHGG FLGKNDGIKT KKELVNKKK HLGPFVEEYQL LLQVITYRDSK 60  
 EKRDRLNPLK LKPLPLWWSH GLIRIIRAKA TTDNSLNGV LQCTCEDSYT WFPFSCLDPO 120  
 NCYLHTAGAL PSCECHLNNL SQSVNFCERT KIWGTFKINE RFTNDLLNSS SAIYSKYANG 180  
 IEIQLKKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALHK 240  
 LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 300  
 LSLLEELNKN FSMIVGNATE AAVSSFVQNL SVIIRQNPST TVGNLASVVS ILSNISLSL 360  
 ASHFRVSNST MEDVISIADN ILNSASVTNW TVLLREEKYA SSRLLLETLEN ISTLVPPAL 420  
 PLNFSRKFDI WKGIPIVNSQ LKRGYSYQIK MCPQNTSIPI RGRVLIGSDQ FQRSLPETII 480  
 SMASLTGNI LPVSKNGNAQ VNGPVIPTVI QNYSINEVFL FFSKIESNLS QPHCVFWDFF 540  
 HLQWNDAGCH LVNETQDIVT CQCTHLTSFS ILMSPFVPSF IFPVVKWITY VGLGISIGSL 600  
 ILCILIEALF WKGIKKSQTS HTRRICMVNI ALSLLIADVW FIVGATVDTT VNPSPGVCTAA 660  
 VFFTHFFYLS LFFWMLMLGI LLAYRIILVF HHMAQHLMA VGFCLGYGCP LIISVITIAV 720  
 TQPSNTYKRK DVCWLNWSNG SKPLLAFFVP ALAIVAVNFV VLLVLTKLW RPTVGERLSR 780  
 DDKATIRRVG KSLIILTPLL GLTWGFGIGT IVDSQNLAWH VIFALLNAFQ GFFILCFGIL 840  
 LDSKLRQLLF NKLSALSSWK QTEKQNSSDL SAKPKFSKPF NPLQNKGHYA FSHGTGDSSDN 900  
 IMLTQFVSNE

Seq ID NO: 176 DNA sequence  
 Nucleic Acid Accession #: AB035089.1  
 Coding sequence: 9845..10219

1 11 21 31 41 51  
 GGGCATGCAG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA 60  
 CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAGAAGG 120  
 CCAAGAGGAA TTAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTGGT 180  
 TTGGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG CAGTGTGTTG CAGAGTAGGA 240  
 AGGAGGAAGG GAGGCAAGAG ATAATATCAT TTTCTCTGTG CTCCAACCTGT ACTTACATAT 300  
 GAGACTATTT CCCTCTCTGC TTTTCAAACC TTACTGGAGT TGTTTTCCCT CATGAAAACC 360  
 AAGAAAGGAA AGCTAGTTAG TCTTGTCTCT AGGTTGTTCA ATGTATACAT ATCTATATCT 420  
 GTAGACAGAA TCCTTGGGAA TACAGTAATT GACATATATT CTGTTATTGT ATGCTTGAAA 480  
 AATCTCTCTC ACTAACCACT TCCCTATAG ATTGCCACAA GCACATAATA AGAAACAATA 540  
 AATAAAATGT TCTCTGACTT TTGTTACTTA ACAATGCTGA GAAACCTTTA CAGCCTTCAT 600  
 AAGGAAGTGA GGTCCAGGAA AATCTAGGAG ATATTTCTTA ACCAATCTAT AAAGGCATTA 660  
 GTAATGACAG GATATTTCCT GAAAGTGTA TTTCCCATTT AGGATTGTTT TTTAATTTCT 720  
 GGATTCTCTG AGCCAATGAA GTTGGTGTAT GTTTATGAAA TATCAAGAGA CATAAGTTGG 780  
 CAAGTGTTCA TATGCAAAAA CTCTCTGGAA TTTCTGAGTT CTCTGTGGCA ATATATGACA 840  
 TCAGGATATG TCCAGTCTCA CACACCAGGA TATGTCTCTT CTAGCCTGTC TATCACATGC 900  
 TAGGAGAACT ATTTAGGAAC AGAAAAAAT GCCTGAAATG ATTTCTCAT TGAACCTATC 960  
 CAAGCTTTCT CTAAATTTAA GCAAACTCCT GGTCAATTTT AGTAGTACC TTTCTTAAAG 1020  
 TTCAACCTTC AGGGCAAACC TCCGTGCCCTC AGACGTTTAG CCATAGTCTG AAATCTCTT 1080  
 CCATAGATTG GTCCCCGTGA ACCCCGGTTT GTCTCAGCTT GTTATCTCTG TTTTCTCTTC 1140  
 CCTCCATTCC CAGGATGAGC TTGTTGCTTC TGTCTATGTA GACATTAGAT TCCTTTTCTT 1200  
 TGGTACCCGA GTAAATCCAT CACTACTCAA TAGAGGAAGG TCATTTTTGT TCTTATAGCG 1260  
 CTGGATGTCG ACTCAGCTGA GAAGACCATT ATTCATTTTT GGAATTTCTT ATCTCAGATA 1320  
 TTTCTCTCTT TTTCTTTTTC TTCTATCTTT GGATTTTATG TCCATCAACG CCCCATTAGT 1380  
 CTATTCCCGG ACTTCAATCA GGGAACTTAT ACCTCTTAAA CTCATTGAGA GACTCAAAC 1440  
 ATATATATTG ATACAGGAGA CCTAAGAAGA GCATGTCTTG GGGGTTGAGG AAACAGGCAG 1500  
 GTGAGAAATT TCCAGATTGG AAACACAGCT TCCTTTCTCC CATCCAGCCC CTACTTTCAG 1560  
 CCTATGTGTT TCTGGCACCT TGTGTAGAT AAATCTCCCT TGACTTTGTG ATGTGCTGAG 1620  
 AAAACAAACT CACGGCTGGT GTTAAAAAGG GCCCATGACA ATACCAAGTG TTGGGGAGAA 1680  
 TGTGGAGAAA TCAGAACTCT ATTACGGTCT GGTGGAATG CACACTGTG CAGAATTTCTA 1740  
 TGGAGAAGAG TCTGGCATTT CTCAAAATG TTAACCTGGA TTTACCATAT GACCCAGCGA 1800  
 TTTCAATCAT AGGTTTATAC TCAAAAGAAA TGAAGAAATA TGCCATGCAA AAAAATGTAT 1860  
 ATGAAAGGTC ACAACATCAT TATTCATAAT AGTAAAGGGA TGGAAACAAC ACAAAATGTC 1920  
 ATCAACTTAT GATTAAAGAA AATCTGGTCT ATTCATAGAA TGGAAATATTA TTCGACCACA 1980

	AAAAGGAATG	ATGTACTGAT	CCATGCAATG	ATGTGGACAA	ACCATGAAAA	TAACACTAGA	2040
	TTAAGAAGC	CAGTCACAAA	AGGACTTACT	GTATGATTCC	ATTTACCTGA	AATGTTTGGA	2100
	ATAGGCAAA	CCATAGAAAC	AGGAGSTAGA	TTCTGGTTT	CCAGGGTCTC	CAGGAAGGGA	2160
5	AGAATGAAGT	ACAAGATTTC	TTTGGAGGT	AGTGAAATTG	TTGTGGAATG	AGATCATGAT	2220
	GATGATAGCA	CAACTTTGTG	AATATAATAA	AATCATTGAA	TTGTACAGTT	GAATTTATGG	2280
	TATATAAATT	ATATGTTAAT	AAAAAGGGGG	TCCACAAAAC	AAACAGCCCC	CCACTCTGGT	2340
	TGTCAGGGAG	ATATTGGATT	AAATGGCCTT	GGACAACAAC	CCCTCTCCCT	GGCCACAGAC	2400
	ATTCTTCAGA	TTACAAGATA	TTCCAGGGGA	AACACTGGAA	TGAGTCTGAA	GCCAGGTGCT	2460
10	AAACAGAAGG	ACCATTGAGA	AATGTTGTGA	TCCTGACAGG	TCAAGCAATT	TATTTTTCCG	2520
	CTTCATTTTT	AAATGTAAAA	TTAGAAAGCT	GCCATTAAAA	ATGGCCCCGC	TGTTTCAATT	2580
	GCTCTTCTCA	GTGTCAGCCT	GTTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATACCT	GAGACTGGCA	AGAAAAAGAG	GTTTAATTGG	GCTTAGAGTT	CCACGTGATT	2700
	GGGAGGCGCT	CAGAATCACA	GTAGGAGGCA	AAAGTTATTCT	TTACATGGTG	GCTGCAAGAG	2760
15	AAGATGAGGA	AGAAGCAAAA	GAAGAAACCC	CTGATAAACCC	CATCGGATCT	CCTGAGGCTT	2820
	ATTAACATATC	ATGAGAATAG	CACAAGAAAG	ACCGCCCCCC	ATGATTCAAT	TACCTCTACC	2880
	TGGGTCCCTC	CAATAACATG	TGGAAATCTT	GGTAGATACA	ATTCAAGTTG	AGATTTGGGT	2940
	GGGAACACAG	CCAAACCATA	TCACCTCAGCA	AGGCAGATAA	CTTTCTCACT	GAGCCTATGC	3000
	AAACAGAAAC	CATCTGGGAT	GGTTGTAAAG	GGCACAGGAA	GTGACTGGTA	GGATCACTGC	3060
20	CAAAAGCTGAG	CACCTCAGGAG	AAGGCAATAG	AATCCTATTCT	TCCATAGTAT	GCTATAAGAT	3120
	ACTGAAGTAC	ACTTCTTCAC	TATCTCTTTG	GACTTAGAAT	TAGCACTACA	TTCTTTGTTA	3180
	TACAGAAAAA	TTACTAAGGA	AATTCATAGG	ATGACAAAAA	CTTTCAGAAC	TGAAAAACAG	3240
	GAAATGTAAG	CTTTTGTAGT	CTTTGGTATT	CGAAGTATGC	CTAAAAGACA	ATGCAAAATC	3300
	CAAGAAAAGA	ATGGTGGGGT	TTTTGTTTTGT	TTGGTTTTGT	TTTTGTTTTA	CAGCTGGAGT	3360
25	AGAATACAAA	GGGATGGAGT	TGAAACAAAT	GAGAGGAAAT	TGGAATTCTA	AACCTATTCT	3420
	CATTGGCATT	AGAAAGGCAC	CTACATGTAT	TTACATGAG	CCGGTGACTG	CTGACTTGCA	3480
	TTCTTATTTT	TTCCCTATAG	ATTAATAAAGG	AGGTACAATG	GTAGAACTGT	AATCCTGTCC	3540
	TTTGTCTATA	ATTTTCATAT	TCATAAAGGT	GAGTGTTAGC	CCGCTGTGTA	AATCTGAAGT	3600
	TGAGTAACTT	CAAAATACTAA	CCACAGAGGG	AAAGGCAGCA	AGAGGAGAGG	CATAAATTTA	3660
30	GGATCTCACC	CTTCATTCCA	CAGACACACA	CAGCCTCTCT	CCCCACCTCT	GCTTCTCTTA	3720
	GGAACACAGG	TAAGAGCTTC	AAGCCTCTCC	AGCTTAATAA	CATGAATTAT	TTTTGAGAAAT	3780
	AATAATGATA	CTGTGTTCTA	TATCATGCAT	CTCCTGCATT	CTGTCTGATT	ATATTTTACT	3840
	TATTCTGCCA	GAGCAAAATT	AAAATACCTA	TTTCATCTGA	TTTGTCCTTT	ATCTAAATG	3900
	CTTAGTTCCA	AGTAAACCAA	GGCCTTTTA	GGAACACAGA	GGGAGAGTGC	CTTGCAAGCA	3960
35	GAGAGTCTTG	AAGGAGATGT	CAGGGACGCA	TCTTAACAGC	TGGTTGGATG	TGATCCACAG	4020
	AGGTCTCCCTG	TTAGCATTTA	TTGTAAGGCC	ATCCTACCTA	GCTCTAGTGT	AACCAGCAAT	4080
	GAAAGAAAGA	TAAAGAGGGT	CGATTACTTA	TTTACAATAG	TCTTTAAAAA	CGTAGTTTTG	4140
	TAAGCCTTCT	AATTAGGACA	TTAATATATT	TAATATATGC	ACATTGTAGA	AAGATTGAAG	4200
	CGTTAAAAAT	AAGAGAAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCATTTT	4260
40	TTTAAGAAAA	TTGTACTACA	AAATACCATT	CCATTATTAT	AAGTCATTCT	GACAGGAATC	4320
	TGATGCTTTT	CCAGGAGTTC	CAGATCACAT	CGAGTTCACC	ATGAATTTCAC	TCAGTGAAGC	4380
	CAACACCAAG	TTTATGTTCC	ATCTGTTCCA	ACAGTTTACA	AAATCAAAAG	AGAACAACAT	4440
	CTTCTATTCC	CCATACAGCA	TCACATCAGC	ATTAGGGATG	GTCTCTTAG	GAGCCAAAGA	4500
	CAACACTGCA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCGTGTCAG	4560
45	TTTTTCTCTG	GTTCCTGTCG	CTAGCACGCA	GATGGTAATA	GATGTGGTGG	TCTGATGGGT	4620
	AGCACAGGGG	GCTGTGCAGG	AATTTCCATA	ACTGTGAGAC	CACCTGACTTA	AACAGATCTT	4680
	TTGAGTAAAG	TTTTCTTGTC	CCGCTTCATG	TCTCTTCCAG	GTCTTTCAC	TTGATCAAGT	4740
	CACAGAGAAC	ACCACAGAAA	AAGCTGCAAC	ATATCATGTG	AGTCACAGAG	CACCTCTGAT	4800
	CAGCTTTAGA	TCCCTGAACA	GGTCATAGTT	TAAACCTGGA	ACTTCACAAA	AACATAAGAAA	4860
50	AGGCCAGTTT	TAGGGAATAAT	CTTGGACACA	AAGATTGAGA	CATACAGAGT	GGGTTGGCAT	4920
	TTTATGTCAC	ATAATTATTA	TTCTCTATTT	CTGCGTTACT	AAAAGACAGT	CAGCACTGTA	4980
	CCTCAGAGCA	TAGGTCTGGA	TCAGGATAGG	CTGGGTTTCA	ACTCCAGCTT	TGCTCTTCAC	5040
	AAATGATGAA	TAAGAGCAGG	ACACAACTGC	TCGGAGTCCC	AGTGACCTCA	TCCCAGAAAA	5100
	CTAAGGGTAA	GAAAAATCTT	GACTCAATAC	ATGCAAAATAC	ATGCAAAATGT	TTACAACAGT	5160
55	GCCTTGCCCA	TAAAAGTCAT	AATAAATGTT	ATTATTATTA	TAAAGTAGCT	ATAATTATAC	5220
	TAATCATATAT	AATGTGAAAA	TAATTTAATT	TTTATTGAGT	CATTAAATGAG	ATTGAGAGGA	5280
	ATAAGCACAA	GTCCAAGTAT	ATTTGGAAA	ATGATTGCTA	TGGAATATAT	TGGTTTAGAG	5340
	CCTTAATAGT	GCAAAATGCT	TTGCTGGAAG	GTAGAAAAGT	CTAGATTTAA	ACAGGCTTAG	5400
	GTTCAAAAC	TGGCACTTCT	AATTTATGTC	TCTATAAACA	GGGTTTTTTT	CCCATTTCTC	5460
60	TGAGCTTTT	TGTGTTTATC	TGAATTGAAC	TAAAGACTTA	GAGTTACCCA	TGTAAAGTCC	5520
	TTAGCCATGG	ACCTGGCATA	CACCTCTCTT	ACGTGCGAGG	AATGACCATC	ATGAGGAAAG	5580
	AGCCACAGAT	CAGTCAATGT	GTCTTACAAG	ATAATAGCAC	CAACAGGTAT	AACAGGGCTT	5640
	CCTGGCATAA	TCTATTTTAA	ATATCCAACC	TTCAACATAC	TCGTATCTTT	GATGACTGTT	5700
	AGAAGTGAAA	TATGTCCTTT	GCCCATAAAG	AGCTGAGAGT	TTAAGTGGGA	AGCTAAACCT	5760
65	AACCCCTTAA	ACCAACAAGG	AGAAAATCTA	CTGGTAGACA	GCGCTGCATC	TTAGTTTCAG	5820
	AAGAGAAAAA	ATTGCAAGTAC	GTTAGAGCAA	GAAGAATTTT	CTGGAAGAA	TCAAATATAA	5880
	GGTGGATTTT	GAAGGGTATT	TGAGGTGAAA	TACACCAATT	ATCAGGGAAT	AACATCAAAG	5940
	GTCCCTCAATG	AGACTACCCAG	CATTTAGGGA	CTGATCTAAC	AGACTTAGCA	TGGGTTTAGT	6000
	ATTTACATTG	ATACAGCAAT	TGAATGATCT	CCTTTTGTGA	TGTTTGAAGG	TTGATAGGTC	6060
70	AGGAAATGTT	CATCACCAGT	TTCAAAAGCT	TCGACTGAA	TTCAACAAAT	CCACTGATGC	6120
	ATATGAGCTG	AAGATCGCCA	ACAAGCTCTT	CGGAGAAAAG	ACGTATCAAT	TTTTACAGGT	6180
	AAATTTACCT	GGCCTACCCA	CATTTTCAAT	GCATCCTGAT	GTCTGTGTCT	CTGAGTGGCC	6240
	AAATGGAAGA	AAGCAAGGCA	GATGAGCCTG	GCCGACCCAG	GTGGAGAGCA	TTTACTCAGA	6300
	GTGCATTAGC	TCCATTTTCCA	CAACTCTCCC	CCACTGGAGT	GTCCCAGACC	CCAACGATAC	6360
75	ATCACTGAAG	TGTGGATTTA	GGGATAATCT	TGTGATAAAA	GAGGAGGTTG	TGTAATAGAG	6420
	TGAGTAAGAG	TAATAAGTAA	TAAAGATCCA	TCGATAAACT	GGCACTGACT	CAGTCACATA	6480
	CGATACATCT	TGGTGGGAAA	TGTATGACTA	ATGGGATATT	ATTGGAATGG	GCAGGCTTGG	6540
	GTGAGTTCCT	GAGAATAGTT	GAGGAAGTAC	CAGGAAATAT	TGAATGCACA	GGATGAAAGA	6600
	CAAAAACAAA	GATCAGAAAC	ATCATGGTTA	AAATTACTGG	AGAGAAGTCT	GAGAAGCAAT	6660
80	GAATCTCCTT	CAGGGAAGCC	TGCTCTGCAG	TTTGCAAAAC	ACAGCCTCTT	CTGCTTCTGC	6720
	CTTTTGCCAA	GATGATATTG	ACCTTCAGTG	ACCTCTTCTT	TGTGCCAGCC	CACATTCCCC	6780
	TTTTGCATTG	CCTACATGAC	ACCTGTATAA	AAATATCCAT	GGACAGGAGA	TACTGCATCT	6840
	ATTGAGGGTC	TGAGATTGAG	TTACTGTTGT	TACAAATAAG	TAAGTTTGGT	AATATATAGT	6900
	TACATAAATT	ACTCCTAATT	CCTACTCTCT	CTTACATATC	TCAAAGGAAT	ATTTAGATGC	6960
	CATCAAGAAA	TTTTTACCAGA	CCAGTGTGGA	ATCTACTGAT	TTTGCAAAATG	CTCCAGAAGA	7020

AAGTCGAAAG AAGATTAACT CCTGGGTGGA AAGTCAAACG AATGGTAGGA GAGCCACCCA 7080  
 TTATAGAAAC ACCTTTGAGA AACCTATGCC AGTGAGCCTT GTGCTTGACA CTGCATGGGG 7140  
 GAACAGGTGT GGGGATTGAG ATGGGTTTGC AGGGAGGGCT GAAGAGGGCA CTCCAGATGA 7200  
 5 AGGATTTGTC CAAATGAATA TGAAGAGAGC CTAGGGGAGC CAAGGAGGAA ATCACAGGAA 7260  
 GCCAATTAGA TGGAAACACA TCTGGAGAA TATTTGCTTA TGGCCCTGCA TGACAATAGC 7320  
 TTTGTGGATC CCTGTCTCC GCTCAGACCT ATTTTGAGAT CATATCCTTT ACTTTAAATC 7380  
 AGACTCAAT TTTTATGATG AATATTTAAT AGAAAACATT AGAAAGCGTC TCTCGTCTCC 7440  
 TTTACTAATT GGGAAACAAG CAGCTCTCTG GTAAATCACC CTTTTGTCTC TGAGCTGGAG 7500  
 10 CTGCCTGGAT CACATCTGTA GCCAATGTGT TCTGCAGGGA TTATCACAGC TCTCTTCCCC 7560  
 ATCAAGGGCA AAGAGGCTGA CAAAGTCTCC ATTCTACAGA CATCTTCTTT ACCTCCCACC 7620  
 TCTCATTACA GGGCAAACTT ACAGCAACTC AACATGAGAG TGAATAGGAA GATACCCCCG 7680  
 GAAGTAGTGT CTGACAGCAC AGGACATGCG TTTCATATTA CAGAGCTCAA GTCACTCATC 7740  
 CTAAATGCA ATCAGGGCCT CCTTCTCTG AATGGGGACC CCGTAGTTAA AAAAAATAA 7800  
 15 AAGTAGGAAG AGGAGGGAGG GAGAAAGGAA AGACACATGT TGGAAAGAGT GACAAATCA 7860  
 GTTATCAGT ATTTCAAAATC AGATGATTGG AGACATTCAT ACACAGAGAA CGTGAACCTC 7920  
 TTCTCTATCA CAAGAAGTGA TGTCTCCATC AAGGGTAACT TTATACGACT GGAGCCTTGA 7980  
 AGAAAGCTGC ATCTGGTGAA CCACTGGTCA GTGAGTCTAA CAATTCAAAG ATCAAAGTCA 8040  
 GTGAGTCTCA AGCAGGGATT TGGGTCAATA ATTAACGATC AGTCACGAAC ATTTGCAAG 8100  
 20 CATCTTCCAG ACAAGCCATT TGTAGCTTGT GTAAAGACT CTTTTATCT TCCCTTGCA 8160  
 GAAAAATTA AAAACCTATT TCCTGATGGG ACTATTGGCA ATGATACGAC ACTGGTTCTT 8220  
 GTGAACGCAA TCTATTTCAA AGGGCAGTGG GAGAATAAAT TTAATAAAGA AAACACTAAA 8280  
 GAGGAAAAAT TTTGGCCAAA CAAGGTATTG TCTATATTTT ATTTATATAG TGTAAATATG 8340  
 25 TAATACATGG AATGTTAAAC ATTTCTGATG GAATGTAACA TGATAAGTAA AAAATAAAAA 8400  
 TTGTTCAATG CTGTTATTTT GTTGTTTTAC TCTTATAACT TTATTTAGTT AGGAATACCT 8460  
 GAAAAACTAT TGTTTCTAAC TCATGGAATT CCTGGGTTAT TTCTTAGAAG AAGAAGGATG 8520  
 TGTGTCTATC TCAATAATAT TATCTTTTAT GTCTTGTGTT TCACGTGTTA TTTGTTGGAC 8580  
 ACATTGATTT ATTGCAGAA ACATACAAAT CTGTACAGAT GATGAGGCAA TACAATTCCT 8640  
 30 TTAATTTTGC TTCTCTGGAG GATGTACAGG CCAAGTCTCT GGAATATCCA TACAAAGGCA 8700  
 AAGATCTAAG CATGATTGTG CTGCTGCCAA ATGAAATCGA TGGTCTGCAG AAGGTAAGAA 8760  
 CTTGCATCTA CAATCTTCTC TTCTACTGCC GGACATTTT CCAGAGATAC CAAGTTTAAA 8820  
 CAAGGTAAAA GCTTATGACC GAGTTGCCCT AAAATGATGA AAAATTTCTAA ATGAGGAATG 8880  
 ATGACTCACC TCTATATTAC AAATATTGTA GCATAGGGCC TGACACAAC TGAAAGCTTA 8940  
 35 GTTTTGTGTT GTTTGTTTGT TTTTATTATT ATTATTATA TACTTTAAGC TTTAGGGTAC 9000  
 ATGTGCACAA TGTGCAGGTT AGTTACATAT GTATACATGT GCCATGCTGG TGTGCTGCAC 9060  
 CCAATTAATC ATCATTTAGC GTTAGGTATA TCTCCTAATG CTATCCCTCC CCCCTCCCC 9120  
 CACCCACCAA CAGTCTCAG AGTGTGATGT TACCTTCTGT TGTCCAAGTG TTCTCATGTT 9180  
 TCAATTTCCA TCTATGATTT AATTCCATCT ATGGCTTAGT TAATGATTAA TTTATTAGAG 9240  
 TTACATGCAT TGGATATCAA TTTGATGATA TTATTATGCA GCAATTTAAA CTTGACTGGG 9300  
 40 AGAAATATAT ACCAATGTGA GGAAGTTTAA CAAATAGGCC GAGTAGAAAA GGAATACAAA 9360  
 ATTTAGGAAT TTAGGGAATT ACAATTTAAT AATTGCAATG TGTACTAAAT AATGTATACA 9420  
 GAAAAATATG ATGAGCCTAT TAAAAATTGA CACATGTAGT AGGCTGTTGG CACAGAAGAT 9480  
 AGTGATACAT ACAGTTCATT GTGTACAAA TAATGTAATC ATATTTTACA TGTGTATCAT 9540  
 ACAGTTGTAT ACATACATAT GTACACATAT ACATATACGT AAAACATGA TTCTGTTTTT 9600  
 45 ACATACATGT ATATACATAT ACACATATAA CCAATGTAT TTATATATTC AGGACTCATA 9660  
 TTTTACCTAT TAGAATAATA ATGTCTATTA AAGTGAACCT TCTGTATTTC ACATTTATTG 9720  
 CCAAAATAAC GAATCTCCAC ATAGTCAATT CATTGTTAAG GTGTATTAGA GATCGACAGT 9780  
 TAGTCATATC AGTTTCTTTT TTCCATTTGT ATAGCTTGAA GAGAAACTCA CTGCTGAGAA 9840  
 ATTGATGGAA TGGACAAGTT TGCAGAATAT GAGAGAGACA TGTGTCGATT TACACTTACC 9900  
 50 TCGGTTCAAA ATGGAAGAGA GCTATGACCT CAAGGACAGC TTGAGAACCA TGGGAATGGT 9960  
 GAATATCTTC AATGGGGATG CAGACCTCTC AGGCATGACC TGGAGCCAG GTCTCTCAGT 10020  
 ATCTAAAGTC CTACACAAGC CCTTTGTGGA GGTCACTGAG GAGGGAGTGG AAGCTGCAGC 10080  
 TGCCACCGCT GTAGTAGTAG TCGAATTATC ATCTCCTTCA ACTAATGAAG AGTTCTGTTG 10140  
 TAATCACCTT TTCTTATCT TCAATAGGCA AAATAAGACC AACAGCATCC TCTTCTATGG 10200  
 55 CAGATTCTCA TCCCATAGA TGCAATTAGT CTGTCACTCC ATTTAGAAAA TGTTCACTTA 10260  
 GAGGTGTTCT GGTAAACTGA TTGCTGGCAA CAACAGATTCT TCTTGGCTCA TATTTCTTTT 10320  
 CTATCTCATC TTGATGATGA TAGTCATCAT CRAGAATTTA ATGATTAAAA TAGCATGCCT 10380  
 TTCTCTCTTT CTCTTAATAA GCCACATAT AAATGTACTT TTCTTCCAG AAAAATTTC 10440  
 CTTGAGGAAA AATGTCCAAG ATAAGATGAA TCATTTAATA CCGTGTCTTC TAAATTGAA 10500  
 60 ATATAATCT GTTCTTGACC TGTTTTAAAT GAACCAAAACC AAATCATACT TTCTCTTCAA 10560  
 ATTTAGCAAC CTAGAAACAC ACATTTCTTT GAATTTAGGT GATACCTAAA TCCTTCTTAT 10620  
 GTTCTTAAT TTTGTGATTC TATAAAACAC ATCATCAATA AAATAATGAC ATAAAAATCAT 10680  
 TTTTGCTTTA CTTGTTTTCT CTCTGGAAAG GGCAAGTGT CAGTTACACA TAGGAAAGAT 10740  
 AATTTAGAGA TATATTAATC ATATATAAAG GAAAAATAA AACAGAGTAG TTCATGATGA 10800  
 65 GCCTGGAGTA GAAGGCATAT CCCAGAACAG GAGGAGCCTT GTAAACCACA TAGGAACTTC 10860  
 CTATTTTATG CTAAGGGAT AAGAACTCA TTACAGGCTT TGATGGTTGT TTGTCAAAGA 10920  
 GGGGCATAAA ATTATCATAT CCACATCTAG AAAATACATC TCTGGCTACG CTGATATCAA 10980  
 TGGATGCGAG GAAAGAACAG TGTGGTTACC ATATATAAAT TAGGAAATCA TTAGAGTATT 11040  
 70 GGGAGTGGAA ATGGAGAGAA AGAAAGAGCC TGGGGGAATT ATTTAGGAAA TAATAGTTAC 11100  
 AGAAGACAT CTAAGTTGCT GACCTATCTG ACTGGATGGA TGGAAAGATA TCTTGTCTCT 11160  
 GAGAGAAAAA AAGACTTTGG GTTTAAATTT GTACTTGATG AATTAAGGTA CTTTAAATAT 11220  
 TCAATGGAT TTGCTGGCA GGCACCTGAA GATATTAGTC TAAATCTCAG AAACAGAATA 11280  
 TGATCTGAAG CTCATAATTT GTGATATCA ATATAAATAC TTTAGAGTCA TTTGGATAAA 11340  
 75 TATGGTAGTT GTAGCTAAAA GCAAAAATAA GATACTAGGG AGAAAGGATA AAGTTAGAAG 11400  
 AAAGAAGAA CTAGAATTGA CCTTGAAGTA TATCAGCATG TGTAAAGATC AGGAATTGAT 11460  
 CATTTTATT TTCCAGAAAG TAGCTTTTCT TAGGGTTCCA TATTTACTCC CATAGATTCT 11520  
 TCCC

Seq ID NO: 177 Protein sequence  
 Protein Accession #: BAB21525.1

1 11 21 31 41 51  
 | | | | |  
 MNSLSEANTK FMFDLQQFR KSKENNIFYS PISITSALGM VLLGAKDNIA QQISKVLHFD 60  
 QVTENTTEKA ATYHVDRSGN VHHQFQKLLT EFNKSTDAYE LKIANKLFE KTYQFLQEYL 120

DAIKKFYQTS VESTDFANAP EESRKKINSW VESQTNEKIK NLFPDGTIGN DTTLLVLNVAI 180  
 YFKGQWENKF KKENTKEEFK WPNKNTYKSV QMMRQYNSFN FALLEDEVQAK VLEIPYKGD 240  
 LSMIVLLPNE IDGLQKLEEK LTAEKLEMEWT SLQNMRETCTV DLHLPRFKME ESYDLKDTLR 300  
 TMGMVNIIFNG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAAATAVV VVELSSPSTN 360  
 EEFCCNHPFL FFRQNKNTNS ILFYGRFSSP

Seq ID NO: 178 DNA sequence  
 Nucleic Acid Accession #: NM\_001910.1  
 Coding sequence: 50..1240

1 11 21 31 41 51  
 | | | | |  
 GGAGAGAAGA AAGGAGGGGG CAAGGGAGAA GCTGCTGGTC GGACTCACAA TGAACACGCT 60  
 CCTTCTTTTG CTGCTGGTGC TCCTGGAGCT GGGAGAGGCC CRAAGGATCCC TTCACAGGGT 120  
 CCCCCTCAGG AGGCATCCGT CCTCAAGAA GAAGCTGCGG GCACGGAGCC AGCTCTCTGA 180  
 GTTCTGGAAA TCCCATTAAT TGGACATGAT CCAGTTCAACC GAGTCTTGCT CAATGGACCA 240  
 GAGTGCCAAG GAACCCCTCA TCAACTACTT GGATATGGAA TACTTCGGCA CTATCTCCAT 300  
 TGCTCCCCCA CCACAGCACT TCACTGTCTT CTTCGACACT GGCTCCTCCA ACCTCTGGGT 360  
 CCCTCTGTGT TACTGCACTA GCCCAGCCTG CAAGACGCAC AGCAGGTTC AGCCTTCCCA 420  
 GTCCAGCACA TACAGCCAGC CAGGTCAATC TTTCTCCATT CAGTATGGAA CCGGGAGCTT 480  
 GTCGGGATC ATTGGAGCCG ACCAAGTCTC TGTGGAAGGA CTAACCGTGG TTGGCCAGCA 540  
 GTTTGGAGAA AGTGTACACG AGCCAGGCCA GACCTTTGTG GATGCAGAGT TTGATGGAAT 600  
 TCTGGGCGCTG GGATACCCCT CCTTGGCTGT GGGAGGAGTG ACTCCAGTAT TTGACAACAT 660  
 GATGGCTCAG AACCTGGTGG ACTTGGCGAT GTTTCTGTCT TACATGAGCA GTAACCCAGA 720  
 AGGTGGTGCG GGGAGCGCAG TGATTTTTGG AGGCTACGAC CACTCCCAT TCTCTGGGAG 780  
 CCTGAATTGG GTCCCACTCA CCAAGCAAGC TTACTGGCAG ATTGCCTGG ATAACATCCA 840  
 GGTGGGAGGC ACTGTTATGT TCTGCTCCGA GGGCTGCCAG GCCATTGTGG ACACAGGGAC 900  
 TTCCCTCATC ACTGGCCCTT CCGACAAGAT TAAGCAGCTG CAAAACGCCA TTGGGGCAGC 960  
 CCCCCTGGAT GGAGAATATG CTGTGGAGTG TGCCAACCTT AACGTCATGC CGGATGTCAC 1020  
 CTTCAACCAT AACCGAGTCC CCTATACCCCT CAGCCCAACT GCCTACACCC TACTGGACTT 1080  
 CGTGGATGGA ATGCAAGTTCT GCAGCAGTGG CTTTCAAGGA CTTGACATCC ACCCTCCAGC 1140  
 TGGGCCCTCT TGATCTCTGG GGGATGTCTT CATTCGACAG TTTTACTCAG TCTTTGACCG 1200  
 TGGGAATAAC CGTGTGGGAG TGGCCCGCAG AGTCCCTTAA GGAGGGGCTT TGTGTCTGTG 1260  
 CCTGCCTGTC TGACAGACCT TGAATATGTT AGGCTGGGGC ATTCTTTTACA CCTACAAAAA 1320  
 GTTATTTTCC AGAGAATGTA GCTGTTTCCA GGGTTGCAAC TTGAATTAAG ACCAAACAGA 1380  
 ACATGAGAAT ACACACACAC ACACACATAT ACACACACAC ACACCTTACA CATACACACC 1440  
 ACTCCACCA CCGTCATGAT GGAGGAATTA CGTTATACAT TCATATTTTG TATGATTTT 1500  
 TGATTATGAA AATCAAAAAT TTTCACATTT GATTATGAAA ATCTCCAAAC ATATGCACAA 1560  
 GCAGAGATCA TGGTATAATA AATCCCTTTG CACTCCACT CAGCCCTGAC AACCATCCA 1620  
 CACACGGCCA GGCCTGTTTA TCTACACTGC TGCCCACTCC TCTCTCCAGC TCCACATGCT 1680  
 GTACCTGGAT CATTCGAAG CAAATCCGA GCATTACATC ATTTGTGTTA TAAATATTTT 1740  
 TAACATCCTT AAATATACAA TCGGAATTCA AGCATCTCCC ATTGTCCAC AAATGTTTGG 1800  
 CTGTTTTTGT AGTTGGATTCT TTTGTATTAG GATTCAAGCA AGGCCCATAT ATTGCATTTA 1860  
 TTTGAAATGT CTGTAAGTCT CTTTCCATCT ACAGAGTTTA GCACATTGA ACGTTGCTGG 1920  
 TTGAAATCCC GAGGTGTCTT TTGACATGGT TCTCTGAAC TATCTTTCTT ATAAATGGT 1980  
 AGTTAGATCT GAGAGTCTGA TTTTGTGGCA AAAATACTTC CTAGGTGGTG CTGGGTACTT 2040  
 CTTGTGTCAT CCTGTCAAGA GGCAGATAAT GCTGGTGCCT CTCTATTGGT AATGTTAAGA 2100  
 CTGCTGGGTG GGTTTGGAGT TCTTGGCTTT AATCATTCAT TACAAAGTTC AGCATTTT

Seq ID NO: 179 Protein sequence  
 Protein Accession #: NP\_001901.1

1 11 21 31 41 51  
 | | | | |  
 MKTLLLLLLL LLELGEAQGS LHRVPLRRHP SLKKKLRRAS QLSEFWKSHN LDMIQFTESC 60  
 SMDQSAKEPL INYLDMEYFG TISIGSPPQN FTVIFDTGSS NLWVPSVYCT SPACKTHSRF 120  
 QPSQSTYSYQ PGQSFSIQYG TGSLSGIIGA DQVSVEGLTV VQQQFGEVST BPGQTVDVDA 180  
 FDGILGLGYP SLAVGGVTFV PDNMMAQNLV DLPMSVYMS SNPEGAGSE LIFGGYDHS 240  
 FSGSLNWVPV TKQAYWQIAL DNIQVGGTVM FCSBGCAIV DTGTSITIGP SDKIKQLQNA 300  
 IGAAPVDGEY AVECANLNMV PDVFTINGV PYTLSPXTAT LLDFVDGMQF CSSGFQGLDI 360  
 HPPAGPLWIL GDVFIRQFYS VFDRGNRRVG LAPAVP

Seq ID NO: 180 DNA sequence  
 Nucleic Acid Accession #: NM\_018058.1  
 Coding sequence: 319..1575

1 11 21 31 41 51  
 | | | | |  
 TACGCGCTGC GGGACCGGCA GGGGAACGCC ATCGGGGTCA CAGCCTGCGA CATCGACGGG 60  
 GACGGCCGGG AGGAGATCTA CTTCTCAAC ACCAATAATG CCTTCTCGGG GGTGGCCAGC 120  
 TACACCGACA AGTTGTTCAA GTTCCGCAAT AACCGGTGGG AAGACATCCT GAGCGATGAG 180  
 GTCACCGTGC CCGCTGGTGT GGCACGCCTC TTGCGCGGAC GCTCTGTGGC CTGTGTGGAC 240  
 AGAAAGGGCT CTGGACGCTA CTCTATCTAC ATTGCCAATT ACGCCTACGG TAATGTGGGC 300  
 CCTGATGCCC TCATTGAAAT GGACCTGAG GCCAGTGACC TCTCCCGGG CATTCGTGGC 360  
 CTCAGAGATG TGGCTGTCTG GGCTGGGGTC AGCAAATATA CAGGGGGCCG AGGCGTCAGC 420  
 GTGGGCCCCA TCCTCAGCAG CAGTGCCTCG GATATCTTCT GCGACAATGA GAATGGGCCT 480  
 AACTTCCTTT TCCACAACCG GGGCGATGGC ACCTTTGTGG ACGTGCGGC CAGTGTGGT 540  
 GTGGACGACC CCCACGACA TGGCGAGGT GTCGCCCTGG CTGACTTCAA CCGTGTGGC 600  
 AAAGTGGACA TCGTCTATGG CAACTGGAAT GGCCCCCACC GCCTCTATCT GCAAATGAGC 660  
 ACCCATGGGA AGGTCCGCTT CCGGGACATC GCCTCACCCA AGTTCTCCAT GCCCTCCCT 720  
 GTCCGACCGG TCATCAGCTG CGACTTTGAC AATGACGAGG AGCTGGAGAT CTTCTTCAAC 780  
 AACATGCTCT ACCGAGCTCT CTCAGCCAAC CGCCTCTTCC GCGTCATCCG TAGAGAGCAC 840  
 GGAGACCCCT CCGATCGAGA GCTCAATCCC GGCAGCGCCT TGGAGCCTGA GGGCGGGGCG 900  
 ACAGGGGGTG TGGTGACCGA CTTGACGAGA GACGGGATGC TGGACCTCAT CTTGTCCCAT 960



5 GGAGAGTCCA TGGCTCAGCC GCTGTCCGTC TTCCGGGGCA ATCAGGGGCTT CAACAACAAC 1020  
 TGGCTGCGAG TGGTGCCACG CACCCGGGTT GGGGCCTTGG CCAGGGGAGC TAAGTTCGTG 1080  
 CTCTACACCA AGAAGAGTGG GGCCCACTCG AGGATCATCG ACGGGGGCTC AGGCTACCTG 1140  
 TGTGAGATGG AGCCCGTGGC ACACITTTGGC CTGGGGAAGG ATGAAGCCAG CAGTGTGGAG 1200  
 GTGACGTGGC CAGATGGCAA GATGGTGAGC CGGAACGTGG CCAGCGGGGA GATGAACTCA 1260  
 GTGCTGGAGA TCCTCTACCC CCGGGATGAG GACACACTTC AGGACCCAGC CCCACTGGAG 1320  
 ACACCAATGA ATGCATCCAG TTCCCATTCG TGTGCCCTCG AGACAAGCCC GTATGTGTCA 1380  
 ACACCTATGG AAGCTACAGG TGCCGGACCA ACAAGAAGTG CAGTCGGGGC TACGAGCCCA 1440  
 ACGAGGATGG CACAGCCTGC GTGGGGGACTC TCGGCCAGTC ACCGGGGCCC CGCCCCACCA 1500  
 10 CCCCACCGC TGCTGCTGCC ACTGCCGCTG CTGCTGCCGC TGCTGGAGCT GCCACTGCTG 1560  
 CACCGGTCCT CGTAGATGGA GATCTCAATC TGGGGTCGGT GGTTAAGGAG AGCTGCGAGC 1620  
 CCAGCTGCTG AGCAGGGGTG GGACATGAAC CAGCGGATGG AGTCCAGCAG GGGAGTGGGA 1680  
 AAGTGGGCTT GTGCTGCTGC CTAGACAGTA GGGATGTAAA GGCTTGGGAG CTAGACCCCTC 1740  
 15 CCCAAGCCCA TCCATGCACA TTACTTAGCT AACAAATTAGG GAGACTCGTA AGGCCAGGCC 1800  
 CTGTGCTGGG CACATAGCTG TGATCACAGC AGACAGGGTC GCTGCCCTGA TGGCGCTTAC 1860  
 ATTCAGTGG GTCTAATGAC CATATCTTAG GACACAGATG TGCCGAGGGA GTGGTGTGTA 1920  
 CTGCACAGGA AGTATGAGGA CTTTAGTGTC CTGAGTTCAA ATCCTGATTG AGGAACTCAC 1980  
 AAAGCTATGT GACCTTACAC CAGTCACTTA ACTTGTTAGC CATCCATTAT CGCATCTGCA 2040  
 20 AAATGGGGAT TAAGAAATAGA ATCTTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA 2100  
 GACACTTGGC ACAAACCTTG GCACATAGTA AAGGCTCAAT AAAAACAAGT GCCTCTCACT 2160  
 GGGCTTTGTC AACACGTG

Seq ID NO: 181 Protein sequence  
 Protein Accession #: NP\_060528.1

25 1 11 21 31 41 51  
 MDPEASDLR GILALRDVAA EAGVSKYTGG RGVSVGPILS SSASDIFCDN ENGNPFLFHN 60  
 RGDGTFVDAA ASAGVDDPHQ HGRGVALADF NRDGKVDIVY GNWNGPHRLY LQMSTHGKVR 120  
 30 FRDIASPKFS MSPFVRTVIT ADFDNDQELE IFNNIAYRS SSANRLFRVI RREHGDPLIE 180  
 ELNPGDALEP EGRGTGGVVT DFDGDMLDL ILSHGESMAQ PLSVFRGNQ FNNNWLRRVP 240  
 RTRVGAFARG AKVVLYTKKS GAHLRIIDGG SGYLCMEPEV AHFGLGKDEA SSVEVTWPDG 300  
 KMSVRNVASG EMNSVLEILY PRDEDTLQDP APLETPMNAS SSHSCALET S PVSSTPMEAT 360  
 GAGPTRSAVG ATSPTRMAQP AWGLSASHRA PAPPPPPLLL PLPLLLPLLE LPLLHRSR

Seq ID NO: 182 DNA sequence  
 Nucleic Acid Accession #: AJ279016  
 Coding sequence: 1..1962

40 1 11 21 31 41 51  
 ATGTCCAGGA TGTACCGTT CCTGCTGCTG CTCTGGTTTC TGCCCATCAC TGAGGGGTCC 60  
 CAGCGGGCTG AACCCATGTT CACTGCAGTC ACCAACTCAG TTCTGCCTCC TGACTATGAC 120  
 45 AGTAATCCCA CCCAGCTCAA CTATGGTGTG GCAGTTACTG ATGTGGACCA TGATGGGGAC 180  
 TTTGAGATCG TCGTGGCGGG GTACAATGGA CCCAACCTGG TTCTGAAGTA TGACCCGGGC 240  
 CAGAAGCGGC TGGTGAACAT CGCGGTGATG GAGCGCAGCT CACCCTACTA CGCGCTGCGG 300  
 GACCGGCAGG GGAACGCCAT CGGGGTCACT GCCTGCAGCA TCGACGGGGA CGGCGGGGAG 360  
 GAGATCTACT TCCTCAACAC CAATAATGCC TTCTCGGGGG TGGCCACGTA CACCGACAAG 420  
 50 TTGTTCAGT TCCGCAATAA CCGGTGGGAA GACATCCTGA GCGATGAGGT CAACGTGGCC 480  
 CGTGGTGTGG CCGAGCCTTT TGCCGGACGC TCTGTGGCCT GTGTGGACAG AAAGGGCTCT 540  
 GGACGCTACT CTATCTACAT TGCCAATTAC GCCTACGGTA ATGTGGGCCC TGATGCCCTC 600  
 ATTGAAATGG ACCCTGAGGC CAGTGACCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660  
 GCTGCTGAGG CTGGGGTCAG CAAATATACA GGGGGCCGAG GCGTCAGCGT GGGCCCCATC 720  
 55 CTCAGCAGCA TGCGCTCGGA TATCTTCTGC GACAATGAGA ATGGGCTTAA CTTCCTTTTC 780  
 CACAACCGGG GCGATGGCAC CTTTGTGGAC GCTGCGGCCA GTGCTGGTGT GGACGACCCC 840  
 CACCAGCATG GGCAGAGTGT CGCCCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900  
 GTCTATGGCA ACTGGAATGG CCCCCACCGC CTCTATCTGC AAATGAGCAC CCATGGGAAG 960  
 60 GTCCGCTTCC GGGACCTGCG CTCACCCAAG TTCTCCATGC CCTCCCCTGT CCGCACGGTC 1020  
 ATCACCGCCG ACTTTGACAA TGACCAGGAG CTGAGATCT TCTTCAACAA CATTGCCCTAC 1080  
 CGCAGCTCCT CAGCCAACCG CCTCTTCCGC GTCATCCGTA GAGAGCACGG AGACCCCTC 1140  
 ATCGAGGAGC TCAATCCCGG CGAGCCCTTG GAGCCTGAGG GCCGGGGCAC AGGGGGTGTG 1200  
 GTGACCGACT TCGACGGAGA CGGGATGCTG GACCTCATCT TGTCCCATGG AGATGCCATG 1260  
 65 GCTCAGCCG TGTCCTCTTT CCGGGGCAAT CAGGGCTTCA ACAACAAGT GCTGCGAGTG 1320  
 GTGCCACGCA CCCGGTTTGG GGCCTTTGCC AGGGGAGCTA AGGTCTGTCT CTACACCAAG 1380  
 AAGAGTGGGG CCCACCTGAG GATCATCGAC GGGGGCTCAG GCTACCTGTG TGAGATGGAG 1440  
 CCCGTGGGAC ACTTTGGCCT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGCCA 1500  
 GATGGCAAGA TGGTGAAGCG GAACGTGGCC AGCGGGGAGA TGAACCTAGT GCTGGAGATC 1560  
 70 CTCTACCCCC GGGATGAGGA CACACTTCAG GACCCAGCCC CACTGGAGTG TGGCCAAGGA 1620  
 TTCTCCAGC AGGAAATAGG CCATTGCAATG GACACCAATG AATGCATCCA GTTCCCATTTC 1680  
 GTGTGCCCTC GAGACAAGCC CGTATGTGTC AACACCTATG GAAGCTACAG GTGCCGGACC 1740  
 AACAAAGAAT GCAGTCGGGG CTACGAGCCC AACGAGGATG GCACAGCCTG CGTGGGGACT 1800  
 CTCGGCCAGT CACCGGGCCC CCGCCCCACC ACCCCACCGC CTGCTGCTGC CACTGCCGCT 1860  
 75 GCTGCTGCCG CTGCTGGAGC TGCCACTGCT GCACCGGTCC TCGTAGATGG AGATCTCAAT 1920  
 CTGGGGTCCG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980  
 CCAGCGGATG GAGTCCAGGA GGGGAGTGGG AAAGTGGGCT TGTGCTGCTG CTTAGACAGT 2040  
 AGGGATGTAA AGCCCTGGGA GCTAGACCTT CCCCAGCCCC ATCCATGCAC ATTACTTAGC 2100  
 TAACAATTAG GGAGACTCGT AAGGCCAGGC CTTGTGCTGG GCACATAGCT GTGATCACAG 2160  
 CAGACAGGGT CGCTGCCCTG ATGGCGCTTA CATTCCAGTG GGTCTAATGA CCATATCTTA 2220  
 80 GGACACAGAT GTGCCCAGGG AGGTGGTGTG ACTGCACAGG AAGTATGAGG ACTTTAGTGT 2280  
 CCTGAGTTCA AATCCTGATT CAGGAACTCA CAAAGCTATG TGACCTTACA CCAGTCACTT 2340  
 AACTTGTTAG CCATCCATTA TCGCATCTGC AAAATGGGGA TTAAGAATAG AATCTTGGGG 2400  
 TTAGTGTGGA GATTAGATTA AATGTATGTA AGACACTTGG CACAAAACCT GGCACATAGT 2460  
 AAAGGCTCAA TAAAAACAAG TGCCCTCTAC TGGGCTTTGT CAACACG

Seq ID NO: 183 Protein sequence  
Protein Accession #: CAC08451

5	1	11	21	31	41	51	
	MSRMLPFLLL	LWFLPITEGS	QRAEPMFTAV	TNSVLPPDYD	SNPTQLNYGV	AVTDVDHGD	60
	FEIVVAGYNG	PNLVLYKIDRA	QKRLVNIADV	ERSSPYYALR	DRQNAIGVT	ACDIDGDGRE	120
	EIYFLNTNNA	FSGVATYTDK	LFKFRNNRWE	DILSDEVNVA	RGVASLFAGR	SVACVDRKGS	180
	GRYSIIYANY	AYGNVGPDAL	IEMDPEASDL	SRGILALRDV	AAEAGVSKYT	GGRGVSVGPI	240
10	LSSASDIFC	DNENGNPFLF	HNRGDGTFVD	AAASAGVDDP	HQHGGRGVALA	DFNRDGVKDI	300
	VYGNWNGPHR	LYLQMSHGHK	VRFRDIASPK	FSMPSPVVRTV	ITAFEDNDQE	LEIFFNNIAY	360
	RSSSANRLFR	VIRREHGDPL	IEELNPGDAL	EPEGRGTGGV	VTDGFDGDMGL	DLILSHGESM	420
	AQPLSVFRGN	QGFNNNWLVR	VPRTFRGFAFA	RGAKVVLVTK	KSGAHLRIID	GGSGYLCEME	480
	PVAHFGLGKD	EASSVEVETWP	DGKMVSRNVA	SGEMNSVLEI	LYPRDEDTLQ	DPAPLECGQG	540
15	FSQQENGHCN	DTNECIQFF	VCPDKPVVCV	NTYGSYRCRT	NKKCSRGYEP	NEDGTACVGT	600
	LGQSPGPRPT	TPTAAAATAA	AAAAAGAATA	APVLVDGDLN	LGSVVKESCE	PSC	

Seq ID NO: 184 DNA sequence  
Nucleic Acid Accession #: FGENESHH  
Coding sequence: 1..4794

20	1	11	21	31	41	51	
	ATGGCGTGTC	CGGGAGGACT	CCCAGCCCCGT	TGCTCTGGTT	GGATGGGACT	GGGTGGGCCC	60
25	AGCGGCTCCT	CCCCAGCATC	CCCTCCCCAT	TCCTCCTCCA	GGTACAATGG	ACCCCAACCTG	120
	GTTCTGAAGT	ATGACCCGGC	CCAGAAGCGG	CTGGTGAACA	TCGCGGTCTGA	TGAGCGCAGC	180
	TCACCTACT	ACGCGCTGG	GGACCGGCAG	GGGAACGCCA	TCGGGTCTAC	AGCCTGCGAC	240
	ATCAGCGGG	ACGGCCGGGA	GGAGATCTAC	TTCTCAACA	CCAATAATGC	CTTCTCGGGC	300
	CACAGCAGCT	CAGCGCAGGT	CCCTCTGGG	CTCCACAGAA	ACAGGCCTGT	GCTGAAGCCT	360
30	CCACCTACAA	CCCCTGCAAG	CCTCCTGGGT	CTGCCTCCAC	TCAGCGGAAG	GGACTTTTCC	420
	TCCTCCCTGG	GTCAGGCTTC	TCCGGACAGC	AGGCAGGGAG	AGAGGGTGCC	GGTTCCCTGC	480
	TGTCGGGGTG	GACTGAGACC	TACCATGAA	CCAGAACCAT	TTCTTCTGAG	ACCCAAATCA	540
	GGGGTGGCCA	CGTACACCGA	CAAGTTGTTC	AAGTTCGCA	ATAACCGGTG	GGAAAGACATC	600
	CTGAGCGATG	AGGTCAACGT	GGCCCGTGGT	GTGGCCAGCC	TCTTTGCCGG	ACGCTCTGTG	660
35	GCCTGTGTGG	ACAGAAAGGG	CTCTGGACGC	TACTCTATCT	ACATTGCCAA	TACGCTTAC	720
	GGTAATGTGG	GGCCTGATGC	CCTCATTGAA	ATGGACCCCTG	AGGCCAGTGA	CCTCTCCCGG	780
	GGCATTCTGG	CGCTCAGAGA	TGTGGCTGCT	GAGGCTGGGG	TACGAGAAATA	TACAGAAGGC	840
	TTCTCCCA	CTGCCTCTCC	AAGCATTTGGT	GAGATATCTG	GCAGAACCGA	GGAGCGGGAA	900
40	GGAGAGAGACC	CAGAGGAGGC	AGATGAGGAG	CACAGTGGGG	ATGGAAGCAC	CAGCCAACTG	960
	TGCCGGCTGG	GCTGGAAGGA	CGGGCAGTTC	AAGGAAGAAG	CAGCAGCTTT	GGTGGAGGAA	1020
	CAGAGGGAGG	CTGGGGCAGC	TGGCGTGCCC	AGAGGACGTG	TTGGAACAGC	TCTGCAGACT	1080
	TCCAAAAGCC	ATTGTGCTGA	CAAGAACCTA	TTTGGCCCA	CATGTTACTA	TTCTGTCTGC	1140
	GGCCTTCTC	CAGCCACACC	TTTCCCTGCC	CGCCAAGCCC	CCCAACACTA	CCCTGTAGCC	1200
	CCCCTTGTCA	CTCAGCTAAT	GACACATGGA	CGTCTGGCTG	GAAAACTAGC	CCGGAGTGTC	1260
45	CCCCACCCC	GAGCCCCAGG	AATGGACCCC	AAATGTAAGG	GCGCCCATGC	TGAGCCCCGC	1320
	CTGATGGCTG	AGGCTTTGGG	CGCGTGCCCA	GCCTCAGCA	CCACTGTGGT	GCCAGGGGGC	1380
	CTGAGAAGCT	GGGAGGAAAG	CAGGCAGAAAG	GGGCAGGCCA	TGTCCAGATG	TGCATCAGG	1440
	GAGCTGGGAG	GTCCCTGGAG	CCAAGCCACA	CAGCACCTGC	CTGCTAGAGA	GCTGTATGAC	1500
	CTGGGAGAAC	CTCCCATTTT	ACAAAGAACA	GACGGAGATC	CAGGGAGGAG	AAGGGACTCG	1560
50	CCCAAGGTCA	CACAGGATG	CCATCTAGTG	GCCACCATGC	CAGCTCTCGG	GGGACTCGAG	1620
	GGCCCCGGGA	GGGTGGCCAA	CGGAGAGATT	GGGAGAGAGA	CTGGGGCAGT	AGGAAGACCA	1680
	CTCTCCCATC	CCCTGTCTCC	CAACTTCCCC	AGCTGCTTGA	GGCCTCTTGA	AGCCGGGACA	1740
	GTGCCGGGAG	CTGCCCTGCC	TGGGAATCCT	GGGAAGTGGG	TTCTGGACAT	GGCCAAGGCC	1800
	CTGGCGTGG	ACAGATGGA	AAAAGAGGAG	GGGAAGATT	ATGGAGACCA	TGAGCCCA	1860
55	TTTAGGCTCA	GGAAAGCAGG	GGAAAGCAGG	TTCCCCCAG	GCTCCTCTGA	GGAGCCTCTG	1920
	CTGCAGTTCC	CCTCAGGCT	CAGAGGAGC	CCTGTCTCTC	AGGTGGGCCT	GGGGCTTGCT	1980
	CTTGCCACTC	ACTGTGGGTC	GATGTCTTTT	CTAGGGGGCC	GAGGCGTCAG	CGTGGGCCCC	2040
	ATCCTCAGCA	GCATGCTCTC	GGATATCTTC	TGCGACAATG	AGAATGGGCC	TAACTTCTCT	2100
	TTCCACAACC	GGGCGATGAG	CACCTTTGTG	GACGCTGCGG	CCAGTGTCTGA	ACGTCGTTTA	2160
60	GCCTTCATCG	TTCACTCA	ATATCACTC	TGCAGAGATT	TTCTCACTC	CCTGTGCCAC	2220
	CTAGCAGAAA	CTGGTCTCTC	CTCCTCTCTC	TGCCCGTGGC	ATGCACGTCT	TCTTCAGGCT	2280
	CCACATTGCC	ATCATGTTT	GTCTATGAGC	TTTACAAGGA	CCGGGTCAAG	GTTCTATTCA	2340
	TTCTTGACGC	AAGGCTTGGC	CTCCAGTGCC	CACCGGAGGA	CACCTCAGCT	CCAGGGTTCT	2400
	CAGGGGGCCC	CACCTGCCT	TCTGGCAAGA	GCTCCCTGTG	TCTTGGGGTC	TCTGATCCCC	2460
65	ACTGCCATT	ACATTGTCTT	GTGGTCTGCC	ATCCAGAGA	GCCTGATGAC	CCACAGCTAT	2520
	TTGTCTCTG	AAAGAGTCAA	CGTGGGTGTG	GACGACCCCC	ACCAGCATGG	GCGAGGTGTC	2580
	GCCTTGCTG	ACTTCAACCG	TGATGGCAAA	GTGACATCG	TCTATGGCAA	CTGGAATGGC	2640
	CCCCACGCC	TCTATCTGCA	AATGAGCACC	CATGGGAAGG	TCCGCTTCCG	GGACATCGCC	2700
70	TCACCCAAGT	TCTCATGCC	CTCCCTGTG	CGCACGGTCA	TCACCGCCGA	CTTGACAAAT	2760
	GACCAGGAGC	TGGAGATCTT	CTTCAACAAC	ATTGCCTACC	GCAGCTCTC	AGCCAAACCGC	2820
	CTCTTCCGAT	GCTCCATCTT	GGCTCGTGGC	TCTTCATCCT	TGACAGCTGG	TGGAGGAAAC	2880
	GGTCAGGGAG	AAGGTTTAA	AATCAGAAAG	GGAGGGTTC	CAGGGCCAGG	GGGTCAAGCC	2940
	AAGGTCAACA	CAGGTCCCTT	GATGAAGAAA	CAGAAAGGAA	GGAAGGACGA	GGACTGGGCA	3000
75	AGAGGCTGTG	GGAAATGCAAG	GCAAAAGCCTG	GCCAAAGGAGC	CGGCCTCTGC	TATTGCAGGG	3060
	AAAGGGAGG	GAAATGTGGC	CCAAAGTGTG	CCCAGAACCC	AAGCGCCACA	AGATACAAAG	3120
	CCACACTACC	ACAAAAGGGG	GCTACAGGGT	CCAATCACTA	CCAGGAAAG	GGGCTACGGG	3180
	GTCCAATCAC	TACCAGGAAA	AGGGGCTACG	GGGTCCAATC	ACTACCAGGA	AAAGGGGCTA	3240
	CGGGGTCCAA	TCACTACCAG	GAAAAGGGGC	TACGGGGTCC	AATCACTACC	AGGAAAAGGG	3300
	GCTACGGGCT	CCACTACACTA	CCAGGAAAAG	GGGCTACAGG	GTCCAATCAC	TACCAGGAAA	3360
80	AGGGGCTACG	GGCTCCAATC	ACTACCAGGA	AAAGGGGCTA	CAGGGTCCAA	TCACTACCAC	3420
	AGAAAGGGG	TACGGGGCTC	AATCACTACC	AGGAAAAGGG	GCTACGGGGT	CCAATCACTA	3480
	CCAGGAAAAG	GGGCTACAGG	GTCCAATCAC	TACCAGGAAA	AGGGGCTACG	GGGTCCAATC	3540
	ACTACCAGGA	AAAGGGGCTA	CGGGCTCCAA	TCACTACCAG	GAAAAGGGGC	TACGGGGTCC	3600
	AATCACTACC	AGGAAAAGGG	GCTACAGGGT	CCAATCACTA	CCAGGAAAAG	GGGCTACAGG	3660

	GTCCAATCAC	TACCACAGAA	AGGGGCTACG	GGCTCCAATC	ACTACCAGGA	AAAGGGGCTA	3720
	CGGGGTCCAA	TCACTACCA	GAAAAGGGG	TACGGGCTCC	AATCACTACC	AGGAAAAGAG	3780
	GCTATGGGGT	CCAATCACTA	CCAGGAAAAG	GGGCTACGGG	CTCCAATCAC	TACCAGGAAA	3840
5	AGGGGCTATG	GGGTCCAATC	ACTACCACAG	AAAGGGGCTA	CGGGGTCCAA	CGTCATCCGT	3900
	AGAGAGCACG	GAGAGCCCC	CATCGAGGAG	CTCAATCCCC	GCGACGCCCT	GGAGCCTGAG	3960
	GGCCGGGGCA	CAGGGGGTGT	GGTGACCGAC	TTCGACGGAG	ACGGGATGCT	GGACCTCATC	4020
	TTGTCCCATG	GAGAGTCCAT	GGCTCAGCCG	CTGTCCGTCT	TCCGGGGCAA	TCAGGGCTTC	4080
	AACAACAAC	GGCTGCGAGT	GGTGCCACGC	ACCCGGTTTG	GGGCCCTTGC	CAGGGGAGCT	4140
10	AAAGTCTGTC	TCTACACCAA	GAAGAGTGGG	GCCCACCTGA	GGATCATCGA	CGGGGGCTCA	4200
	GGCTACCTGT	GTGAGATGGA	GCCCGTGGCA	CACTTTGCCC	TGGGGAAGGA	TGAAGCCAGC	4260
	AGTGTGGAGG	TGACGTGGCC	AGATGGCAAG	ATGGTGAGCC	GGAACGTGGC	CAGCGGGGAG	4320
	ATGAACCTAG	TGCTGGAGAT	CCTCTACCCC	CGGGATGAGG	ACACACTTCA	GGACCCAGCC	4380
	CCACTGGAGT	GTGGCCAAGG	ATTCTCCCAG	CAGGAAAATG	GCCATTGCAT	GGACACCAAT	4440
15	GAATGCATCC	AGTTCCCAT	CGTGTGCCCT	CGAGACAAGC	CCGTATGTGT	CAACACCTAT	4500
	GGAGCTACA	GGTGCCGGAC	CAACAAGAAG	TGCAGTCGGG	GCTACGAGCC	CAACGAGGAT	4560
	GGCAGACGCT	GCCTGGGTAC	TGAGCTAGGC	TCTAGGCATA	CAATGACGTG	GAAACCAAGG	4620
	CCCAAAAAGG	AGCTGCAACT	TTCCCAAGGC	ATCTGCACCC	CCGTCTGGTC	CTTTTCTCTG	4680
	CCGGTTTGGC	GGCTGCTCCT	CAAAAGAGCT	CAGCTCCAGG	CTGCTCCCAG	CACCCCTCTC	4740
20	CAGAAAGCTC	CAGGTATTCC	AGAAGCCCAA	GTGTATGAAC	AAGATCAGGA	ATAA	

Seq ID NO: 185 Protein sequence  
Protein Accession #: FGENESHH

	1	11	21	31	41	51	
25	MACPGGLPAR	CSGWMGLGPP	SGSSPASPPH	SSSRYNGPNL	VLKYDRAQKR	LVNIAVDERS	60
	SPYYALRDRQ	GNAIGVTACD	IDGDGREEIY	PLNTNNAFSG	HSSSAQVPSG	LHRNRPVLKP	120
	PPTTPAGLLG	LPPLSGRDFS	SSLGQASPDS	RQGERVPVPC	CRGGLRPTHE	PEPFLLRPKS	180
30	GVATYTDKLF	KFRNNRWED	LSDEVNVARG	VASLFAGRSV	ACVDRKSGSR	YSIYIANYAY	240
	GNVGPDALIE	MDPEASDLR	GILALRDVA	EAGVSKYTEG	FSHTASPSIG	EISGRTEERE	300
	GGDPEEADDE	HSGDGSTSQL	CRLGWKDGQF	KEEAALVEE	QREAGAAGVP	RGRVRTALQT	360
	SKSHLADKNL	FGPPCYYSVC	APSPAHPFFA	RQAPQHYPPA	PLVTQLMTHG	RLAGKLARSV	420
	PHPRAPGMDP	KCKGRHAEPG	LMAEALGAWP	ALSTTVVPGG	LRSWEESRQK	QAMSRCALR	480
	ELGGPWSQAT	QHLPAELEYD	LGEPPILQRT	DGDPGRRRDS	PKVTQECHLV	ATMPALGGLE	540
35	GPRVAKREI	GRETGAVGRP	LSHPLVPNFP	SCLRPLEAGT	VPGALPGNP	GNWVLDMAKA	600
	LAWNQMEKEE	GKIHGDHEPR	FRLRKAREAE	FPFGSSEEP	LQFPSSGLRGS	PVLQVGLGLA	660
	SATHCGSMSP	LGGRGVSVGP	ILSSASDIF	CDNENGNPFL	FHNRGDGTFF	DAAAASAERRL	720
	AFIVHLKVHL	CRDFPHSLCH	LAETGPSSSC	CPWHARLLQA	PHCHHGLSMS	FTRTGSRFYS	780
	FLTQGLASSA	HRRTLSLQGS	QGAPPCLLAR	APCVLGSLLP	TAYYIVLWSA	IPESLMTHSY	840
40	LSSERVNVGV	DDPHQHGRRV	ALADFNRDGK	VDIVYGNWNG	PHRLYLQMS	HGKVRFRDIA	900
	SPKFSMPSPV	RTVITADFDN	DQLEIFFNN	IAYRSSSANR	LFRCSILARG	SSSLTAGGRN	960
	GQGGELRIIR	GGFPGPGGQA	KVNTGPLMKK	QKGRKDEDA	RCCGNAGQSL	AKEPASAIA	1020
	KGKGNVAQSV	PRTQAPQDTK	PHYHKKGLQG	PITTRKRGY	VQSLPGKGAT	GSNHVQEKGL	1080
45	RGPITTRKR	YGVQSLPGKG	ATGNSHYQEK	GLQGPITTRK	RGYGLQSLPG	KGATGNSHYH	1140
	RKGLRAPITT	RKRGYGVQSL	PGKGATGSNH	YQEKGLRGPI	TTRKRGYGLQ	SLPGKGATGS	1200
	NHYQEKGLQG	PITTRKRGY	VQSLPGKGAT	GSNHVQEKGL	RGPITTRKR	YGLQSLPGKE	1260
	AMGNSHYQEK	GLRAPITTRK	RGYGVQSLPG	KGATGNSNVR	REHGDPLIEE	LNPGDALPEE	1320
	GRGTGGVVTD	FDGDGMLDLI	LSHGESMAQP	LSVFRGNQGF	NNNWLRRVPR	TRFGAFARGA	1380
50	KVVLTYTKSG	AHLRIIDGGS	GYLCEMEPVA	HFGLGKDEAS	SEVETWPDGK	MVSRNVASGE	1440
	MNSVLEILYP	RDEDTLQDPA	PLECGGQFSQ	QENGHCMDTN	ECIQFPFVCP	RDKPVCVNTY	1500
	GSYRCRTNKK	CSRGYEPNED	GTACVGTETG	SRHTMTWKPR	PKKELQLSQG	ICTPVWSSFLL	1560
	PGCRLLLKRA	QLQAAPSTLL	QKAPGIPEAQ	VYEQDQE			

Seq ID NO: 186 DNA sequence  
Nucleic Acid Accession #: NM\_000584.1  
Coding sequence: 75..374

	1	11	21	31	41	51	
60	AGCAGAGCAC	ACAAGCTTCT	AGGACAAGAG	CCAGGAAGAA	ACCACCGGAA	GGAACCATCT	60
	CACGTGTGTG	AAACATGACT	TCCAAGCTGG	CCGTGGCTCT	CTTGGCAGCC	TTCTGATTTT	120
	CTGCAGCTCT	GTGTGAAGGT	GCAAGTTTGC	CAAGGAGTGC	TAAAGAACTT	AGATGTCAGT	180
	GCATAAAGAC	ATACTCCAAA	CCTTCCACCC	CCAAATTAT	CAAAGAACTG	AGAGTGATTG	240
65	AGAGTGGACC	ACACTGCGCC	AACACAGAAA	TTATTGTAAA	GCTTCTGAT	GGAAGAGAGC	300
	TCTGTCTGGA	CCCCAAGGAA	AACTGGGTGC	AGAGGGTTGT	GGAGAAGTTT	TTGAAGAGGG	360
	CTGAGAATTC	ATAAAAAAT	TCATTCTCTG	TGGTATCCAA	GAATCAGTGA	AGATGCCAGT	420
	GAAACTTCAA	GCAAACTAC	TTCAACACTT	CATGTATTGT	GTGGGTCTGT	TGTAGGGTTG	480
	CCAGATGCAA	TACAAGATTC	CTGGTTAAAT	TTGAATTTC	GTAACAATG	AATAGTTTTT	540
70	CATTGTACCA	TGAAATATCC	AGAACATACT	TATATGTAAA	GTATTATTTA	TTTGAATCTA	600
	CAAAAAACAA	CAAAATAATT	TTAAATATAA	GGATTTTCTT	AGATATTGCA	CGGGAGAAAT	660
	TACAAATAGC	AAAATTGAGC	CAAGGGCCAA	GAGAATATCC	GAACTTTAAT	TTACGGAATT	720
	GAATGGGTTT	GCTAGAATGT	GATATTGAA	GCATCACATA	AAAATGATGG	GACAAATAAT	780
	TTTGCCATAA	AGTCAAATTT	AGCTGGAAT	CCTGGATTTT	TTTCTGTTAA	ATCTGGCAAC	840
75	CCTAGTCTGC	TAGCCAGGAT	CCACAAGTCC	TTGTTCCTCT	GTGCCTTGGT	TTCTCTTTTA	900
	TTTCTAAGTG	AAAAAAGTAT	TAGCCACCAT	CTTACCTCAC	AGTGATGTTG	TGAGGACATG	960
	TGGAAGCACT	TAAAGTTTTT	TCATCATAAC	ATAAATTATT	TTCAAGTGTA	ACTTATTAAC	1020
	CTATTTATTA	TTTATGTATT	TATTTAAGCA	TCAAATATTT	GTGCAAGAAT	TTGAAAAAAT	1080
	AGAAGATGAA	TGATGTATTG	AATAGTTATA	AAGATGTTAT	AGTAAATTTA	TTTATTTTAA	1140
80	GATATTAAT	GATGTTTTAT	TAGATAAATT	TCAATCAGGG	TTTTTAGATT	AAACAAAGAA	1200
	ACAATTGGGT	ACCCAGTTAA	ATTTTCATTT	CAGATAAACA	ACAAATAATT	TTTATGATTA	1260
	AGTACATTAT	TGTTTATCTG	AAAGTTTATA	TTGAACTAAC	AATCCTAGTT	TGATACTCCC	1320
	AGCTCTGTCA	TGTCAGCTGC	TGTTGGTAGT	GCTGTGTTGA	ATTACGGAAT	AATGAGTTAG	1380
	AACATATTA	ACAGCCAAAA	CTCCACAGTC	AATATTAGTA	ATTTCTTGCT	GGTTGAAACT	1440
	TGTTTATTAT	GTACAAATAG	ATTCCTTATA	TATTATTTAA	ATGACTGCAT	TTTATAAATC	1500

AAGGCTTTAT ATTTTAACT TTAAGATGTT TTTATGTGCT CTCCAAATTT TTTTACTGT 1560  
 TTCTGATTGT ATGGAAATAT AAAAGTAAAT ATGAAACATT TAAATATATA TTTGTTGTCA 1620  
 AAGTAAAAAA AAAAAAAA

Seq ID NO: 187 Protein sequence  
 Protein Accession #: NP\_000575.1

1 11 21 31 41 51  
 MTSKLAVALL AAFILISAALC EGAVLPSAK ELRCQCIKY SKPFHPKFIK ELRVIESGPH 60  
 CANTEIIVKL SDGRELCCLDP KENWVQRVVE KFLKRAENS

Seq ID NO: 188 DNA sequence  
 Nucleic Acid Accession #: NM\_003661.1  
 Coding sequence: 1..1152

1 11 21 31 41 51  
 ATGAGTGCAC TTTTCCTTGG TGTGGGAGTG AGGGCAGAGG AAGCTGGAGC GAGGGTGCAA 60  
 CAAACCGTTC CAAGTGGGAC AGATACTGGA GATCCTCAAA GTAAGCCCTC CGGTGACTGG 120  
 GCTGCTGGCA CCATGGACCC AGAGAGCAGT ATCTTTATTG AGGATGCCAT TAAGTATTTC 180  
 AAGGAAAAAG TGAGCACACA GAATCTGCTA CTCCTGCTGA CTGATAATGA GGCCTGGAAC 240  
 GGATTCGTGG CTGCTGCTGA ACTGCCCAGG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG 300  
 GACAACTTGG CAAGACAAAT GATCATGAAA GACAAAAACT GGCACGATAA AGGCCAGCAG 360  
 TACAGAAACT GGTTCCTGAA AGAGTTTCCT CGGTTGAAAA GTGAGCTTGA GGATAACATA 420  
 AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAAGGCAC CACCATCGCC 480  
 AATGTGGTGT CTGGCTCTCT CAGCATTTCC TCTGGCATCC TGACCTCGT CGGCATGGGT 540  
 CTGGCACCCT TCACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA 600  
 ATCAGAGCCG CTTTGACCCG GATTACCAGC AGTACCATTG ACTACGGAAA GAAGTGGTGG 660  
 ACACAGCCCC AAGCCACAGA CCTGGTCATC AAAAGCCTTG ACAAATTGAA GGAGGTGAGG 720  
 GAGTTTTTGG GTGAGAACAT ATCCAACTTT CTTTCTTAG CTGGCAATAC TTACCAACTC 780  
 ACACGAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA 840  
 GTACCGCATG CCTCAGCCTC ACGCCCCCGG GTCACTGAGC CAATCTCAGC TGAAAGCGGT 900  
 GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCCTGAAAA TGAGCAGAGG AGTCAAGCTC 960  
 ACGGATGTGG CCCTCTAAG CTTCTTCTT GTGCTGGATG TAGTCTACCT CGTGTACGAA 1020  
 TCAAAGCACT TACATGAGGG GGCAGAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT 1080  
 CAGGAGCTGG AGGAGAAGCT AAACATTTCT AACATAATT ATAAGATTCT GCAGGCGGAC 1140  
 CAAGAAGTGT GA

Seq ID NO: 189 Protein sequence  
 Protein Accession #: NP\_003652.1

1 11 21 31 41 51  
 MSALFLGVGV RAEEAGARVQ QNVPSGTDGT DPQSKPLGDW AAGTMDPES IFIEDAIKYF 60  
 KEKVTQNL LLTLDNEAWN GFVAAELPR NEADELRKAL DNLARQMIMK DKNWHDKGQQ 120  
 YRNVFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGLSIS SGILTLVGMG 180  
 LAPFTEGGS LLEPFGMELG ITAALTGITS STMDYGKKWW TQAQAHDLVI KSLDKLKEVR 240  
 EFLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPIAESG 300  
 EQVERVNEPS ILEMSRGVKL TDVAPVSFFL VLDVVYLVE SKHLHEGAKS ETAEELKKVA 360  
 QLEBEKLNIL NNNYKILQAD QEL

Seq ID NO: 190 DNA sequence  
 Nucleic Acid Accession #: NM\_014452.1  
 Coding sequence: 1..1968

1 11 21 31 41 51  
 ATGGGGACCT CTCGAGCAG CAGCACCACC CTCGCCTCCT GCAGCCGCAT CGCCCGCCGA 60  
 GCCACAGCCA CGATGATCGC GGGCTCCCTT CTCCTGCTTG GATTCCCTAG CACCACCACA 120  
 GCTCAGCCAG AACAGAAGGC CTCGAATCTC ATTGGACATC ACCGCCATGT TGACCGTGCC 180  
 ACCGGCCAGG TGCTAACCTG TGACAAGTGT CCAGCAGGAA CCTATGTCTC TGAGCATGTG 240  
 ACCAACACAA GCCTGCGCGT CTGCAGCAGT TGCCCTGTGG GGACCTTTAC CAGGCATGAG 300  
 AATGGCATAG AGAAATGCCA TGACTGTAGT CAGCCATGCC CATGGCCAAT GATTGAGAAA 360  
 TTACCTTGTG CTGCCTTGAC TGACCGAGAA TGCCTTGCC CACCTGGCAT GTTCCAGTCT 420  
 AACGCTACCT GTGCCCCCA TACGGTGTGT CCTGTGGGTT GGGGTGTGCG GAAGAAAGGG 480  
 ACAGAGACTG AGGATGTGCG GTGTAAGCAG TGTGCTCGGG GTACCTTCTC AGATGTGCCT 540  
 TCTAGTGTGA TGAATGCAG AGCATACACA GACTGTCTGA GTCAGAACCT GGTGGTGATC 600  
 AAGCCGGGGA CCAAGGAGAC AGACAACGTC TGTGGCACAC TCCCGTCCTT CTCCAGTCTC 660  
 ACCTCACCTT CCCCTGGCAC AGCCATCTTT CCAAGCCCTG AGCAGATGGA AACCCATGAA 720  
 GTCCCTTCTT CCACCTATGT TCCCAAAGGC ATGAACTCAA CAGAATCCAA CTCTTCTGCC 780  
 TCTGTAGAC CAAAGGTACT GAGTAGCATC CAGGAAGGGA CAGTCCCTGA CAACACAAGC 840  
 TCAGCAAGGG GGAAGGAAGA CGTGAACAAG ACCCTCCCAA ACCTTCAGGT AGTCAACCAC 900  
 CAGCAAGGCC CCCACACAG ACACATCCTG AAGCTGCTGC CGTCCATGGA GGCCACTGGG 960  
 GGCAGAGAGT CCAGCAGGCC CATCAAGGGC CCAAGAGGGG GACATCCTAG ACAGAACCTA 1020  
 CACAAGCATT TTGACATCAA TGAGCATTTG CCCTGGATGA TTGTGCTTTT CTGCTGCTG 1080  
 GTGCTTGTGG TGATTGTGGT GTGCAGTATC CGGAAAGCT CGAGGACTCT GAAAAAGGGG 1140  
 CCCCAGCAGG ATCCAGTGC CATTGTGGAA AAGGCAGGGC TGAAGAAATC CATGACTCCA 1200  
 ACCCAGAACG GGGAGAAATG GATCTACTAC TGCAATGGCC ATGGTATCGA TATCCTGAAG 1260  
 CTGTAGCAG CCCAAGTGGG AAGCCAGTGG AAAGATATCT ATCAGTTTCT TTGCAATGCC 1320  
 AGTGAGAGGG AGGTTGCTGC TTTCTCCAAT GGGTACACAG CCGACCACGA GCGGGCTTAC 1380  
 GCAGCTCTGC AGCACTGGAC CATCGGGGC CCGAGGCCA GCCTCGCCCA GCTAATTAGC 1440  
 GCCCTGCGCC AGCACCAGG AAACGATGTT GTGGAGAAGA TTCGTGGGCT GATGGAAGAC 1500  
 ACCACCCAGC TGGAACTGA CAACTAGCT CTCCGATGA GCCCAGCCC GCTTAGCCG 1560

AGCCCCATCC CCAGCCCCAA CGCGAACTT GAGAATTCG CTCTCCTGAC GGTGGAGCCT 1620  
 TCCCCACAGG ACAAGAACAA GGGCTTCTTC GTGGATGAGT CGGAGCCCT TCTCCGCTGT 1680  
 GACTCTACAT CCAGCGGCTC CTCCGCGCTG AGCAGGAACG GTTCTTTTAT TACCAAAGAA 1740  
 AAGAAGGACA CAGTGTTCG CGAGGTACGC CTGGACCCCT GTGACTTGCA GCCTATCTTT 1800  
 GATGACATGC TCCACTTTCT AAATCCTGAG GAGCTGCGGG TGATTGAAGA GATTCCCCAG 1860  
 GCTGAGGACA AACTAGACCG GCTATTCGAA ATTATGGAG TCAAGAGCCA GGAAGCCAGC 1920  
 CAGACCCTCC TGGACTCTGT TTATAGCCAT CTTCCTGACC TGCTGTAG

Seq ID NO: 191 Protein sequence  
 Protein Accession #: NP\_055267.1

1 11 21 31 41 51  
 | | | | |  
 MGTSPSSSTA LASCRIARR ATATMIAGSL LLLGFLSTTT AQPEQKASNL IGTyrHVDRA 60  
 TGQVLTCDKC PAGTYVSEHC TMTSLRVCSS CPVGTFTTRHE NGIEKCHDCS QPCPWPMEIK 120  
 LPCAALTDRE CTCPPGMFQS NATCAPHTVC PVGWGVRKKG TETEDVRCKC CARGTFSQVDP 180  
 SSVMKCKAYT DCLSNLNVVI KPGTKETDNV CGTLPSFSSS TSFSPGTAIF PRPEHMETHE 240  
 VPSSTYVPKG MNSTSNSSA SVRPKVLSSI QEGTVPDNTS SARGKEDVNH TLPNLQVNVH 300  
 QQGPHRHRL KLLPSMEATG GEKSSTPIKG PKRGHPRQNL HKHFDINEHL PWMIVLFLLL 360  
 VLVVIVVCSI RKSSRTLKKG PRQDPSAIVE KAGLKKSMTP TQNREKIYY CNGHGIDILK 420  
 LVAAQVGSQW KDIYQFLCNA SEREVAAFSN GYTADHERAY AALQHWITRG PEASLAQLIS 480  
 ALRQHRNDV VEKIRGLMED TQLETDKLA LPMSPSPLSP SPIPSPNAKL ENSALLTVEP 540  
 SPQDKNKGF VDESEPLLRC DSTSSGSSAL SRNGSFITKE KKDTVLRLQVR LDPCDLQPIF 600  
 DMLHFLNPE ELRVIIEIPQ AEDKLDRLFE IIGVKSQEAS QTLLDVSVYSH LPDLL

Seq ID NO: 192 DNA sequence  
 Nucleic Acid Accession #: XM\_044533  
 Coding sequence: 238..2751

1 11 21 31 41 51  
 | | | | |  
 GCTCTGCCCA AGCCGAGGCT GCGGGGCGGG CGCCGCGCGG AGGACTGCGG TGCCCCGCGG 60  
 AGGGGCTGAG TTTGCCAGGG CCCACTTGAC CCTGTTTCCC ACCTCCCGCC CCCAGGTGCC 120  
 GGAGGCGGGG GCCCCGCGGG CGACTCGGGG GCGGACCGCG GGGCGGAGCT GCCGCCCGTG 180  
 AGTCCGCGCG AGCCACCTGA GCCGAGCCGG CCGGACACCG TCGCTCCTGC TCTCCGAATG 240  
 CTGCGCACCG CGATGGGCGT GAGGAGCTGG CTGCGCGCCC CATGGGGCGC GCTGCGGCCT 300  
 CGGCCACCGC TGTGCTGCTC CTGCTCCTGC TGCAGCCGCC GCCTCCGACC 360  
 TGGGCGCTCA GCCCCGCGAT CAGCCTGCCT CTGGGCTCTG AAGAGCGGCC ATTCTCTAGA 420  
 TTCGAAGCTG AACACATCTC CAACTACACA GCCCTTCTGC TGAGCAGGGA TGGCAGGACC 480  
 CTGTACGTGG GTGCTCGAGA GGCCTCTTT GCACCTAGTA GCAACCTCAG CTTCTCGCCA 540  
 GGGCGGGAGT ACCAGGAGCT GCTTTGGGGT GCAGACGCGA AGAAGAAACA GCAGTGCAGC 600  
 TTCAAGGGCA AGGACCCACA GCGCGACTGT CAAACTACA TCAAGATCCT CCGCCGCGTC 660  
 AGCGGCAGTC ACCTGTTTCA CTGTGGCACA GCAGCCTTCA GCCCATGTG TACCTACATC 720  
 AACATGGAGA ACTTCACCTT GGCAGGGGAC GAGAAGGGGA ATGTCTCTCT GGAAGATGGC 780  
 AAGGGCGGTT GTCCCTTCGA CCCGAATTTC AAGTCCACTG CCCTGGTGGT TGATGGCGAG 840  
 CTCTACACTG GAACAGTCTC CAGCTTCCAA GGGAAATGACC CGGCCATCTC GCGGAGCCAA 900  
 AGCCTTCGCC CCACCAAGAC CGAGAGCTCC CTCAACTGGC TGCAAGACCC AGCTTTTGTG 960  
 GCCTCAGCCT ACATTCCTGA GAGCCTGGGC AGCTTGCAAG GCGATGATGA CAAGATCTAC 1020  
 TTTTCTTCTA GCGAGACTGG CCAGGAATTT GAGTCTTTTG AGAACACCAT TGTGTCCCGC 1080  
 ATTGCCGCGA TCTGCAAGGG CGATGAGGGT GGAGAGCGGG TGCTACAGCA GCGCTGGACC 1140  
 TCCTTCTCTA AGGCCAGCT GCTGTGCTCA CGGCCGACG ATGGCTTCCC CTTCAACGTG 1200  
 CTGCAGGATG TCTTCACGCT GAGCCCCAGC CCCAGGACT GGCCTGACAC CCTTTTCTAT 1260  
 GGGGTCTTCA CTTCCAGTGT GCACAGGGGA ACTACAGAAG GCTCTGCGGT CTGTGCTTTC 1320  
 ACAATGAAGG ATGTGCAGAG AGTCTTCAGC GGCCTCTACA AGGAGGTGAA CCGTGAGACA 1380  
 CAGCAGTGGT ACACCGTGAC CCACCCGGTG CCCACACCCC GGCTTGGAGC GTGCATCACC 1440  
 AACAGTGCCC GGGAAAGGAA GATCAACTCA TCCCTGCAGC TCCCAGACCG CGTGTGAAC 1500  
 TTCCTCAAGG ACCACTTCTT GATGGACGGG CAGGTCCGAA GCCGCTGCT GCTGTGCAG 1560  
 CCCAGGCTC GCTACCCAGC CGTGCTGTA CACCGCGTCC CTGGCTGCA CCACACTTAC 1620  
 GATGTCTCTT TCCTGGGAC TGGTGACGGC CGGCTCCACA AGGCAGTGAG CGTGGGCCCC 1680  
 CGGGTGACCA TCATTGAGGA GCTGCAGATC TTCTCATCGG GACAGCCCGT GCAGAATCTG 1740  
 CTCTGGACA CCCACAGGGG GCTGCTGTAT GCGGCCCTAC ACTCGGGCGT AGTCCAGGTG 1800  
 CCCATGGCCA ACTGCAGCTC GTACAGGAGC TGTGGGACT GCCTCCTCGC CCGGACCCC 1860  
 TACTGTGCTT GGAGCGGCTC CAGCTGCAAG CACGTACGCC TCTACCAGCC TCAGCTGGCC 1920  
 ACCAGGCCGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGCTCT 1980  
 TCGGTTGTGT CCCGCTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC 2040  
 CAGCCCAACA CAGTGAACAC TTTGGCCTGC CCGCTCCTCT CCAACCTGGC GACCCGACTC 2100  
 TGGCTACGCA ACGGGGCCCC CGTCAATGCC TCGGCTCCTT GCCACGTGCT ACCCACTGGG 2160  
 GACCTGCTGC TGGTGGGAC CCAACAGCTG GGGGAGTTCC AGTGCTGGTC ACTAGAGGAG 2220  
 GGCTTCCAGC AGCTGGTAGC CAGCTACTGC CCAGAGGTGG TGGAGGACGG GGTGGCAGAC 2280  
 CAAACAGATG AGGGTGGCAG TGTACCCGTC ATTATCAGCA CATCGCGTGT GAGTGCACCA 2340  
 GCTGTGGGCA AGGCAGCTG GGGTGACAGC AGGTCTTACT GGAAGGAGTT CCTGGTGATG 2400  
 TGCACGCTCT TTGTGCTGGC CGTGCTGCTC CCAGTTTAT TCTTGCTCTA CCGGACCCGG 2460  
 AACAGCATGA AAGTCTTCTT GAAGCAGGGG GAATGTGCCA GCGTGACCCC CAAGACCTGC 2520  
 CCTGTGGTGC TGCCCCCTGA GACCCGCCCA CTCACCGGCC TAGGGCCCCC TAGCACCCCG 2580  
 CTCGATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCG AGTCTTCACT 2640  
 GAGTCAGAGA GTGGGCACT CAGCATCCAA GACAGCTTCG TGGAGGTATC CCGAGTGTGC 2700  
 CCCCAGCCCC GGGTCCGCTT TGGCTCGGAG ATCCGTGACT CTGTGGTGTG AGAGCTGACT 2760  
 TCCAGAGGAC GCTGCCCTGG CTTCAGGGGC TGTGAATGCT CGGAGAGGGT CAACTGGACC 2820  
 TCCCTCCGCG TCTGCTCTTC GTGGAACACG ACCGTGGTGC CCGGCCCTTG GGAGCCTTGG 2880  
 GGCCAGCTGG CTGTGCTCTC TCCAGTCAAG TAGCGAAGCT CTACACCCC AGACACCCAA 2940  
 ACAGCCGCTG CCCCAGAGGT CTTGGCCAAA TATGGGGGCC TGCCTAGGTT GGTGGAACAG 3000  
 TGCTCTTAT GTAAACTTGA CCCTTTGTTT AAAAAACAAT TCCAAATGTG AACTAGAAAT 3060  
 GAGAGGGAAG AGATAGCATG GCATGCAGCA CACACGCGTG CTCCAGTTCA TGGCCTCCCA 3120  
 GGGGTGCTGG GGATGCATCC AAAGTGGTTG TCTGAGACAG AGTGTGAAAC CCTCACCAAC 3180

TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT 3240  
 CAGGACCAGC TTGGGCTGCG TCGCTTCTGC CTTGCCAGTC AGCCGAGGAT GTAGTGTGTG 3300  
 GTGCCGTCTT CCCACCACCT CAGGGACCAG AGGGCTAGGT TGGCACTGCG GCCCTCACC 3360  
 5 GTGCTTGGG CCGGACCCAA CTCCTGGACC TTCCAGCCT GTATCAGGCT GTGGCCACAC 3420  
 GAGAGGACAG CGCGAGCTCA GGAGAGATTT CGTGACAATG TACGCCCTTC CCTCAGAATT 3480  
 CAGGGAAGAG ACTGTGCGCT GCCTTCTCTC GTTGTGTGCGT GAGAACCCGT GTGCCCCCTC 3540  
 CCACCATATC CACCTCGCT CCATCTTGA ACTCAAACAC GAGGAACATA CTGCACCTG 3600  
 GTCTCTCTCC CAGTCCCCAG TTCACCTCC ATCCCTCACC TTCCTCCATT CTAAGGGATA 3660  
 10 TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG 3720  
 ATGCACCTTA TGTATTTTT TAATAAAGTC TGAAGAATTA CTGTTT

Seq ID NO: 193 Protein sequence  
 Protein Accession #: XP\_044533.3

1 11 21 31 41 51  
 MLRTAMGLRS WLAAPWGALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60  
 RFEAHISNY TALLLRDGR TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC 120  
 20 SFKGDQPDQR CQNYIKILLP LSGSHLFTCG TAAFSPMCTY INMENFTLAR DEKGNVLLED 180  
 GKGRCPFDN FKSTALVVDG ELYTGTVSSF QGNDDPAISRS QSLRPTKTES SLNWLQDPAF 240  
 VASAYIPESL GSLQGGDDKI YFFFSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300  
 TSFLKAQLLC SRPDDGFPPN VLQDVFTLSP SPQDWRDRLF YGVFTSQWHR GTTEGSAVCV 360  
 FTMKDVQRFV SGLYKEVNRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420  
 25 NFLKDHFLMD GQVRSRMLLL QPQARYQVRA VHRVPLHHT YDVLFLGTGD GRLHKAIVSVG 480  
 PRVHIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540  
 PYCAWSGSSC KHVSLYQPL ATRPWQDIE GASAKDLCSA SSVVSPSFVP TGEKPCBQVQ 600  
 FQNTVNTLA CPLLNSLATR LWLRNGAPVN ASASCHVLPT GDLLLVTGTTQ LGFEQCSWLE 660  
 EGFQQLVASV SPEVVEDGVA DQTEGGGSPV VIISTSRVSA PAGGKASWGA DRSYWKFLV 720  
 30 MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780  
 PLDHRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSV

Seq ID NO: 194 DNA sequence  
 Nucleic Acid Accession #: NM\_022819.1  
 Coding sequence: 1..635

1 11 21 31 41 51  
 ATGGCAGATG GGGCAAAGGC CAACCCCAAA GGGTTCAAAA AGAAGGTGCT GGATAGATGC 60  
 TTCTCTGGGT GGAGGGGCCC ACGCTTCGGG GCCTCCTGTC CTTCAAGAAC CTCCAGGTCT 120  
 40 AGCCTGGGTA TGAAGAAGTT CTTACCGTG GCCATCCTTG CTGGCAGCGT TCTGTCCACA 180  
 GCTCACGGCA GCTCTGCTCAA CCTGAAGGCC ATGTTGGAGG CCGTCACAGG GAGGAGCGCC 240  
 ATCCTGTCTCT TCGTGGGCTA CGGTTGCTAC TGTGGGCTGG GGGGCCGTGG CCAGCCCAAG 300  
 GATGAGGTGG ACTGTTGCTG CCACGCCCAC GACTGCTGCT ACCAGGAAC CTTTGACCAA 360  
 45 GGCTGTCAAC CCTATGTGGA CCACTATGAT CACACCATCG AGAACAACAC TGAGATAGTC 420  
 TGCAGTGACC TCAACAAGAC AGAGTGTGAC AAGCAGACAT GCATGTGTGA CAAGAACATG 480  
 GTTCTGTGCC TCATGAACCA GACGTACCGA GAGGAGTACC GTGGCTTCCT CAATGTCTAC 540  
 TGCCAGGGCC CCACGCCCAA CTGCAGCATC TATGAACCGC CCGCTGAGGA GGTCACTGTC 600  
 AGTCACCAAT CCCAGCGCC CCCCGCCCT CCCTAG

Seq ID NO: 195 Protein sequence  
 Protein Accession #: NP\_073730

1 11 21 31 41 51  
 MADGAKANPK GFKKKVLDRC FSGWRGPRFG ASCPSRTSRS SLGMKKFFTV AILAGSVLST 60  
 AHGSLNLKA MVEAVTGRSA ILSFVGYGCV CGLGGRGQPK DEVDWCCAH DCCYQELFDQ 120  
 GCHPYVDHYD HTIENNTIIV CSDLNKTECD KQTCMCDKNM VLCLMNQTYR EBYRGFLNVY 180  
 CQGPTPNCSI YEPPEEVEVC SHQSPAPPAP P

Seq ID NO: 196 DNA sequence  
 Nucleic Acid Accession #: XM\_028196.1  
 Coding sequence: 1315..1791

1 11 21 31 41 51  
 GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60  
 GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCCTTTCTGT CTGTCTCCTT GCTCTGCCCC 120  
 AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180  
 70 ATGGCCTGGG CTGGGCCCCG GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAGG 240  
 CTCTTGTGGG CAAAGCAGGG GAGGCCCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG 300  
 CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCTG 360  
 GGGTCACCGT AGGCCCATG TAGCACCTG GTTCCCTGCT CTGTAGGTGA CAGGAGCCAG 420  
 CCCAGCCAGG TGTGCTCCTT CCCCAGGCC TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480  
 75 CGCCCGCCCC ACCTCTCTTC CCACCCACAT GCCGAAGGGT GGCCAGGCAG GCAGGTGGAC 540  
 GAGTCCAGGC AGCGGCTGAG TCAGTGTGTG TGAATGTTC TGGCCGCTCC CAGCTGCACC 600  
 CTGCCCTTAC CTGCCACCAC CTCACCTTCA TCCTCAGGCG CTGCGGCCCT GAGCCCTGCT 660  
 CAGGAATGCA CCTTAGCCAC AGGCCTGCTC AGTGAGCTCC GCCGACAGCC AGCCCTGCTC 720  
 CTCCCGCAT GACCTGTCAG ACCCTCTG GCTTCCAAGT TCCTGGGGGC TGCAGTGAAC 780  
 80 ATGCTCCACC TGCAATGGCTG GCAAACCATG GTGGGCCCCA GCTGTGGTGC GTGCTGGGGT 840  
 AGAGGCAAGG AAGTGATGGG ACCGCAGAGA TGAGACCCCC AGGGATGAGA TGGGACCCCC 900  
 AGGCAGGGCC CAGGTCCAG GGCACAGGAG AGAGAAGCAG GGAGGGAGAG AGCTTCTG 960  
 TGGAGGAGC ATCTTACAGT GGGGGCAAG GTGCTCTGAG GTCCGGTGAA GGCAGGGACT 1020  
 AGGCTGCCCA GGCCCTGCCT GCTTGGCTGG GGCTGGGGGC TGCTGGGAGG TGGCTGGGAG 1080  
 GCTGGGCGCT GGCAGCTAAG CTGGAGCTTT GGCCAGGGTC CAGAGCCTCC CTCCTTCAG 1140

5 CTTCCTGCTG CACAGAACCC TCGCCCTGG CCACCCCGTG CTGCCCTCTT GCCCTGGCAG 1200  
 ACCCAGCACT GGCTGCTGCT AGTCAGATGG GGTAGCGGGC AGGGGCCGGA GGGGCCACCC 1260  
 TCCCAGCTGA CCCAGCCTCC TGGGCCCGCTT CTTCCAAACC AGCAGGGTAG AAAGATGGGG 1320  
 CACCCACCCAG TCTCTCCAG TGGCCCGGCC CCAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380  
 ATTCCAGACC TTGTCGCCGG GACCCCTGT GAGTTGTGGG ATTCCCAAGA GGGGTGTGGG 1440  
 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC 1500  
 CCAGGGCCCC GCTGGGCTCT CATTGCCGGC GCCCTTGCCG CGGGCGTCTT CCTCGTCTCC 1560  
 TGCTCTCTCT GTGCTGCTG CTGCTGCTGC CGCCGCCACA GGAAGAAGCC CAGGGACAAG 1620  
 10 GAGTCCGTGG GTCTGGGCAG TGCCCGCGGC ACCACCACCA CCCACCTGGT GAGGAGCGGC 1680  
 TCCTTGCTCA CTCAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740  
 GGGCAGTTCA GCCCCAGGGA TGGTTTAACC CCCACAGAGG CAGGGCGTTG AGGACCTTCC 1800  
 TGGCAGGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCAT 1860  
 GGGCCCGAGG GAGCCACAGC GGGTTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT 1920  
 TTTGGGTGGG TTTGGCCGGT CTCACAGAGC GAAGCCGACG ATTTGTGCCT GTTGGGTGGC 1980  
 15 CTGGCCTGGA GTGCGGGGGT CTTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCACGGG 2040  
 CTCTGATGAG GCATGATGTC AGCACCACCT GCCCTTGTC CCAACTCACT CCAGGTGCAA 2100  
 CCTGATGTGG ATGCCCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGCGG GTGCCCTGAG 2160  
 CTCTCCCTGG AGTTTCGACTT TGAAGCCAG GAGGTGAAGG GCCCCGCTGC GCAGGACCCAG 2220  
 CGGTTCTGCG AGTTTCCGGA AAGGGTGACG GGGGAAGGGC AGACCCCATG CCCTGGGTGG 2280  
 20 TGGGAGCTG ACAGGGCAGG GGCCTTGGC TGAGCCCAAC CCGCTGGCTC CCAGATCAGG 2340  
 GTGGGCCTGA GGCAGGCAGC CGACTGAGG CCTGGGGCA CCGTGGACCC CTATGCCCGG 2400  
 GTCAGCGTCT CCACCCAGGC CGGACACAGA CATGAGACAA AAGTGCACCG AGGCACGCTC 2460  
 TGCCCCGTGT TTGACGAGAC CTGCTGCTTC CACGTGAGTC AGGATGCTC GGTGGGTGG 2520  
 25 GCCTGGACGG CTGATGGGG CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGCCTGGGCA 2580  
 GCTGGGTGGG CCTGAGCTAG GGCAGCAGG CCTGGCTCAC GCCGTGCCT CAGATCCCGC 2640  
 AGGCGGAGCT GCCAGGGGCC ACCCTGCAGG TGCAGCTTTT CAACTTCAAG CGCTTCTCGG 2700  
 GGCATGAGCC CCTGGGTGAG CTCGCTGTC CACTGGGCAC CGTGGATCTG CAGCATGTTT 2760  
 TGGAGCACTG GTACCTGCTG GGCCTGCGCG CTGCCACTCA GGTGAGGTGC TGGTCACCCAG 2820  
 30 GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CCTGCCCTAT GGGCCATCGG AAAGACAGGC 2880  
 CTGATGGGCA GCATTTTCGG GGGTCTGAGC CCCAACTCGG CCAAGATCAC CCTCCCGGGC 2940  
 TGAAGCCCTT CTGCTGCCCC ACAGCCCGAG CAGGTGCGGG AGCTGTGCTT CTCTCTCCGG 3000  
 TACGTGCCCA GCTCAGGCCG GCTGACCGTG GTGGTGTCTG AGGCTCGAGG CCTGCGTCCA 3060  
 35 GGACTTGCAG AGCCCTACGT GAAGTCCAG CTCATGCTGA ACCAGAGGAA GTGGAAGAAG 3120  
 AGAAAGACAG CCACCAAAAA GGCACGCGC GCCCCTACT TCAATGAGGC CTTACCTTC 3180  
 CTGGTGCCCT TCAGCCAGGT CCAGAATGTG GACCTGGTGC TGGCTGTCTG GGACCCGAGC 3240  
 CTGCCGCTCC GAACTGAGCC CGTAGGCAAG GTGCACCTGG GTGCCCGGGC CTCGGGGCAG 3300  
 CCCCTGCAGC ACTGGGCAGA CATGCTGGCC CACGCCCGGC GGGCCATGTC CCAGCGGCAC 3360  
 40 CCCCTGCCGC CAGCCAGGGA GGTGGACCGC ATGCTGGCCC TGCAGCCCCG CCTTCGCTCG 3420  
 CGCCTGCCCT TGCCCCACTC CTGAATGCAC CACATGCCCT TGTCTCCCG CTGAGCCAG 3480  
 GCATTTGCCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC

Seq ID NO: 197 Protein sequence

Protein Accession #: XP\_028196.1

45 1 11 21 31 41 51  
 | | | | | |  
 MGHPVPVSPA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAGWGL QLSTDALSIA 60  
 STPGPRWALI AGALAAGVLL VSCLLCAACC CRRHRKKPR DKESVGLGSA RGTTHLVR 120  
 50 SGLSLTQRE GLKSLRLQSPG QRGEFSPRDG LTPTEAGR

Seq ID NO: 198 DNA sequence

Nucleic Acid Accession #: NM\_000612.2

Coding sequence: 553..1095

55 1 11 21 31 41 51  
 | | | | | |  
 TTCTCCCGCA ACCTTCCCTT CGCTCCCTCC CGTCCCCCCC AGCTCCTAGC CTCGACTCC 60  
 CTCCCCCCT CACGCCCGCC CTCTCGCCTT CGCCGAACCA AAGTGGATTA ATTACACGCT 120  
 60 TTCTGTTTCT CTCCTGCTG TTCTCTCCCG CTGTGCGCCT GCCCGCCTCT CGCTGTCTCT 180  
 TCTCCCCCTC GCCCTCTCTT CGGCCCCCCC CTTTCACGTT CACTCTGTCT CTCCCACTAT 240  
 CTCTGCCCCC CTCTATCCTT GATACAAACAG CTGACCTCAT TTCCCGATAC CTTTTCCTCC 300  
 CCGAAAAGTA CAACATCTGG CCGGCCCCAG CCCGAAGACA GCCCGTCTCT CTTGGACAAT 360  
 CAGACGAATT CTCCCCCCCC CCCCAAAAA AAAAGCCATC CCCCCTCTCT GCCCGGTGCG 420  
 65 ACATTGCGCC CCCGCGACTC GGCCAGAGCG GCGCTGGCAG AGGAGTGTCC GGCAGGAGGG 480  
 CCAACGCCCG CTGTTCCGTT TCCGACACGC AGCAGGGAGG TGGGCGGCAG CGTCGCCCGC 540  
 TTCCAGACAC CAATGGGAAT CCCAATGGGG AAGTCGATGC TGGTGCTTCT CACTTCTTGT 600  
 GCCTTCGCCT CGTGCTGCAT TGCTGCTTAC CGCCCAAGTG AGACCCTGTG CGGCGGGGAG 660  
 CTGGTGGACA CCTCCAGTT CGTCTGTGGG GACCGCGGCT TCTACTTTCAG CAGGCCCGCA 720  
 70 AGCCGTGTGA GCCGTCCGAG CCGTGGCATC GTTGAAGAGT GCTGTTTCCG CAGCTGTGAC 780  
 CTGGCCCTCC TGGAGACGTA CTGTGCTACC CCGCCCAAGT CCGAGAGGGA CGTGTCCGAC 840  
 CCTCCGACCG TGCTTCCGGA CAACCTCCCC AGATACCCCG TGGGCAAGTT CTTCAATAT 900  
 GACACCTGGA AGCAGTCCAC CCAGCGCCTG CGCAGGGGCC TGCCCTGCCCT CCTGCGTGCC 960  
 CGCCGGGGTC ACGTGTCTCG CAAGGAGCTC GAGGCGTTCA GGGAGGCCAA ACGTCAACGT 1020  
 75 CCCCTGATAT CTCTACCCAC CCAAGACCCC GCCACGGGG GCGCCCCCCC AGAGATGGCC 1080  
 AGCAATCGGA AGTGAGCAA ACTGCCGCAA GTCTGCAGC CGGCGCCACC ATCTGTCAGC 1140  
 CTCCTCTGTA CCACGGACGT TTCCATCCCG AAAATCTCTC GGTTCACAGT 1200  
 CCCCCGTTGG CTCTCTCTGA CCCAGTCCCC GTGCCCGGCC TCCCGGAAAC AGGCTACTCT 1260  
 80 CCTCGGCCCC CTCCATCGGG CTGAGGAAGC ACAGCAGCAT CTTCAACAT GTACAAAATC 1320  
 GATTGGCTTT AAACACCCCT CACATACCCCT CCCCCC

Seq ID NO: 199 Protein sequence

Protein Accession #: NP\_000603.1

1 11 21 31 41 51

MGIPMGKSM | VLLTFLAFAS | CCIAAYRPSE | TLCGGELVDT | LQFVCGDRGF | YFSRPASRVS 60  
 RRSRGIVEEC | CFRSCLLALL | ETYCATPAKS | ERDVSTPPTV | LPDNFPRYPV | GKFFQYDTWK 120  
 QSTQRLRRGL | PALLRRARRH | VLAKELEAFR | EAKRHRPLIA | LPTQDPAHGG | APPEMASNRK

Seq ID NO: 200 DNA sequence  
 Nucleic Acid Accession #: AK057131.1  
 Coding sequence: 61..1146

1 11 21 31 41 51  
 AGTCTGGGCG | TTTAGGTCAG | AACTACCCCG | GTAGCCTGAC | AGCAGGAGCT | CGAGAGAAGC 60  
 ATGGCTCAGC | GGTGCGTTTG | CGTGCTGGCC | CTGGTGGCTA | TGCTGCTCCT | AGTTTTCCCT 120  
 ACCGTCTCCA | GATCGATGGG | CCGGAGGAGC | GGGGAGCATC | AAAGGGCGTC | GCGAATCCCT 180  
 TCTCAGTTCA | GCAAAGAGGA | ACGCGTCGCG | ATGAAAGAGG | CGCTGAAAGG | TGCCATCCAG 240  
 ATTCCAACAG | TGACTTTTAG | CTCTGAGAAG | TCCAATACTA | CAGCCCTGGC | TGAGTTCGGA 300  
 AAATACATTC | ATAAAGTCTT | TCCTACAGTG | GTCAGCACCA | GCTTTATCCA | GCATGAAGTC 360  
 GTGGAAGAGT | ATAGCCACCT | GTTCACTATC | CAAGGCTCGG | ACCCCAGCTT | CGAGCCCTAC 420  
 CTGCTGATGG | CTCACITTTGA | TGTGGTGCCT | GCCCTGAAG | AAGGCTGGGA | GGTGCCCCCA 480  
 TTCTCTGGGT | TGGAGCGTGA | TGGCGTCATC | TATGGTTGGG | GCACACTGGA | CGACAAGAAC 540  
 TCTGTGATGG | CATTATCGCA | GGCCTTGGAG | CTCCTGCTGA | TCAGGAAGTA | CATCCCCCGA 600  
 AGATCTTTCT | TCATTCTCTT | GGGCCATGAT | GAGGAGTCAT | CAGGGACAGG | GGCTCAGAGG 660  
 ATCTCAGCCC | TGCTACAGTC | AAGGGGCGTC | CAGCTAGCCT | TCATTGTGGA | CGAGGGGGGC 720  
 TTCATCTTGG | ATGATTTTCT | TCCTAACTTC | AAGAAGCCCA | TCGCCTTGAT | TGCAGTCTCA 780  
 GAGAAGGGTT | CCATGAACCT | CATGCTGCAA | GTAAACATGA | CTTCAGGCCA | CTCTTCAGCT 840  
 CCTCCAAAGG | AGACAAGCAT | TGGCATCCTT | GCAGCTGCTG | TCAGCCGATT | GGAGCAGACA 900  
 CCAATGCCTA | TCATATTTGG | AAGCGGGACA | GTGGTGAAGT | TATTGCAGCA | ACTGGCAAAAT 960  
 GAGGTTTATG | GAGAGAAATC | CCTAAACCAA | TGCAATAATC | AGGACCACCA | CGGCACTCAC 1020  
 CATATTTCAA | GCAGGGGTCA | AGTTCAATGT | CATCCCCCCA | GTGGCCGAGG | CCACAGTCAA 1080  
 CTTCGGGATT | CACCCCTGGC | AGACAGTCCA | AGAGGTCTTA | GAACTCACGA | AGAATCATGT 1140  
 GGTGATAAAG | AGAGTCCAGT | TCCATGTGTT | GAGTGCCTTT | GACCCCTCTC | CCGTCAGCCC 1200  
 TTCTGATGAC | AAGGCCTTGG | GCTACCAAGT | GCTCCGCCAG | ACCGTACAGT | CCGTCTTCCC 1260  
 GGAAGTCAAT | ATTACTGCCC | CAGTTACTTC | TATTGGCAAC | ACAGACAGCC | GATTCTTTAC 1320  
 AAACCTCACC | ACTGGCATCT | ACAGGTTCTA | CCCCATCTAC | ATACAGCCTG | AAGACTTCAA 1380  
 ACCGATCCAT | GGAGTCAACG | AGAAAACTTC | AGTCCAAGCC | TATGAGACCC | AAGTGAATTT 1440  
 CATCTTTGAG | TTGATTCAGA | ATGCTGACAC | AGACCAGGAG | CCAGTTTCTC | ACCTGCACAA 1500  
 ACTGTGAGGT | CAAGGGGCGT | GCTGGGTTAG | GCATGCCCGA | CCCCGGGACA | GGACTAAGCC 1560  
 AAGGGGGAAA | GCTAGTGTGG | ATGAAACTTT | TGATCAAAAC | CACATTGTAA | AACATTGCCC 1620  
 ATCTGTCTTG | CTCATCTTTA | AACTCTCCCA | AGAACAAGGC | CGGGGTAAGG | TAAAGTCAGC 1680  
 AGAAATCTGG | CTCTCCCTTT | CCTCCCGACA | TCTGCATCCC | TTGATCCACT | GGCATTGCTC 1740  
 GCCCTCTTGT | CCCTTATCTG | TCTTATGCTG | GTTATTTTAC | TGCTTCACCT | TCCAGGCTTG 1800  
 ACTTAAACAA | TGTAGATTTG | AGAAATCTCA | ACCAGTTGTT | ACCTGATAGG | AGTCTTTAAT 1860  
 TTAGGGCAGT | TTTGCTGGGA | TGCTTTCTCC | AGAGCTTATA | TATTCTCTCT | TACTAGAACT 1920  
 TTCTTCCCCC | CTTTATTTCC | CTCTCTTCTT | GGACTCATGA | GCTGTCTCTT | CATCTCTCCT 1980  
 CTCTCTCTCT | CATCTCTCCC | CTTACTCTTC | AATTTATCTT | ACTTCTGGAC | CTGGACTTAC 2040  
 CCAAACTGTG | ATACTACCAT | AATTGTCAAC | ATAATCAGTC | AAATAAAGTG | ATCTGTGCAT 2100

Seq ID NO: 201 Protein sequence  
 Protein Accession #: BAB71368.1

1 11 21 31 41 51  
 MAQRVCVCLA | LVAMLLLVFP | TVSRSMGPRS | GEHQRASRIP | SQFSKEERVA | MKEALKGAIQ 60  
 IPTVTFSEK | SNTTALAEFG | KYIHKVFPTV | VSTSFQHEV | VEEYSHLFTI | QGSDPSLQPY 120  
 LLMAHFDVVP | APEBGWVFP | FSGLERDGI | YGWGLDDKN | SVMALLQALE | LLLIRKYIPR 180  
 RSFFISLGH | EESSGTGAQR | ISALLQSRGV | QLAFLVDEGG | FILDDFIPNF | KKPIALIAVS 240  
 EKGSMNMLQ | VNMSTGSHSA | PPKETSIGIL | AAASVRLQ | PMP1IFSGST | VVTVLQQLAN 300  
 EVYGEKSLN | Q | CNNQDHHGTH | HIQSRGQVQC | HPPSGPGHSQ | LPDSEWTDSP | RGPRTHEHC 360

Seq ID NO: 202 DNA sequence  
 Nucleic Acid Accession #: NM\_004217.1  
 Coding sequence: 58..1092

1 11 21 31 41 51  
 GGCCGGGAGA | GTAGCAGTGC | CTTGGACCCC | AGCTCTCCTC | CCCCTTTCTC | TCTAAGGATG 60  
 GCCCAGAAAG | AGAACTCCTA | CCCCTGGCCC | TACGGCCGAC | AGACGGCTCC | ATCTGGCCTG 120  
 AGCACCTGCG | CCCAGCGAGT | CCTCGGAAA | GAGCCTGTCA | CCCCATCTGC | ACTTGTCTCT 180  
 ATGAGCCGCT | CCAATGTCCA | GCCCACAGCT | GCCCTGGGCC | AGAAGGTGAT | GGAGAATAGC 240  
 AGTGGGACAC | CCGACATCTT | AACCGGGCAC | TTCACAAATG | ATGACTTTGA | GATTGGGCGT 300  
 CCTCTGGGCA | AAGGCAAGTT | TGGAAACGTG | TACTTGGCTC | GGGAGAAGAA | AAGCAATTTT 360  
 ATCGTGGCGC | TCAAGGTCTT | CTTCAAGTCC | CAGATAGAGA | AGGAGGGCGT | GGAGCATCAG 420  
 CTGGCGAGAG | AGATCGAAAT | CCAGGCCAC | CTGCACCATC | CCAACATCCT | CGCTCTCTAC 480  
 AACTATTTT | ATGACCGGAG | GAGGATCTAC | TTGATTCTAG | AGTATGCCCC | CCGCGGGGAG 540  
 CTCTACAAGG | AGCTGCAGAA | GAGCTGCACA | TTTGACGAGC | AGCGAACAGC | CACGATCATG 600  
 GAGGAGTTGG | CAGATGCTCT | AATGTACTGC | CATGGGAAGA | AGGTGATTCA | CAGAGACATA 660  
 AAGCCAGAAA | ATCTGCTCTT | AGGGCTCAAG | GGAGAGCTGA | AGATTGCTGA | CTTGCGCTGG 720  
 TCTGTGATG | CGCCCTCCTT | GAGGAGGAAG | ACAATGTGTG | GCACCCCTGA | CTACCTGCCC 780  
 CCAGAGATGA | TTGAGGGGCG | CATGCACAA | GAGAAGGTGG | ATCTGTGGTG | CATGGAGTGG 840  
 CTTTGCTATG | AGCTGCTGGT | GGGGAACCCA | CCCTTTGAGA | GTGCATCACA | CAACGAGACC 900  
 TATCGCCGCA | TCGTCAAGGT | GGACCTAAG | TTCCCGCTT | CTGTGCCAC | GGGAGCCAG 960  
 GACCTCATCT | CCAAACTGCT | CAGGCATAAC | CCCTCGGAAC | GGCTGCCCTT | GGCCAGGTC 1020



TCAGCCCACC CTTGGGTCCG GGCCAACTCT CGGAGGGTGC TGCCTCCCTC TGCCCTTCAA 1080  
 TCTGTGCGCT GATGTGCCCT GTCAATCACT CGGGTGCCTG TGTTTGTATG TCTGTGTATG 1140  
 TATAGGGGAA AGAAGGGATC CCTAATGTGT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200  
 TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 203 Protein sequence  
 Protein Accession #: NP\_004208

1 11 21 31 41 51  
 | | | | |  
 MAQKENSYPW PYGRQTAPSG LSTLPQRVLR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN 60  
 SSGTDPDILTR HFTIDDFEIG RPLGKGKFGN VYLAREKKSH FIVALKVLPK SQIEKEGVEH 120  
 QLRREIEIQH HLHHPNLRRL YNYFYDRRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI 180  
 MEELADALMY CHGKKVIHRD IKPENLLGL KGBELKIADFG WSVHAPSLRR KTMCGTLDYL 240  
 PPEMIEGRMH NEKVDLWCIG VLCYELLVGN PPFESASHNE TYRRIVKVDL KFPASVPTGA 300  
 QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPSPAL QSWA

Seq ID NO: 204 DNA sequence  
 Nucleic Acid Accession #: AK055663  
 Coding sequence: 38..1423

1 11 21 31 41 51  
 | | | | |  
 AGAACGGCTT CCGGCGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTCG 60  
 AAAACACCAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA 120  
 CCGAAGGTCC TGAAGATAC TGCTCTTTGG TGTAAATAAAC TTGATATGTA CTGGCTTCCT 180  
 GCTTATGTGG TGCACTTCTA CTAATAGTAT AGCTTTAACT GCCTATACTT ACCTGACCAT 240  
 TTTTGTATCT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAACAT TGAGGAAACC 300  
 TAGCCCTGTC TATTCATTTG GGTTTGAAAG ATTAGAAGTC CTGGCTGTAT TTGCCCTCCAC 360  
 AGTCTTGGCA CAGTTGGGAG CTCTCTTTAT ATTAAGAGAA AGTGCAGAAC GCTTTTGGGA 420  
 ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA 480  
 CCTGTTTACG ATGCTTTCTA TTCGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG 540  
 TACGAGCTGG CTTCAGAGAG ATGTTGCAGA TCTTAGTCGA AGCTTGTGTG GAATTATTCC 600  
 GGGACTTAGC AGTATCTTCC TTCCCGAAT GAATCCATTT GTTTGATTG ATCTTGCTGG 660  
 AGCATTTGCT CTTTGTATTA CATATATGCT CATTGAAATT AATAATTATT TTGCCGTAGA 720  
 CACTGCCTCT GCTATAGCTA TTGCCTTGAT GACATTTGGC ACTATGTATC CCATGAGTGT 780  
 GTACAGTGGG AAAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATTGGTC AGTTGGACAA 840  
 ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTTAGAA GTCCGAAATG AACATTTTGG 900  
 GACCTTAGGT TTTGGCTCAT TGGCTGGATC AGTGCATGTA AGAATTCGAC GAGATGCCAA 960  
 TGAACAAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTCTAGTGT CTACTCTAAC 1020  
 TGTTCAAAT TTCAAGGATG ACTGGATTAG GCCTGCCTTA TTGCTGCGC CTGTTGCAGC 1080  
 CAATGTCTTA AACTTTTCAG ATCATCACGT AATCCCAATG CCTCTTTTAA AGGGTACTGA 1140  
 TGATTTGAAC CCACTTACAT CACTCCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC 1200  
 ATTTAACACT CCTGGGAAAA ATGTGAACCC AGTTATTCTT CTAAACACAC AAACAAGGCC 1260  
 TTATGGTTTT GGTCTCAATC ATGGACACAC ACCTTACAGC AGCATGCCTA ATCAAGGACT 1320  
 TGGAGTTCCA GGAATTGGAG CACTCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG 1380  
 TAGATATGGA ACTAATAATA GAATTGGACA ACCAAGACCA TGATAGACTC TAACCTTATT 1440  
 TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTTAG TAATCCAAC TTGCATTGAC 1500  
 TGTTAATCA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACATT TCATGAAACC 1560  
 TATGAACTA TATTTTGTGA AAATGTATTT GTGACAGTGA AATCCTCGTA AATGTTAAAG 1620  
 GCTTTAAATA GGCTCTCTTT AGAAAATGTG TTTCTTTAAA TTTGGATTTT GGTATCTTTG 1680  
 GTTTTGTAGT TGACTGCACT GTGATGTGAC CTACCTTTA TAAGAGCCAC TTGATGGAGT 1740  
 AGATCTGTCA CATTACTAAG ATACGATATT TCTTTTCTTT TCCGAGACGG AGTCTTGCTC 1800  
 TGCCACTGTG CCCGGCCAAT ACATTATTAT TAACCTAAGG CTGTACTTTA TTAAGGCTTC 1860  
 CTTAGTTTTT GTTTTGTATT GTTTTGTGAG ATGGAGTCTC ACTCTGTCGC CCAGGCTGGA 1920  
 ATGCAGTGGC ATGATCTCAG CTCACTGCAA CCTCTGCCCT CTGAGTTCAA ATGATTCTCC 1980  
 TGCCTCAGCC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCACGCC AGCTAATTTT 2040  
 TGTATTTTGA GTAAAGACGG GGGATTTCAC CATGTTGGCC AGGCTGGTCT TGAACCTCTG 2100  
 ACCTCATGAT CCACCCACCT TAGCCTCCCA AAGTGCTGGG ATTAGGTGTG AGCCACCGCA 2160  
 CCTGGCCGAT ATTTTCTTTA ATGAAATTTA TAAATATGCT TCTTGAATAA TACACATTTT 2220  
 GGGAAAGGGA AAAATGTCTG TTCAAAAAGT AAAGTCTCT TTTATAGCTT TTCCAAACTT 2280  
 AATTGCTAAA TTTTCTTTTG AGGTCTCTCT GAATTATGTC TTACAACTA AAAGCAAAA 2340  
 TTTTATGAGC AAATTTTGGG ATACATTCTA TCTAGCACAA TTTGAATTTT TAATTATCAA 2400  
 GATTTTTGTT AAAGTTTCTC TCCTTAAAA ATTTTAGTAC ATTTGTAAT

Seq ID NO: 205 Protein sequence  
 Protein Accession #: BAB70980.1

1 11 21 31 41 51  
 | | | | |  
 MGTIHLFRKP QRSFPGKLLR EFRLVAADRR SWKILLFGVI NLICTGFLM WCSSTNSIAL 60  
 TAYTYLTIFD LFSLMTCCLIS YWVTLRKPSF VYSFGFERLE VLAVFASTVL AQLGALFILK 120  
 ESAERFLEQP BIHTGRLLVG TFVALCFNLF TMLSIRNKP FAYVSEAAST WLQEHVADLS 180  
 RSLCGIIPGL SSIFLPRMNP FVLIDLAGAF ALCITYMLIE INNYFAVDTA SAIAIALMTF 240  
 GTMYPMSVYS GKVLQTPFP HVIGQLDKLI REVSTLDGVL EVRNEHFNTL GFGLSLAGSVH 300  
 VRIRRDANQ MVLARVITNRL YTLVSTLTQV IFKDDWIRPA LLSGPPVAANV LNFSDHHVIP 360  
 MPELLKGTDDL NPVTSTPAKP SSPPEFSFN TPGKNVNPVI LNTQTRPYG FGLNHGHTPY 420  
 SSMLNQGLGV PGIGATQGLR TGFTNIPSRV GTNNRIGQPR P

Seq ID NO: 206 DNA sequence  
 Nucleic Acid Accession #: NM\_016361.1  
 Coding sequence: 397..1662

1 11 21 31 41 51

5  
10  
15  
20  
25  
30

	GGAACTCAGG		GCCGGCTCCT		GTTCCTTCAA		GAGTGTGGA		GGCCAAACTT		GAAATACAAG	60
	TTTAATGTTC		CTCGTCGGGC		AAAAGATAAG		GATCCGATCT		CCCCCGGCC		GGTGTGCAGC	120
	AGGAGCGACC		AACCCCGACC		CGGGTTAAAA		CTCCAGGGA		CTCTTCGCTG		CTGCCACCTC	180
	TTGTTCTCTC		CCCCGTTCCT		ACTCGGGGTC		TCCCTCAGGG		CCGGGAGGCA		CAGCGGTCCC	240
	TGCTTGCTGA		AGGGCTGGAT		GTACGCATCC		GCAGGTTCCC		GCGGACTTGG		GGGCGCCCGC	300
	TGAGCCCCGG		CGCCCCGAGA		AGACTTGTGT		TTGCCTCCTG		CAGCCTCAAC		CCGGAGGCAG	360
	CGAGGGCCTA		CCACCATGAT		CACTGGTGTG		TTCAGCATGC		GCTTGTGGAC		CCCAGTGGGC	420
	GTCTGACCT		CGCTGGCGTA		CTGCCTGCAC		CAGCGGCGGG		TGGCCCTGGC		CGAGCTGCAG	480
	GAGGCCGATG		GCCAGTGTCC		GGTCGACCGC		AGCCTGCTGA		AGTTGAAAAT		GGTGCAGGTC	540
	GTGTTTCGAC		ACGGGGCTCG		GAGTCTCTC		AAGCCGCTCC		CGCTGGAGGA		GCAGGTAGAG	600
	TGGAACCCCC		AGCTATTAGA		GGTCCCACCC		CAAACCTCAGT		TTGATTACAC		AGTCACCAAT	660
	CTAGCTGGTG		GTCCGAAACC		ATATTCTCCT		TACGACTCTC		AATACCATGA		GACCACCTTG	720
	AAGGGGGCCA		TGTTTGTGG		GCAGCTGACC		AAGGTGGGCA		TGCAGCAAAAT		GTTTGCCTTG	780
	GGAGAGAGAC		TGAGGAAGAA		CTATGTGGAA		GACATTCCCT		TTCTTTCAAC		AACCTTCAAC	840
	CCACAGGAGG		TCPTTATTCG		TTCCACTAAC		ATTTTTCGGA		ATCTGGAGTC		CACCCGTTGT	900
	TTGCTGGCTG		GGCTTTTCCA		GTGTCAAGAA		GAAGGACCCA		TCATCATCCA		CACTGATGAA	960
	CGAGATTGAG		AAGTCTTGTA		TCCCAACTAC		CAAAGCTGCT		GGAGCCTGAG		GCAGAGAACC	1020
	AGAGGCCGGA		GGCAGACTGC		CTCTTTACAG		CCAGGAATCT		CAGAGGATTT		GAAAAAGGTG	1080
	AAGGACAGGA		TGGGCATTGA		CAGTAGTGAT		AAAGTGGACT		TCTTCATCCT		CCTGGACAAC	1140
	GTGCTGCCG		AGCAGGCACA		CAACCTCCCA		AGCTGCCCCA		TGCTGAAGAG		ATTGTCACGG	1200
	ATGATCGAAC		AGAGAGCTGT		GGACACATCC		TTGTACATAC		TGCCCAAGGA		AGACAGGGAA	1260
	AGTCTTCAGA		TGGCAGTAGG		CCCATTCTCT		CACATCCTAG		AGAGCAACCT		GCTGAAAGCC	1320
	ATGACTCTG		CCACTGCCCC		CGACAAGATC		AGAAAGCTGT		ATCTCTATGC		GGCTCATGAT	1380
	GTGACCTTCA		TACGCTCTT		AATGACCTTG		GGGATTTTTG		ACCACAAATG		GCCACCGTTT	1440
	GCTGTGACC		TGACCATGGA		ACTTTACCAG		CACCTGGAAT		CTAAGGAGTG		GTTTGTGCAG	1500
	CTCTATTACC		ACGGGAAGGA		GCAGGTGCCG		AGAGGTTGCC		CTGATGGGCT		CTGCCCCTG	1560
	GACATGTTCT		TGAATGCCAT		GTCAGTTTAT		ACCTTAAGCC		CAGAAAAATA		CCATGCACCT	1620
	TGCTCTCAAA		CTCAGGTGAT		GGAAGTTGGA		AATGAAGAGT		AACCTGATTA		TAAAAGCAGG	1680
	ATGTGTTGAT		TTTAAATATA		AGTGCCTTTA		TACAAAAAAA		AAAAAAAATA		A	

Seq ID NO: 207 Protein sequence  
Protein Accession #: NP\_057445.1

35  
40  
45

	1		11		21		31		41		51	
	MRLWTPVGV		LSLAYLQHR		RVALAELQEA		DGQCPVDRSL		LKLMVQVVF		RHGARSPLKP	60
	LPLEBQVEWN		POLLEVPPQT		QFDYTVTNLA		GGPKPYSPYD		SQYHETTLKG		GMFAGQLTKV	120
	GMQMQFALGE		RLRKNYVEDI		PFLSPTFNPO		EVFIRSTNIF		RNLESTRCLL		AGLFQCQKEG	180
	PIIIHTDEAD		SEVLYPNYQS		CWSLRQRTRG		RQQTASLQPG		ISEDLKKVKD		RMGIDSSDKV	240
	DFFIILLDNVA		AEQAHLNLPSC		PMLKRFARM		EQRAVDTSLY		ILPKEDRESL		QMAVGPFLHI	300
	LESNLLKAMD		SATAPDKIRK		LYLYAAHDVT		FIPLLMTLGI		FDHKWPPFAV		DLTMELYQHL	360
	ESKEWFVQLY		YHGKEQVPRG		CPDGLCPLDM		FLNAMSVMYTL		SPEKVHALCS		QTQVMEVGNE	420
	E											

Seq ID NO: 208 DNA sequence  
Nucleic Acid Accession #: CAT cluster

50  
55  
60

	1		11		21		31		41		51	
	TTTGAGGGGG		TGGTGGGGCG		AGTTTAATTC		ATAAAGAAGC		CTCCTGATCA		GAAAGGGGCC	60
	TAACAGCCTG		CCCTTGAGGA		GAAGTCCTTC		CTTGAGGATA		AGGCCTCCCA		GGGGAGGAGG	120
	TGCTGGGGGC		CAGTGTTAGG		CTTCAGGCCA		TCCCTGGAGG		CCAGTCCTGT		GCTCAGCAAG	180
	TAGTGGCAGA		GCCTGGAGTG		ATGAGTGGGA		TGGCCTTCTC		AGGTACAGGA		CTGTGCTGCT	240
	TCGGCTGCT		CTTGCAATTTG		CATTTGCCAC		TCAGAACTGC		CGCATCCCA		GCAATGGCCA	300
	GGAGCCCTCC		GCAGATCAGT		CCGCTCAGCT		GCAGGTTTTT		CCAGTCATAG		TAGAAGGGAT	360
	CGTCTTTTAT		GGCAAAATGG		TCATTGGCTT		CCAAGGCAGT		CAGGCCAACT		GTGTGACTCT	420
	GCAGGTTCTC		CACTGCTCCT		TCACCACTGT		CCTGCGAGGT		CACCTTGGCG		AGGGCTCACC	480
	TGAGCTGGCA		GCGCAG									

Seq ID NO: 209 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..564

65  
70  
75  
80

	1		11		21		31		41		51	
	ATGGAGCCCT		GGGCGTGGCT		GCAGGGTTTA		AAGAGCCGAC		CCACGTGCCC		AGCAGCCTCC	60
	TCAGATCCGT		TCTCTGCGCT		GCCAGCTCAG		GACACTGGTG		AAGGAGCAGT		GAGGAACCTG	120
	CAGAGTCACA		CAGTTGGCCT		GACTGCCTTG		GAAGCCAATG		ACCCATTTCG		CAATAAAGAC	180
	GATCCCTTCT		ACTATGACTG		GAAAAACCTG		CAGCTGAGCG		GACTGATCTG		CGGAGGGCTC	240
	CTGGCCATTG		CTGGGATCGC		GGCAGTTCTG		AGTGGCAAAT		GCAAAATGCAA		GAGCAGCCAG	300
	AAGCAGCACA		GTCCTGTACC		TGAGAAGGCC		ATCCCACTCA		TCACTCCAGG		CAGATTCTCT	360
	ACCTTGGCCA		AATCAAATAA		ACCTTTATCT		CCAAGCACCT		TTGTCTTGGT		GTTTGGCATC	420
	AGCTACACAT		CAGTCTTCCG		AGTGCTCTT		TCTGCGTCCC		TGTACCTGTC		GATTCCTGGT	480
	GATGCTGCTG		CCCTCACATC		AGGCCATCCA		AGCATGCAGA		ACATAAGCAT		GCAGAACACT	540
	GGAACGAAGG		GCTGTACCTA		ATGA							

Seq ID NO: 210 Protein sequence  
Protein Accession #: FGENESH predicted

	1		11		21		31		41		51	
	MEPWAWLQGL		KSRPTCPAAS		SDPFSALPAQ		DTGEGAVRNL		QSHTVGLTAL		EANDPFANKD	60
	DPFYDWNKLN		QLSLGICGGL		LAIAGIAAVL		SGKCKCKSSQ		KQHSFVPEKA		IPLITPGRFL	120

TLAKSNKPLS PSTFVLVFGI SYTSVFRVPL SASLYPAIPG DAAALTSQHP SMQNISMQNT 180  
GTRGCT

Seq ID NO: 211 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..318

10 1 11 21 31 41 51  
| | | | | |  
ATGCCCGGCC ACCCCGTCTG TGAAGTGAGG AGCACCTCTG CCCGGCTGCC CCGTCTGGGA 60  
AGTGAGGAGC GCCTCTGCCC GGCTGCCACC CCGTCTGTGA GTGCCCTGCTG CGCTGGGCCC 120  
AGGCCGCCCG TGCCCTGCCA GGCCCTCCCG CCCCCACCT TCCACCCAG GGCCTGCTCC 180  
TCACCCAGG GTTCCATCTC CTTAGTTTCC ACCAGAGACT GGGTCTTCAT TCTCACCTCG 240  
15 CTACACAGCC CCTACCAGAA CGTTCTGAAA TGCAAACCTA ACAACTGTCT CACCCAGCA 300  
GGAAACTCCC CAGGGTCCCG GGCCCCCTGC GGGGTTCAG GCCTCACTCT TCGCGCCCAT 360  
CCCTCCGCCCT TGACGCCCT GAGCTCGCCC CCAGTGCTGG CCCTTCACGT CCAGTTATCC 420  
CTCCAGCCT CCAAGTCCC CGTTACCGAA GACCGCCACC ATCAGACAT AGCGCAGCAC 480  
ATATGGGACA CTGGTGAAG AGCAGTGAGG AACCTGCAGA GTCACACAGT TGGCCTGACT 540  
GCCTTGAAG CCAATGACCC ATTTGCCAAT AAAGACGATC CCTTCTACTA TGACTGGAAA 600  
20 AACCTGCAGC TGAGCGGACT GATCTGCGGA GGGCTCTGG CCATTGCTGG GATCGCGGCA 660  
GTTCTGAGTG GCAATGCAA ATGCAAGAGC AGCCAGAAGC AGCAGAGTCC TGTACTGTAG 720  
AAGGCCATCC CACTCATCAC TCCAGGCAGA TTTCTCACCT TGGCCAAATC AAATAAACCT 780  
TTATCTCCAA GCACCTTTGT CTTGGTGTGT GGCATCAGCT ACACATCAGT CTTCCGAGTG 840  
25 CCTCTTCTG CGTCCCTGTA CCCTGCCAT CTGTGTGATG CTGCTGCCCT CACATCAGGC 900  
CATCCAAGCA TGCAGAACAT AAGCATGCAG AACACTGGAA CGAAGGGCTG TACCTAA

Seq ID NO: 212 Protein sequence  
Protein Accession #: FGENESH predicted

30 1 11 21 31 41 51  
| | | | | |  
MPGHPVCEVR STSARLPRLG SEERLCPAAT PSVSACCAGP RPPVPCQALR PPTFHPRACS 60  
SPQGSISLVS TRDWVFILTL LHSPYQNVLK CKPNNCLTPA GNSPGSRAPC GVAGLTTLRAH 120  
35 PSALTALSSP PVLAHLVQLS LPASKVPVTE DRHHHDIAQH IWDTEGAVR NLQSHTVGLT 180  
ALEANDPFAN KDDPFYDWNK NLQLSGLICG GLLAIAAGIAA VLSGKCKCKS SQKQHSVPPE 240  
KAIPLITPGR FLTAKSNKP LSPSTFVLVF GISYTSVFRV PLSASLYPAI PGDAAALTSQ 300  
HPSMQNISMQ NTGTGCT

Seq ID NO: 213 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..1758

45 1 11 21 31 41 51  
| | | | | |  
ATGATGGGGT CTCATGTTGC CCAGGCTGGT CTGAACTCC TGGGCTCGAG TGACCTCCT 60  
GCCTTGGCCT CCGAAAGTGC TGGGATTACA GGACTGTTAT TACAGGAATC CATAACACTG 120  
GAGGATGTGG CTGTGGACTT CACTTGGGAG GAGTGGCAAC TCCTGGGCGC TGCTCAGAAG 180  
GACCTGTACC GGGATGTGAT GTTGAGAAAC TACAGCAACC TGGTGGCAGT GGGGTATCAA 240  
50 GCCAGCAAC CCGATGCACCT CTTCAAGTTG GAACAAGGAG AACAACTGTG GACAAATTGAA 300  
GATGGAATCC ACAGTGGAGC CTGTTCAAGT TCTCCAAAGG TCCCGTTCTC CATTCTCTCA 360  
TCTGTGCCCT TCACTCTTCA AAATTGCCTT CATTCTAACA TATGGAAAGT TGATCATGTG 420  
CTGGAGCGCT TGCAGAGTGA AAGCCTGGTG AACAGAAGGA AACCATGTCA TGAACATGAT 480  
GCATTGAAA ATATTGTTCA TTGCAGCAAA AGTCAGTTTC TGTTAGGGCA AAATCATGAT 540  
55 ATATTGACT TACGTGGAAA AAGTTTGAAA TCCAATTTAA CTTTAGTTAA CCAGAGCAAA 600  
GGCTATGAAA TAAAGAACTC TGTTGAGTTT ACTGGAATG GGGACTCCTT TCTTCATGCT 660  
AACCATGAAC GACTTCATAC TGCAATTAAT TTCCCTGCAA GTCAAAAAC CATCAGCACT 720  
AAGTCCCAAT TCATCAGTCC CAAGCATCAG AAAACACGAA AATTAGAGAA GCATCATGTG 780  
TGCAGTGAAT GTGGGAAAGC CTTTCATCAG AAGTCTTGGC TAACTGATCA CCAGGTAATG 840  
60 CATACAGGAG AGAAACCCCA CAGATGTAGT CTATGTGAGA AAGCCTTCTC CAGAAAGTTT 900  
ATGCTACTG AACATCAGCG AACTCATACA GGAGAAAAAC CTTATGAATG CCCTGAATGT 960  
GGCAAGCCT TTCTCAAGAA ATCAGCGCTC AACATACATC AGAAAACACA TACCGGAGAG 1020  
AAACCCTATA TATGCAGTGA ATGTGAAAAA GGCTTCATCC AGAAAGGAAA TCTCATTGTA 1080  
CACCAGCGAA TTCATACAGG TGAGAAACCT TATATATGCA ATGAATGTGG AAAAGGCTTC 1140  
65 ATTCAGAAGA CGTGTCTCAT AGCAGATCAG AGATTTCACA CAGGAAAGAG GCCCTTTGTG 1200  
TGCACTGAAT GTGGAAAATC CTGTTCTCAG AAATCAGGTC TCATTAAACA TCAAAGAATT 1260  
CACACAGGAG AGAAACCCCT TGAATGTAGT GAATGTGGGA AAGCCTTTAG CACAAGCAA 1320  
AAGCTCATGT TCCATCAAAG GACTCATACA GGAGAGAGAC CCTATGGCTG TAACGAGTGT 1380  
GGGAAAGCGT TTGCGTATAT GTCGTGTCTG GTTAAGCATA AGAGAATACA CACAAGGAG 1440  
70 AAACAAGAGG CAGCAAGGT GGAAAATCCT CCTGCAGAGA GGCACAGCTC ATTACACACC 1500  
AGTGATGTCA TGCAGGAGAA AAACCTCTGCT AACGGGGCGA CTACACAAGT GCCTCTGTG 1560  
GCCCTCAGA CATCATTAAT CATCAGCGGC CTCCTCGCAA ACAGGAACGT AGTCCTTTGT 1620  
GGACAGCCAG TGGTCAGATG TGCAGCCTCA GGAGATAACA GAGGATTTGC ACAGGACAGA 1680  
75 AACCTTGTGA ATGCAGTGAA TGTGGTTGTG CCTTCCGTGA TCAATATGT CTTATTTTAT 1740  
GTTACAGAAA ACCCATAG

Seq ID NO: 214 Protein sequence  
Protein Accession #: FGENESH predicted

80 1 11 21 31 41 51  
| | | | | |  
MMGSHVAQAG LELLGSSDPP ALASESAGIT GLLQESITL EDVAVDFTWE EWQLLGAAQK 60  
DLYRDVMLEN YSNLVAVGYQ ASKPDALFKL EQGEQLWTIE DGIHSGACSG SPKVFFSIFS 120  
SVPFTLQNL HSNLWKVDHV LERLQSESLV NRRKPCHEHD AFENIVHCSK SQFLGLQNH 180  
IFDLRGKSLK SNLTLVNQSK GYEIKNSVEF TNGKDSFLHA NHERLHTAIK FPASQKLIST 240

KSFQFISPKHQ KTRKLEKHHV CSECGKAFIK KSWLTDHQM HTGEKPHRCS LCEKAFSRKF 300  
 MLTEHQRTHT GEKPYECPEC GKAFLLKSRLL NIHQKTHTGE KPYICSECGK GFIOKGNLIV 360  
 HQRIHTGEKP YICNECGKGF IQKTCLIAHQ RFHTGKTPFV CSECGKSCSQ KSLGIKHQRI 420  
 HTGEKPFECB ECGKAFSTKQ KLIVHQRTHT GERPYGCNEC GKAFAYMSCL VKHKRIHTRE 480  
 QGEAAKVENP PAERHSSSLHT SDVMQEKNSA NGATTQVPSV APQTSNLISG LLANRNVVLV 540  
 GQPVVRCAS GDNRGFAQDR NLVNAVNVVV PSVINYLIFY VTENP

Seq ID NO: 215 DNA sequence  
 Nucleic Acid Accession #: NM\_032190.1  
 Coding sequence: 502..1332

1	11	21	31	41	51	
GATTCCGTGT	TCTTGGCCAT	GTTAGCCATA	ATATCCTGTG	CAGTATGTTT	TTCCTGTGCA	60
GAGGCAAAAA	CATATTGGGC	ATATGTTCCC	AAGCCCCCAG	CAGTATGACC	CATACCTTTGG	120
AGTGACACTC	CTCCTAAGAT	TTATCATGAT	TAAGGAGCAT	GGGCTCCAGG	ACCCCTAACT	180
CCACCTGACA	TAGAACAGTT	AGACTCTCAG	AATAATGTCA	TTAATTATAC	CGCTCCATTG	240
GAAGGACTTC	CTTTGTGTGT	CACCACAAAG	ACATCACTCA	GCCATAGCTG	TCTTACAGTT	300
CAAGCTCACA	CATGGTTGAG	TCACTATGGG	AAAATCATGT	ACTTTATTAAG	TCTTGGTTAT	360
ATTAATGTAA	CCGGTGTGCT	AACCAACCAT	TCCTGGCCCA	ATCGCCTTCA	TTGTGCTGAC	420
TATACAGAA	GGATTCCCTT	CAATAGTTCC	TACCCCCCTC	CATAGACCCA	GTGTCTTGCC	480
CCACTGGCTA	GAAACAATC	TATGTTAACT	GGAGACATTG	TGGATTGGGG	ACCTAAAGGC	540
CAATTAGATG	GAAAGAAGA	AAATCAGAAA	TCGTGGCACA	AACCTTGCTG	GCATTGGTGG	600
CAAGCTTTTA	ATGCTTCTTC	TTTATATAAC	ACTGGGATCC	AATCCCAGTC	GGCCGCCCAG	660
ATTGCTTGGC	ATGGAGCAGG	CTTTAGCCCG	CCTCTTCCCTC	AGTGGCATT	TCTAGGGAGG	720
AAAGGACCAA	TCAAAAGAT	GATATGGAAG	GCAGCATTC	CATTTATGAA	TGGCAACATC	780
TGGGTGCGCA	TAATACTATC	CAATAATAGC	AATAGTAAGC	AACACAGTCT	TAATGTTACA	840
TTTGTAAGA	ATATCACCAC	TCAATTTACA	GTTTGTGTTT	TTAATCCTTA	TGTGTTTTTG	900
GCAGCTAAGA	AGGACACAGT	CCAGGTAAAC	AATACCCAAT	TGACCTGTAA	ATCTTGCCAG	960
TTATATCACT	GCATTAACTA	TAGCACATTG	CAAAACACATA	ATATCTCTAC	TTTGATGATT	1020
TTAGGTTGCA	TCCCTGGGCT	ATGGATTCCCT	GTTAATCTGT	CTGAGCCATG	GGCTGCCACA	1080
ATTGCTTTAC	ATTTTGTGAA	ACTTCTTCTA	ACTCAGTTTA	CTCATTGTGT	CCGTAGAGGC	1140
TTAGGCATGA	TAATTTTGTG	TATTGTTTAC	TTGGTCACAC	TAATAATTTT	TGTTGTGATG	1200
TCCTCTGTAG	CTTTGCATAG	TTCTATTCAA	ACAGCTCAGT	ATGTGGAGAA	CTGGACACGC	1260
ACAGTCAACC	AAGGGTGGCT	ACTTGAGAA	AAAATTAACA	CTGAGTTACA	AACTGAAGTG	1320
GCAGTGTAT	AAICCCAGAT	TCTATGGTTA	GGGGAACAAG	TACAAAGCTT	GCAATTGCAG	1380
CAGTAATTGT	GTTGTCAATT	TAATCACACT	CATATTTGTG	TAACCAACTT	AGAATATAAC	1440
CAAAGTGAGT	ATCCATGGGA	TCTTGTGAAA	GCCCATTTGC	AGGGAGCTTT	CACATCCGAC	1500
ATCACCTTTG	ATATTGGTGA	ATTACAAAAC	AAAATCTTGT	ATTTAAATAA	ACAAATTTCA	1560
GAGTTTCAGC	CTTCTTTAGA	AGACTGGACT	GAATTCAGC	AAGGCCTGGA	GAGCGTCAAC	1620
CCTTGGACCT	ATCTAAAGCA	CCACATTAAC	ATCTTATATA	TAGTTCTTGG	ATAATGTTG	1680
TTTTGTCTCT	GCTCTCTGTT	CATAGTCTGT	AAAATCGGAT	GGACTGCCAA	TCGGAGAATG	1740
AAAGCTACCC	AGCCTGGCCT	TACATTCTTT	CACCTAATAC	ATAAACAAGA	AGGGGGAAT	1800
GTTGGGAGCC	AAAAAGGCCA	AAGGGATGGT	GACCAACTCA	GCATTCCACT	GGAGGCTACA	1860
TGATCAAAACA	GCAAACTGTT	TATCATGAAT	ACAGAAATGTG	GGCAAACTCG	CTTCTGTGCC	1920
TGCCCAGAAG	GTTTGTCTAG	GGCCATCGCT	CCCTGGCCCC	GGCTCCTTGA	GGTTATCTAC	1980
TGGGACATCT	AGAGCCTATT	GTTGAGGAA	TGCAGTCTTG	CAAGCCTACT	CTGGACCGAG	2040
CAGCTGACCT	CTTCTTCCAC	ACCCCTTCTC	ACTATCTCTT	TTGCCTAATA	AATATGGAGG	2100
GCTGTGTAAA	GCTCAGGGCC	CTTGTCCACT	AGAGGCAAGG	TGTCCTCTGA	CCCTTCTTCC	2160
AAACAT						

Seq ID NO: 216 Protein sequence  
 Protein Accession #: NP\_115566.1

1	11	21	31	41	51	
MLTGDIVDWG	PKGQLDGKEE	NQKSWHKLW	HWQAFNASS	LYNTGIQSQS	AAQIAWHGAG	60
FSPPLPQWHY	LGRKGPQIKM	IWKAAFPFMN	GNIIWVAILL	NNSNSKQHS	NVTFVKNIIT	120
QFTVCLFNPY	VFLAAKDKQL	QVNNLTQLCK	SCQLYHCINH	STLQTHNIST	LMILGCIPLG	180
WIPVNLSEPW	AATIALHFPV	LLLTQFTHCV	RRGLGMIIFA	IVYLVTLIIS	VVMSSVALHS	240
SIQTAQYVEN	WTRTVNQGWL	LENKINTELO	TEVAVL			

Seq ID NO: 217 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..1566

1	11	21	31	41	51	
ATGGTGAACC	CCAAATCCAC	TTCCTCCCTC	TTCAGGTTAT	GTTTTTTGCT	CCTGAGGAGT	60
CAGAACCTGT	GGGTGGAAGA	GCAAATTCAC	TGCAAAAACA	TATTGGGCAT	ATGTTCCCAA	120
TCCCCAGACA	GTATGGCCTA	TACTTTGGAG	CTCACTCCCTC	CTGAGATTTA	TCACGATCAG	180
GGAGAGTGGG	CTCCAGGACC	CCTAACTCCC	CGTGACATAG	AAAAGTTAGA	CTCTCAGAAC	240
AATGTCATTA	ATTATACCAC	TCCACTGGAA	GGACTCCCTT	TGTTTATCAC	CACAAAGACG	300
TCGTCAGACC	ATAGCTGTCT	TGCAATTCAA	GCTCAAACAT	GGTTGAGTCA	CTATGGAAAA	360
ATTATGTACT	TATTAGGCTC	TGGTCTTATT	AATGTAACCTG	GTGTGCTAAC	CAATCATTTCC	420
CAGTCAGTFC	ACCTTAATGT	TGCTGATTAT	ACAGAAATGA	TTCCATTCAA	TAGTTCTTAC	480
CCCACTCTGT	GGACCCAGTG	TCTTGATCCA	CTGGCTAGTA	AACAATATAT	GTCAACTGAA	540
GACACTGTGG	ATTGGGAACC	TAAAGGTCAA	TTAGATGGAA	AAGGTGAAG	TCAGAAATCA	600
TGGCAAAAC	TTCATCTGGA	TTGGCGGCAA	GCTTTTAATG	CTTCTCTTTT	ATACACACGC	660
AGAATCCAAT	CCCACTCTGC	TGCTCAGATT	GCTTGGCATG	GAGCAGGCTT	TAGCCCACTT	720
CTTCTCAGT	TGCATTATCT	GGGGAGGAAA	GGACCAATTC	AAGAACTAT	ATGGAAGGCA	780
GCACTCCCAT	TTATGAATGG	CAACATCTGG	ATTGGAACAC	TGTCTAATAA	TAGCAATAGT	840
AAGCAACACA	GTCTTAATGT	TGCATTGTGA	AAGAATATCA	CAACTCAGTT	TACAGTTTGT	900
GTTTTTAATC	CTTATGCCTT	TTTGGCAGCT	AAGAAGAACC	AGCTTCAGGT	GGAGAATTGG	960

ACACGCACAG CTGACCAAGC GAGGCTACTT CAGAATAAAA TTAACACTGA GTTACAAACT 1020  
 GAAGTGGCAA TGGTGAATC CATGGTCTGT TGGTTAGGAG AACAGGTACA AAGCTTGCAG 1080  
 TTGCAGCAGC AATTGCGTCA TCATTTTAAT CACATTCATA TTTGCGTAAC TAACTCAGAA 1140  
 TATAACCAAA GTGAGTATCC GTGGGACCTT GTGAAAGCCC ATTTGCAAGG AGCTTTCACA 1200  
 TCCAACATCA CCTTTGATAT TGGTGAATTA CAAAACAAAA TTATTGATT AAATAGGCAA 1260  
 ACTCAAGAAT TTCAGCCTTC TTTAGAAGAC TGGACCGAAT TCCAGGAAGG CCTGGAGAGC 1320  
 CTCACCCCTT GGACCTATCT AAGGCACCAC ATTAACATCT TATATGTAGT TCTTGGAAATA 1380  
 ATGTTTGTTT GTCTCTGTCT TCGGTTTATA GTCTGTAAAA TCGGATGGAC CACCAATTGG 1440  
 AGAATGAGAG CCTCCAGGCC CAGCCTTACA TTCTTTCAAT TAATACATAA ACAGAAAGGG 1500  
 GGATATGCAG GGAGCCAAAG GCCTGTGGGA CGTGACCAAC TCAGCATTCCT GCTGGAGGCT 1560  
 ATATGA

Seq ID NO: 218 Protein sequence  
 Protein Accession #: FGENSESH predicted

1 11 21 31 41 51  
 | | | | |  
 MVNPKSTSSL FRLCFLLLRS QNLWVEEQIQ CKNILGICSQ SPSSMAYTLE LTPPEIYHDQ 60  
 GEWAPGGLTP RDIEKLDSQN NVINYTPLE GLPLFITTKT SLSHSCLAIQ AQTWLSHYGK 120  
 IMYLLGLGSI NVTVGLTNHS QSSHPNCADY TEWIPFNSSY PTLWTQCLDP LASKQYMSTE 180  
 DTVDWEFKQG LDGKGESQKS WHKLHWHWRQ AFNASSLYNS RIQSQAQAI AWHGAGFSPP 240  
 LPQLHYLGRK GPIQETIWK AALPFMNGNIW IGTLSNNSNS KQHSNLNVAFV KNITTQFTVC 300  
 VFNPYAFLLA KKNQLQVENW TRTADQARLL QNKINTELQT EVAMLKSMVL WLGEQVQSLQ 360  
 LQQQLRHHFN HIIKICVTNSE YNQSEYPWDL VKAHLQGAFT SNITFDIGEL QNKIIDLNRQ 420  
 TQEFQPSLED WTEFQEGLES LNPWTYLRHH INILYVVLGI MLFCLCLRFI VCKIGWTTNW 480  
 RMRASQPSLT FFQLIHKQKG GYAGSQRPVG RDQLSILLEA I

Seq ID NO: 219 DNA sequence  
 Nucleic Acid Accession #: FGENSESH predicted  
 Coding sequence: 1..900

1 11 21 31 41 51  
 | | | | |  
 ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60  
 CCGCGCGCGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC 120  
 GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180  
 CGGCCCACTG CGCTGGACAC CTTCTCTGGT ACGTACGTTT AATCGCCCGT GCGGCGCGCT 240  
 GGCTGCGCGC GGGCTGTGCA CCGGGGAGCT GGGGCGGGCG TCTCGGCGGG AGGGCGCAGA 300  
 GGACCCCGGG GAGGAGACTG GAGCAGGCCC CGAGGTGGCG CTGGTGCGGC CCAGGACGCT 360  
 CTTCTAACT CAGGCTCTCC CCGCCCCGCC CCTGCAGTGC AAGTCCTGGT GGTATGGAGCT 420  
 CCGGTGCGCA TTGAGCTCTG GGACACAGCG GGACAGGAGG ATTTTGACCG ACTTCGTTC 480  
 CTTTGCTACC CGGATACCGA TGTCTTCTGT GCGTGCTTCA GCGTGCTGCA GCGCAGCTCC 540  
 TTTCAAAACA TCACAGAGAA ATGGTGCCCC GAGATCGCA CGCACAAACC CCAGGCGCCT 600  
 GTGCTGCTGG TGGGCACCCA GGCCGACCTG AGGGACGATG TCAACGTACT AATTCAGCTG 660  
 GACCAGGGGG GCCGGGAGGG CCCCCTGCCC CAACCCAGG CTCAGGGTCT GGCCGAGAAG 720  
 ATCCGAGCTG GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAACTT GAAGGAAGTA 780  
 TTTGACTCGG ERTATCTCAG TGCCATTGAG CACAAAGCCC GGCTGGAGAA GAAACTGAAT 840  
 GCCAAAGGTG TGCGCACCTT CTCCCGCTGC CGCTGGAAGA AGTTCTTCTG CTTCTGTTGA

Seq ID NO: 220 Protein sequence  
 Protein Accession #: FGENSESH predicted

1 11 21 31 41 51  
 | | | | |  
 MPPRELSEAB PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60  
 RPTALDTFSG TYVQSPVRPR GCGGAVHRGA GAGVSAGRRR GPRGGDWSRP RGGAGAAQDA 120  
 LPNSGSPRPA PAVQVLVDGA PVRIELWDTA GQEDFDRLLS LCYPDTDFVL ACFSVVQPSS 180  
 FQNITEKWL P ERTTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGPVP QPQAQGLAEK 240  
 IRACCYLECS ALTQKNLKEV FDSAILS AIE HKARLEKKLN AKGVRTLSRC RWKKFFCFV

Seq ID NO: 221 DNA sequence  
 Nucleic Acid Accession #: XM\_063832.2  
 Coding sequence: 1..711

1 11 21 31 41 51  
 | | | | |  
 ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60  
 CCGCGCGCGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC 120  
 GCCGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180  
 CGGCCCACTG CGCTGGACAC CTTCTCTGTG CAAGTCCTGG TGGATGGAGC TCCGGTGGCG 240  
 ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTCGTTT CTTTGTCTAC 300  
 CCGGATACCG ATGTCTTCTT GCGGTGCTTC AGCGTGGTGC AGCCAGCTC CTTTCAAAAC 360  
 ATCACAGAGA AATGGCTGCC CGAGATCCGC ACGCACACCC CCCAGGCGCC TGTGCTGCTG 420  
 GTGGGCAACC AGGCCGACCT GAGGGACGAT GTCAACGTAC TAATTCAGCT GGACCAAGGG 480  
 GCGCCGGAGG GCCCCGTGCC CCAACCCAGG GCTCAGGGTC TGGCCGAGAA GATCCGAGCC 540  
 TGTGCTTACC TTGAGTGCTC AGCCTTGACG CAGAAGAAGT TGAAGGAAGT ATTTGACTCG 600  
 GCTATTCTCA GTGCCATTGA GCACAAAGCC CGGCTGGAGA AGAAACTGAA TGCCAAAGGT 660  
 GTGCGCACCC TCTCCCGCTG CCGCTGGAAG AAGTTCTTCT GCTTCGTTTG A

Seq ID NO: 222 Protein sequence  
 Protein Accession #: XP\_063832.1

1 11 21 31 41 51  
 | | | | |

MPPRELSEAE PPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60  
 RPTALDTFSV QVLVDGAPVR IELWDTAGQE DFDRLRLSLCY PDTDVFLACF SVVQPSFQON 120  
 ITEKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGPVPQPQ AQGLAEKIRA 180  
 CCYLECSALT QKNLKEVFD S AILSAIEHKA RLEKKLNAKG VRTLSCRWKF KFCFCV

Seq ID NO: 223 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1161

1 11 21 31 41 51  
 | | | | | |  
 ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG 60  
 TTCCGAGATG ACTTCATTGC CAAGGTGTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTT 120  
 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTCTGTGT TCCACCTCAA GTCTTGAAA 180  
 15 TCCAGCCGGA TTTTCTGTCT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 240  
 CCGTTCGTGA TGGACTACTA TGTGCGGCGT TCAGACTGGA AGTTTGGGGA CATCCCTTGC 300  
 CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 360  
 GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420  
 20 AATTGGACAG CAGCCATCAT CTCTTGCTT CTGTGGGGCA TCACTGTGTG CCTAACAGTC 480  
 CACCTCTGTA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 540  
 AGCATCTGCC ATACCTTCCG GTGGCAGCAA GCTATGTTCC TCCTGGAGTT CCTCTGCCC 600  
 CTGGGCATCA TCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660  
 GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720  
 25 GTCATCTGCT TCCTTCCAG CGTGGTTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT 780  
 TCGGGCAGCG AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTCTT TATCACTCTC 840  
 AGCTTCACCT ACATGAACAG CATGCTGGAC CCCGTGGTGT ACTACTTCTC CAGCCCATCC 900  
 TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 960  
 CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC 1020  
 30 GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080  
 ACCTCAAATA ACCATTCCAA GAAGGGACAT TGTACCAAG AACCAAGCATC TCTGGAGAAA 1140  
 CAGTTGGGAT GTTCATCGA G

Seq ID NO: 224 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | | |  
 MNRHHLQDHF LEIDKKNCCV FRDDFIKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK 60  
 SSRIFLFNLA VADFLLIICL PFLMDNYVRR WDWKFGDIPC RLMLFMLAMN RQGSIIIFLTV 120  
 40 VAVDRYFRVV HPHHALNKIS NRTAAIISCL LWGITVGLTV HLLKKKLIQ NGPANVCISF 180  
 SICTHFRWHE AMFLLEFFLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFIMVVAIVF 240  
 VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SFTYMNSMLD PVVYFSSPS 300  
 FPNFFSTLIN RCLQRKMTGE PDNNRSTSV L TGDPNKTRG APEALMANSG EPWSPSYLGP 360  
 45 TSNHSHKKGH CHQEPASLEK QLGCCIE

Seq ID NO: 225 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1092

1 11 21 31 41 51  
 | | | | | |  
 ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG 60  
 TTCCGAGATG ACTTCATTGT CAAGGTGTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTC 120  
 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTCTGTGT TCCACCTCAA GTCTTGAAA 180  
 55 TCCAGCCGGA TTTTCTGTCT CAACCTGGCA GTGGCTGACT TTCTACTGAT CATCTGCCTG 240  
 CCCTTCTCTG TGGACAACTA TGTGAGGCGT TGGGACTGGA AGTTTGGGGA CATCCCTTGC 300  
 CGGCTGATGC TCTTCATGTT GGCTATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 360  
 GTGGCGGTAG ACAGGTATTT CCGGTGGTGC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420  
 60 AATCGGACAG CAGCCATCAT CTCTTGCTT CTGTGGGGCA TCACTATTGG CCTGACAGTC 480  
 CACCTCTCTG AGAAGAAGAT GCCGATCCAG AATGGCGGTG CAAATTTGTG CAGCAGCTTC 540  
 AGCATCTGCC ATACCTTCCA GTGGCAGCAA GCCATGTTCC TCCTGGAGTT CTTCTGCCC 600  
 CTGGGCATCA TCTGTTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660  
 GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720  
 65 GTCATCTGCT TCCTTCCAG CGTGGTTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT 780  
 TCGGGCAGCG AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTCTT TATCACTCTC 840  
 AGCTTCACCT ACATGAACAG CATGCTGGAC CCCGTGGTGT ACTACTTCTC CAGCCCATCC 900  
 TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 960  
 CCAGATAATA ACCGCAGCAC GAGCGTCGAG CTCACAGGGG ACCCCAACAA AACCAGAGGC 1020  
 70 GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080

Seq ID NO: 226 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | | |  
 MNRHHLQDHF LEIDKKNCCV FRDDFIVKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK 60  
 SSRIFLFNLA VADFLLIICL PFLMDNYVRR WDWKFGDIPC RLMLFMLAMN RQGSIIIFLTV 120  
 80 VAVDRYFRVV HPHHALNKIS NRTAAIISCL LWGITIGLTV HLLKKKMPIQ NGGANLCSF 180  
 SICTHFRWHE AMFLLEFFLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFIMVVAIVF 240  
 VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SFTYMNSMLD PVVYFSSPS 300  
 FPNFFSTLIN RCLQRKMTGE PDNNRSTSV L TGDPNKTRG APEALMANSG EPWSPSYLGP 360  
 TSP

Seq ID NO: 227 DNA sequence  
Nucleic Acid Accession #: NM\_006018  
Coding sequence: 61..1224

```

5      1      11      21      31      41      51
|      |      |      |      |      |
CGCCACTTTG CTGGAGCATT CACTAGGCGA GCGCTCCAT CGGACTCACT AGCCGCACTC 60
ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAATAG ACAAGAAGAA CTGCTGTGTG 120
TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCCGGTGT TGGGGCTGGA GTTTATCTTT 180
GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCTGGAAAA 240
TCCAGCCGGA TTTTCTGTGT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 300
CCGTTCTGTA TGGACTACTA TGTGCGGCGT TCAGACTGGA ACTTTGGGGA CATCCCTTGC 360
CGGCTGGTGC TCTTCACTGT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 420
GTGGCGGTAG ACAGGTATTG CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 480
15 AATTGGACAG CAGCCATCAT CTCTTGCCCT CTGTGGGGCA TCACGTGTGG CCTAACAGTC 540
CACCTCCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 600
AGCATCTGCC ATACCTTCCG GTGGCAGCAA GCTATGTTCC TCCTGGAGTT CCTCCTGCCC 660
CTGGGCATCA TCTGTCTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 720
20 GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 780
GTCATCTGCT TCCTTCCCAG CGTGGTGTGT CGGATCCGCA TCTTCTGGCT CCTGCACACT 840
TCGGGCACGC AGAATGTGTA AGTGATCCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC 900
AGCTTCACCT ACATGAACAG CATGCTGGAC CCGTGGTGTG ACTACTTCTC CAGCCCATCC 960
TTTCCCAACT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 1020
25 CCAGATAATA CCGCAGACAG GAGCGTCGAG CTCACAGGGG ACCCAACAA AACCAGAGGC 1080
GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCC 1140
ACCTCAAATA ACCATTCCAA GAAGGACAT TGTACCAAG AACCAGCATC TCTGGAGAAA 1200
CAGTTGGGCT GTTGATCGA GTAATGTAC TGGACTCGGC CTAAGTGTTC CTGGAACCTT 1260
CAGATTGAGA GAATCTGATT TAGGGAAACT GTGGCAGATG AGTGGGAGAC TGGTTGCAAG 1320
30 GTGTGACCA AGGAATCCTG GAGGAACAGA GAGTAAAGCT TCTAGGCATC TGAAACTTGC 1380
TTTATCTCTG ACGCTCGCAG GACTGAAGAT GGGCAAATTG TAGGCGTTTC TGCTGAGCAG 1440
AGTTGGAGCC AGAGATCTAC TTTGACTTGT TTGGCCTTCT TCCACATCT GCCTCAGACT 1500
GGGGGGGGCT CAGCTCCTCG GGTGATATCT AGCCTGCTTG TGAGCTCTAG CAGGGATAAG 1560
GAGAGCTGAG ATTGGAGGGA ATTGTGTTGC TCCTGGAGGA AGCCAGGCA TCATTAAACA 1620
35 AGCCAGTAGG TCACCTGGCT TCCGTGGACC AATTCACTCT TCAGACAAGC TTAGAGAAAA 1680
TGGACTCAGG GAAGAGACTC ACATGCTTTG GTTAGTATCT GTGTTTCCGG TGGGTGTAAT 1740
AGGGGATTAG CCCCAGAGG GACTGAGCTA AACAGTGTTA TTATGGGAAA GGAAATGGCA 1800
TTGCTGCTTT CAACAGAGCA CTAATGCAAT CCATTCTCTC CTGTTTATA GTAATCTAAG 1860
GGTTGAGCAG TTAACACGGC TTCAAGATAG AAAGCTGTTT CCCACCTGTT TCGTTTACC 1920
40 ATTAAGAGG AAACGTGCCT CTGCCCCACG GGTAGAGGGG GTGCAGGTTT CTCTGGTTT 1980
CTTCGCTTGT GTTCTGTGAC TTACCAAAAA TCTACCACTT CAATAAATTT TGATAGGAGA 2040
CAAAAAAAA A

```

Seq ID NO: 228 Protein sequence  
Protein Accession #: NP\_006009.1

```

45      1      11      21      31      41      51
|      |      |      |      |      |
MNRHHLQDHF LEIDKKNCCV FRDDFIKVL PPVLGLEFIF GLLGNGLALW IFCFHLKSWK 60
SSRIPLFNLA VADFLLIICL PFVMDYVRR SDWNFGDIPC RLVLFMFAMN RQGSIIIFLT 120
50 VAVDRYFRVV HPHHALNKIS NWTAAIISCL LWGITVGLTV HLLKKLLIQ NGPANVCISF 180
SICHTFRWHE AMPLLEFLLP LGIILFCSAR IIWSLRQRQM DRHAKIKRAI TFMVVAIVF 240
VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFITL SFTYMSMLD PVVYFSSPS 300
FPNFFSTLIN RCLQRKMTGE PDNNRSTSV LITGDPNKRTRG APEALMANSG EPWSPSYLGP 360
55 TSNHSHKKGH CHQEPASLEK QLGCCIE

```

Seq ID NO: 229 DNA sequence  
Nucleic Acid Accession #: NM\_014398.1  
Coding sequence: 64..1314

```

60      1      11      21      31      41      51
|      |      |      |      |      |
GGCACCATTG CCGGGCCTGC CCGGACTTCG CCGCACGCTG CAGAACCTCG CCCAGCGCCC 60
ACCATGCCCC GGCAGCTCAG CGCGGCGGCC GCGCTCTTCG CGTCCCTGGC CGTAATTTTG 120
65 CACGATGGCA GTCAAAATGAG AGCAAAAGCA TTTCCAGAAA CCAGAGATTA TTCTCAACCT 180
ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACAGC TAAGCAAGCA 240
CCTCACCAAA CTTTAGCAGC AAGATTCAAT GATGTCATA TCACCTTTCA AACAGCGGCC 300
ACAGTAAAAA TTCCAACAAC TACCCAGCA ACTACAAAAA AACTGCAAC CACCAGCCCA 360
ATTACTTACA CCCTGGTCAC AACCCAGGCC ACACCAACA ACTCACACAG AGCTCTCTCA 420
70 GTTACTGAAG TTACAGTCGG CCTAGCTTA GCCCTTATT CACTGCCACC CACCATCACC 480
CCACCAGCTC ATACAGCTGG AACAGTTTCA TCAACCGTCA GCCACACAAC TGGGAACACC 540
ACTCAACCCA GTAACAGAC CACCCTTCCA GCAACTTTAT CGATAGCACT GCACAAAAGC 600
ACAACCGGTC AGAAGCCTGA TCAACCCACC CATGCCCCAG GAACAACGGC AGCTGCCACC 660
AATACCAACC GCACAGCTGC ACCTGCCTCC ACGGTTCTCG GGCCACCCCT TGCACCTCAG 720
CCATCGTCAG TCAAGACTGG AATTATCAG GTTCTAAACG GAAGCAGACT CTGTATAAAA 780
75 GCAGAGATGG GGATACAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAAATCC 900
AACCTTCTGT TGAATTTTCA GGGCGGATTT GTGAATCTCA CATTTACCAA GGATGAAGAA 960
TCATATTATA TCAGTGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
CAAGGAATTA AACATGCGGT GGTGATGTTT CAGACAGCAG TCGGGCATTC CTTCAAGTGC 1080
80 GTGAGTGAAC AGAGCCTCCA GTTGTGAGCC CACCTGCAGG TGAAACAAAC CGATGTCCAA 1140
CTTCAAGCCT TTGATTTTGA AGATGACCAC TTTGGAAATG TGGATGAGTG CTCGTCTGAC 1200
TACACAATTG TGTCTCTGTG GATTGGGGCC ATCGTGGTTG GTCTCTGCCT TATGGGTATG 1260
GGTGTCTATA AAATCCGCCT AAGGTGTCAA TCATCTGGAT ACCAGAGAA CTAATGTGTG 1320
CCCGGGGGGA ATGAAAATAA TGAATTTAG AGAACTCTTT CATCCTTACC AGGATGGATG 1380

```

5 TTGGGAAATT CCCTCAGAGT GTGGGTCCTT CAAACAATGT AAACCACCAT CTTCTATTCA 1440  
 AATGAAGTGA GTCATGTGTG ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACTTTT 1500  
 GTTTATTTTA TGAAAGATAT AGTGAGCTGT TTATTTTCTA GTTTCCTTTA GAATATTTTA 1560  
 GCCACTCAAA GTCACATTTT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620  
 AGCCTTCAAA TTATAAACC AAGGTCAATT GTAACATAA CTAAGTGTG TGCATTGAAG 1680  
 ATTTTATTTT ACCCTTGATC TTAACAAAGC CTTTGCTTTG TTATCAAATG GACTTTCAGT 1740  
 GCTTTTACTA TCTGTGTTT ATGGTTTCAT GTAACATACA TATTCCTGGT GTAGCACTTA 1800  
 10 ACTCCTTTTC CACTTTAAAT TTGTTTTGT TTTTGGAGC GGAGTTTCAC TCTTGTACC 1860  
 CAGGCTGGAG TACAGTGGCA CGATCTCGGC TTATGGCAAC CTCCGCCTCC CGGGTTCAG 1920  
 TGATTCTCCT GCTTCAGCTT CCCGAGTAGC TGGGATTACA GGCACACACT ACCACGCTG 1980  
 GCTAATTTT GTATTTTAT TATAGACGGG TTTCACCATG TTGGCCAGAC TGGTCTTGAA 2040  
 CTCTTGACCT CAGGTGATCC ACCCACCTCA GCCTCCCAA GTGCTGGGAT TACAGGCATG 2100  
 AGCCATTGCG CCCGCGCTTA AATGTTTTT TTAATCATCA AAAAGAACA CATATCTCAG 2160  
 15 GTTGTCTAAG TGTTTTTATG TAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTTAT 2220  
 CTGTGATGACT CCTGCTCCAG AATTGCTAGA CTAAGAATTA GGTGGCTACA GATGGTAGAA 2280  
 CTAACAATA AGCAAGAGAC AATAATAATG GCCCTTAAT ATTAACAAAG TGCCAGAGTC 2340  
 TAGGCTAAGC ACTTTATCTA TATCTCATTT CATCTCACA ACTTATAAGT GAATGAGTAA 2400  
 ACTGAGACTT AAGGGAAGT AATCACTTAA ATGTCACCTG GCTAACTGAT GGCAGAGCCA 2460  
 20 GAGCTTGAAT TCATGTGGT CTGACATCAA GGTCTTTGGT CTTCTCCCTA CACCAAGTTA 2520  
 CCTACAAGAA CAATGACACC ACACTCTGCC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580  
 CTACCTTACA GGGAAATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640  
 AGCTTTGCAG ATAACAAAT AGCCTATCCT TAATAATCC TCCACTCTCT GGAAGGAGAC 2700  
 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTTA TGGGATTGCT TAGCTGGGCT 2760  
 25 GTAAAGATGA AGGCATCAA TAAACTCAA GTATTTTAA ATTTTGTGA TAATAGAGAA 2820  
 ACTTCGCTAA CCAACTGTTT TTTCTTGAGT GTATAGCCCC ATCTTGTGGT AACTTGCTGC 2880  
 TTCTGCACTT CATATCCATA TTCTCTATTG TTCACCTTAT TCTGTAGAGC AGCCTGCCAA 2940  
 GAATTTTATT TCTGCTGTTT TTTTGTCTGC TAAAGAAAGG AACTAAGTCA GGATGTTAAC 3000  
 AGAAAAGTCC ACATAACCCT AGAATCTTGA GTCAAGGAAT AATTCAAGTC AGCCTAGAGA 3060  
 30 CATGTTGAC TTTCTCATG TGTTCCTTA TGACTCAGTA AGTTGGCAAG GTCTGCACTT 3120  
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAACT TACTTTGG

Seq ID NO: 230 Protein sequence

Protein Accession #: NP\_055213.1

35 1 11 21 31 41 51  
 | | | | | |  
 MPROLSAAAA LFLASLAVILH DGSQMRKAF PETRDYSQPT AAATVQDIKK PVQPPAKQAP 60  
 HQTLAARFMD GHITFQTAAT VKIPTTTPAT TKNTATTSPI TYTLVTTQAT PNNSHAPPV 120  
 40 TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHTTGNTT QPSNQTTLPA TLSIALHKST 180  
 TGQKPDQPTH APGTAAAHN TTRTAAPAST VPGPTLAPQP SSVKTGIYQV LNSRLCIKA 240  
 EMGIQLIVQD KESVFSRRY FNIDPNATQA SGNCGRKSN LLLNFQGGFV NLFTTKDEES 300  
 YYISEVGAYL TVSDPEVYQ GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTDDVQL 360  
 QAFDFEDDFH GNVDECSSDY TIVLPVIGAI VVGLCLMGMG VYKIRLRCSQ SGYQRI

Seq ID NO: 231 DNA sequence

Nucleic Acid Accession #: NM\_005409.3

Coding sequence: 94..378

50 1 11 21 31 41 51  
 | | | | | |  
 TTCCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60  
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120  
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180  
 55 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCCTCC 240  
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT 300  
 AAAGGACAA GATGCTTAAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360  
 GAAAGAAAAG ATTTTAAAA ATATCAAAC ATATGAAGTC CTGGAAGAGG GCATCTGAAA 420  
 AACCTGAAC AAGTTAACT GTGACTACTG AATGACAAAG AATTCTACAG TAGGAAACTG 480  
 60 AGACTTTTCT ATGGTTTTGT GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540  
 GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCTGAAT GAATGACAAT CAGAATTCCA 600  
 CTGCCCAAAG GAGTCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660  
 GGTTACCATG GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTGTGAT ATACATTCAT 720  
 GCATTCTCAG CTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780  
 65 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840  
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900  
 CATCTATGTC TCGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAATACAC ACTTCTTTCC 960  
 CCAAAATATCA TGTAGACAT CAATATGTAG GGAAACATTC TTATGCATCA TTTGGTTTGT 1020  
 TTTATAACCA ATTCATTAAA TGTAAATTCAT AAAATGTACT ATGAAAAAA TTATACGCTA 1080  
 70 TGGGATACTG GCAACAGTGC ACATATTTCA TAACCAAAAT AGCAGCACCG GTCTTAATTT 1140  
 GATGTTTTTC AACTTTTAT CATTGAGATG TTTTGAAAGCA ATTAGGATAT GTGTGTTTAC 1200  
 TGACTTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGAC ACATTGAAA 1260  
 TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAATG TATACCTAGC 1320  
 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380  
 75 TTGTTTCATG CTATATACG TAAAAATTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440  
 GTCATTTTTT TCTCTAATAA ACTACCACAA CTTTCTTTT TTAATAAAAA AAA

Seq ID NO: 232 Protein sequence

Protein Accession #: NP\_005400.1

80 1 11 21 31 41 51  
 | | | | | |  
 MSVKGMAIAL AVILCATVVQ GFPMFKRGRG LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60  
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF



Seq ID NO: 233 DNA sequence  
Nucleic Acid Accession #: NM\_000577.1  
Coding sequence: 41..520

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      GGCACGAGGG  GAAGACCTCC  TGTCTATCA  GGCCCTCCCC  ATGGCTTTAG  AGACGATCTG  60
      CCGACCTCT  GGGAGAAAAT  CCAGCAAGAT  GCAAGCCTTC  AGAATCTGGG  ATGTTAACCA  120
10     GAAGACCTTC  TATCTGAGGA  ACAACCAACT  AGTTGCCGGA  TACTTGCAAG  GACCAAATGT  180
      CAATTTAGAA  GAAAAGATAG  ATGTGGTACC  CATTGAGCCT  CATGCTCTGT  TCTTGGGAAT  240
      CCATGGAGGG  AAGATGTGCC  TGTCTGTGT  CAAGTCTGGT  GATGAGACCA  GACTCCAGCT  300
      GGAGGCAGTT  AACATCACTG  ACCTGAGCGA  GAACAGAAAG  CAGGACAAGC  GCTTCGCCTT  360
      CATCCGCTCA  GACAGTGGCC  CCACCACAG  TTTTGAGTCT  GCCGCCTGCC  CCGTTGGTT  420
      CCTCTGCACA  GCGATGGAAG  CTGACCAGCC  CGTCAGCCTC  ACCAATATGC  CTGACGAAGG  480
15     CGTCATGCTC  ACCAAATTCT  ACTTCCAGGA  GGACGAGTAG  TACTGCCAG  GCCTGCCTGT  540
      TCCCATTCTT  GCATGGCAAG  GACTGCAGGG  ACTGCCAGTC  CCCCTGCCCC  AGGGCTCCCG  600
      GCTATGGGGG  CACTGAGGAC  CAGCCATTGA  GGGGTGGACC  CTCAGAAGGC  GTCACAACAA  660
      CTGGTGCACA  GGACTCTGCC  TCCTCTTCAA  CTGACCAGCC  TCCATGCTGC  CTCAGAATG  720
      GTCTTTCTAA  TGTGTGAATC  AGAGCACAGC  AGCCCCTGCA  CAAAGCCCTT  CCATGTCGCC  780
20     TCTGCATTCA  GGATCAAACC  CCGACCACCT  GCCCAACCTG  CTCTCCTCTT  GCCACTGCCT  840
      CTTCTCCCT  CATTCACCT  TCCCATGCC  TGGATCCATC  AGGCCACTTG  ATGACCCCA  900
      ACCAAGTGGC  TCCACACCC  TGTTTTACAA  AAAAGAAAAG  ACCAGTCCAT  GAGGGAGGTT  960
      TTTAAGGGTT  TGTGGAAAAT  GAAAATTAGG  ATTCATGAT  TTTTTTTTTT  CAGTCCCGT  1020
25     GAAGGAGAGC  CCTTCATTG  GAGATTATGT  TCTTCGGGG  AGAGGCTGAG  GACTTAAAT  1080
      ATTCTGCTAT  TTGTGAAATG  ATGGTGAAAG  TAAGTGGTAG  CTTTCCCTT  CTTTCTCTC  1140
      TTTTCTGTG  ATGTCCCAAC  TTGTAAAAAT  TAAAAGTTAT  GGTACTATGT  TAGCCCCATA  1200
      ATTTTCTTT  TCCTTTTAAA  ACACTTCCAT  AATCTGGACT  CCTCTGTCCA  GGCACTGCTG  1260
      CCCAGCCTCC  AAGCTCCAT  TCCACTCCAG  ATTTTTTACA  GCTGCCTGCA  GTACTTTACC  1320
30     TCCTATCAGA  AGTTTCTCAG  CTCCCAAGGC  TCTGAGCAAA  TGTGGCTCCT  GGGGGTCTT  1380
      TCTTCTCTG  CTGAAGGAAT  AAATGTCTCC  TTGACATTGT  AGAGCTTCTG  GCACCTGGAG  1440
      ACTGTATGA  AAGATGGCTG  TGCCTCTGCC  TGTCTCCCC  ACCAGGCTGG  GAGCTCTGCA  1500
      GAGCAGGAAA  CATGACTCGT  ATATGTCTCA  GGTCCCTGCA  GGGCCAAGCA  CCTAGCCTCG  1560
      CTCTTGCGAG  GTACTCAGCG  AATGAATGCT  GTATATGTTG  GGTGCAAAAG  TCCTACTTTC  1620
35     CTGTGACTTC  AGTCTCTGTT  TACAATAAAA  TCTTGAATAA  GCCTAAAAAA  AAAAAAAAAA  1680
      AAAAAAAAAA  AAAAAAAAAA  AAAAAAAAAA  AAAAAA

```

Seq ID NO: 234 Protein sequence  
Protein Accession #: NP\_000568.1

```

40     1      11      21      31      41      51
      |      |      |      |      |      |
      MALETICRPS  GRKSSKMQAF  RIWDVNQKTF  YLRNNQLVAG  YLQGPVNLE  EKIDVVPIEP  60
      HALEFLGIHGG  KMLCLSCVKS  DETRLQLEAV  NITDLSENRK  QDKRFAFIRS  DSGPTTSFES  120
45     AACPGWFLCT  AMEADQPVS  L  TNMPDEGVMV  TKFYFQEDE

```

Seq ID NO: 235 DNA sequence  
Nucleic Acid Accession #: NM\_001840.1  
Coding sequence: 149..1567

```

50     1      11      21      31      41      51
      |      |      |      |      |      |
      GGGGACTACG  GAGAGCTCTG  CAGGGAGCCG  AGGCCCCCGC  CCGGGCCAAG  GGAGCTTCTG  60
      TCCCGAGGAC  CAGGGGATGC  GAAGGGATTG  CCCCTGTGG  GTCACCTTCT  CAGTCATTTT  120
55     GAGCTCAGCC  TAATCAAAGA  CTGAGGTTAT  GAAGTCGATC  CTAGATGSCC  TTGCAGATAC  180
      CACCTTCCGC  ACCATCACCA  CTGACCTCCT  GTACGTGGGC  TCAAATGACA  TTCAGTACGA  240
      AGACATCAAA  GGTGACATGG  CATCCAAATT  AGGGTACTTC  CCACAGAAAT  TCCCTTTAAC  300
      TTCCTTTAGG  GGAAGTCCCT  TCCAAGAGAA  GATGACTGCG  GGAGACAACC  CCCAGCTAGT  360
      CCCAGCAGAC  CAGGTGAACA  TTACAGAATT  TTACAACAAG  TCTCTCTCGT  CCTTCAAGGA  420
      GAATGAGGAG  AACATCCAGT  GTGGGAGAAA  CTTTATGGAC  ATAGAGTGT  TCATGGTCTC  480
60     GAACCCACG  CAGCAGCTGG  CCATTGCACT  CCTGTCCCTC  ACGCTGGGCA  CCTTCACGGT  540
      CCTGGAGAAC  CTCCTGGTGC  TGTGCGTCAT  CCTCCACTCC  CGCAGCCTCC  GCTGCAGGCC  600
      TTCCTACCAC  TTCATCGGCA  GCCTGGCGGT  GGCAGACCTC  CTGGGGAGTG  TCATTTTGT  660
      CTACAGCTTC  ATTGACTTCC  ACGTGTTC  CCGCAAAGAT  AGCCGCAACG  TGTTCCTGTT  720
      CAAACTGGGT  GGGGTACAGG  CCTCCTTCA  TGCCTCCGTG  GGCAGCCTGT  TCCTCACAGC  780
65     CATCGACAGG  TACATATCCA  TTCACAGGCC  CCTGGCCTAT  AAGAGGATTG  TCACCAGGCC  840
      CAAGGCCGTG  GTGGCGTTTT  GCCTGATGTG  GACCATAGCC  ATTGTGATCG  CCGTGTGCC  900
      TCTCTGGGC  TGGAACTGCG  AGAAACTGCA  ATCTGTTTGC  TCAGACATTT  TCCACACAT  960
      TGATGAAACC  TACCTGATGT  TCTGGATCGG  GGTCAACAGC  GTACTGCTTC  TGTTCATCGT  1020
70     GTATGCGTAC  ATGTATATTC  TCTGGAAGGC  TCACAGCCAC  GCCGTCCGCA  TGATTACGCG  1080
      TGGCACCAG  AAGAGCATCA  TCATCCACAC  GTCTGAGGAT  GGGAGGGTAC  AGGTGACCCG  1140
      GCCAGACCAA  GCCCGCATGG  ACATTAGGTT  AGCCAAGACC  CTGGTCCTGA  TCCTGGTGGT  1200
      GTTGATCATC  TGCTGGGGCC  CTCTGCTTGC  AATCATGGTG  TATGATGTCT  TTGGGAAGAT  1260
      GAACAAGCTC  ATTAAGACGG  TGTTTGCATT  CTGCAGTATG  CTCTGCCTTC  TGAACCTCC  1320
75     CGTGAACCCC  ATCATCTATG  CTCTGAGGAG  TAAGGACCTG  CGACACGCTT  TCCGGAGCAT  1380
      GTTTCCTCT  TGTGAAGGCA  CTGCGCAGCC  TCTGGATAAC  AGCATGGGGG  ACTCGGACTG  1440
      CCTGCACAAA  CACGCAACCA  ATGCAGCCAG  TGTTCACAGG  GCCGCAGAAA  GCTGCATCAA  1500
      GAGCAGGTC  AAGATTGCCA  AGGTAACCAT  GTCTGTGTCC  ACAGACACGT  CTGCCAGGCC  1560
      TCTGTGAGCC  TGATGCCTCC  CTGGCAGCAC  AGGAAAAGAA  TTTTTTTTTT  TAAGCTCAA  1620
80     ATCTAGAAGA  GTCATATTGC  TCCTTGGTTA  TATTTTTTTA  ACTTTACCAT  GCTCAATGAA  1680
      AAGGTGATTG  CCACATGTCA  CTTATTGTCT  TAGTTTCCGT  TGGGCTAAT  CTTCCGGGGT  1740
      TCGTAGGAAA  CCTTT

```

Seq ID NO: 236 Protein sequence  
Protein Accession #: NP\_001831.1

	1	11	21	31	41	51	
5	MKSILDGLAD	TTFRITITDL	LYVGSNDIQY	EDIKGDMSK	LGYFPQKFPL	TSFRGSPFQE	60
	KMTAGDNPQL	VFPADQVNITE	FYNKSLSSFK	ENEENIQCGE	NFMDIECFMV	LNPSQQLAIA	120
	VLSLTGLTFT	VLENLLVLCV	ILHSRSLRCR	PSYHFIGSLA	VADLLGSVIF	VYSFIDFHFV	180
	HRKDSRNVFL	FKLGGVTASF	TASVGSFLFT	AIDRYISIHR	PLAYKRIVTR	PKAVVAFCLM	240
	WTIAIVIAVL	PLLGNWCEKL	QSVCSDFPH	IDETYLMEWI	GVTSVLLLF	VYAYMYILWK	300
10	AHSHAVRMQ	RGTKSIIH	TSDEGKVQVT	RPDQARMDIR	LAKTLVLILV	VLIICWGPLL	360
	AIMVYDVFGK	MNKLIKTVFA	FCSMLCLLNS	TVNPIIYALR	SKDLRHAERS	MFPSCGTAQ	420
	PLDMSMGDS	CLHKHANNAA	SVHRAAESCI	KSTVKIAKVT	MSVSTDTSAE	AL	

Seq ID NO: 237 DNA sequence

Nucleic Acid Accession #: NM\_016083.2

Coding sequence: 64..1482

	1	11	21	31	41	51	
20	GATTGCCCCC	TGTGGGTCAC	TTTCTCAGTC	ATTTTGAGCT	CAGCCTAATC	AAAGACTGAG	60
	GTTATGAAGT	CGATCCTAGA	TGGCCTTGCA	GATACCACTT	TCCGCACCAT	CACCACTGAC	120
	CTCCTGTACG	TGGGCTCAAA	TGACATTCAG	TACGAAGACA	TCAAAGGTGA	CATGGCATCC	180
	AAATTAGGGT	ACTTCCCA	GAAATTCCTT	TTAACTTCCT	TTAGGGGAAG	TCCCTTCCAA	240
	GAGAAGATGA	CTGGGGGAGA	CAACCCCAAG	CTAGTCCCA	CAGACCAGGT	GAACATTACA	300
25	GAATTTTACA	ACAAGTCTCT	CTCGTCTTC	AAGGAGAATG	AGGAGAACAT	CCAGTGTGGG	360
	GAGAACTTCA	TGGACATAGA	GTGTTTCATG	GTCTTGAACC	CCAGCCAGCA	GCTGGCCATT	420
	GCAGTCTGT	CCCTCACGCT	GGGCACCTTC	ACGGTCCCTG	AGAACCTCCT	GGTGTCTGTC	480
	GTCATCTCTC	ACTCCCGAG	CCTCCGCTGC	AGGCCTTCCT	ACCACTTCAT	CGGCAGCTCG	540
	GCGGTGGCAG	ACCTCCTGGG	GAGTGTCAAT	TTTGTCTACA	GCTTCATGTA	CTTCCACGTG	600
30	TTCACCCGCA	AAGATAGCCG	CAACGTGTTT	CTGTTCAAAC	TGGGTGGGGT	CACGCCCTCC	660
	CTCACTGCTG	CCGTGGGAG	CCTGTTCTTC	ACAGCCATCG	ACAGGTACGT	ATCCATTAC	720
	AGGCCCTGG	CCTATAAGAG	GATTGTCAAC	AGGCCCAAGG	CCGTGGTGGC	GTTTGTGCTG	780
	ATGTGGACCA	TAGCCATTGC	GATCGCCGTG	CTGCCTCTCC	TGGGCTGGAA	CTGCGAGAAA	840
	CTGCAATCTG	TTTGCTCAGA	CATTTTCCCA	CACATTGATG	AAACCTACCT	GATGTTCTGG	900
35	ATCGGGGTCA	CCAGCGTACT	GCTTCTGTTC	ATCGTGTATG	CGTACATGTA	TATTCTCTGG	960
	AAGGCTCAG	GCCAGCCGCT	CCGCATGATT	CAGCGTGGCA	CCCAGAAGAG	CATCATCATC	1020
	CACACGTCTG	AGGATGGGAA	GGTACAGGTG	ACCCGCCAG	ACCAAGCCCG	CATGGACATT	1080
	AGGTTAGCCA	AGACCCTGGT	CCTGATCCTG	GTGGTGTGTA	TCATCTGCTG	GGGCCCTTTG	1140
	CTTGCAATCA	TGGGTATATG	TGTCTTTGGG	AAGATGAACA	AGCTCATTA	GACGGTGTTC	1200
40	GCATTTCTGA	GTATGCTCTG	CCTGCTGAAC	TCCACCGTGA	ACCCCATCAT	CTATGCTCTG	1260
	AGGAGTAAGG	ACCTGCGACA	CGCTTTCCGG	AGCATGTTTC	CCTCTTGTGA	AGGCACTGCG	1320
	CAGCCTCTGG	ATAACAGCAT	GGGGGACTCG	GACTGCCTGC	ACAAACACGC	AAACAATGCA	1380
	GCCAGTGTTC	ACAGGCGCGC	AGAAAGCTGC	ATCAAGAGCA	CGGTCAAGAT	TGCCAAGGTA	1440
	ACCATGTCTG	TGTCCACAGA	CACGTCTGCC	GAGGCTCTGT	GAGCCTGATG	CCTCCCTGGC	1500
45	AGCACAGGAA	AAGAATTTT	TTTTTAAGC	TCAAAATCTA	GAAGAGTCTA	TTGTCTCCTT	1560
	GGTTATATTT	TTTTAACTTT	ACCATGCTCA	ATGAAAAGGT	GATTGTCAAC	ATGATCACTT	1620
	ATCAGTTTGC	TAATGTTTCC	ATAGTTTAGG	TACTCAAAC	CCATTCTCCA	GGGGTTTACA	1680
	GTGAAGAAAG	CCGTGTGTTT	AAGTACTGA	ACGATCCTTC	AAAGTCTCAA	TGAATAGGTA	1740
	GGGAAACCTT	TGGCTACACA	ATTGGAAGTC	TAAGAACCCA	TGGAAAAATG	CCATCAAATG	1800
50	AATAATGCTT	TTGTAACCA	AACTTTCACT	ATAATGTGAA	ATGTAACGTG	CCGTAGTATC	1860
	AGAGATGCTT	ATTTTACAAA	GTTATAGTAC	TAGAGATATT	TTGTAAAATG	TATTATGTCC	1920
	TGTGAGATGT	GTATCAGTGT	TTATGTGCTA	TTAATATTTG	TTTAGTTTCA	CAAAACTGAA	1980
	AGGTAGACTT	TTATGAGAAC	AATGGACRAG	CAGTGGATAC	GTGTCAATGT	GTGCACTTTT	2040
	TTTCTATATT	ATTGCCCATG	ATATAACTTT	AGAAATAAAC	CTTAATATTT	CTTCAATAT	2100
55	CTCTATTATA	TTTTGACACT	GAAATAACCG	TAAAGGTTTA	TTTTTCTGTT	ACCTCAACAA	2160
	GAAGAATTTG	AAGACTTCAA	AATATTGAGC	AGAATTTCAT	CATACTTAAA	AATTTATTAG	2220
	CCCTGCATTT	TCATAGGAAG	ACACATTATC	TTCTGGACTA	TAGCTGTTCT	AATGGATTAT	2280
	AATCAGAAAT	GAAGAGAGAA	AGCATATTGA	CTTTTTTTGA	GCGACATCTC	TGACTTTCTT	2340
	TAGTCTTTAG	CTATTACTGG	ATCTCTTAAG	ACAGCATGTG	TAACTCTTAA	TGTATATCGT	2400
60	TATCACTGTG	CAGTGTCTGT	TTACTTGAAT	AGTATTGTGT	TCCTATATTC	CAGGTTTAA	2460
	TAGATTTTCA	GCCTGGGTGG	CCAAACAACA	GTCTTCATTT	TTTTTAATTG	AAAAGAAAGTA	2520
	GTGTCTGGAT	CAGTAAAAAT	ATACTGTGTG	TGAGTGTGAA	TATAAATGTG	TGTATGTGTG	2580
	TTTCTGTCCG	TAACGTGTTAC	AGTAATGTCA	TAAAGTGAGA	AAACTGTGAC	CAAGTATAAA	2640
	CTTTTACCAC	TGCTGTCACT	CTTGACATG	GATTCAAGTT	CTAAAATTGA	GTTCTTCTGT	2700
65	TAATCTTGTT	GATAAAAATA	CTGACTCCAA	CCATTCAAAA	ATTTCAACCC	ATCCCTCCTT	2760
	AAGAGATTGG	ATCAAGTATT	ACTAAATTGA	CCTTTAGGTA	TTACACAAGA	CCAGTGCTTA	2820
	GCAAAAAATA	ATGACAGGCA	TCCAAGGAAG	GGATGTATTT	GTAGTGTAT	TGCCAGGAAA	2880
	GGAGAGTACT	TTGGTTTCTG	AGCACCGAAT	ATTGAGCAAT	ATGTCAGTCA	CTAAAAGGAA	2940
	GACAGTTCTA	CAGAAAAACA	AATGGTAACA	TTTTTCAATA	GCGTGTGTAG	ATAGTATGCA	3000
70	CTATATACAT	CACGTAAAG	TAGGACTATC	ACACCAGGCC	CATGTGGCTA	AAAAAGCTGA	3060
	ATCAGACAGT	GGATGAGACA	CACAACGGCA	GTGAAGAACC	GATACACTTG	GCATTGACGT	3120
	CTAGCTATGC	TGTATCTGTG	CTTTGCCAC	ATGCCCTTGG	TGACAGCTGA	GCACCCAGCT	3180
	CTGTCTTGTT	AGGTTTGGGC	TAAGGAACAA	ATCTCTCCTT	TGCTCGTGGT	TAGCAAGATA	3240
	CACTCAAGCA	TGAAGATAAA	CACAGCTGCT	TTCTTCTTAC	ACCCCGGTCT	CATGCTCCTT	3300
75	AATGGCGCCA	TGGGTGCTTG	TTGGGCCTTT	TTCCAGTAAG	GAATGATATT	GCTGAAGAA	3360
	CTACTTAAAC	CTGACAAAT	TTAATTATA	TCTCTCTTA	TACAGATAAA	ACATGACTCC	3420
	TACAAGGCC	CAAGGTTTAC	ATAGTCTGAA	GTGAAGTACA	GAGCTGGCAT	CTATCTGGTG	3480
	ATTTCTAGCT	CTCGAGATAC	CCAAGCAGCC	TGATGGGGCA	GTTCCCTTTC	TTACGGTTCA	3540
	CGCTCTAAGG	CAGGATGTGG	CTTATGAGAT	ACTTTGCATT	GTCTGTCTGC	ACACCTTGAA	3600
80	TCTGCTGCT	GGCTCCCTTA	CTTTACCTCT	CTGTCAATGC	CAGATGAAGG	CTCAGGGTGC	3660
	TAGAGGATTA	GTAAGATCTC	TTTCTAAAGA	CAGGAGAGAT	TATTTACAAG	AAGAACTCAC	3720
	CAGGGTTTAG	TTTGCAATTA	AGAATTGCCA	GTCTTTTGTC	CTGCATCATC	TTGAACATTA	3780
	ATCCACATGT	TTCAGAGCTC	ACCAGGCAGT	ACCAATGCTC	TTTTACAGC	TATGAAGAGC	3840
	TAGAGAAAT	CTTGTTATGG	TAGAAAAAT	TCACGGTTCA	TTTTTGAAAC	TGCATTTGTG	3900
	CGTATGCAGT	GTAGATTTTA	TAGTGTGTTG	TGCTTTCAAG	ATCTAAATCA	TATATAATA	3960

ATTAAGGGAC AATGGGGCTG ACAGCACTAA ACTTGGTGCT TATTGATATT CTAAGAAATA 4020  
 TCTGTGAAAT ATCATCACGT ATGTTATACA ACCTTCATTT AAAAAGGTTT AAAACTAGTT 4080  
 AGATTCACTT TGACACTTTT CATATCATTT CTTAACCCAA GTGACGAAAA CATTGTCCCC 4140  
 AATGAATATA CTCATTAGAA TTACCATTTG TTAATATCAC TCATTAATTA ACCCCATAAT 4200  
 TAGATCCATT AATTTAAATG ATTTAAATT AAGTAAGTTT TATAAGGTCT GACATCAGAG 4260  
 GTATCTTACT TTCTCTGAG GATGATGTAC TTGCCCTGAC CATGCATTTT ACCATCACAC 4320  
 ATGTTCAGAA AGGGCCAAAT TCCCAACCTG CTCATTTTTT TTTTATCAG AGTCATGATG 4380  
 AATCAGTCCT AGAATGTTTC ATTTGCACAA GTAGGGCTGC CTCCAAGAGG AACCTCTGAT 4440  
 TTATTTTGTA TGAATATAT GTGAAAGGAT ATGAATCTGA GAGATGCTGT AGACATCTGT 4500  
 CCTACACTTG AGATGATTTT CAAGCCTCTC TGGCACTTTG AGTTAAGTCT ATCTGGTATT 4560  
 AAATGCCAAG GACCTTTTGC TGCCTAAATC CACTCTGCAG GAAATAGGCC CAACCCACAG 4620  
 ATGAGAATTA GGCCCTGGAT GAGTAGCGCT ATAGTTACTG TCCTGTTGAT TAATTTCTGC 4680  
 CATTTCATGT CCATAAAGA GACCACCCAT ATCATGCACA CAATTAGATT TCTCACACTC 4740  
 TAACGTGATA TTTGTATGAT ATTTTAAAT CTCTTAAATG CTGGGCAATG GCTATTAAAC 4800  
 ATTAATGTCT TTGCACTGGC CTCTGATGA AATGTTAACA ATGCCTATTG TAATATAGAA 4860  
 AAAAACATTCT TATCTACTGA TTTGGGCTGA ATGTATGTAA ATAGGTTTCT AAAAAGTCAG 4920  
 ATGTTTGGAG AGTGGGCTAC AAATCAGTAA TTTTCGGGTG GGAGAGTTTC TTTACATTGC 4980  
 CGTGGCATCT TAAAGCTAT CTTCATGTAA ATTGACTGTA CTAGGCTTAC TGGGGATCAG 5040  
 AGTTCCTAAG AAAGGAAACC TTTTCTTGTA TCTGGATTCA AATTTATTTC CAATGTTTCA 5100  
 AGCGGGAAC ATGACTCTTT ATTGTCTGTA AATCTAACAT TATTACTTTT CCTCTTAGAA 5160  
 GAATATTGTA TTGTTAGAGC TTTGTTGAGC TGGTAACATC GTTGCAACCA CTGCAATATC 5220  
 TTCGTTAGTA ATCTGTATAA TACTTTGTAT ACAAGTACTG GTAAGATTGT TATTAAATGT 5280  
 AGCTTCAGTC ATTAAATTAC TATAGCAAAG TAGTACTTCT TCTGTAAATAT TTACAATGTA 5340  
 TTAAGCCAC AGTATATTTT ATTTCAATGT AATTAACCTG TTAACCTATT CAAAGAGAAA 5400  
 ACATCTCATC ATGTCTATTG TCCAAAGTTA CCTGGAATCA AATAAAATTT CTAGATTACC 5460  
 ATGAAGAACA TA

Seq ID NO: 238 Protein sequence  
 Protein Accession #: NP\_057167.1

1 11 21 31 41 51  
 | | | | |  
 MKSILDGLAD TTFRTITTDL LYVGSNDIQY EDIKGDMASK LGYFPQKFPPL TSFRGSPFQE 60  
 KMTAGDNPQL VPADQNVITE FYNKSLSEFK ENEENIQCGE NFMIDIECFMV LNPSQQLAIA 120  
 VLSLTLTGFT VLENLLVLCV ILHSRSLRCR PSYHFIGSLA VADLLGSVIF VYSFIDFHFV 180  
 HRKDSRNVFL FKLGGVTASL TASVGSFLFT AIDRYVSIHR PLAYKRIVTR PKAVVAFCLM 240  
 WTIAIAIAVL PLLGWNCEKL SVCSDFPH IDETYLMEFI GVTSVLLLFV VYAYMYILWK 300  
 AHSHAVRMIQ RGTQKSIH TSEDGKVQVT RPDQARMDIR LAKTLVLILV VLIIICWGPLL 360  
 AIMVYDVFGK MNLIKTVFA FCSMLCLLNS TVNPIIYALR SKDLRHAERS MPFSCGTAQ 420  
 PLDSMGGSD CLHKHANNA SVHRAAESCI KSTVKIAKVT MSVSTDTSAE AL

Seq ID NO: 239 DNA sequence  
 Nucleic Acid Accession #: NM\_033181.1  
 Coding sequence: 17..1252

1 11 21 31 41 51  
 | | | | |  
 ATGAAGTCGA TCCTAGATGG CCTTGCAGAT ACCACCTTCC GCACCATCAC CACTGACCTC 60  
 CTGTACGTGG GCTCAAAATGA CATTCACTAC GAAGACATCA AAGGAGAATG AGGAGAACAT 120  
 CCAGTGTGGG GAGAACTTCA TGGACATAGA GTGTTTCATG GTCCTGAACC CCAGCCAGCA 180  
 GCTGGCCATT GCAGTCCFTG CCTCACGCT GGGCACCTTC ACGTCTCTGG AGAACCTCCT 240  
 GGTGCTGTGC GTCATCCTCC ACTCCCGCAG CCTCCGCTGC AGGCCTTCTC ACCACTTCAT 300  
 CGGCAGCCTG GCGGTGGCAG ACCTCCTGGG GAGTGTCTAT TTTGTCTACA GCTTTCATTGA 360  
 CTTCCACGTG TTCCACCGCA AAGATAGCCG CAACGTGTTT CTGTTCAAAC TGGGTGGGGT 420  
 CACGGCCTCC TTCATCGCCT CCGTGGGCAG CCGTCTCTC ACAGCCATCG ACAGGTACAT 480  
 ATCCATTAC AGGCCCTTGG CCTATAAGAG GATTGTCAAC AGGCCCAAGG CCGTGGTGGC 540  
 GTTTTGCCTG ATGTGGACCA TAGCCATTGT GATCGCCGTG CTGCCTCTCC TGGGTGGGAA 600  
 CTGCGAGAAA CTGCAATCTG TTTGCTCAGA CATTTTCCCA CACATTGATG AAACCTACCT 660  
 GATGTTCTGG ATCGGGGTCA CCAGCGTACT GCTTCTGTTC ATCGTGTATG CGTACATGTA 720  
 TATTCTCTGG AAGGCTCACA GCCACGCCGT CCGCATGATT CAGCGTGGCA CCCAGAAGAG 780  
 CATCATCATC CACACGCTCG AGGATGGGAA GGTACAGGTG ACCCGGCCAG ACCAAGCCCG 840  
 CATGGACATT AGGTTAGCCA AGACCTTGTT CCTGATCCTG GTGGTGTGTA TCATCTGCTG 900  
 GGGCCCTCTG CTTGCAATCA TGGTGTATGA TGTCTTTGGG AAGATGAACA AGCTCATTAA 960  
 GACCGTGTCT GCATTCTGCA GTATGCTCTG CTGCTGAAC TCCACCGTGA ACCCATCAT 1020  
 CTATGCTCTG AGGAGTAAGG ACCTGCGACA CGCTTTCCGG AGCATGTTTC CCTCTGTGTA 1080  
 AGGCACTGCG CAGCCTCTGG ATAACAGCAT GGGGGACTCG GACTGCTGTC ACAAACACGC 1140  
 AAACATGCA GCCAGTGTTC ACAGGGCCGC AGAAAGCTGC ATCAAGAGCA CGGTCAAGAT 1200  
 TGCCAAGGTA ACCATGTCTG TGTCCACAGA CACGTCTGCC GAGGCTCTGT GA

Seq ID NO: 240 Protein sequence  
 Protein Accession #: NP\_149421.1

1 11 21 31 41 51  
 | | | | |  
 MALQIPPSAP SPLTSCITWQ MTFSTKTSKE NEENIQCGEN FMDIECFMVL NPSQQLAIAV 60  
 LSLTLTGFTV LENLLVLCVI LHSRSLRCR SYHFIGSLAV ADLLGSVIFV YSFIDFHFVH 120  
 RKDSRNVFLF KLGGVTSFT ASVGSFLFTA IDRYISIHPR LAYKRIVTRP KAVVAFCLMW 180  
 TIAIVIAVL PLLGWNCEKL SVCSDFPHI DETYLMFVIG VTSVLLLFV YAYMYILWKA 240  
 HSHAVRMIQ RGTQKSIH TSEDGKVQVT RPDQARMDIR AKTLVLILV LIICWGPLLA 300  
 IMVYDVFGKM NKLIKTVFA FCSMLCLLNS VNPIIYALRS KDLRHAERSM FPFSCGTAQP 360  
 LDNSMGGSD CLHKHANNA SVHRAAESCI STVKIAKVT SVSTDTSAE L

Seq ID NO: 241 DNA sequence  
 Nucleic Acid Accession #: NM\_003596.1

Coding sequence: 82..1194

	1	11	21	31	41	51	
5	GTAGACTGTC	CATGGCCTGA	ACATTTTCCG	AAAATCATT	TGAGCAAAAT	ATCTGTTTAA	60
	TAACAAGATA	ACCACATCAA	GATGGTTGGA	AAGCTGAAGC	AGAACTTACT	ATTGGCATGT	120
	CTGGTGATTA	GTTCTGTGAC	TGTGTTTAC	CTGGGCCAGC	ATGCCATGGA	ATGCCATCAC	180
	CGGATAGAGG	AACGTAGCCA	GCCAGTCAAA	TTGGAGAGCA	CAAGGACCAC	TGTGAGAACT	240
10	GGCCTGGACC	TCAAAGCCAA	CAAAACCTTT	GCCTATCACA	AAGATATGCC	TTTAATATTT	300
	ATTGGRGGTG	TGCTCTGGAG	TGGAACCACA	CTCATGAGGG	CCATGCTGGA	CGCACATCCT	360
	GACATTGCTG	GTGGAGAGGA	AACCAGGGTC	ATTCCTCCGAA	TCCTGGCCCT	GAAGCAGATG	420
	TGGTCACGGT	CAAGTAAAGA	GAAGATCCGC	CTGGATGAGG	CTGGTGTTAC	TGATGAAGTG	480
	CTGGATTCTG	CCATGCAAGC	CTTCTTACTA	GAAATTATCG	TTAAGCATGG	GGAGCCAGCC	540
	CCTTATTTAT	GTAATAAAGA	TCCTTTTGCC	CTGAAATCTT	TAACTTACCT	TTCTAGGTTA	600
15	TTCCCAATG	CCAAATTCT	CCTGATGGTC	CGAGATGGCC	GGGCATCAGT	ACATTCAATG	660
	ATTCTCGAA	AAGTACTAT	AGCTGGATTT	GATCTGAACA	GCTATAGGGA	CTGTTTGACA	720
	AAGTGGAATC	GTGCTATAGA	GACCATGTAT	AACCAGTGTA	TGGAGGTG	TTATAAAAG	780
	TGCAATGTTG	TTCACTATGA	ACAACTTGTC	TTACATCCTG	AACGGTGGAT	GAGAACACTC	840
20	TTAAAGTTCC	TCCAGATTCC	ATGGAACAC	TCAGTATGTC	ACCATGAAGA	GATGATTGGG	900
	AAAGCTGGGG	GAGTGTCTCT	GTCAAAAGTG	GAGAGATCTA	CAGACCAAGT	AATCAAGCCA	960
	GTCAATGTAG	GAGCTCTATC	AAAATGGGTT	GGGAAGATAC	CGCCAGATGT	TTTACAAGAC	1020
	ATGGCAGTGA	TTGCTCTCTAT	GCTTGCCAAG	CTTGGATATG	ACCCATATGC	CAACCCACCT	1080
	AACATCGGAA	AACCTGATCC	CAAAATTATT	GAAAACACTC	GAAGGGTCTA	TAAGGGAGAA	1140
25	TTCCAACCTAC	CTGACTTCT	TAAAGAAAA	CCACAGACTG	AGCAAGTGGG	GATGAGAAC	1200
	CAGGAGCCTC	TTCCATACAT	GAGGAAAGAT	TGCTGCTCTT	TCAGCAGAAG	GGAAATTCCT	1260
	AGGATTGGCT	GTCCCTTGCC	AAGCTTGGTG	GAGCGTCTGC	ACCTTGGCTG	CGCCGCTCTG	1320
	GCATTTGCCA	GTTTCCCTCCC	ACTGAGAGGA	TGGAGGTGTC	CGCACAGCTT	TGGGCTCTCGT	1380
	GAGGATCTG	CCTCCTGAGC	AAAGAGCTCT	TGATCCCGAT	TTCAATGCACA	GCCCTGCAGT	1440
30	AAGGAGCCCA	GAAGGAACAT	GTGTTTCTCT	TTAAACTCTC	TCTTGTCTCT	TTTCTTCTA	1500
	TTATGACGTT	TGTTTTCAAG	GAGAGGGTTT	AAAAATGGGA	TCCTGTAAAG	AGACTTGGGG	1560
	AGTCTCTCTT	TGAAATAGGT	TGCTCTGACA	TGTTCTAATG	TTTGTAGAAA	CACGTGTGCC	1620
	TGTTAAAGTG	TATTGATGTG	AATAATATTA	AATATCCTAA	TTATTTAATT	CATTGTATTG	1680
	TTTCTGAGAA	GTTGGGAAAT	TACCATTATA	CATTTACAAC	CTAATGACTT	TTGTATTTTA	1740
35	TTTTTCAAAA	TAAAGCTTT	CAATGTGA				

Seq ID NO: 242 Protein sequence  
Protein Accession #: NP\_003587.1

	1	11	21	31	41	51	
40	MVGKLGKQNL	LACLVISSVT	VFYLGQHAME	CHHRIEERSQ	PVKLESTRRT	VRTGLDLKAN	60
	KTFAYHKDMP	LIFIGGVPRS	GTTLMRAMLD	AHPDIRCGEE	TRVIPRILAL	KQWRSRSKE	120
	KIRLDEAGVT	DEVLDSAMQA	FLLEIIVKHG	EPAPYLCNKD	PFALKSLTYL	SRLFNPNAFL	180
45	LMVRDGRASV	HSMISRKVTI	AGFDLNSYRD	CLTKWNRAT	TMYNQCMVEG	YKKMLVHYE	240
	QLVLHPRWMM	RTLLKFLQIP	WNHSLVHHEE	MIGKAGGVSL	SKVERSTDQV	IKPVNVGALS	300
	KWVGKIPDPV	LQDMAVIAPM	LAKLGYDPYA	NPPNYGKPD	KIIENTRRVY	KGEFQLPDFL	360
	KEKPQTEQVE						

Seq ID NO: 243 DNA sequence  
Nucleic Acid Accession #: NM\_001492.3  
Coding sequence: 1395..2513

	1	11	21	31	41	51	
55	ACGCGGGGCG	CGCGGCTCCG	TGCGCTACCG	CGGGCGGGCG	CAGGCGACGG	GCACGGCGGG	60
	CGAGCGGGCG	GTATGGCGGC	GGCGGGGCCC	GCGCGGGGCG	CGAGCGGGCC	CGAGCCCATG	120
	CCGAGCTACG	CGCAGCTAGT	GCAGCGCGGC	TGGGGCAGCG	CGCTGGCGGC	GGCGCGGGGC	180
	TGCACGGAAT	GCGGCTGGGG	GCTGGCGCGT	CGCGGCTGGG	CTGAGCACGC	GCACCTGGCG	240
60	CCGCGCGAGC	TGCTGCTGCT	GGCGCTCGGC	CGCGTGGGCT	GGACCGCGCT	GCGCTCCGCG	300
	GCCACTGCGC	GCCCTCTTTC	GCCCTGGCG	AAGCGGTGCT	GCCTCCAGCC	CAGAGATGCC	360
	GCCAAGATGC	CCGAGAGCGC	TTGGAAGTTT	CTCTTCTACC	TGGGCAGCTG	GAGCTACAGT	420
	GCTACCTGTC	TGTTTGGCAC	CGACTACCCC	TTCTTCCATG	ACCCACCATC	TGTCTTCTAC	480
	GACTGGAGCG	CGGGCATGGC	AGTGCCACGG	GACATTGCAG	CCGCCTACCT	GCTCCAGGGA	540
65	AGCTTCTATG	GCCACTCCAT	CTACGCTACG	CTATACATGG	ACACCTGGCG	CAAGGACTCG	600
	GTGGTCTATG	TGCTCCACCA	CGTGGTCACT	CTCATCTCTA	TGCTCTCTCT	CTACGCTTTC	660
	CGGTACCACA	ATGTGGGCAT	CCTTGTGCTC	TTCTTGACAG	ATATCAGTGA	CGTGCAGCTT	720
	GAGTTCACCA	AGCTCAACAT	TTACTTCAAG	TCCCGCGCGC	GCTCCTACCA	TCCGCTGCAT	780
	GCCTTGGCAG	CAGACTTGGG	CTGCCTCAGC	TTCCGGCTTCA	GCTGGTCTCT	GTTCCGCTCT	840
70	TACTGGTTCC	CGCTCAAGGT	CCTGTATGCC	ACCACTCACT	GCAGTCTGCG	CACGGTGCCT	900
	GACATCCCTT	TCTACTTCTT	CTTCAATGCG	CTCCTGTGTC	TGCTCACCTT	TATGAACCTC	960
	TACTGGTTCC	TGTACATCGT	GGCGTTTGCA	GCCAAGGTGT	TGACAGGCCA	GGTGCACGAG	1020
	CTGAAGGACC	TGCGGGAGTA	TGACACAGCC	GAGGCCAGGA	GCCTGAAGCC	CAGCAAGGCC	1080
	GAGAAGCCAC	TGAGGAACGG	CCTGGTGAAG	GACAAGCGCT	TCTGAACCCC	TCCGCCCCCG	1140
75	CCCCGTGGAC	CCGGCCCCAC	CCCGAATACC	CCGGCCACGC	TCCCCGTCCT	TGGCCGCCCC	1200
	TCCACCCCTC	CCAACCTGCG	TCCTCTAGGG	CCGCCGCCAC	CTCCCTGGG	ACCCCGCCCC	1260
	CTCATCTGTC	CTCCATTTC	CGGCCACGCC	CCCCAGGACC	CCTGCCCTTC	CGGGGACACC	1320
	GGCCCCGCCC	TCAGCCCACT	GGTCCCGGGC	CGCCGCGGAC	CCTGCGCACT	CTCTGTGTCAT	1380
	CGCTGGGAG	GAAGATGCCA	CGCCGCGAGC	AAGTCCCTG	CGGCCACCAC	CTCTCTCTCC	1440
80	TCCTGGCCCT	GCTGCTGCCC	TCGCTGCCCC	TGACCCGCGC	CCCCGTGCCC	CCAGGCCACG	1500
	CCGCCGCTCT	GCTCCAGGCT	CTAGGACTGC	GCGATGAGCC	CGAGGGTGCC	CCCAGGCTCC	1560
	GGCCGCTTCC	CTCCGCTCAT	TGGCGCTGTG	TTCCAGCGCC	GGACCCACAG	GAGACCAGTG	1620
	CTGGCTGCGG	GCGGACGTCC	CCAGGGGTCA	CCCTGCAACC	GTGCCACGTG	GAGGAGCTGG	1680
	GGGTGCGCGG	AAACATCGTG	CGCCACATCC	CGGACCGCGG	TGGGCCACAC	CGGGCTCTCG	1740
	AGCCTGTCTC	GGCCGCGGGG	CATTGCCCTG	AGTGGACAGT	CGTCTTCGAC	CTGTCCGGCTG	1800

5 TGGAACCCGC TGAGCGCCCG AGCCGGGCCG GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG 1860  
 CGGCAGCCCC GGAGGGCGGC TGGGAGCTGA GCGTGGCGCA AGCGGGCCAG GGCGCGGGCG 1920  
 CGGACCCCGG GCCGTGCTGT CTCCGCCAGT TGGTGGCCCG CCTGGGGCCG CCAGTGCGCG 1980  
 CGGAGCTGCT GGGCGCCGCT TGGGCTCGCA ACGCCTCATG GCCGCGCAGC CTCGCGCTGG 2040  
 CGCTGGCGCT ACGCCCCCGG GCCCTGCGG CCTGCGCGCG CCTGGCCGAG GCCTCGCTGC 2100  
 TGCTGGTGAC CCTCGACCCG CGCCTGTGCC ACCCCTGGC CCGGCGCGCG CGCGACGCGG 2160  
 AACCCGTGTT GGGCGGCGGC CCCGGGGGCG CTGTGCGCGC GCGGCGGCTG TACGTGAGCT 2220  
 TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCCGCG CGGCTTCCTG GCCAACTACT 2280  
 10 GCCAGGGTCA GTGCGCGCTG CCGCTCGCGC TGTGCGGGTC CCGGGGGCCG CCGGCGCTCA 2340  
 ACCACGCTGT GCTGCGCGCG CTCATGCACG CGGCCGCCCG GGGAGCCGCG GACCTGCCCT 2400  
 GCTGCGTGCC CGCGCGCTG TCGCCCATCT CCGTGCTCTT CTTTGACAAC AGCGACAACG 2460  
 TGGTGTCTCG GCAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCCG TAACCCGGGG 2520  
 CGGGCAGGGA CGCGGGCCCA ACAATAAATG CCGCTGGTTC TGCTC

Seq ID NO: 244 Protein sequence  
 Protein Accession #: NP\_001483.2

1 11 21 31 41 51  
 20 MPPFPQQGPGC HLLLLLLALL LPSLPLTRAP VPPGPAAALL QALGLRDEPQ GAPRLRPVPP 60  
 VMWRLFRRRD PQETRSRSGRR TSPGVTLQPC HVEELGVAGN IVRHIPDRGA PTRASEPVSA 120  
 AGHCPEWTVV FDLSAVEPAE RPSRARLELR FAAAAAAPE GWELSVQA GQAGADPGP 180  
 VLLRQLVPAL GPPVRAELLG AAWARNASWP RSLRLALALR PRAPAACARL AEASLLLVTL 240  
 25 DPLRCHPLAR PRRDAEPVLG GPGGACRAR RLYVSFREVQ WHRWIAPRG FLANYCQGGC 300  
 ALPVALSGSG GPALNHAVL RALMHAAAPG AADLPCCVPA RLSPISVLFF DNSDNVVLRLQ 360  
 YEDMVVDECG CR

Seq ID NO: 245 DNA sequence  
 Nucleic Acid Accession #: NM\_021267.1  
 Coding sequence: 17..1125

1 11 21 31 41 51  
 35 ACGCGGGGCG CGCGGCTCCG TCGGCTACCG CGGGCGGGCG CAGGCGACGG GCACGGCGGG 60  
 CGAGCGGGCG GTATGGCGGC GCGGGGGCCC GCGGCGGGCG CGACGGGGCC CGAGCCCATG 120  
 CCGAGCTACG CGCAGCTAGT GCAGCGCGGC TGGGGCAGCG CGCTGGCGGC GCGCGGGGCG 180  
 TGACCGGACT GCGGCTGGGG GCTGGCGCGT CGCGGCTGG CTGAGCACGC GCACCTGGCG 240  
 CCGCCCGAGC TGTGCTGCT GCGCTCGGC GCGCTGGGCT GGACCGCGCT GCGCTCCGCG 300  
 40 GCCACTGCGC GCCTCTTTCG GCCCTGGCG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC 360  
 GCCAAGATGC CCGAGAGCGC TTGGAAGTTT CTCTTCTACC TGGGCAGCTG GAGCTACAGT 420  
 GCCTACCTGC TGTTTGGCAC GCACTACCCC TTCTTCCATG ACCCACCATC TGTCTTCTAC 480  
 GACTGGAGCG CGGGCATGGC AGTGCCACGG GACATTGCAG CCGCCTACCT GCTCCAGGGA 540  
 AGCTTCTATG GCCACTCCAT CTACGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG 600  
 45 GTGGTCATGC TGCTCCACCA CGTGGTCACT CTCATCCTCA TCGTCTCCTC CTACGCCTTC 660  
 CGGTACCACA ATGTGGGCAT CCTTGTGCTC TTCTGTGACG ATATCAGTGA CGTGACGCTT 720  
 GAGTTCACCA AGCTCAACAT TTACTTCAAG TCCCGCGGCG GCTCCTACCA TCGGCTGCAT 780  
 GCCTTGGCAG CAGACTTGGG CTGCCTCAGC TTCGCTTCA GCTGGTTCTG GTTCCGCCTC 840  
 TACTGGTTCC CGCTCAAGGT CCTGTATGCC ACCAGTCACT GCAGTCTGCG CACGGTGCCT 900  
 50 GACATCCCTT TCTACTTCTT CTTCATGCG CTCCTGTGCG TGCTCACCTT TATGAACCTC 960  
 TACTGGTTCC TGTACATCGT GCGTTTGA GCGCAAGGTG TGACAGGCCA GGTGCACGAG 1020  
 CTGAAGGACC TCGGGAGTA TGACACAGCC GAGGCCCAGA GCCTGAAGCC CAGCAAAGCC 1080  
 GAGAAGCCAC TGAGGAACGG CCTGGTGAAG GACAAGCGCT TCTGAACCCC TCGGCCCGCG 1140  
 CCGGTGGAG CCGGCCCCAC CCGGAATACC CCGGCCACGC TCCCGTCTCT TGGCCGCCCC 1200  
 55 TCCACCCCTT CCAACTCTGC TCCTCTAGGG CCGCGGCCAC CTCCTCTGGG ACCCGGCCCC 1260  
 CTATCTCTG CTGCATTTCG CGGCCACGCC CCGCAGGACC CCTGCCCTCT CCGGGACACC 1320  
 GGCCCGGCCC TCAGCCCACT GGTCCCGGGC CGCCGCGGAC CCTGCGCACT CTCTGGTCAT 1380  
 CGCCTGGGAG GAAGATGCCA CCGCGCAGC AAGGTCCCTG CCGCCACCAC CTCCTCTCTC 1440  
 TCCTGGCCCT GCTGCTGCCC TCGCTGCCCG TGACCCGCGC CCGCGTGCCC CCAGGCCAGG 1500  
 60 CCGCGCCCTT GCTCAGGCT CTAGGACTGC GCGATGAGCC CCAGGGTCCC CCCAGGCTCC 1560  
 GGCCGGTTCC CCCGTCATG TGGCGCCTGT TTCGACGCGG GACCCCCAG GAGACCAGGT 1620  
 CTGGCTCGCG GCGGACGCTC CCAGGGTCA CCTGCAACC GTGCCACGTG GAGGAGCTGG 1680  
 GGGTGC CGG AAACATCGTG CGCCACATCC CGGACCGCGG TGCGCCACC CGGGCCTCGG 1740  
 AGCCTGTCTC GGCCGCGGGG CATTGCCCTG AGTGGACAGT CGTCTTCGAC CTGTGCGCTG 1800  
 65 TGGAACCCGC TGAGCGCCCG AGCCGGGCCG GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG 1860  
 CGGCAGCCCC GGAGGGCGGC TGGGAGCTGA GCGTGGCGCA AGCGGGCCAG GGCGCGGGCG 1920  
 CGGACCCCGG GCCGTGCTG CTCCGCCAGT TGGTGGCCCG CCTGGGGCCG CCAGTGCGCG 1980  
 CGGAGCTGCT GGGCGCGGCT TGGGCTCGCA ACGCCTCATG GCCGCGCAGC CTCGCGCTGG 2040  
 CGCTGGCGCT ACGCCCCCGG GCCCTGCGG CCTGCGCGCG CCTGGCCGAG GCCTCGCTGC 2100  
 70 TGCTGGTGAC CCTCGACCCG CGCCTGTGCC ACCCCTGGC CCGGCGCGCG CGCGACGCGG 2160  
 AACCCGTGTT GGGCGGCGGC CCGGGGGGCG CTGTGCGCGC GCGGCGGCTG TACGTGAGCT 2220  
 TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCCGCG CGGCTTCCTG GCCAACTACT 2280  
 GCCAGGGTCA GTGCGCGCTG CCCGTGCGCG TGTGCGGGTC CCGGGGGCCG CCGGCGCTCA 2340  
 ACCACGCTGT GCTGCGCGCG CTCATGCACG CGGCCGCCCG GGGAGCCGCG GACCTGCCCT 2400  
 75 GCTGCGTGCC CGCGCGCTG TCGCCCATCT CCGTGCTCTT CTTTGACAAC AGCGACAACG 2460  
 TGGTGTCTCG GCAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCCG TAACCCGGGG

Seq ID NO: 246 Protein sequence  
 Protein Accession #: NP\_067090.1

1 11 21 31 41 51  
 80 MAAAGPAAGP TGPEPMPSYA QLVQRGWGSA LAAARGCTDC GWGLARRGLA EHAHLAPPEL 60  
 LLLALGALGW TALRSAATAR LFRPLAKRCC LQPRDAAKMP ESAWKFLFYL GSWSYSAYLL 120  
 FGTDYPFFHD PPSVFIYDWTG GMAVPRDIAA AYLLQGSFYG HSIYATLYMD TWRKDSVVML 180

LHHVVTLLILI VSSYAFRYHN VGILVLFLHD ISDVQLEFTK LNIYFKSRGG SYHRLHALAA 240  
 DLGLSFGFS WFWRLYWFP LKVLATSHC SLRTVPDIPF YFFFNALLLL LTLMLNLYWFL 300  
 YIVAFAPAKVL TGVHLEKDL REYDTAEAS LKPSKAEKPL RNLVVKDKRF

5

Seq ID NO: 247 DNA sequence  
 Nucleic Acid Accession #: NM\_002081.1  
 Coding sequence: 222..1898

10 1 11 21 31 41 51  
 | | | | |  
 GGCTGCCCGA GCGAGCGTTC GGACCTCGCA CCCCGCGCGC CCCCGCGCGC CGCCGCGCGC 60  
 GGCTTTTGT GTCTCCGCTT CCTCGGCCGC CGCCGCTCTT GGACCCGCGAG CCGCGCGCGC 120  
 CGGGACCTTG GCTCTGCCCT TCGCGGGCGG GAACTGCGCA GGACCCGCGC AGGATCCGAG 180  
 15 AGAGGCGCGG GCGGGTGGCC GGGGGCGCGG CCGGCCCGGC CATGGAGTTC CGGGCCCGAG 240  
 GCTGGTGGCT GCTATGTGCG GCGGCAGCGC TGGTCCGCTG CGCCCGCGGG GACCCGGCCA 300  
 GCAAGAGCCG GAGCTGCCGC GAGGTCCGCC AGATCTACGG AGCCAAGGCG TTCAGCCTGA 360  
 GCGAGCTGCC CCAGGCGGAG ATCTCGGGTG AGCACTGCG GATCTGTCCC CAGGGCTACA 420  
 CCTGCTGCAC CAGCGAGATG GAGGAGAACC TGGCCAACCG CAGCCATGCC GAGCTGGAGA 480  
 CCGCGCTCCG GGACAGCAGC CGCGTCCCTGC AGGCCATGCT TGCCACCAGC CTGCGCAGCT 540  
 20 TCGATGACCA CTTCCAGCAC CTGCTGAACG ACTCGGAGCG GACGCTGCAG GCCACCTTCC 600  
 CCGGCGCCTT CGGAGAGCTG TACACGAGA ACGCGAGGGC CTTCCGGGAC CTGTACTCAG 660  
 AGCTGCGCCT GTACTACCGC GGTGCCAACC TGCACCTGGA GGAGACGCTG GCCGAGTTCT 720  
 GGGCCCGCCT GCTCGAGCGC CTCTTCAAGC AGCTGCACCC CCAGCTGCTG CTGCCTGATG 780  
 25 ACTACCTGGA CTGCCTGGGC AAGCAGGCGG AGGCGCTGCG GCCCTTCGGG GAGGCCCGGA 840  
 GAGAGCTGCG CCGCGCGGCC ACCCGTGCC TCGTGGCTGC TCGCTCCTTT GTGCAGGGCC 900  
 TGGGCGTGCG CAGCGACTG GTCCGAAAG TGGCTCAGGT CCCCCTGGGC CCGGAGTGCT 960  
 CGAGAGCTGT CATGAAGCTG GTCTACTGTG CTCACTGCCT GGGAGTCCCC GGGCCAGGC 1020  
 CCTGCGCTGA CTATTGCCGA AATGTGCTCA AGGGCTGCCT TGCCCAACCA GCGGACCTGG 1080  
 30 ACGCCGAGTG GAGGAACCTC CTGGACTCCA TGGTGTCTAT CACCGACAAG TTCTGGGGTA 1140  
 CATCGGGTGT GGAGAGTGTG ATCGGCAGCG TGCAACACGT GCTGCGGAG GCCATCAACG 1200  
 CCCTCCAGGA CAACAGGAGC ACGCTCACGG CCAAGGTCAT CCAGGGCTGC GGAACCCCA 1260  
 AGGTCAACCC CAGGGCCCTT GGGCCTGAGG AGAAGCGGCG CCGGGGCAAG CTGGCCCGCG 1320  
 GGGAGAGGGC ACCTTCAGCG ACGCTGAGGA AGCTGGTCTC TGAAGCCAAG GCCCAGCTCC 1380  
 35 GCGACGTCCA GACTTCTGAG ATCAGCCTCC CAGGGACACT GTGCAGTGAG AAGATGGCCC 1440  
 TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGGATGGC CAGAGGCCGG TACCTCCCCG 1500  
 AGGTATGAGG TGACGGCCTG GCCAACCAAG TCAACAACCC CGAGGTGGAG GTGGACATCA 1560  
 CCAAGCCGGA CATGACCATC CGGCAGCAGA TCATGCAGCT GAAGATCATG ACCAACCCGC 1620  
 TGCGCAGCGC CTACAACGGC AACGACGTGG ACTTCCAGGA CGCCAGTGAC GACGCGAGCG 1680  
 40 GCTCGGGCAG CCGTGATGCG TGTCTGGATG ACCTCTGCGG CCGGAAGGTC AGCAGGAAGA 1740  
 GCTCCAGCTC CTGCGACGCC TTGACCCATG CCTTCCGAG CCGTGCAGAG CAGGAAGGAC 1800  
 AGAAGACCTC GGTCTGCCAG TGCCCCCAGC CCCCAGCCTT CCTCTGCCCC CTCTCTCTCT 1860  
 TCCTGGCCCT TACAGTAGCC AGGCCCGGT GCGGTAACT GCCCAAGGC CCCAGGACA 1920  
 GAGGCCAAGG ACTGACTTTG CCAAAAATAC AACACAGACG ATATTTAATT CACCTCAGCC 1980  
 45 TGAGAGGGCC TGGGGTGGGA CAGGGAGGGC CCGCGGCTCT GAGCAGGGGC AGGCGCAGAG 2040  
 GTCCAGCCCC CAGGCTGCTG CTGCGCTGCC TTCTGCTCTT TTAATTTTGT ATGAGTCTCT 2100  
 CAGGTGAGCT GGGAGCCAGT GTGCCCAAAA GCCATGTATT TCAGGGACCT CAGGGGCACC 2160  
 TCCGGCTGCC TAGCCCTCCC CCCAGCTCCC TGCACCGCGG CAGAAGCAGC CCTCGAGGC 2220  
 50 CTACAGAGGA GGCCTCAAG CAACCCGCTG GAGCCACAG CGAGCCTGTG CCTTCTCTCC 2280  
 CGCTCTCTCC CACTGGGACT CCCAGCAGAG CCCACAGGCC AGCCCTGGCC CACCCCCAG 2340  
 CCTCCAGAGA AGCCCGCAC GGGCTGTCTG GGTGTCCGCC ATCCAGGGTC TGGCAGAGCC 2400  
 TCTGAGATGA TGCATGATGC CCTCCCTCA GCGCAGGCTG CAGAGCCCGG CCCACCTCC 2460  
 CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGGTGACGCC TGAGACAGCA CCACTGCTGA 2520  
 GGAGTCTGAG GACTGTCTCT CCACAGACCC TGCAGTGAGG GGCCCTCCAT GCGCAGATGA 2580  
 55 GGGGCCACTG ACCACCTGCG GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAGAGCCAG 2640  
 GGAGGACGCG TGGGCTCTCG CAATGTGGGC TGCCCTTCGC ACACAGGGCT CACAGGCGAG 2700  
 GCCTTGCTGG GGTCCAGGGC TGTGGAGGA CCCCAGGGGC TGAGGAGCAG CCAGGACCCG 2760  
 CCTGCTCCCA TCCTCACCCA GATCAGGAAC CAGGGCCTCC CTGTTACAGG TGACACAGGT 2820  
 CAGGGCTCAG AGTGACCTCT GGCTGTCAAC TGCTCACAGG GATGCTGGTG GCTGGTGAGA 2880  
 60 CCCGCACTG CACACGGGAA TGCTAGGTG CCTTCCCGAC CCAGCCAGCT GCACTGCAGG 2940  
 GCACGGGGAC CTGGATAGTT AAGGGCTTTT CCAACATGCT ATCCATTTC TGACACTTCC 3000  
 TGTCTTGTG CATGGAGAGC TGTTCGCTCC TCCAGATGG CTTCCGAGGC CCGCAGGGCC 3060  
 CACCTTGGAC CCTGGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120  
 CTGACCGGGC CCTCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GGAGGGGTGG 3180  
 65 TGTGGTGTG GGAAGGGGTC CTGCAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG 3240  
 TCCTGAACCG ACTGACCTTG AGGAGGCCGC TTAGTGCTGC TTTGCTTTTC ATCACCCTCC 3300  
 CGCACAGTGG ACGGAGGTCC CCGTTGCTG GTCAAGTCCC CATGGCTTGT TCTCTGGAAC 3360  
 CTGACTTTAG ATGTTTGGG ATCAGGAGCC CCAACACAG GCAAGTCCAC CCCATAATAA 3420  
 CCCTGCCAGT GCCAGGGTGG GCTGGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG 3480  
 70 CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CTAACGCTCA 3540  
 TCTCTGGAAG GGGCAGCCCT GAGTGGTCACT TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT 3600  
 CCTTCTCCA CAAGGTCCCC CCACCGCTCA GTGTCAGCGG GTGACGTGTG TTCTTTTGGAG 3660  
 TCCTGTATG AATAAAGGC TGAACCTA AA

75

Seq ID NO: 248 Protein sequence  
 Protein Accession #: NP\_002072.1

80

1 11 21 31 41 51  
 | | | | |  
 MELRARGWLW LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSVDP QAEISGEHLR 60  
 ICPQGYTCTT SEMEENLANR SHAELETALR DSSRLVQAML ATQLRSFDDH FOHLNDSESR 120  
 TLQATFPFPAF GELYTQNARA FRDLYSELRL YYRGNLHLE ETLAEFWARL LERLFLKQLHP 180  
 QLLLLDDYLD CLGKQAEALR PFGEAPREL RLRATRAFAA RSFVQGLGVA SDVVRKVAQV 240  
 PLGPBCSRAV MKLVYCAHCL GVPGARPCPD YCRNVKGLCL ANQADLDAEW RNLLDSMVL I 300  
 TDKFWGTSGV ESVGSVHTW LAEAINALQD NRDTLTAKVI QCGNPKVNP QGPGEPEKKR 360

RGKLA PRERP PSQTLEKLVS EAKAQLRDVQ DFWISLPGTL CSEKMALSTA SDDRCWNMGMA 420  
 RGRYLPVEMG DGLANQINNP EVEVDITKPD MTIROQIMQL KIMTNRLRSA YNGNDVDFQD 480  
 ASDDGSGSGS

Seq ID NO: 249 DNA sequence  
 Nucleic Acid Accession #: NM\_001492.3  
 Coding sequence: 8..1864

1	11	21	31	41	51	
GAAGGCCATG	GTCTCCCCAC	GGATGTCCGG	GCTCTCTCTC	CAGACTGTGA	TCCTAGCGCT	60
CATTTTCTCT	CCCCAGACAC	GGCCCGCTGG	CGTCTTCGAG	CTGCAGATCC	ACTCTTTCGG	120
GCCGGGTCCA	GGCCCTGGGG	CCCCGCGGTC	CCCCTGCAGC	GCCCGGCTCC	CCTGCCGCCT	180
CTTCTTCAGA	GTCTGCCTGA	AGCCTGGGCT	CTCAGAGGAG	GCCCGCGAGT	CCCCGTGCGC	240
CCTGGGCGCG	GCGCTGAGTG	CGCGCGGACC	GGTCTACACC	GAGCAGCCCG	GAGCGCCCGC	300
GCGTGATCTC	CCACTGCCCC	ACGGGCTCTT	GCAGGTGCCC	TTCCGGGACG	CCTGGCCTGG	360
CACCTTCTCT	TTCATCATCG	AAACCTGGAG	AGAGGAGTTA	GGAGACCAGA	TTGGAGGGCC	420
CGCCTGGAGC	CGCTGGCGC	GCGTGGCTGG	CAGGCGGCGC	TTGGCAGCCG	GAGGCCCGTG	480
GGCCCCGGAC	ATTACGCGCG	CAGGCGCCTG	GGAGCTGCGC	TTCTCGTACC	GCGCGCGCTG	540
CGAGCGGCCT	GCCGTGCGGA	CCGCGTGCAC	GCGCCTCTGC	CGTCCGCGCA	GCGCCCCCTC	600
GCGGTGCGGT	CCGGGACTGC	GCCCCTGCGC	ACCGCTCGAG	GACGAATGTG	AGGCGCCGCT	660
GGTGTGCCGA	CGAGGTGCA	GCCCTGAGCA	TGGCTTCTGT	GAACAGCCCG	GTGAATGCCG	720
ATGCCTAGAG	GGCTGGACTG	GACCCCTCTG	CACGGTCCCT	GTCTCCACCA	GCAGCTGCCT	780
CAGCCCCAGG	GGCCCTCTCT	CTGTACACAC	CGGATGCCCT	GTCCCTGGGC	CTGGGCCCTG	840
TGACGGGAAC	CGGTGTGCCA	ATGGAGGCAG	CTGTAGTGAG	ACACCCAGGT	CCTTTGAATG	900
CACCTGCGCG	CGTGCGTTCT	ACGGGCTGCG	GTGTGAGGTG	AGCGGGGTGA	CATGTGCAGA	960
TGGACCTGCG	TTCAACGCGC	GCTTGTGTGT	CGGGGTGCA	GACCCGACT	CTGCCTACAT	1020
CTGCCACTGC	CCACCTGGTT	TCCAAGGCTC	CAACTGTGAG	AAGAGGGTGG	ACCGGTGCAG	1080
CCTGCAGCCA	TGCCGCAATG	GCGGACTCTG	CCTGGACCTG	GGCCACGCCC	TGCGCTGCCG	1140
CTGCCGCGCG	GGCTTCCGCG	GTCTCTGCTG	CGAGCACGAC	CTGGACGACT	GCGCGGGCCG	1200
CGCTTGCCTC	AACGGCGGCA	CGTGTGTGGA	GGCGCGCGCG	GCGCACCGCT	GCTCCTGCGC	1260
GCTGGGCTTC	GGCGGCGCGC	ACTGCCGCGA	GCGCGCGGAC	CCGTGCGCCG	GCGGCCCTTG	1320
TGCTACGGCG	GGCCGCTGCT	ACGCCCACTT	CTCCGGCCTC	GTCTGCGCTT	GCGCTCCCGG	1380
CTACATGGGA	GCCGCGTGTG	AGTTCACAGT	GCACCCGACG	GCGCGAAGCG	CCTTGCCCGC	1440
GGCCCCGCGG	GGCTCAGGCG	CCGGGAGACC	TCAGCGCTAC	CTTTTGCTCT	CGGCTCTGGG	1500
ACTGCTCGTG	GCCGCGGGCG	TGGCCGCGCG	TGCGCTCTTG	CTGGTCCACG	TGCGCGCCCG	1560
TGGCCACTCC	CAGGATGCTG	GGTCTCGCTT	GCTGGCTGGG	ACCCCGGAGC	CGTCAGTCCA	1620
CGCACTCCCG	GATGCACTCA	ACAACCTAAG	GACGCGAGGAG	GGTTCCGGGG	ATGGTCCGAG	1680
CTCGTCCGTA	GATTGGAATC	GCCCTGAAGA	TGTAGACCTT	CAAGGGATTG	ATGTCAATATC	1740
TGCTCCTTCC	ATCTACGCTC	GGGAGGTAGC	GACGCCCTTT	TTCCCCCGCG	TACACACTGG	1800
CGCGCTGGG	CAGAGGCAGC	ACCTGCTTTT	TCCTACCTCT	TCCTCGATTC	TGTCGGTGAA	1860
ATGAATTGGG	TAGATCTCT	GGAAGGTTTT	AAGCCCATTT	TCAGTTCTAA	CTTACTTTCA	

Seq ID NO: 250 Protein sequence  
 Protein Accession #: NP\_058637.1

1	11	21	31	41	51	
MVSPRMSGLL	SQTIVILALIF	LPQTRPAGVF	ELQIHSFPGP	PGPGAPRSPC	SARLPCLRFF	60
RVCLKPLGLSE	EAAESPCALG	AALSARGPVY	TEQPGAPAPD	LPLPDGLLQV	PFRDAWPETF	120
SFIETWREE	LGDQIGGPAW	SLLARVAGRR	RLAAGGPWAR	DIQRAGAWEL	RFSYRARCEP	180
PAVGTACTRL	CRPRSAPSRC	GPGLRPCAPL	EDECEAPLVC	RAGCSPHGF	CEQPGECL	240
EGWTGPLCTV	PVSTSSCLSP	RGPSSATTGC	LVPFGPGCDG	NPCANGGSCS	ETPRSFECTC	300
PRGFYGLRCE	VSGVTGADGP	CFNGGLCVGG	ADPDSAYICH	CPPGFQGSNC	EKRVDRCSLQ	360
PCRNGLCLD	LGHALRCR	AGFAGPRCEH	DLDDCAGRAC	ANGGTCVEGG	GAHRCSCALG	420
FGGRDCRERA	DFCAARPCAH	GGRCYAHFSG	LVCACAPGYM	GARCEFPVHP	DGASALPAAP	480
PGLRPGDPQR	YLLPPLGALL	VAAGVAGAAL	LLVHVRRRGH	SQDAGSRLLA	GTPBPSVHAL	540
PDALNNLRTO	EGSGDGPSSS	VDWNRPEVD	PQGIYVISAP	SIYAREVATP	LFPPLHTGRA	600
GQRQHLLFPY	PSSILSVK					

Seq ID NO: 251 DNA sequence  
 Nucleic Acid Accession #: CAT cluster

1	11	21	31	41	51	
GAAATATAAC	CATTGCAATT	AGAAAATATC	CAAAATAGCC	TGTTATCTTC	CACGTGGCCT	60
AGATTATTGA	CAATCCCAAA	TATACAATTT	TTCTTTAAAA	GTAGTACAAT	TTCTTTTGTA	120
GCTTCAATTC	CTTATATGAC	TTCAAGCTGG	AGAAGCCTGT	TAAACCACTG	TTAGTTTCAG	180
TTAGAAAGTC	TGAGAGACTT	TATACATAAA	TTCTCAATTT	GGCTGCTGTA	CACGTGCCAG	240
AGTTTTACTA	CTGTAGTGAC	CGTTGAGAAG	ACCCTTGTTT	ATTTACATTT	GAAGCACTGT	300
TTGTGCAAAAC	AACCTTTTCAT	TGTTAAGTGC	CTGTATTCCCT	TTCAATTACT	TCATGTCCAG	360
GGGTGCTATT	TACCTAGAAC	CATTGTCTAC	TACAATTAAC	ATTTACATTA	CAAAGTGTGT	420
GGTTTTCTTT	TTCAAGGAGG	TTCAATTAAG	GCAATAAGAT	GTTTGCTGGA	GAAACCTATT	480
GTTTACTGAA	AGCACTCAAT	GAAAGTCAAT	TACTGAAGCT	TTTGCTTACA	TCTTGGTCTT	540
TTATGTAAAT	ATGTTAAATA	TAACATCTAA	GGAAAATAAA	CAATATTATA	ATTATGTGTT	600
TGCCATTGTC	ATATCAAACT	TGCTTTGTAT	CATACTAATG	TTACATAACT	TATCGATCAA	660
TAAAAATACA	TTTCAATGTT	AAAAAATAAA	AAAAAATAAA			

Seq ID NO: 252 DNA sequence  
 Nucleic Acid Accession #: Eos sequence

1	11	21	31	41	51	
AGGTACTGCC	AGAAAGGATC	AGGACCTGGA	GTCTGGCAAG	AGGAAGACAG	AGGCCGTGTG	60

5 GGAAGCGAG TTGTTATCTT TGGTTATCTA GCTGTATGAG TGTATTGGTC TTCATAAAGC 120  
 TAGATAACCG AAAGTAAAAA CTTCTTCAAG ATCGCCGGGG AGCGTGTGAG AATGAAAGAC 180  
 TACAGCCGAG AGACAGTAAA AACCAGAAAG GTCAGGAATA CTTATTGAAT CTAACCTTGT 240  
 TTTTGTGTTG TTTTTCCTT TATGATTAAA GGTGGGATGA GAGAAAAATTA AATGACACAC 300  
 10 ACATGCTAAA ATATCAAGGT TCCAGATATG TCTTGAGAGG GGTGTGTGCA GCTGCAAGG 360  
 AGAAGTGAT AGTGATAATG AGTAAAGATG CATGTGCAGT TTGTTCTATT TTAAGGCAAA 420  
 AGTTATATCA GGGATTTTTT TCTAGAAAAG GTGTTGCAGA GATGCTCGGT ACCTAGTTTA 480  
 AAAATGATTC CATAATATGT AGACTTGGGC AGTTCTTTG GGAGGCACCT CCCTCTCAAA 540  
 ATTTGAAGAT TGTGCTTGGA AATTACTTTA CATGTATTTG GGTGTATGT CAATTTGTAC 600  
 GAAATTAGAG TTTTCAGAAA GTTTATACTG GAAGGTTAAT AATTGTATC TACTGAGGAC 660  
 TTAGAGCTAG CAGGCAAAAT GAAAAAAR GAAAGGCTGA TTTTATTTCT 720  
 TCTATTCAAA ATACAAGGAC AGATGCTTCT CTGTTCCAAG AGGGTTTCTT TGAGGAAGCT 780  
 ACTGAAGCAG AAAGACATGA TGGAGACGAG ATCGCCTCCC CTCTGTCAA AGTGTAAAA 840  
 15 AAATGTTCTG TCTTACTCTG CGCTTAGCAT TGGAAATGAA AGTGACATTT ACGCCACAAC 900  
 CCAGTGTGCG GCGTCTCTCT TTTTGTGTTA AGGATGATCA GGTCTATCCA GGAACACGCT 960  
 CTGGCATCCC AAAGTGAAT AATTAGGACG TATATAGACC TGACAAAAAT GGAAGGGGG 1020  
 TGGGGAATCT GAGGGTCTGT CTGTCCTAAT TGATTCGCT AAACGGAATG CAGGAGATGT 1080  
 GAACGGCAGG ACCTCCGAT TCCCACGCTC GGGGGCAAGT GATAAAGCGG GCGCGGCAG 1140  
 20 CCTATGACAG ACAGCCTCTG TGGGGGTGG GGGTATGAAA AAAACATCAA GTGCACACAC 1200  
 CATACTCATC TCCATCGCTT AAGAAAGTAA AGGCATTTC CACCCACAGC CATCTGCAGC 1260  
 TTCCCAAATG CGAGACCAA CTGCTCTGTA GCTGCTACAT AGTCTGCTTC TGTAAATTTT 1320  
 TTAACCACTG TTTAATCTGG CCATAATTA GTTTGGCTTT CTTCGTTGTT TGAGATTTTC 1380  
 AGAATTCAAG CCAAGCTAGT AGAAAGCAAT TCCAAGAAAG TCCCATGACT GCCTGCCCTT 1440  
 25 AATGTCAAAA TCTCAGTCCA TGAGATTATG GCCTTGTGAC CACATTTTGT CTTTGTGTTT 1500  
 GGGTGGGCAA ATGTGTATAG AGATAAAATA CATATCTCTA TATAACAGTC GTTATTATAA 1560  
 TTTCTAGAG CTTTTACCT CTTAACATGA TACATCTAGG AACTTGGTCT AATTGTGCTA 1620  
 GTAGATATAC ACTAGAAGTA AAACATATAA GTCATTAGCC TGTAGAAAGT TGATTATGAT 1680  
 AACAAATATG TAAAAAGTTT GTTTTGAAT AGTCTCAGCT AGATGGGCTT AAATAGCCAT 1740  
 30 TTTAATGTAA TCTAAAAATA ACACATATGCC TAGCAGAAAC TTTGGCGCTT TGGAGGTCCC 1800  
 CATGTGCGCC TTTTCATAAA AGTCCCTAAG TTTTCCATAT GTCACCAAGC AAACATTGTT 1860  
 ATAGGCATT ACACAGAAAT ATAACCATG CAATTAGAAA ATATCCAAAA TAGCTGTGTA 1920  
 TCTTCCACGT GGCCTAGATT ATTGACAATC CCAATATATC AATTTTCTT TAAAAGTAGT 1980  
 ACAATTTCTT TTGTAGCTTC AATTCCTTAT ATGACTTCAG ACTGGAGAAG CCTGTTAAAC 2040  
 35 CACTGTAGT TCTCAGTTAGA AAGTCTGAGA GACTTTATAC ATAAATTCTC AATTGGCTG 2100  
 CTGTACAGCT GCCAGAGTTT TACTACTGTA GTGACCGTTG AGAAGACCCT TGTTATTGTA 2160  
 CATTTGAAGC ACTGTTTGTG CAAACAACCT TTCATTGTTA AGTGCCTGTA TTCCTTTTCA 2220  
 TTACTTCATG TCCAGGGGTT CTATTTACCT AGAACCATTG TCTACTACAA TTAACATTAT 2280  
 CATTACAAAG TGTTGTGTTT TCTTTTCAA GAGGTTCAA TTAAGGCAAT AAGATGTTTG 2340  
 40 CTGGAGAAAC CTATTGTTTA CTGAAAGCAC TCAATGAAGT CAAATTACTG AAGCTTTTGC 2400  
 CTACATCTTG GTCCTTTATG TAAATATGTT AAATATAACA TCTAAGGAAA ATAAACAATA 2460  
 TTATAATTAT GTGTTTGCCA TTGTCATATC AAACCTTGCTT TGTATCATAC TAATGTTACA 2520  
 TAACCTATCG ATCAATAAAA ATACATTCCA ATGTT

Seq ID NO: 253 DNA sequence

Nucleic Acid Accession #: NM\_001650.2

Coding sequence: 40.1011

50 1 11 21 31 41 51  
 | | | | |  
 GGGGAGGCA ATGAGAGCTG CACTCTGGCT GGGGAAGGCA TGAGTGACAG ACCCAGCA 60  
 AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCTTTCAA 120  
 GGGGTCTGGA CTCAGGCTTT CTGGAAGCA GTCACAGCGG AATTCTGGC CATGCTTATT 180  
 TTTGTCTCC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240  
 55 GTCGACATGG TTCTCATCTC CCTTTGCTTT GGACTCAGCA TTGCAACCAT GGTGTCAGTGC 300  
 TTTGGCCATA TCAGCGGTGG CCACATCAAC CTGTCAGTGA CTGTGGCCAT GGTGTGCACC 360  
 AGGAAGATCA GCATCGCCAA GTCTGTCTTC TACATCGCAG CCCAGTGCCT GGGGGCCATC 420  
 ATTGGAGCAG GAATCCTCTA TCTGGTCACA CCTCCAGTG TGGTGGGAGG CCTGGGAGTC 480  
 ACCATGGTTT ATGGAATCT TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA 540  
 60 TTTCAATTGG TGTTTACTAT CTTTGCCAGC TGTGATTCCA AACGGAAGT TGTCACTGGC 600  
 TCAATAGCTT TAGCAATTGG ATTTTCTGTT GCAATTGGAC ATTTATTTGC AATCAATTAT 660  
 ACTGGTGCCA GCATGAATCC CGCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTGG 720  
 GAAAACCATT GGATATATTG GGTGGGCCC ATCATAGGAG CTGTCTCTGC TGGTGGCCTT 780  
 TATGAGTATG TCTTCTGTCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC 840  
 65 AAAGCTGCCC AGCAACAAA AGGAAGCTAC ATGGAGGTGG AGGACAACAG GAGTCAGGTA 900  
 GAGACGGATG ACCTGATTCT AAAACCTGGA GTGGTGCATG TGATTGACGT TGACCGGGGA 960  
 GAGGAGAAGA AGGGGAAAGA CCAATCTGGA GAGGTATTGT CTTAGTATG ACTAGAAGAT 1020  
 CGCACTGAAA GCAGACAAAG CTCCTTAGAA CTGTCCTCAG ATTTCTCTCC ACCCATTAAG 1080  
 GAAACAGATT TGTATAAAT TAGAAATGTG CAGGTTGTT GTTTCATGTC ATATTACTCA 1140  
 70 GTCTAAACAA TAAATATTTC ATAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200  
 TCCAATCTA AAAAAAGAAA TATTTTAAAG ATGTTCTTAA GCAATATAT ACCTATTTTA 1260  
 TCTAGTTACC TTTTCTTAA ACACCAATTT AACCGTGTGT CAAGATTGGA TTAAGTCTTG 1320  
 CCTGACAGAA CTCAAAGACA CGTCTATCAG CTATTCTCT CTCTACTGGA ATATTGGTAT 1380  
 AGTCAATTCT TATTGAATA TTTATTCTAT TAAACTGAGT TTAACAATGG C

Seq ID NO: 254 Protein sequence

Protein Accession #: NP\_001641.1

80 1 11 21 31 41 51  
 | | | | |  
 MDRPTARRV GKCGPLCTRE NIMVAFKGVW TQAFWKAVTA EFLAMLIFVL LSLGSTINWG 60  
 GTEKPLEPDM VLLSLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTRKI SIAKSVFYIA 120  
 AQCLGAIIGA GILYLVTPPS VVGGLGVMTV HGNLTAGHGL LVELIITFQL VFTIFASCDS 180  
 KRTDVTGSIA LAIGFSAVIG HLFAINYTGA SMNPARSFPG AVIMGNWENH WIYWVGPIIG 240  
 AVLAGGLYIE VFCDPVEFKR RFKEAFSKAA QQTKGSYMEV EDNRSQVETD DLLKPGVVH 300



VIDVDRGEEK KGKQDSGEVL SSV

Seq ID NO: 255 DNA sequence

Nucleic Acid Accession #: U26742.1

Coding sequence: 325..1449

5

1	11	21	31	41	51	
CAGGAAACCC	TGGTACTGGC	AGCAGCCAGC	CTCTGCTGTG	CCCACATGAC	CCACAACCTCT	60
GGCAGCGGAC	CCGGCCTTTC	CAACATTATT	AAATAATAAG	AAAGCGGCTC	CTACTCCAGG	120
CTCAAACCTC	CCTGCAGACC	AATGGACACC	TTCTAAGAGT	TTGGCGAGTC	AGTGACTGAA	180
GGCCCCGTCC	ATTCCAAGAT	AAATAGGATT	TACCAATCCT	TGGATGAAAGT	GCTTGGGAAG	240
TCITTTAAGTG	CCATAATCAA	CTGCCATTTC	AAAGAATATA	GATGGTTTTG	AAAAGTTCAT	300
GCTGTCCCTT	CATTGAATTT	TAGAATGATT	GAAGATAGTG	GGAAAAGAGG	AAATACCATG	360
GCAGAAAGAA	GACAGCTGTT	TGCAGAGATG	AGGGCTCAAG	ATCTGGATCG	CATCCGACTC	420
TCCACCTACA	GAACAGCATG	CAAGCTTAGG	TTTGTTTCAGA	AGAAATGCAA	TTTGCACCTG	480
TGGGACATAT	GGAATGTCAT	AGAAGCATTG	CGGGAAAATG	CTCTGAACAA	CCTGGACCCA	540
AAACACTGAAC	TCAACGTGTC	CCGCTTAGAG	GCTGTGCTCT	CCACTATTTT	TTACCAGCTC	600
AACAAACGGA	TGCCAACCCAC	TCACCAAATC	CATGTGGAGC	AGTCCATCAG	CCTCCTCCTT	660
AACTTCTCTG	TTGCAGCGTT	TGATCCGGAA	GGCCATGGTA	AAATTTTCAGT	ATTGTCTGTC	720
AAAATGGCTT	TAGCCACATT	GTGTGGAGGG	AAGATCATGG	ACAAATTAAG	ATATATTTTC	780
TCAATGATTT	CTGACTCCAG	TGGGGTGATG	GTTTATGGAC	GATATGACCA	ATTCCTTCGG	840
GAAGTTCTCA	AACTACCCAC	GGCAGTTTTT	GAAGTCTCTT	CATTTGGTTA	CACAGAACAC	900
TCAGCCAGAT	CCTGTTTCTC	CCAACAGAAA	AAAGTCACGT	TAAATGGTTT	CTTGGACACG	960
CTTATGTCAG	ATCCTCCCCC	GCAAGTGTCTG	GTCTGGTTGC	CTCTTCTGCA	TCGACTAGCA	1020
AATGTGGAAA	ATGCTTTCCA	TCCGGTTGAG	TGTTCTTACT	GCCACAGTGA	GAGTATGATG	1080
GGATTTTCGCT	ACCGATGCCA	ACAGTGTAC	AATTACCAGC	TCTGTGAGGA	CTGCTTCTGG	1140
AGGGGACATG	CCGGTGGTTC	TCATAGCAAC	CAGCACCAAA	TGAAAGAGTA	CACGTATGAG	1200
AAATCACCTG	CTAAGAAAGT	GACTAATGCA	TTAAGCAAAGT	CCCTGAGCTG	TGCTTCCAGC	1260
CGTGAACCTT	TGCACCCCAT	GTTCCAGAT	CAGCCTGAGA	AGCCACTCAA	CTTGGCTCAC	1320
ATCGTTGATA	CTTGGCCTCC	CAGACCTGTA	ACCAGCATGA	ACGACACCTT	GTTCTCCAC	1380
TCGTGTTCCCT	CCTCAGGAAG	TCCTTTTATT	ACCAGGAGCT	CGGACGGTGC	TTTTGGTGGA	1440
TGCGTCTAGA	TGGATAACAT	GACTTCTTCT	ACCCTAAAAAT	ATTCTCTATA	TACTTTGAGC	1500
TGTTCTGGTT	CCTCCAGGGT	GCAATGGTACC	CATTAACCCA	AAATATGATT	ATTTCCTTTT	1560
TTTCCCATTT	TCAGTCATTT	TGGAATGTTT	TCTGTGAACC	ACAGTTGGGT	TGTTTAAAGC	1620
TCACATTTCT	TTTCTGTACC	ACAGAGATTG	GCCTACGGTT	TCTGTTTGA	GGGTGCTGTT	1680
CAATAAAGCT	GTGTACACTA	AATGTCC				

Seq ID NO: 256 Protein sequence

Protein Accession #: AAC50424.1

40

1	11	21	31	41	51	
MIEDSGKGRN	TMAERRQLFA	EMRAQDLDR	RLSTYRTACK	LRFVQKKCNL	HLVDIWNVIE	60
ALRENALNNL	DPNTELVNVR	LEAVLSTIFY	QLNKRMPPTH	QIHVEQSISL	LLNFLLAAFD	120
PEGHGKISVF	EKKMALATLC	GGKIMDKLRY	IFSMISDSSG	VMVYGRYDQF	LREVLKLPFA	180
VFEGPSFGYT	BQSARSCFSP	QKKVTLNGFL	DTLMSDPPFP	CLVNLPLLHR	LANVENVFHP	240
VECSYCHSES	MMGFYRRCQQ	CHNYQLCQDC	FWRGHAGGSH	SNQHQMKEYT	SWKSPAKKLT	300
NALSKSLSCA	SSREPLHPMF	PDQPEKPLNL	AHIVDTWPPR	PVTSMNNTLF	SHSVSPSGSP	360
FITRSDGAF	GGCV					

Seq ID NO: 257 DNA sequence

Nucleic Acid Accession #: NM\_004172.1

Coding sequence: 179..1807

55

1	11	21	31	41	51	
GCGGATTGTT	GCTCCGTTGT	ACCTGCTGGG	GAATTCACCT	CGTTACTGCT	TGATATCTTC	60
CACCCCTTAC	AAAATCAGAA	AAGTTGTGTT	TTCTAATACC	AAAGAGGAGG	TTTGGCTTTC	120
TGTGGGTGAT	TCCCAGACAC	TGAAGTGCAA	AGAAGAGACC	CTCCTAGAAA	AGTAAATAT	180
GACTAAAAGC	AATGAGAGAG	AGCCCAAGAT	GGGGGGCAGG	ATGGAGAGAT	TCCAGCAGGG	240
AGTCCGTAAA	CGCACACTTT	TGGCCAAGAA	GAAAGTGCA	AACATTACAA	AGGAGGATGT	300
TAAAAGTTAC	CTGTTTCGGA	ATGCTTTTGT	GCTGCTCACA	GTCACCGCTG	TCAATGTGGG	360
TACAATCCTT	GGATTATACC	TCCGACCATA	CAGAATGAGC	TACCGGGAAG	TCAAGTACTT	420
CTCCTTTCTT	GGGGAACTTC	TGATGAGGAT	GTTACAGATG	CTGGTCTTAC	CATTATCAT	480
CTCCAGTCTT	GTCAACAGAA	TGGCGGCGCT	AGATAGTAAG	GCATCAGGGA	AGATGGGAAT	540
GCGAGCTGTA	GTCTATTATA	TGACTACCAC	CATCATTGCT	GTGGTGATG	GCATAATCAT	600
TGTCTATCAT	ATCCATCCTG	GGAAGGGCAC	AAAGGAAAAC	ATGCACAGAG	AAGGCAAAAT	660
TGTACGAGTG	ACAGCTGCAG	ATGCCTTCCT	GGACTTGATC	AGGAACATGT	TCCCTCCAAA	720
TCTGGTAGAA	GCCTGCTTTA	AACAGTTTAA	AACCAACTAT	GAGAAAGAGAA	GCTTTAAAGT	780
GCCCATCCAG	GCCCAACGAA	CGCTTGTGGG	TGCTGTGATA	AACAATGTGT	CTGAGGCCAT	840
GGAGACTCTT	ACCCGAATCA	CAGAGGAGCT	GGTCCCAGTT	CCAGGATCTG	TGAATGGAGT	900
CAATGCCCTG	GGTCTAGTTG	TCTTCTCCAT	GTGCTTCGGT	TTTGTGATG	GAAACATGAA	960
GGAACAGGGG	CAGGCCCTGA	GAGAGTTCTT	TGATTCTCTT	AACGAAGCCA	TCATGAGACT	1020
GGTAGCAGTA	ATAATGTGTT	ATGCCCCCGT	GGGTATTCTC	TTCTCTGATT	CTGGGAAGAT	1080
TGTGGAGATG	GAAGACATGG	GTGTGATTGG	GGGGCAGCTT	GCCATGTACA	CCGTGACTGT	1140
CATTGTTGGC	TTACTCATTC	ACGCAGTTCAT	CGTCTTGCCA	CTCCTCTACT	TCTTGGTAAC	1200
ACGGAAAAAC	CCTTGGGTTT	TTATTGGAGG	GTGTGTCGAA	GCACTCATCA	CCGCTCTGGG	1260
GACCTCTTCA	AGTCTTGCCA	CCCTACCCAT	CACCTTCAAG	TGCCTGGAAG	AGAAACAATGG	1320
CGTGGACAAG	CGCGTCACCA	GATTCGTGCT	CCCCGTAGGA	GCCACCATT	ACATGGATGG	1380
GACTGCCCTC	TATGAGGCTT	TGGCTGCCAT	TTTCAATTGCT	CAAGTTAACA	ACTTTGAACT	1440
GAACTTCGGA	CAAATTATTA	CAATCAGCAT	CACAGCCACA	GCTGCCAGTA	TTGGGGCAGC	1500
TGGAATTCTT	CAGGCGGGCC	TGGTCACTAT	GGTCATTGTG	CTGACATCTG	TCGGCCTGCC	1560
CACTGACGAC	ATCACGCTCA	TCATCGCGGT	GGACTGTTTC	CTGGATCGCC	TCCGGACACC	1620

CACCAACGTA CTGGGAGACT CCCTGGGAGC TGGGATTGTG GAGCACTTGT CACGACATGA 1680  
 ACTGAAGAAC AGAGATGTTG AAATGGGTAA CTCAGTGATT GAAGAGAATG AAATGAAGAA 1740  
 ACCATATCAA CTGATTGCAC AGGACAATGA AACTGAGAAA CCCATCGACA GTGAAACCAA 1800  
 GATGTAGACT AACATAAAGA AACACTTTCT TGAGCACCAG GTGTAAAAAA CCATTATAAA 1860  
 5 ATCTTTCCAT CTCTATACAG CTCATTGCT CCAGCAAGCC CGTCATCTTC CCTTCTCTCC 1920  
 CTCTCGATAA GACTGGAAAA TAGTCTCTCA AAACACAAGG GAGGATTTTG GGTGGCCCAA 1980  
 GTGTACAATT TTCTCCAC AAATGAAATT TTTAAATCAT TTCATGTTAG TCTTACCGAA 2040  
 TAAGGTACCA AGATCACAAA TAGTGTGTAG CAGATCTTAC AAGTTTATGT GGCACACAAT 2100  
 10 TCCTATAAAT GTGATTTTTT TATATAAGTT AAAGAGACAA ATAGTAGGCT AAAAACATTT 2160  
 TAAAATCAAC TTTTGAAATT TAAAAATCTT TCAGAATACA ATTCAGTTTT AGTTTCAAAA 2220  
 TGTTAACAACT TTGAATTACA ACCGGTTATC AGTTGGACAG TAAGATTTTA TCCCTTTCTC 2280  
 TTCTGACTGG TATACCTATT TCATTAGTAG CTAGGTGCAC ATATACATCT AGCAGAGCTG 2340  
 TGAGGACAGA CAGAAGGCAA AGTTTCCATG TGGCCTTGAG CAAGTCCCAT CTCACCTCTA 2400  
 15 GGCCTCAGTG TCCTCATCTA TAAATGAGG GACTTCCCTA GAAGTCTTCA TGGTCTCTTC 2460  
 CAGCCCAGAC ATCTGTGTAT GTCATGAAAG CACCTGCCCT CTGTTTCCCC TCAGAACACC 2520  
 CTGTACCATC CATGGAGCAC GAGGCCTTCA GAAAAGACAC TTCAATGGGA GTGAACATTT 2580  
 CTAACAAAG ACAGGATGGC TGTGTGTGTT GGTCAACCAG TCCTGTGAGC AAAGTGCAGG 2640  
 TTATGCAAGT CGCCAGGCAG GAGGCCATTC CAGGAGTGGG ATTATTCATC AAACCTTTTG 2700  
 CCCAGTTTCA CCCAATGGGG GAAGTATTCC CTCTTTTCTT ACTCTGGGAA GAATGTCTCC 2760  
 20 TGCCACTCCT CAACGTATGA TAGACTTCGA AAACAGATGA GAAGACTAGC AGCTAGCAAG 2820  
 GGTGCTTGTA GTCACACTGT GGAACACTAA AGAGCTAGGA AAGAGTTGAG CACAGGCCAA 2880  
 ATTACAAACA AAGGATTTGA AAACACCAAG AGTACAGGTC TTTCTTAAGG AAGAATAAAA 2940  
 AAGAAGAGGT TCATTTTTCT GGCTTTTTTT TTCACCTGAA ACACTTTTTC TCGAGTCCAA 3000  
 AATCATTTCC CCCGTGAAGT CTGCTTACCA AAACATAAGA CGACTTATAT ATTTGAAAGA 3060  
 25 AGTCAAATGA ATGAGCTCTC TAATAGAAGT CCATGAGTTG AGTGGGTATT TCTTATTGTA 3120  
 AAGTGTTTTT CTTTAATCAA AAGTCTTAG AATGAGGGAA ACAAATATTT TATTGTGTTT 3180  
 GGAATCCAC TTATCAAACT ATTCAAACT TTCAGCTGGA GTGGGGTTTG CTTTGTGTTT 3240  
 GTTTGTGTCC ATAAGAGAAA TGGTAGAAGA TGAATCAGTA TGAAGACT GTCAATGAGG 3300  
 30 TTATGAGAAA AAAACAGCAG GGGCATTAGT TTCAGGCAAG GCAGCTCCCA GGTTAGAGA 3360  
 TTAATTTTTA CCCCTAAGG AATATCCAGT CAAAGACGCT GAGTGGGAGC TGTCAGGCAG 3420  
 TAGCAGCTGT GTTTGAGTTT CTGGCTGAAA ATGGTGAAGA ATGGACTTAA TTATGCTAAC 3480  
 AAACGAAAA ATCTAGACAT AGATCCTCTG ATATACAATT AGAGATATTT TTATATAGAC 3540  
 CCCAAGCATT CTGTGCATAA AAGTTAACAT TAGGCTGTGG TGCAAGTACC ATTTAATGTC 3600  
 35 GAGGCTCTAT TTCGGAATTA CACTACAAAT GTTAAAGTAC GTGGCTGTCC TCTTAAGACA 3660  
 CTAGTAGAGC AAAGACTTAA TCATATCAAC TTAATCTGT TACACAATAT GTGTTTTTTA 3720  
 ATATACTAAC CATTTCTTAT GGAAAGGTCC TGTGGGAGC CCATCTCTC GCCAAGCCAT 3780  
 CACAGGCTCT GCATACACAT GCACTCAGT TGGACTGGGA AGCATTACTT TGTAGATGTA 3840  
 TTTTCAATAA AGAAAAAAT AGTTTTACAT T

Seq ID NO: 258 Protein sequence  
 Protein Accession #: NP\_004163.1

1 11 21 31 41 51  
 45 MTKSNGEPEK MGRMERFQQ GVRKRTLLAK KKVQNITKED VKSYLFRNAF VLLTVTAVIV 60  
 GTILGFTLRP YRMSYREVKY FSFPBELLMR MLQMLVPLI ISSLVTGMAA LDSKASGKMG 120  
 MRADVYMTT TIIAVVIGII IVIIHPGKG TKENMHREGK IVRVTAADAF LDLIRNMFPF 180  
 NLVEACFKQF KTNYEKRSFK VPIQANETLV GAVINNVESEA METLTRITEE LVPVPGSVNG 240  
 50 VNALGLVVFV MCFGFIIGNM KEQGQALREF FDSLNEAIMR LVAVIMWYAP VGILFLIAGK 300  
 IVEMEDMGVI CCGQLAMTVT VIVGLLIHAV IVLPLLYFLV TRKNPNWVFI GLLQALITAL 360  
 GTSSSSATLP ITFKCLEENN GVDKRVTRFV LPVGATINMD GTALYEALAA IFIAQVNMFE 420  
 LNFQIIITIS ITATAASIGA AGIPQAGLVT MVIVLTSVGL PTDDITLIIA VDWFLLRLRT 480  
 TTNVLGDSLQ AGIVEHLRSH ELKNRDVEMG NSVIEENEMK KPYQLIAQDN ETEKPIDSET 540  
 KM

Seq ID NO: 259 DNA sequence  
 Nucleic Acid Accession #: NM\_021948.1  
 Coding sequence: 48..2783

60 1 11 21 31 41 51  
 TGTGGCACTG CTTGCGTACC CAACCCAGC CCTGGGTAGC CTGCAGCATG GCCCAGCTGT 60  
 TCTTGCCCTT GCTGGCAGCC CTGGTCTTGG CCCAGGCTCC TGCAGCTTTA GCAGATGTTT 120  
 65 TGGAAAGGAGA CAGCTCAGAG GACCGCGCTT TTCGCGTGCG CATCGCGGGC GACCGGCCAC 180  
 TGCAGGGCGT GCTCGGCGGC GCCCTCACCA TCCCTTGCCA CGTCCACTAC CTGCGGCCAC 240  
 CGCCGAGCCG CCGGGCTGTG CTGGGCTCTC CGCGGGTCAA GTGGACTTTC CTGTCCCGGG 300  
 GCCGGGAGGC AGAGGTGCTG GTGGCGCGGG GAGTGCCTGT CAAGGTGAAC GAGGCCTACC 360  
 GGTTCGCGT GGCACCTGCT GCGTACCCAG CGTCGCTCAC CGACGTCTCC TTGGCGCTGA 420  
 70 GCAGACTGCG CCCCAACGAC TCAGGTATCT ATCGCTGTGA GGTCCAGCAC GGCAATCGATG 480  
 ACAGCAGCGA CGCTGTGGAG GTCAAGGTCA AAGGGGTCTT CTTTCTCTAC CGAGAGGGCT 540  
 CTGCCCCGTA TGCTTTCTTC TTTTCTGGGG CCCAGGAGGC CTGTGCCCCG ATTGGAGCCC 600  
 ACATCGCCAC CCCGGAGCAG CTCTATGCCG CCTACCTTGG GGGCTATGAG CAATGTGATG 660  
 CTGGCTGGCT GTCCGATCAG ACCGTGAGGT ATCCCATCCA GACCCACGAG GAGGCCTGTT 720  
 75 ACGGAGACAT GGATGGCTTC CCCGGGGTCC GGAACATATG TGTGGTGGAC CCGGATGACC 780  
 TCTATGATGT GTACTGTTAT GCTGAAGACC TAAATGGAGA ATTGTTCTCT GGTGACCCCTC 840  
 CAGAGAAGCT GACATTGGAG GAAGCACGGG CGTACTGCCA GGAGCGGGGT GCAGAGATTG 900  
 CCACCAAGGG CCAACTGTAT GCAGCTGGG ATGGTGGCCT GGACCATGCG AGCCCAAGGT 960  
 GGCTAGCTGA TGGCAGTGTG CGCTACCCCA TCGTCAACCC CAGCCAGCGC TGTGGTGGGG 1020  
 80 GCTTGCTGGT TGTCAAGACT CTCTTCTCTT TCCCCAACCA GACTGGCTTC CCCAATAAGC 1080  
 ACAGCCGCTT CAACGTCTAC TGCTTCCGAG ACTCGGCCCA GCCTTCTGCC ATCCCTGAGG 1140  
 CCTCCAACCC AGCCTCCAAC CCAGCCTCTG ATGGACTAGA GGCTATCGTC ACAGTGACAG 1200  
 AGACCTGGA GGAACCTGCA CTGCCTCAGG AAGCCACAGA GAGTGAATCC CGTGGGGCCA 1260  
 TCTACTCCAT CCCCATCATG GAGGACGGAG GAGGTGGAAG CTCCACTCCA GAAGACCCAG 1320  
 CAGAGGCCCC TAGGACGCTC CTAGAATTG AAACACAATC CATGTTACTT CCCACGGGT 1380

5	TCTCAGAAGA	GGAAAGGTAAG	GCATTGGAGG	AAGAAGAGAA	ATATGAAGAT	GAAGAAGAGA	1440
	AAGAGGAGGA	AGAAGAAGAG	GAGGAGGTGG	AGGATGAGGC	TCTGTGGGCA	TGGCCACGCG	1500
	AGCTCAGCAG	CCCCGGCCCT	GAGGCCTCTC	TCCCCACTGA	GCCAGCAGCC	CAGGAGGAGT	1560
	CACTCTCCCA	GGCGCCAGCA	AGGGCAGTCC	TGCAGCCTGG	TGCATCACCA	CTTCCTGATG	1620
	GAGAGTCAGA	AGCTTCCAGG	CCTCCAAGGG	TCCATGGACC	ACCTACTGAG	ACTCTGCCCA	1680
	CTCCCAGGGA	GAGGAACCTA	GCATCCCCAT	CACCTTCCAC	TCTGGTTGAG	GCAAGAGAGG	1740
	TGGGGAGGCG	AACCTGGTGT	CCTGAGCTAT	CTGGGGTCCC	TCGAGGAGAG	AGCGAGGAGA	1800
	CAGGAAGCTC	CGAGGGTGCC	CCTTCCCTGC	TTCCAGCCAC	ACGGGCCCCCT	GAGGGTACCA	1860
10	GGGAGCTGGA	GGCCCCCTCT	GAAGATAATT	CTGGAAGAAC	TGCCCCAGCA	GGGACCTCAG	1920
	TGCAGGCCCA	GCCAGTGTCTG	CCCACTGACA	GCGCCAGCCG	AGGTGGAGTG	GCCGTGGTCC	1980
	CCGCATCAGG	TGACTGTGTC	CCCAGCCCCCT	GCCACAATGG	TGGGACATGC	TTGGAGGAGG	2040
	AGGAAGGGGT	CCGCTGCCTA	TGTCTGCCTG	GCTATGGGGG	GGACCTGTGC	GATGTTGGCC	2100
	TCCGCTTCTG	CAACCCCGGC	TGGGACGCCT	TCCAGGGCGC	CTGCTACAAG	CACTTTTCCA	2160
15	CACGAAGGAG	CTGGGAGGAG	GCAGAGACCC	AGTGCCGGAT	GTACGGCGCG	CATCTGGCCA	2220
	GCATCAGCAG	ACCCGAGGAA	CAGGACTTCA	TCAACAACCG	GTACCGGGAG	TACCACTGGA	2280
	TCGGACTCAA	CGACAGGACC	ATCGAAGGCG	ACTTCTTGTG	GTCCGATGGC	GTCCCCCTGC	2340
	TCTATGAGAA	CTGGAACCTT	GGGCAGCCTG	ACAGCTACTT	CCTGTCTGGA	GAGAACTGCG	2400
	TGGTCATGGT	GTGGCATGAT	CAGGGACAAT	GGAGTGACGT	GCCCTGCAAC	TACCACCTGT	2460
20	CCTACACCTG	CAAGATGGGG	CTGGTGTCTT	GTGGGCCGCC	ACCGGAGCTG	CCCCTGGCTC	2520
	AAGTGTTCGG	CCGCCACGCG	CTGCCGTATG	AGGTGGACAC	TGTGCTTCGC	TACCGGTGCC	2580
	GGGAAGGACT	GGCCACGCGC	AATCTGCCGC	TGATCCGATG	CCAAGAGAAC	GGTCGTTGGG	2640
	AGGGCCCCCA	GATCTCCTGT	GTGCCAGAAA	GACCTGCCCG	AGCTCTGCAC	CCAGAGGAGG	2700
	ACCCAGAAAG	ACGTCAAGGG	AGGCTACTGG	GACGCTGGAA	GGCGCTGTTG	ATCCCCCTTT	2760
25	CCAGCCCCAT	GCCAGGTCCC	TAGGGGGCAA	GGCCTTGAAC	ACTGCCGGCC	ACAGCACTGC	2820
	CCTGTCACCC	AAATTTTCCC	TCACACCTCG	CGCTCACCAC	AGGAAGTGAC	AACATGAC	

Seq ID NO: 260 Protein sequence  
Protein Accession #: NP\_068767.1

30	1	11	21	31	41	51	
	MAQLFLPLLA	ALVLAQAPAA	LADVLEGDSS	EDRAFRVRIA	GDAPLQGVLG	GALTIPCHVH	60
	YLRPPPSRRA	VLGSPRVKWT	FLSRGREAEV	LVARGVRVKV	NEAYRFRVAL	PAYPASLTDV	120
35	SLALSELRPN	DSGIYRCBVQ	HGIDSSDAV	EVKVKGVVFL	YREGSARYAF	SFSGAQEACA	180
	RIGAHIAIPE	QLYAYLGGY	BQCDAGWLS	QTVRYPIQTP	REACYGDMDG	FPGVNRNYGVV	240
	DPDDLVDVYC	YAEIDLNGELF	LGDPPPEKLT	EEARAYCQER	GAEIATTNQL	YAANDGGLDH	300
	CSPGWLADGS	VRYPIVTPSQ	RCGGGLPGVK	TLFLFPNQTG	FPNKHRSRNV	YCFRDSAQPS	360
	AIPEASNPA	NPASDGLLEAI	VTVTETLEEL	QLPQEAETSE	SRGAIYSIPI	MEDGGGGSST	420
40	PEDPAEAPRT	LLEFETQGMV	PPTGFSEEEG	KALEEBEEKYE	DEEBKEEBEE	EEVEDEALW	480
	AWPSELSPFG	PEASLPTEPA	AQEEELSQA	ARAVLQPGAS	PLPDGESEAS	RPPRVHGPFT	540
	ETLPTPRENR	LASPSPTLV	EAREVGEATG	GPESLGVPRG	ESEETGSSEG	APSLLPATRA	600
	PEGTRELEAP	SEDNSGRAP	AGTSVQAQPV	LPTDSASRGG	VAVVPASGDC	VPSFCHNGGT	660
	CLEEEEGVRC	LCLPGYGGDL	CDVGLRFCNP	GWDAFQGACY	KHFSTRRSWE	EAETQCRMVY	720
45	AHLASISTPE	BQDFINNRYR	EYQWIGLND	TIEGDFLWSD	GVPLLYENWN	PGQPD SYFLS	780
	GENCVVMVWH	DQGNQSDVPC	NYHLSYTKCM	GLVSCGPPPE	LPLAQVFGRP	RLRYEVDTVL	840
	RYRCREGLAQ	RNLPLIRCQE	NGRWEAPQIS	CVPRRPARAL	HPEDDEPEGRQ	GRLLGRWKAL	900
	LIPSSPMFPG	P					

Seq ID NO: 261 DNA sequence  
Nucleic Acid Accession #: NM\_004386.1  
Coding sequence: 2..3967

55	1	11	21	31	41	51	
	GATGGGGGCC	CCGTTTGTCT	GGGCCTTGGG	CCTTTTGATG	CTGCAGATGC	TGCTCTTTGT	60
	GGCTGGGGAA	CAGGGCACAC	AGGATATCAC	CGATGCCAGC	GAAAGGGGGC	TCCACATGCA	120
	GAAAGCTGGG	TCTGGGTGAG	TGCAGGCTGC	GCTGGCGGAG	CTGGTGGCCC	TGCCCTGTCT	180
	CTTTACCCTG	CAGCCACGGC	CAAGCGCAGC	CCGAGATGCC	CCTCGGATAA	AGTGGACCAA	240
60	GGTGCGGACT	CGCTCGGGCC	AGCGACAGGA	CTTGCCCATC	CTGGTGGCCA	AGGACAAATG	300
	CGTGAGGPTG	GCCAAAAGCT	GGCAGGGACG	AGTGTCACTG	CCTTCTTACC	CCCGCGCGCG	360
	AGCCAACGCC	ACGCTACTTC	TGGGGCCACT	GAGGGCCAGT	GACTCTGGGC	TGTACCGCTG	420
	CCAGGTGGTG	AGGGGCATCG	AGGATGAGCA	GGACCTGGTG	CCCTTGGAGG	TGACAGGTGT	480
	TGTGTTCCAC	TACCGATCAG	CCCGGGACCG	CTATGCATCG	ACCTTCGCTG	AGGCCACGGA	540
65	GGCCTGCCGT	CTCAGCTCAG	CCATCATTGC	AGCCCTCGCG	CATCTACAGG	CTGCCTTTGA	600
	GGATGGCTTT	GACAACTGTG	ATGCTGGCTG	GCTCTCTGAC	CGCACTGTTC	GGTATCCTAT	660
	CACCCAGTCC	CGTCTGTGTT	GCTATGGCGA	CCGTAGCAGC	CTTCCAGGGG	TTCGGAGCTA	720
	TGGGAGGCGC	AACCCACAGG	AACTCTACGA	TGTGTATTGC	TTTGCCCGGG	AGCTGGGGGG	780
	CGAGGTCTTC	TACGTGGGCC	CGGCCGCGCG	CCTGACACTG	GCCGCGCGCG	GTGCACAGTG	840
70	CCGCCGCGAG	GGTGCCGCGC	TGGCCTCGGT	GGGACAGCTG	CACCTGGCCT	GGCATGAGGG	900
	CCTGGACCA	TGCGACCGCG	GCTGGCTGGC	CGACGGCAGC	GTGCGCTACC	CGATCCAGAC	960
	GCCGCGCCGG	CGCTGCGGGG	GGCCAGCCCC	GGGCGTGCGC	ACCGTCTACC	GCTTCGCTAA	1020
	CCGACCGCGC	TTCCCTCTAC	CCGCCGAGCG	CTTCGACGCC	TACTGCTTCC	GAGCTCATCA	1080
	CCCAACGTCA	CAACATGGAG	ACCTAGAGAC	CCCATCTCT	GGGATGAGG	GGGAGATTCT	1140
75	GTCAGCAGAG	GGGCCCCCAG	TTAGAGAACT	GGAGCCCACC	CTGGAGGAGG	AAGAGGTGGT	1200
	CACCCCTGAC	TTCCAGGAGC	CTCTGGTGTG	CAGTGGGGAA	GAAGAAACCC	TGATTTTGTG	1260
	GGAGAAGCAG	GAGTCTCAAC	AGACCCTCAG	CCCTACCCCT	GGGGACCCCA	TGCTGGCTGA	1320
	ATGGCCCACT	GGGGAAGTGT	GGCTAAGCAC	GGTGGCCCCC	AGCCCTAGCG	ACATGGGGGC	1380
	AGGCACTGCA	GCAAGTTTCA	ACACGGAGGT	GGCCCCAACT	GACCCTATGC	CTAGGAGAAG	1440
80	GGGGCGCTTC	AAAGGGTTGA	ATGGGCGCTA	CTTCCAGCAG	CAGGAACCGG	AGCCGGGGCT	1500
	GCAAGGGGGG	ATGAGAGGCC	GCGCCAGACC	CCCCACCTCA	GAGGCTGCAG	TGAACCAATG	1560
	GGAGCCTCCG	TTGGCCATGG	CAGTCACAGA	GATGTTGGGC	AGTGGCCAGA	GCCCGAGCCC	1620
	CTGGGCTGAT	CTGACCAATG	AGGTGGATAT	GCCTGGAGCT	GGTTCGTGCT	GTGGCAAGAG	1680
	CTCCCCAGAG	CCCTCGCTGT	GGCCCCCTAC	CATGGTCCCA	CCCAGCATCT	CAGGCCACAG	1740
	CAGGGCCCCCT	GTCTCTGGAG	TAGAGAAAGC	CGAGGGCCCC	AGTGCCAGGC	CAGCCACCCC	1800

5 AGACCTGTTT TGGTCCCCT TGGAGGCCAC TGTCTCAGCT CCCAGCCCTG CCCCTGGGA 1860  
 GGATTCCTCT GTGGCCACCT CCCAGATCT CCCTATGATG GCCATGCTGC GTGGTCCAA 1920  
 AGAGTGGATG CTACCACACC CCACCCCAT CTCCACCGAG GCCAATAGAG TTGAGGCACA 1980  
 TGGTGGAGCC ACCGCCACGG CTCACCCCTC CCTGTGTCGA GAGACCAAGG TGTATTCCCT 2040  
 GCCTCTCTCT TTGACCCCAA CAGGACAGGG TGGAGAGGCC ATGCCACAA CACCTGAGTC 2100  
 CCCAGGGCA GACTTCAGAG AAAGTGGGGA GACCAGCCCT GCTCAGGTCA ACAAGCTGA 2160  
 GCCTCCAGC TCCAGCCCAT GGCCTTCTGT AAACAGGAAT GTGGCTGTAG GTTTGTCCC 2220  
 CACTGAGACT GCCACTGAGC CAACGGGCTT CAGGGGTATC CCGGGGTCTG AGTCTGGGGT 2280  
 10 CTTGACACCA CGAGAAGGCC CCACTTCTGG CTTGCAGGCC ACTGTAGATG AGGTGCAGGA 2340  
 CCCTGGCCCC TCAGTTTACA GCAAAGGGCT GGATGCAAGT TCCCCATCTG CCCCCCTGGG 2400  
 GAGCCCTGGA GTCTTCTTGG TACCCAAAGT CACCCCAAT TTGGAGCCTT GGGTTGCTAC 2460  
 AGATGAAGGA CCCACTGTGA ATCCCATGGA TTCCACAGTC ACGCCGGCCC CCAGTGTATG 2520  
 TAGTGGAATT TGGGAACCTG GATCCCAGGT GTTTGAAGAA GCCGAAAGCA CCACCTTGAG 2580  
 15 CCCTCAGGTG GCCTGGATA CAAGCATGTG GACGCCCTC ACGACCTGG AGCAGGGGGA 2640  
 CAAGGTGGA GTTCCAGCCA TGCTACACT GGGCTCCTCA AGCTCCCAAC CCCACCCAGA 2700  
 GCCAGAGGAT CAGGTGGAGA CCCAGGGAAC ATCAGGAGCT TCAGTGCTC CGCATCAGAG 2760  
 CAGTCCCCTA GGGAAACCGG CTGTTCTCTC TGGGACACCG ACTGCAGCCA GTGTGGGCGA 2820  
 GTCTGCCTCA GTTTCCTCAG GGGAGCCTAC GGTACCGTGG GACCCCTCCA GCACCTTGCT 2880  
 20 GCCTGTCACT CTGGGCATAG AGGACTTCGA ACTGGAGGTC CTGGCAGGGA GCCCGGGTGT 2940  
 AGAGAGCTTC TGGGAGGAGG TGGCAAGTGG AGAGGAGCCA GCCTGTCAG GACCCCTAT 3000  
 GAATGCAGGT GCGGAGGAGG TGCACTCAGA TCCCTGTGAG AACAACCTTT GTCTTCATGG 3060  
 AGGACATGT AATGCCAATG GCACCATGTA TGGCTGTAGC TGTGATCAGG GCTTCGCCGG 3120  
 GGAGAACTGT GAGATTGACA TTGATGACTG CCTTGCAGC CCCTGTGAGA ATGGAGGCAC 3180  
 25 CTGTATTGAT GAGGTCAATG GCTTTGTCTG CTTTGTCTC CCAGCTATG GGGGCACTT 3240  
 TTGTGAGAAA GACACCGAGG GCTGTGACCG CGGCTGGCAT AAGTTCAGG GCCACTGTTA 3300  
 CCGCTATTIT GCCCACCGGA GGGCATGGGA AGATGCCGAG AAGGACTGCC GCGCCGCTC 3360  
 CCGCCACCTG ACCAGCCTCC ACTCACCGGA GGAACACAGC TTCATTAATA GCTTGGGCA 3420  
 TGAACACAGC TGGATCGGCC TGAACGACAG GATCGTGGAG AGAGATTTC AGTGGACGGA 3480  
 30 CAACACCGGG CTGCAATTGG AGAAGTGGC AGAGAACCAG CCGGACAATT TCTTCGCGGG 3540  
 TGGCGAGGAC TGTGTGGTGA TGGTGGCGCA TGAAGCGGG CGCTGGAACG ATGTCCCTCTG 3600  
 CAACTACAACT CACCTCTATG TCTGCAAGAA GGGCACAGTG CTCTGTGGTC CCCCTCCGGC 3660  
 AGTGGAGAAT GCCTCACTCA TCGGTGCCCG CAAGGCCAAG AACATATGTC ATGCCACTGT 3720  
 AAGGTACCAG TGCAATGAAG GATTGTGCCA GCACCATGTG GTCACCATTC GATGCCGGAG 3780  
 35 CAATGGCAAG TGGACAGGAG CCCAAATTGT CTGCACCAA CCCAGACGTT CACATCGGAT 3840  
 GCGGGGACAC CACCACCACT ACCAACACCA CCACCAGCAT CACCACCACA AATCCCGCA 3900  
 GGAGCGCAGA AAACACAAGA AACACCCAAC GGAGGACTGG GAGAAGGACG AAGGGAATTT 3960  
 TTGCTGAAGA ACCAGAAAAA AGAAGACACA ACACCTTCC CATGCCCTCT CTGGAGCCTT 4020  
 CGCCTGGGGA GACAGAACC AGAGAGAAAC AAGAGAGTCC AGAAGTCCCT GAACCCCAA 4080  
 40 CTGTTCTCGC AAAAAAATA TTCTTTGAA CAAAGGTCTT CTTTCTCTTT TTTTACATAC 4140  
 ACAAGATCTT CTTGGCAGGT GGAGCCAGGT GTCTGAAAAG TTCATTCTCG TCTGGCTGAA 4200  
 CTCTGGGAGT GTGTCCAGC TGAGGGAAGC ACAAGTAGCA AAGCTCATTT GTCTGGTCTC 4260  
 TTGTTTGCCA GTGTGATGA AGCAGGCCCT GATGAGGGTG CATGAGTGA TGTTTGCATT 4320  
 CACATGAAGG AATGTCTTT CACACCAGAA ATTCAGACTT AGTCAATGTT GGCTGAATTC 4380  
 45 CTAATCCAG GAAGAAGCCT GGAGCTAGGG TCATTAGCTT TGGGAATAGA AGGCTACACA 4440  
 GAAGCACACT GTTTTGTGAC TTGACAACAG CTCTCCCTTT ACCCTGGACT TCAGCCCAAG 4500  
 TTCCGTCTTT GGTCTTGTG GATAAACACA CAGTGTGGAG ATCCACAGTA CTGCATTTA 4560  
 GGGATGTTTT TAGGACAACC TCCCTCCATG CCTTCAGAGT TAGGAGTGA AATGATACCA 4620  
 GCAATATGTA GGTGATGGAG GGAGAGTGA TTGCTAACCC TTCCAGGTCT AGTCCAGCGC 4680  
 50 TGAGATTGGG TGTTTCTGCA TGTGTGATGA ATCTCTTCA CACAAATAGA CGAGAGGATA 4740  
 TTTAGGGCTA GATGAGCCCA GATTCTTCC CCTCCATCT CTCAGGGAGA CAAAGAACCT 4800  
 CCTTCTGGA CCAAGGAGGT GCTGCCAAGT TTTCTAGCCC AGTGACATA CCCAGTCTCT 4860  
 AAGCAGACTT TGGTAGTGCC CCGGCCCTGG GTCCCACTCC TGCCCCACCC CACCTTGTCT 4920  
 CTGGGCCATT GCCTGGTGGT CTAGAAACAC TTAACACTTG AAGTAGTGAC ACCTACCTGC 4980  
 55 GGTCAATTTG TAGAGAGATG CTCAGTGTTA AAAGTGAAC ACACAAACAC ACACACACAC 5040  
 ACATTTTTCT CTGTAGATT TTAATTTTTT AAGTGGGAAA GAACCTACCT TGCCTTCTCT 5100  
 CCCCAAATGT GCAACCTGTA AAAGTCTCT CCACACCAGG GGCCAGGATC CAGTTCCTCT 5160  
 ATCTCTGGCA GGAAGAGATC ACAGCTTTTC CTCCATGTCT GTTACTACTT TTCAGCAGTC 5220  
 CGGGTAAAT CTGTGGATCA GGGTTAAAAA AGCACCCTGG AGAATGGCCC TCTTCAGGAA 5280  
 60 AGAAAAATAA GCAACTGAAT GGTCCACCTA GGGGTTCAGT AAAGAAAGAA ATGTGTTAAC 5340  
 TGAGCCTGAA TCCCTCTGG GAAGTAATAA TGACCAATTGA CAACTAAGAA GTAGACCA 5400  
 TGCTAAAGAC TTACATACAA TCTCCTTGAA TCTTCTCAAT AGCCCATGTA CTTAGAAACT 5460  
 GTTACTTTCC CATTTTACAC ACAGTGAAAC TGAGGCTCAG ATATAAAGGA AAGGTACTGG 5520  
 CTTGAAGTCA CAACCAAGC AGGAGTAAGG ATTTGGAATA AGGATTGGT CCTGTTTTCT 5580  
 65 GGACCAATC CTACTCTGG CTCTGCTTAC ACTTCTCTC CATCACCATA TCCTTACTCC 5640  
 AAATCCAGAA GTCAGAGCCA ACTCCCATCT TGGTCTGAC CCAATCCTG CTCTGGACTC 5700  
 TGGAGAGGAG ATTGAATAT AATTGCACCC TCATACACAT TTAGGAAATG GTTAAGAAGT 5760  
 GTAAACTGAA CCTTATCTCT TGTCTTCAAT CTTCCTCCCT GTAGACATCT ATCTTATTAT 5820  
 GGTATTATT CAGAAAACCC AGGGATACAG GTTGTCTTC TTACTTTGAT AACTCTTCTT 5880  
 70 AGTTTAAAT AATAATAATA ACACATCTTT GGTCTCTAT GTACACAAA AATTTTCTCT 5940  
 TGTTCGCGG GGGCTGGGGA TGCAAGTGT TTTGGGGGGT CTGTTTAT GCTCCCTGCC 6000  
 CTTAGCCCC TCAGCCGTTT GCCCTGCCCC CACCTCGGCT CCATGGTGGG AGGGGGCTCT 6060  
 GGTCTTTTCT AAAGTGGGCG GTTGTCTTT TGATCTTCC CTTTGGATG TGCGTGTGTG 6120  
 TCTGCGTGTG CCATGTGCGT GGCACGCATA TGAGTGTGTG TGCGTGTGAA CGGCTTGGG 6180  
 75 TCTGCTGGT TTTGCTGTGA GCTGCAAGT TCTGTGGGTC TGTGGTATCT GACACTGTGG 6240  
 ACATTAAATG ACTTCTTGA CATTTTAATA AATTTTAA CAGTTCAAAA AAAAAA 6300  
 AAAAAA

Seq ID NO: 262 Protein sequence  
 Protein Accession #: NP\_004377.1

1 11 21 31 41 51  
 | | | | |  
 MGAPFVWALG LLMLQMLLFV AGEQGTQDIT DASERGLHMQ KLGSGSVQAA LAELVALPCL 60

5	FTLQPRPSAA	RDAPRIKWT	VRTASGQRQD	LPILVAKDNV	VRVAKSWQGR	VSLPSYPRRR	120
	ANATLLGLPL	RASDSGLYRC	QVVRGIEDEQ	DLVPLEVTGV	VFHYRSARDR	YALTFAAEQE	180
	ACRLSSAIIA	APRHQAFAFE	DGFNDNCDAGW	LSDRTVRYPI	TQSRPGCYGD	RSSLPGVRSY	240
	GRNRPQELYD	VYCFARELGG	EVFYVGPARR	LTLAGARAQC	RRQGAALASV	GQLHLAWHEG	300
	LDQCDPGLWA	DGSVRYPIQT	PRRRCGGPAP	GVRTVYRFAN	RTGFPSPAER	FDAYCFRAHH	360
	PTSQHGDLST	PSSGDEGEIL	SAEGPPVREL	EPTLEEEEVV	TPDFQEPLVS	SGEEETLILE	420
	EKQESQQTLS	PTPGDPMPLAS	WPTGEVWLST	VAPSPSDMGA	GTAASSHTIEV	APTDPMPRRR	480
	GRFKGLNGRY	FQQQEPEFGL	QGGMEASAPQ	PTSEAAVNQM	EPPLAMAVTE	MLGSGQSRSP	540
10	WADLTNEVDM	PGAGSAGGKS	SPEPWLWPPT	MVPPSISGHS	RAPVLELEKA	EGPSARPATP	600
	DLFWSPLEAT	VSAFSPAPWE	AFPVATSPDL	PMMAMLRGFK	EWMLPHPTPI	STEANRVEAH	660
	GEATATAPPS	PAAETKVYSL	PLSLTPTGGG	GEAMPTTPES	PRADFRETGE	TSPAQVNKAE	720
	HSSSSPWPSV	NRNVAVGFVP	TETATEPTGL	RGIPGSESGV	FDTAESPTSG	LQATVDEVQD	780
	PWPSVYSKGL	DASSPSAPLG	SPGVFLVPKV	TPNLEPWVAT	DEGPTVNPMD	STVTPAPSDA	840
15	SGIWEFGSQV	FEAEESTTLS	PQVALDTSIV	TPLTLEQGD	KVGVPAMSTL	GSSSSQPHPE	900
	PEDQVETQGT	SGASVPPHQS	SPLGKPAVVP	GTPTAASVGE	SASVSSGEPT	VPWDPSSTLL	960
	PVTGLIEDFE	LEVLAGSPGV	ESFWEEVASG	EEPALPGTPM	NAGAEVHSD	PCENNPLCHG	1020
	GTCNANGTMY	GCSCDQGFAG	ENCEIDIDDC	LCSPCEGGT	CIDEVNGFVC	LCLPSYGGSF	1080
	CEKTEGDCR	GWHKFQGHY	RYFAHRRRAWE	DAEKDCRRRS	GHLTSVHSPE	EHSFINSFGH	1140
20	ENTWIGLNDR	IVERDFQWTD	NTGLQFENWR	ENQPDNFFAG	GEDCVVMVAH	ESGRWNDVPC	1200
	NYNLFPYVCK	GTIVLCGPPPA	VENASLIGAR	KAKNNVHATV	RYQCNEGFAQ	HHVVTIRCRS	1260
	NGKWDRPQIV	CTKPRRSHRM	RGHHHHHQHH	HQHHHHSRK	ERRKHKHPT	EDWEKDEGNF	1320
	C						

Seq ID NO: 263 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 7..2085

30	1	11	21	31	41	51	
	GCCGCGATGG	CCAGCACCAG	GAGTATCGAG	CTGGAGCACT	TTGAGGAACG	GGACAAAAGG	60
	CCGCGGCCGG	GGTCGCGGAG	AGGGGCCCCC	AGCTCCTCCG	GGGGCAGCAG	CAGCTCGGGC	120
	CCCAAGGGGA	ACGGGCTCAT	CCCCAGTCCG	GCGCACAGTG	CCCACTGCAG	CTTCTACCGC	180
	ACGCGGACCC	TGCAGGCCCT	CAGCTCGGAG	AAGAAGGCCA	AGAAGGCGCG	CTTCTACCGG	240
	AACGGGGACC	CTACTTCAA	GGGCTTGGTG	TTTGCCATCT	CCAGCGACCG	CTTCCGGTCC	300
35	TTGATGCGC	TCCTCATAGA	GCTCACCCGC	TCCCTGTCTG	ACAACGTGAA	CCTGCCCCAG	360
	GGTGTCCGCA	CTATCTACAC	CATCGACGGC	AGCCGGAAGG	TCACCAAGCT	GGACGAGCTG	420
	CTGGAAGGTG	AGAGTTACGT	GTGTGCATCC	AATGAACCAT	TTCGTAAAGT	CGATTACACC	480
	AAAAATATTA	ATCCAAACTG	GTCTGTGAAC	ATCAAGGGTG	GGACATCCCG	AGCGCTGGCT	540
	GCTGCCTCCT	CTGTGAAAG	TGAAGTAAAG	GAAAGTAAAG	ATTTCATCAA	ACCCAAGTTA	600
40	GTGACTGTGA	TTGGAAGTGG	AGTGAAGCCT	AGAAAAGCCG	TGCGGATCCT	TCTGAATAAA	660
	AAGACTGTCT	ATTCTTTTGA	ACAAGTCTTA	ACAGATATCA	CCGAAGCCAT	TAAACNAGCC	720
	TACAGAGTGG	TCAAGAGGCT	CTGCACCCCT	GATGGAAAGC	AGGTGAGAGT	TACGTGTGTG	780
	CATCTGCCAG	ACTTTTTTGG	TGATGACGAT	GTTTTTATTG	CATGTGGACC	AGAAAAATTT	840
	CGTTATGCCC	AAGATGACTT	TGTCCTGGAT	CATAGTGAAT	GTCTGTCTCT	GAAGTCATCT	900
45	TATTCTCGAT	CCTCAGCTGT	TAAATATTCT	GGATCCAAAA	GCCTTGGGCC	CTCTCGACGC	960
	AGCCAGATTT	CTGCTCATGG	CAGATCTTCT	TCCAATGTAA	ACGGTGGACC	TGAGCTTGAC	1020
	CGTTGCATAA	GTCTTGAAG	TGTGAATGGA	AACAGATGCT	CTGAATCATC	AACCTCTTCT	1080
	GAGAAATACA	AAATTTGAAA	GGTCATTGGT	GATGGCAATT	TTGCAAGTAGT	CAAAGAGTGT	1140
	ATAGACAGGT	CCACTGGAAA	GGAGTTTGCC	CTAAAAGATT	TAGACAAAAGC	CAATGTTTGT	1200
50	GGAAAGGAAC	ACCTGATTGA	GAATGAAGTG	TCAATCTGCG	GCCGAGTGAA	ACATCCCAAT	1260
	ATCATTATGC	TGCTCGAGGA	GATGGAAACA	GCAACTGAGC	TCCTTCTGGT	GATGGAATTG	1320
	GTCAAAGGTG	GAGATCTCTT	TGATGCAATT	ACTTCGTCGA	CCAAGTACAC	TGAGAGAGAT	1380
	GGCAGTGCCA	CTTAGCCAA	CTTAGCCAA	GCCCTCAGGT	ATCTCCATGG	CCTCAGCATC	1440
	GTGCACAGAG	ACATCAAAAC	AGAGAATCTC	TTGGTGTGTG	AATATCCTGA	TGGAACCAAG	1500
55	TCCTTGAAC	TGGGAGACTT	TGGCCTTGCG	ACTGTGGTAG	AAGGCCCTTT	ATACACAGTC	1560
	TGTGGCACAC	CCACTTATGT	GGCTCCARAA	ATCATTGCTG	AACTGGCTA	TGGCCTGAAG	1620
	GTGGACATTT	GGGCAGCTGG	TGTGATCACA	TACATACTTC	TCTGTGGATT	CCCACCATTC	1680
	CGAAGTGAGA	ACAATCTCCA	GGAAGATCTC	TTCCAGCAGA	TCTTGGCTGG	GAAGCTGGAG	1740
	TTTCCGGCCC	CCTACTGGGA	TAACATCACG	GACTCTGCCA	AGGAATTAAT	CAGTCAAAATG	1800
60	CTTCAGGTAA	ATGTTGAAGC	TCCGTGTACC	GCGGGACAAA	TCCTGAGTCA	CCCCTGGGTG	1860
	TCAGATGATG	CCTCCAGGGA	GAATAACATG	CAAGCTGAGG	TGACAGGTAA	ACTAAAACAG	1920
	CACTTTAATA	ATGCGCTCCC	CAACAGAAAC	AGCACTACCA	CCGGGGTCTC	CGTCATCATG	1980
	GTGAGTGGAA	GCGCGCAGGT	CTGGCCTGAC	TGCGGAGCCG	GCCTTGAAGT	TTTTGAATTA	2040
	GGTAGCCGGG	AGCTGCCCTC	ACATGGAAGT	TGGTGCCTTC	CGTAGTCCTA	TTTCATATGA	2100
65	AGATTGGCTT	GGCATGTGGA	GGGCACTCAT	TCGGCAACTC	CCAGGCTTTG	GGCACTGTGT	2160
	GGAGGGGCTT	GTGTAGGGAC	CAGCAGGCCT	GGTGTGAGGG	GTCCAGGCGT	CAAGGAGCTC	2220
	CTGGCTGGGC	CCTCTGGGCA	GCTGCTTCCA	CTCTTGTCTC	TGCTTCTCTA	TCTAGAGAGA	2280
	CTCCCAAGCC	CTGGAGGGGT	GTGTTGTGTT	AGGAATTAAC	TCCCTGCCTA	CCCCAAGGCC	2340
70	TCAGAAATAG	ATTATTAGAG	ATGTGAATTA	TTCTTTGAGA	CTTGGGATAA	GAAACAGCCA	2400
	AAGCTAAACA	TATTTCAAGT	TTAAAAATC	AGTGTTTTAT	AAAACACAGT	TTGGGGCTTT	2460
	TAAAGGTACA	TAACTCAAGG	AAAAAATATA	TATTCATTTT	TCAGGGTTGG	TAAACATTTA	2520
	TGAGATGTCA	GTGACAAACA	TGGCCTTATT	TTTTTTCAGC	TTTTTCTCTT	CCAAAATGTT	2580
	TCTTAAGGCA	ACTCTCTTAA	ATACATAAAC	ACAACAAATT	AAAATGAAAA	GTGACATGAG	2640
75	AGTAAATGAA	TCAAAGGAAA	AAAACATTGA	ACCAGAGGTG	AGGGCAGCAC	ACCCGAGACA	2700
	GCTGTCCAGG	CCTGAGCCAA	TGCAACCTTG	GGCGGGAAGG	CCAGCTCACC	GTGAGCAGGT	2760
	AGAAGCCAGC	CAGCCACCCA	GGCAGGGACC	TTGGTCTCTC	CCACACACTC	CCAGGAGCAG	2820
	GGAAACAGGG	TGGAGTGGCC	TTTCCAGAG	CTGGAGTTGG	CTGCAGCAGC	TTTCAATCA	2880
	GACCTGCCAA	GGTGAATGGC	GTCTGAGTTT	CACATCTGGG	CCCCCGTGA	CCCCACTGAG	2940
	TCCTGACAGC	TAAGATGGGG	CCACCTCCAC	AGCTCCGTCA	CTCGTACTTG	GGACAGGCTC	3000
80	CTCATCTCT	GGGAAGGTCC	TCCTTGTTC	CTACCCAAC	AGAAGGGAAA	CAGTGGCATA	3060
	TTCTCATGGT	ACATGGTTGT	CTGAAAGCCT	TACCTAGGAA	GACGCAGGGT	CTAGATAGAA	3120
	GCTATAAGCA	AGCCACACAC	ATAACCCACA	TCCCCACACC	CCCAACATCC	CCCACACTCC	3180
	CCACACCCCC	CACACCCCC	ACATCCCCAC	CATAATTACC	CCCACCTCCA	AATATCTCAT	

Seq ID NO: 264 Protein sequence  
Protein Accession #: Eos sequence

5	1	11	21	31	41	51	
	MASTRSIELE	HFEERDKRPR	PGSRRGAPSS	SGGSSSSGPK	GNGLIPSPAH	SAHCSFYRTR	60
	TLQALSSEKK	AKKARFYRNG	DRYFKGLVFA	ISSDRFRSFD	ALLIELTRSL	SDNVNLPQGV	120
	RTIYTIDGSR	KVTSLEDELLE	GESYVCASNE	PFRKVDYTKN	INPNWSVNIK	GGTSRALAAA	180
	SSVKSEVKES	KDFIKPKLVT	VIRSGVKPRK	AVRILLNKKT	AHSFEQVLTD	ITEAIKXASG	240
10	VVKRLCTLDG	KQVRVTCVHL	PDDFGDDVDF	IACGPEKFRY	AQDDFVLDS	ECRVLKSSYS	300
	RSSAVKYSGS	KSPGFSRRSQ	ISAHGRSSSN	VNGGPELDRC	ISPEGVNGNR	CSESSTLLEK	360
	YKIGKVIDGD	NFAVVKECID	RSTGKEFALK	IDKAKCCGK	EHLIENEVSI	LRRVKHPNII	420
	MLVEEMETAT	ELFLVMELVK	GGDLFDAITS	STKYTERDGS	AMVYNLANAL	RYLHGLSIVH	480
15	RDIKPENLLV	CEYPDGTGKSL	KLGDGFLATV	VEGPLYTVCG	TPTYVAPXII	AETGYGLKVD	540
	IWAAGVITYI	LLCGFPFPRS	ENNLQEDLFD	QILAGKLEFP	APYWDNITDS	AKELISQMLQ	600
	VNVBARCTAG	QILSHPWVSD	DASQENNMQA	EVTGKLKQHF	NNALEPKQNST	TTGVSVMIVS	660
	GRRQVWPCDG	AGLEVFEGLS	RELPSHGWSW	LP			

Seq ID NO: 265 DNA sequence  
Nucleic Acid Accession #: AB020684.1  
Coding sequence: 1..1744

25	1	11	21	31	41	51	
	CCCCCTTGTC	ATTAATACAT	TAAAAAGATT	CAATCTTTAC	CCTGAGGTAA	TTTTGGCCAG	60
	TGGGTACCCG	ATTTATACCA	AAATAATGGA	CTTGATTGGT	ATTCAAACCA	AGATATGTTG	120
	GACGGTTACC	AGAGGAGAAG	GACTCAGTCC	TATTGAAAGC	TGTGAAGGAT	TGGGAGATCC	180
	TGCTTGCTTT	TATGTTGCTG	TAATTTTTAT	TTTAAATGGA	CTAATGATGG	CATTATTCTT	240
	CATATATGCG	CATATTTTAA	GTGGCAGCCG	ATTAGGAGCG	CTGGTTACAG	TGTTGTGCTT	300
30	CTTTTTCAT	CATGAGAGAT	GTACCCGTGT	AATGTGGACA	CCACCTCTCC	GTGAAAGCTT	360
	CTCATATCCA	TTTCTTGTTT	TTCAGATGTT	GCTAGTGACT	CATATTCTCA	GGGCTACAAA	420
	ACTTTATAGA	GGAAGCTTGA	TTGCACCTCG	CATTTCCTCA	GTATTTTTC	TGCTTCCTTG	480
	GCAGTTTGCT	CAGTTTGTAC	TTCTTACTCA	GATTGCATCA	TTATTGTCAG	TATATGTTGT	540
	CGGGTACATT	GATATATGTA	AATTACGGAA	GATCATTAT	ATACACATGA	TTTCTCTTGC	600
35	ACTTTGTTTT	GTTTTGATGT	TTGGGAAGTC	AATGTTATTA	ACTTCTTATT	ATGCTTCTTC	660
	TTTGGTAATT	ATTTGGGGTA	TTCTGGCAAT	GAAACACAT	TTCCCTGAAA	TAAATGTATC	720
	TGAAGTGTG	TTATGGGTTA	TTCAAGGATG	TTTTTGGTTA	TTTGGAACTG	TCATACTTAA	780
	ATACTTGACA	TCTAAAATTT	TTGGTATTGC	AGATGACGCT	CATATTGGCA	ACTTACTAAC	840
40	ATCAAAATTC	TTTAGTTATA	AGGATTTTGA	TACTTTATTG	TATACCTGTG	CAGCGGAGTT	900
	TGACTTTATG	GAAAAAGAGA	CTCCACTGAG	ATACACAAAG	ACATTATTGC	TTCCAGTTGT	960
	TCTTGTAGTG	TTTGTGTGCTA	TTGTTAGAAA	GATTATTAGT	GATATGTGGG	GTGCTCTTAGC	1020
	TAAACAACAG	ACACATGTAA	GAAAAACCCA	GTTTGATCAT	GGAGAGCTGG	TTTACCATGC	1080
	ATTGCAATTG	TTAGCATATA	CAGCCCTTGG	TATTTTAATT	ATGAGACTAA	AACCTCTCTT	1140
45	GACACCACAC	ATGTGTGTGA	TGGCATCACT	GATCTGCTCA	AGACAGCTAT	TTGGATGGCT	1200
	CTTTTGCAAA	GTACATCTCG	GTGCTATTGT	GTTTGCTATA	TTAGCAGCAA	TGTCAATACA	1260
	AGGTTGAGCA	AATCTGCAAA	CCCAGTGGAA	TATTGTAGGG	GAGTTGAGCA	ATTTGCCCCA	1320
	AGAAGAAGCT	ATAGAAATGA	TCAAATATAG	TACTAAACCA	GATGAGTGT	TTGCGGGTGC	1380
	CATGCCACAG	ATGGCAAGTG	TTAAGCTCTC	TGCACCTCGG	CCCATTGTGA	ATCATCCACA	1440
50	TTATGAAGAG	GCAGGCTTGA	GAGCCAGAAC	AAAAATAGTA	TACTCAATGT	ATAGTCGGAA	1500
	AGCAGCCGAA	GAAAGTGAAGC	GAGAAGTGA	AAAGTTAAAA	GTGAAGTATT	ACATTCTAGA	1560
	AGAGTCATGG	TGTGTAAGAA	GATCCAAGCC	TGGTTGCAGT	ATGCCGAAA	TTTGGGATGT	1620
	AGAAGATCCT	GCCAACTGCT	GGAAAACTCC	CTTATGTAAC	CTCTTGGTGA	AGGATTCCAA	1680
	ACCTCACTTC	ACCACCTGTAT	TCCAGAACAG	TGTTTACAAA	GTCCTAGAAG	TTGTAAAAGA	1740
55	ATGACTGCTA	GTGACCTGTC	TGCTACGGGA	GAACTACATC	TGTAATGGTT	TTAATGTTTT	1800
	GCTAAGTCAT	GTGTGTGTTA	TATCCCAAAA	ACTTTTATAG	GTAAGTGTTC	TCAAATAGAA	1860
	AACGTTTTAT	TTGGTCAATT	TGAATGTCAT	TCTAATTATA	AAAATGACTT	ACACCTTTAT	1920
	CAATTGTTTA	CTATTTCAAT	GCACCTTTTA	AAATTTGCTA	TGCAAAATGAG	TATATGCTTG	1980
	TACTTGACTT	TAATATTGTT	GCTAAAGTGA	GCAAGGCTAC	CTGTATAAAG	AAAACACAGT	2040
60	GGGTTGTGAC	AAGGATGACA	TGAAAATACA	GGACAATTCT	GACAATGTAG	GGGCTGATTT	2100
	TATAGTGTA	GAAGTATTAA	TGCCCTTTCG	TTCTTTTTC	TGCCTCTTGC	TCTTGTCTTT	2160
	TGGACATTTC	AGTGATTGTA	AGTTCTTCGG	TCATGTCAGC	CCCTGTGATC	AACCTGAGTT	2220
	ACAGTAGATG	GGGCAGACAT	GGAGTGTGTT	CTATATAAAA	CTATCTGTTT	GTTTACTTTC	2280
	CTTGTGCGCT	TTTTGTTCTC	TGTTCTCTTG	TTAATGAAGC	TTTTCTGCCC	CATTATTAAT	2340
65	CCAAACTCTT	GGACCTTGTG	GTTAGGAAAT	TCCCTTAAGT	TCCAGCCATA	TGGCATTATC	2400
	GTGTCCTTTT	CTCTCTCTCT	CTTGCTCTCT	CTCTCTCTCT	CTTCCCCATA	TTTTCTGTCA	2460
	AATAAGTACT	GTTTACTCAT	TTAGTTGCTT	ATCAAGTACT	TATCTCTGGT	TTTTAAAAAA	2520
	ATTAATGGTA	ACTGTATTTT	TCTCATTTTT	AGCATTATTC	AAATGTTTAT	ATTTTAATAC	2580
	CTTTAAACCA	CTTTAAAGTT	TTTTCATGTT	TAATTATAGT	TTTAAGAAAA	ACTATTTTGA	2640
70	ACAACCCCAA	ATATAGTGCA	TCTAGAAACT	AATGTATATT	TGATTAGACA	TCATTATATG	2700
	TGGAACAGTA	GAGCTGTAGTA	CATGGTAATT	TTTCTTTTAC	TATTAAGATA	CAATAAAACA	2760
	TGACTAAATT	TGCTGTCAAA	AATGTAAAGA	ATAATGATAA	ATGGAGTTTT	TTATATTTTA	2820
	CTTTTAAGAT	TGCCTGTCTT	TAATAAGACA	AAGCCTTAAG	CCTTATGTTA	TAATTTTGGT	2880
	TCTAAAAACC	ATCATTTTCAG	TATAAGGAAT	AAGTATATTT	CGTCCTCCTC	TTTAGTTTTT	2940
75	TTCTTCCTAT	TTATTTTAT	TTTGAAAAAT	TTCTACACCT	TCTTTGAATT	CCTGTATGTA	3000
	ATTTTGTGTT	CTTAGAAGTT	AATTTGTGTG	AAATGAGATT	CTTCAAAACG	ATGAAACCTC	3060
	ATAGCTCTGA	GAAAAGGTTT	TAGGGTTTTA	AATTTCTAAGC	AAAGCSTGAC	TATGGCTGAC	3120
	AGACTACACA	TTTAATTATA	CAGCTTCTCT	TTCTTAAACA	CAGGCAGATT	AACCTCATTG	3180
	TGGATTGTCC	TTACAGCTTT	AGTCTCTCAG	CATGGTTTCT	GGTGCCCACT	CCTGGAAGCC	3240
80	GCTGTTCCTT	TTTACCTTTC	TTACAGAGC	CCAAGGGCAG	GCCTGGTCCC	GGGGAAGCAG	3300
	CAGCTTGCTG	ACATAAGTCA	GCTGCAAGG	CTGAGGAGTG	TGCCCTCAGA	GAAGCACCGC	3360
	CCCCCAGTCT	TGTGCGCAGC	CCTAGAGCCG	CAGCTCCAG	GGATGCTCCT	TCCCTGGAGG	3420
	CAGCCAGACA	GAGGACACTG	GGCAGCGTTC	TTCAGATTG	TGGCCACTGT	TTCTCATTTG	3480
	CTGGTTGACT	GTTTTTATTT	CTTAGGCTTT	TGCTAGTTTT	AGAAAATAGG	GAAGCAGCCC	3540
	TTGATTGTG	GATTAAGAGC	AACATTGTAG	CGATGATGCA	CAACAGTCCA	GGAAAATGGG	3600

5 CCGTGGACAC TTGAGGCTGA GGATGGGAGT TGACATGAGC AGGGAGAGGG AGGTGCGCGC 3660  
 TGCTTATCTG TGATTGTGTC TCACCTGAGT GTGGCTGATT GTGTACATCC AGCAGTTACA 3720  
 ATTTTAAAAA ATTATACTTT TACATTTATT TTATATTTT CTCACCCCA GTAATTTCTT 3780  
 TCCAAAGAAG TTCACATGTA ATAAGTAGAA ATTTCTGTATA GGAAAAAGC ATTAATAATA 3840  
 CTATTATAAC TGCTTCATTT GCTGGGAACC ATTAAAGTA ATATAAATTA GCTTTTTCCT 3900  
 GAAGGATCCT TTTGTAGCAG TGTTTATGAA TGTAAACCCC AGCAAAATAT GGCTATATAT 3960  
 TAGGGAGCC AGTTTGGAGC AGAGCCCTGA AGGTCCCTGC TATGCAGCCG TGGCCACAGC 4020  
 TCGCAGCCCA AGCACTGTGG AGCATCCACA CCTTTGATGG CAATGCAGAT TGGTAGCAGG 4080  
 10 TTCCATAGCC GTACAAAACA GTATTAAAGC TCAGTGTTTT GCATATTGTT AGCATTTACA 4140  
 AATATTTTGT CTTTAGTATG AGGAAAGTAA GGATGGGCAA AGAAGCGATC AAAATAGCTA 4200  
 TTGCTACAAC ATTTTCGAAA ACAAAGTTGG GGCTGTATTT CTTTAAAAAG ATAAGCCTCT 4260  
 AAAAATGCTT GGCAAAAAAA ATATAGTGTT AAAATAGGCC AGTGATATTA ATGAGAAAAT 4320  
 GAAAGTATGT ATCAGGAATA AAGTGATATT GCATAGGAGT ATTGTATTTT TATGAATTTT 4380  
 15 ATGCCAGTTG TTTACATGTA CTATATATGT TAAATTAATA AAAATCATGA GAAATG

Seq ID NO: 266 Protein sequence  
 Protein Accession #: BAA74900.1

20 1 11 21 31 41 51  
 | | | | |  
 PLVINTLKRF NLYPEVILAS WYRIYTKIMD LIGIQTKICW TVTRGEGLSP IESCEGLGDP 60  
 ACFVVAVIFI LNGLMMAFF IYGYLSGSR LGGLVTVLGF FNNHGECTRV MWTPLRESF 120  
 SYPLVLQML LVTHILRATK LYRGLIALC ISNVFMLPW QFAQFVLLTQ IASLFAVVVV 180  
 25 GYIDICKLRK IYIHMISLA LCFVLMFGNS MLLTSYYASS LVIIWIGILAM KPHFLKINVS 240  
 ELSLWVIGQC FWLFGTVILK YLTSKIFGIA DDAHIGNLLT SKFFSYKDFD TLLYTCAAEF 300  
 DFMKEKTEPLR YTKTLLLPVV LVVFVAIVRK IISDMWGVLA KQOETHVRKHQ FDHGLVYHA 360  
 LQLLAYTALG ILIMRLKLEL TPHMCVMASL ICSROLFGWL FCKVHPGAIV FAILAAMSIQ 420  
 GSNLQQTOWN IVGEFSNLPK BELIEWIKYS TKPDVAFAGA MPTMASVKLS ALRPIVNHHPH 480  
 30 YEDAGLRART KIVSMYSRK AAEVKKRELI KLVKNYYILE ESWCVRRSKP GCSMEPIDV 540  
 EDPANAGKTP LCNLLVKDSK PHFTTVFQNS VYKVLVVKE

Seq ID NO: 267 DNA sequence  
 Nucleic Acid Accession #: U26744.1  
 Coding sequence: 59..1600

35 1 11 21 31 41 51  
 | | | | |  
 CTTCAAAGAA TATAGATGGT TTTGAAAAGT TCATGCTGTC CCTTCATTGA ATTTTAGAAT 60  
 GATTGAAGAT AGTGGGAAAA GAGGAAATAC CATGGCAGAA AGAAGACAGC TGTTTGAGA 120  
 40 GATGAGGGCT CAAGATCTGG ATCGCATCCG ACTCTCCACC TACAGAACAG CATGCAAGCT 180  
 TAGGTTTGTG CAGAAAGAAAT GCAATTGTCG CCTGGTGGAC ATATGGAATG TCATAGAAGC 240  
 ATTGCGGGAA AATGCTCTGA ACAACCTGGA CCCAAACACT GAACCTCAACG TGTCCCGCTT 300  
 AGAGGCTGTG CTCTCCACTA TTTTTCACCA GCTCAACAAA CGGATGCCAA CCACTCACC 360  
 AATCCATGTG GAGCAGTCCA TCAGCCTCCT CCTTAACTTC CTGCTTGAGC CGTTTGATCC 420  
 45 GGAAGGCCAT GGTAAAATTT CAGTATTTGC TGTCAAAATG GCTTTAGCCA CATTGTGTGG 480  
 AGGGAAGATC ATGGACAAAT TAAGATATAT TTTCTCAATG ATTTCTGACT CCAGTGGGGT 540  
 GATGTTTATG GGACGATATG ACCAATTCCT TCGGGAAGTT CTCAAACTAC CCACGGAAGT 600  
 TTTGAGGGGT CCTTCATTG GTTACACAGA ACAGTCAGCC AGATCCTGTT TCTCCCAACA 660  
 50 GAAAAAAGTG ACGTTAAATG GTTCTTGGA CACGCTTATG TCAGATCTCT CCCCGCAGTG 720  
 TCTGCTCTGG TGCCTCTTC TGCATCGACT AGCAAAATGT GAAAAATGCT TCCATCCGGT 780  
 TGAGTGTTC TACTGCCACA GTGAGAGTAT GATGGGATTT CGCTACCGAT GCCAACAGTG 840  
 TCACAATTAC CAGCTCTGTC AGGACTGCTT CTGGAGGGGA CATGCCGGTG GTTCTCATAG 900  
 CAACAGCAC CAAATGAAAG AGTACAGTC ATGGAATCA CCGTCTAAGA AGCTGACTAA 960  
 55 TGCATTAAGC AAGTCCCTGA GCTGTGCTTC CAGCCGTGAA CCTTTGCACC CCATGTTCCC 1020  
 AGATCAGCCT GAGAAGCCAC TCAACTTGGC TCACATCGTT GATACTTGGC CTCCAGAGAC 1080  
 TGTAACACAG ATGAACGACA CCTGTCTCT CCACTCTGTT CCTCTCTCAG GAAGTCTTT 1140  
 TATTACCAG AGCATGCTTG AGAGTTCAAA CCGGCTTGAT GAAGAACACA GGCTAATTGC 1200  
 CAGGTATGCG GCAAGGCTGG CAGCAGAGTC CTCTTCGTCT CAGCCACCTC AGCAGAGAAG 1260  
 60 TGCTCTCTGAC ATCTCTTTCA CCATCGATGC GAATAAGCAG CAAAGGCAGC TGATTGCTGA 1320  
 GCTAGAAAAC AAGAACAGAG AAATCTTACA GGAGATCCAG AGACTTCGGC TAGAGCATGA 1380  
 ACAAGCTTCT CAGCCACAGC CAGAGAAGGC ACAGCAAAC CCCACCCTGC TGGCAGAACT 1440  
 CCGGCTCCTC AGACAGCGCA AAGATGAGCT GGAACAGAGA ATGTCTGCTC TCCAGGAGAG 1500  
 CCGGAGAGAG CTAATGGTCC AGTTGGAGGG TCTCATGAAG CTAATAAGG AAGAAGAACT 1560  
 65 GAAGCAGGGA GTAAGTTATG TCCCCTACTG CAGGTCTTAA CTAACAGTGG AGGGGCTGC 1620  
 CGACCTGCGG TTTTCTCATT GCTTTTGCTC TAATGTATGT TCATGCTTCA GTTTGGAAG 1680  
 AGAAAAAGT CATACTAATT TGCTTCTTTT TCAATGTAGT GCTTGAATTG AGATATATAA 1740  
 ATTTAGCATT TTTTATAACT ATCACTACTA TCCACATCAA AAGAAGAACT ATGACATCTT 1800  
 70 TTAGAAAAAG GAACGAATTG TCATTTATTG GAAACATTTT AGATCCCCAG AGGTATAAGT 1860  
 TTCAAACAG TCTTAGCTTT TCAAGTTGTT GATCAGACCC TTCTCTTAAC AGAGAGATAC 1920  
 CACAGTCACT AGAGATACCC TGAGGTTTCAT GTCATCCCAA AACCCACAGC ACTCAGAAGC 1980  
 TAACCTCTAC ACCACTCAC ACTGTGAGTA TTCAGTTCGS TTTTATTTTA CTGAAAAACCT 2040  
 GTGAAACCTC TTTTATAAAA AATCAGGCAA TTAATCCCT TTTATCACA CAATTATTGA 2100  
 GCCTTGTTC CCATGGCTCA CCAAAATGTG CTCAATTTT TGAGAGAAAG ACTGTACTCC 2160  
 75 ATAACTGACT ATTCAGTCC CATCTTTTGG GCTCTTCCCC AAAGCAGAA CTCTACTGTT 2220  
 GGTGTGACAT AATCTCTTTT TAAAAAGTAA CTCTCAGCTT TTTCTTAGC ACCAGAGCCT 2280  
 TTCGGCTCCG GGAGCAGAGA GGGTCATTAC ATACTTTTTT TTTTCTCTGG AAATAGGGGC 2340  
 ATTGTGACTT TATAGCTTAA ACTGGAGCTG TCTGAACCTG TGCTCAGGCT CAAGAGCCAG 2400  
 CAGGGGGAGC AGCAAACTC

Seq ID NO: 268 Protein sequence  
 Protein Accession #: AAC50426.1

1 11 21 31 41 51  
 | | | | |

MIEDSGKRGN TMAERRQLFA EMRAQDLDR IRLSTYRTACK LRFVQKKCNL HLVDIWNVIE 60  
 ALRENALNNL DPNTLNVSR LEAVLSTIFY OLNKRMPETH QIHVEQSISL LLNPLLAAPD 120  
 PEGHGKISVF AVKMALATLC GKGIMDKLRY IFSMISDSSG VMVYGRYDQF LREVLKLPTE 180  
 VLEGPSEFGYT EQSARSCFSQ QKKVTLNGFL DTLMSDPPPO CLVWLPLLHR LANVENVFHP 240  
 VECSYCHSES MMGFYRRCQ CHNYQLQDC FWRGHAGGSH SNQHQMKEYT SWKSPAKKLT 300  
 NALSKSLSCA SSREPLHPMF PDQPEKPLNL AHIVDTWPPR PVTSMNDTLF SHSVPSGSP 360  
 FITRSMLESS NRLDEEHLRI ARYAARLAAE SSSSQPPQOR SAPDISFTID ANKQQRQLIA 420  
 ELENKNREIL QEIQRLRLHE EQASQPTPEK AQONPTLLAE LRLRLQRKDE LEQRMSALQE 480  
 SRRELMVQLE GLMKLLKEEE LKQGVSYVPY CRS

Seq ID NO: 269 DNA sequence  
 Nucleic Acid Accession #: NM\_001276.1  
 Coding sequence: 127..1278

1 11 21 31 41 51  
 AGTGGAGTGG GACAGGTATA TAAAGGAAGT ACAGGGCCTG GGAAGAGGC CCTGTCTAGG 60  
 TAGCTGGCAC CAGGAGCCGT GGGCAAGGGA AGAGGCCACA CCCTGCCCTG CTCTGCTGCA 120  
 GCCAGAATGG GTGTGAAGGC GTCTCAAACA GGCTTTGTGG TCCTGGTGCT GCTCCAGTGC 180  
 TGCTCTGCAT ACAAACTGGT CTGCTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT 240  
 GGGAGCTGCT TCCCAGATGC CCTTGACCGC TTCCTCTGTA CCCACATCAT CTACAGCTTT 300  
 GCCAATATAA GCAACGATCA CATCGACACC TGGGAGTGGG ATGATGTGAC GCTCTACGGC 360  
 ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTTGTC TGTGCGAGGA 420  
 TGGAACTTTG GGTCTCAAAG ATTTTCCAAG ATAGCCTCCA ACACCCAGAG TCGCCGGACT 480  
 TTCAATCAAG CAGTACCGCC ATTCCTGCGC ACCCATGGCT TTGATGGGCT GGACCTTGCC 540  
 TGGCTCTACC CTGGACGGAG AGACAAACAG CATTTTACCA CCCTAATCAA GGAATGAAG 600  
 GCCGAATTTA TAAAGGAAGC CCAGCCAGGG AAAAAGCAGC TCCTGCTCAG CGCAGCACTG 660  
 TCTGCGGGGA AGGTCAACAT TGACAGCAGC TATGACATTG CCAAGATATC CCAACACCTG 720  
 GATTTCATTA GCATCATGAC CTACGATTTT CATGGAGCCT GCGGTGGGAC CACAGGCCAT 780  
 CACAGTCCCC TGTTCCGAGG TCAGGAGGAT GCAAGTCTCTG ACAGATTGAG CAACACTGAC 840  
 TATGCTGTGG GGTACATGTT GAGGCTGGGG GCTCCTGCCA GTAAGCTGGT GATGGGCATC 900  
 CCCACCTTCG GGAGGAGCTT CACTCTGGCT TCTTCTGAGA CTGGTGTGGG AGCCCCAATC 960  
 TCAGGACCGG GAATTCACGG CCGGTTTACC AAGGAGGCAG GGACCTTGCC CTACTATGAG 1020  
 ATCTGTGACT TCCTCCGCGG AGCCACAGTC CATAGAACC TCAGCCAGCA GGTCCCCTAT 1080  
 GCCACCAAGG GCAACCAAGT GGTAGGATAC GACGACCAGG AAAGCGTCAA AAGCAAGGTG 1140  
 CAGTACCTGA AGGATAGGCA GCTGGCAGGC GCCATGGTAT GGGCCCTGGA CCTGGATGAC 1200  
 TTCCAGGGCT CCTTCTGCGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT 1260  
 GCACTGCTCG CAACGTAGCC CTCTGTCTTG CACACAGCAC GGGGGCCAAG GATGCCCCGT 1320  
 CCCCCTCTGG CTCCAGCTGG CCGGAGCCTC GATCACCTGC CCTGCTGAGT CCCAGGCTGA 1380  
 GCTCAGTCT CCCTCCCTTG GGGCCTATGC AGAGGTCCAC AACACACAGA TTTGAGCTCA 1440  
 GCCCTGGTGG GCAGAGAGGT AGGGATGGGG CTGTGGGGAT AGTGAGGCAT CGCAATGTAA 1500  
 GACTCGGGAT TAGTACACAC TTGTGTATGA TTAATGGAAA TGTTTACAGA TCCCCAAGCC 1560  
 TGGCAAGGGA ATTTCTTCAA CTCCCTGCCC CTTAGCCCTC CTTATCAAAG GACACCATTT 1620  
 TGGCAAGCTC TATACCAAG GAGCCAAACA TCCTACAAGA CACAGTGACC ATACTAATTA 1680  
 TACCCCTGTC AAAGCCAGCT TGAAACCTTC ACTTAGGAAC GTAATCGTGT CCCCTATCCT 1740  
 ACTTCCCTCT CTAATTTCCA CAGCTGCTCA ATAAAGTACA AGAGTTTAA AGTGTGTTGG 1800  
 CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGGACTCAC CTCCCCATC 1860  
 TCTTCTGGGT TCCTTCTCTC GAGCCTTGGG ACCCCTGAGC TTGCAGAGAT GAAGGCCGCC 1920  
 ATGTT

Seq ID NO: 270 Protein sequence  
 Protein Accession #: NP\_001267.1

1 11 21 31 41 51  
 MGVKASQTGF VVLVLLQCCS AYKLVCYYS WSQYREGDGS CFPDALDRFL CTHIISFAN 60  
 ISNDHIDTWE WNDVTLYGML NTLKNRNPENL KTLISVGGWN FGSQRFSKIA SNTQSRRTFI 120  
 KSVPPFLRTH GFDGLDLAWL YPGRRDKQHF TTLIKEMKAE FIKEAQPKK QLLLSAALSA 180  
 GKVTIDSSYD IAKISQHLDF ISIMTYDFHG AWRGTGTGHS PLFRGQEDAS PDRFSNTDYA 240  
 VGYMLRLGAP ASKLVMGIPT FGSRFTLASS ETGVGAPISG PGIPGRFTKE AGTLAYYEIC 300  
 DFLRGATVHR TLGQVVPYAT KGNQWVGYYD QESVKSQVQY LKDRQLAGAM VWALDLDDFQ 360  
 GSFQQLDRF PLTNAIPDAL AAT

Seq ID NO: 271 DNA sequence  
 Nucleic Acid Accession #: NM\_006474.1  
 Coding sequence: 181..669

1 11 21 31 41 51  
 GCTGCCTAGG GTCTGGAAG CTCGGGCACC CTCCTCTCC GGGGCTCCTG CTCCCACCCC 60  
 TCCGGCCCCC CCACCGTCGC GCTCCTCCAG GCTGGGCTG TGGCCGCGGT GCTTTTAATT 120  
 TTCCCCCAGC TCAGAATCTT GCTGCTCGGC CCCAGGAGA GCAACAACTC AACGGGAACG 180  
 ATGTGGAAGG TGTCACTCT GCTCTTCGTT TTGGGAAGCG CGTCGCTCTG GGTCTCTGCA 240  
 GAAGGAGCCA GCACAGGCCA GCCAGAAGAT GACACTGAGA CTACAGGTTT GGAAGGCGGC 300  
 GTTGCCATGC CAGGTGCCGA AGATGATGTG GTGACTCCAG GAACCAGCGA AGACCGCTAT 360  
 AAGTCTGGCT TGACAACTCT GGTGGCAACA AGTGTCAA CA GTGTAACAGG CATTGCAATC 420  
 GAGGATCTGC CAACTTCAGA AAGCACAGTC CACGCGCAAG AACAAAGTCC AAGCGCCACA 480  
 GCCTCAAACG TGGCCACCAG TCACTCCACG GAGAAAGTGG ATGGAGACAC ACAGACAACA 540  
 GTTGAGAAAG ATGGTTTGT CACAGTGACC CTGGTTGGAA TCATAGTTGG GGTCTTACTA 600  
 GCCATCGGTT TCATTGGTGG AATCATCGTT GTGGTTATGC GAAAAATGTC GGAAGGTAC 660  
 TCGCCCTAAA GAGCTGAAGG GTTACGCCCT GCTTGCCAAAC GTGCTTTAAA AAAAGACCGT 720  
 TTCTGACTCT GTGGGAGGCT CCCTGAGCTC GTGGGAGAGG GATGACCCGT GGAACATTGT 780  
 CGGGCCCATC CAGATTCCAC GGTGACTTTC CGTTTGCCAA ATTAACCGAG GAAAGACCTT 840



TCACCAGATT TGGTTCTTAA ACTTT

Seq ID NO: 272 Protein sequence  
Protein Accession #: NP\_006465.1

1	11	21	31	41	51	
MWKVSALLFV	LGSASLWVLA	EGASTGQPED	DTETTGLEGG	VAMPGAEDDV	VTPGTSEDRY	60
KSLGLTLVAT	SVNSVTGIRI	EDLPTSESTV	HAQEQSPSAT	ASNVATSHST	EKVDGDTQTT	120
VEKDGLSTVT	LVGIIVGVLL	AIGFIGGIIV	VVMRKMSGRY	SP		

Seq ID NO: 273 DNA sequence  
Nucleic Acid Accession #: CAT cluster

1	11	21	31	41	51	
GCGGCCGCCA	GCTTGCAAAG	CCGAAGTCTG	GCCGCGCTCT	TCGACTCGCT	GCGCCACGTC	60
CCCAGGGGTG	CCGAGCCGGC	GGGGGGTGAG	GTGGCTGCGC	CGGCGGCCGG	GCTAGGAGGT	120
GCGGGCACTG	GGGGCGCGGG	AGGGGACGTG	GCAGGCCCCG	CGGGGGCCAC	GGCGATCCCA	180
GGGGCCAGGA	AGGTCCCGCT	GCGGGCACGC	AATCTGCCTC	CGTCCTTCTT	CACGGAGCCG	240
TCCCGGGCAG	GCGGCGGGGG	GTGTGGCCCG	TCGGGGCCGG	ACGTGAGCTT	GGGCGACCTG	300
GAGAAGGGCG	CGGAGGCCGT	GGAGTCTCTT	GAGCTGCTGG	GGCCCGACTA	CGGCGCCGGC	360
ACGGAGGGCG	CAGTCTTGCT	TGCCGCCGAG	CCTCTCGACG	TGTTCCCGCC	CGGAGCCTCC	420
GTACTGCGGG	GACCCCGCGA	GCTGGAGCCC	GGCCTCTTTG	AGCCGCCGCC	GGCAGTGGTG	480
GGAAACCTAC	TGTACCCCGA	GCCCTGGAGC	GTCCCGGGCT	GCTCCCCGAC	CAAAAAGAGC	540
CCCTTGACTG	CCCTCCGGGG	CGGGTTGACC	TGGAACGAGC	CCTTGAGCCC	CCTGTACCCC	600
GCCGCTGCGA	ATTTCTCCCG	GCGGGGAGGA	CGGGCCGGGC	CATTGCGCTT	CTTTCGCCCC	660
CTTCTTTCCA	GACTGCGCTT	TGC				

Seq ID NO: 274 DNA sequence  
Nucleic Acid Accession #: Eos sequence

1	11	21	31	41	51	
CAAAGAGGCC	GGGCTCCAGC	TCCGGGGGTC	CCCGCAGTAC	GGAGGCTCCG	GCGGGGAACA	60
CGTCGAGAGG	CTCGGGGGCA	AGCAAGACTG	CCGCTCCCGT	GCCGGCGCCG	TAGTCGGGCC	120
CAGACAGCTC	AAAGAACTCC	ACGGCCTCCG	CGCCCTTCTC	CAGGTCGCCC	AAGCTCACGT	180
CCGGCCCCGA	CGGGCCACAC	CCGCGCCCGC	CTGCCCGGGA	CGGCTCCGTG	AAGAAGGACG	240
GAGGCAGATT	GCGTGCCCGC	AGCGGGACCT	TCCTGGCCCC	TGGGATCGCC	GTGGCCCCCG	300
CGGGGCCTGC	CACGTCCCCCT	CCCGCGCCCC	CAGTGCCCGC	ACCTCCTAGC	CCGGCCGCCG	360
GGCAGCCAC	CTACCCCCC	GCCGGCTCGG	CACCCCGGG	GACGTGGCGC	AGCGAGTCGA	420
AGAGCGCGGC	CAGACTTCGG	CTTTGCAAGC	TGGCGGCCGC			

Seq ID NO: 275 DNA sequence  
Nucleic Acid Accession #: NM\_001118.1  
Coding sequence: 74..1651

1	11	21	31	41	51	
AGCCCAGAGA	CACATTGGGG	CTGACCTGCC	GCTGCTGTCA	GTGGGAGGCC	AGTGGTGCTG	60
GCCAAGAAGT	GTGATGGCTG	GTGTGCTGCA	CGTTTCCCTG	GCTGCTCACT	GCGGGGCGCTG	120
TCCGTGGGGC	CGGGGCGAGC	TCCGCAAGAG	ACGCGCAGCC	TGCAAGTCCG	CGCCCCAGAG	180
ACACATTGGG	GCTGACCTGC	CGCTGCTGTC	AGTGGGAGGC	CAGTGGTGCT	GGCCAAGAAG	240
TGTGATGGCT	GGTGTGCTGC	ACGTTTCCCT	GGTGTCTCTC	CTCCTGCTGC	CTATGGCCCC	300
TGCCATGCTC	TCTGACTGCA	TCTCAAGAA	GGAGCAAGCC	ATGTGCTTGG	AGAAGATCCA	360
GAGGGCCAAT	GAGCTGATGG	GCTTCAATGA	TTCCTCTCCA	GGCTGTCTTG	GATGTGGGA	420
CAACATCAGC	TGTTGGAAGC	CCGCCCATGT	GGGTGAGATG	GTCTTGGTCA	GCTGCCCTGA	480
GCTCTTCCGA	ATCTTCAACC	CAGACCAAGT	CTGGGAGACC	GAAACCATTT	GAGAGTCTGA	540
TTTTGGTGAC	AGTAACCTCT	TAGATCTCTC	AGACATGGGA	GTGGTGAGCC	GGAACTGCAC	600
GGAGGATGGC	TGGTCGGAAC	CCTTCCCTCA	TTACTTTGAT	GCCTGTGGGT	TTGATGAATA	660
TGAATCTGAG	ACTGGGGACC	AGGATTATTA	CTACCTGTCA	GTGAAGGCC	TCTACACGGT	720
TGGCTACAGC	ACATCCCTCG	TACCCCTCAC	CAGTGCCATG	GTGATCTCTT	GTCGCTTCCG	780
GAAGCTGCAC	TGCACACGCA	ACTTCATCCA	CATGAACCTG	TTTGTGTCGT	TGATGCTGAG	840
GGCGATCTCC	GTCTTCATCA	AAGACTGGAT	TCTGTATGCG	GAGCAGGACA	GCAACCACTG	900
CTTCACTCTC	ACTGTGGAAT	GTAAGGCCGT	CATGGTTTTC	TTCCACTACT	GTGTTGTGTC	960
CAACTACTTC	TGGCTGTTCA	TGAGGGGCC	GTACCTCTTC	ACTCTGCTGG	TGGAGACCTT	1020
CTTCCCTGAA	AGGAGATACT	TCTACTGGTA	CACCATCATT	GGCTGGGGGA	CCCCAACTGT	1080
GTGTGTGACA	GTGTGGGCTA	CGCTGAGACT	CTACTTTGAT	GACACAGGCT	GCTGGGATAT	1140
GAATGACAGC	ACAGCTCTGT	GGTGGGTGAT	CAAAGGCCCT	GTGGTTGGCT	CTATCATGGT	1200
TAACCTTTGTG	CTTTTATTTG	GCATTATCGT	CATCCTTGTC	CAGAACTTTC	AGTCTCCAGA	1260
CATGGGAGGC	AATAGTGTCA	GCACTACTTT	GCGACTGGCC	CGGTCCACCC	TGCTGCTCAT	1320
CCCACTATTC	GGAATCCACT	ACACAGTATT	TGCCTTCTCC	CCAGAGAATG	TCAGCAAAAG	1380
GGAAAGACTC	GTGTTTGAGC	TGGGGCTGGG	CTCCTTCCAG	GGCTTTGTGG	TGGCTGTTCT	1440
CTACTGTTTT	CTGAATGGTG	AGGTACAAGC	GGAGATCAAG	CGAAAAATGG	GAAGCTGGAA	1500
GGTGAACCGT	TACTTCGCTG	TGGACTTCAA	GCACCGACAC	CCGTCTCTGG	CCAGCAGTGG	1560
GGTGAATGGG	GGCACCCAGC	TCTCCATCCT	GAGCAAGAGC	AGCTCCCAAA	TCCGCATGTC	1620
TGGCTTCCCT	GCTGACAATC	TGGCCACCTG	AGCCATGCTC	CCCT		

Seq ID NO: 276 Protein sequence  
Protein Accession #: NP\_001109.1

1	11	21	31	41	51	
MAGVVHVSIA	AHCACPWGR	GRLRKGRAAC	KSAAQRHIGA	DLPLLSVGGQ	WCWPRSVMAG	60

VHVSLAALL LLLPAPAMHS DCIFKKEQAM CLEKIQRANE LMGFNDSSPG CPGMWDNITC 120  
 WKPAHVGEV LVSCPELFRI FNPQVWETE TIGESDFGDS NSLDLSDMGV VSRNCTEDGW 180  
 SEFFPHYFDA CGFDEYEST GDQDYVYLSV KALYTVGYST SLVTLTAMV ILRCRFRKLHC 240  
 TRNFHMLNF VSFMLRAISV FIKDWILYAE QDSNHCFFIST VECKAVMVVF HCVVSNYFHW 300  
 LFIEGLYLF LTVETFFPER RYFYWYTIIG WGTPTVCVTV WATLRLYFDD TGCWDMNDST 360  
 ALWWVIKGPV VGSIMVNFVL FIGIIVILVQ KLQSPDMGNN ESSIYLRLAR STLLLIPLFG 420  
 IHYTVFAFSP ENVSKRERLV FELGLGSFQG FVVAVLYCFL NGEVQAEIKR KWRWSKVNRV 480  
 FAVDFKHRHP SLASSGVNGG TQLSILSKSS SQIRMSGPLA DNLAT

Seq ID NO: 277 DNA sequence  
 Nucleic Acid Accession #: NM\_004000.1  
 Coding sequence: 36..1193

1 11 21 31 41 51  
 AGAAGAAGCT GGCCAAGGAT ATGGGAGCAA CCACCATGGA CCAGAAGTCT CTCTGGGCAG 60  
 GTGTAGTGGT CTGTGCTGCT CTCCAGGGAG GATCTGCCTA CAAACTGGTT TGCTACTTTA 120  
 CCAACTGGTC CCAGGACCGG CAGGAACCCAG GAAAATTAC CCCTGAGAA ATTGACCCCT 180  
 TCCTATGCTC TCATCTCATC TATTCATTCG CCAGCATCGA AAACAACAAG GTTATCATCA 240  
 AGGACAAGAG TGAAGTGATG CTCTACCAGA CCATCAACAG TCTCAAAACC AAGAATCCCA 300  
 AACTGAAAT TCTCTGTGCC ATTGGAGGGT ACCTGTTTGG TTCCAAAGGG TTCCACCCTA 360  
 TGGTGGATT TCTACATCA CGCTTGAAT TCATTAACTC CATAATCCTG TTTCTGAGGA 420  
 ACCATAACTT TGATGGACTG GATGTAAGCT GGATCTACCC AGATCAGAAA GAAAACACTC 480  
 ATTTCACTGT GCTGATTCAT GAGTTAGCAG AAGCCTTTC GAAGGACTTC ACAAAATCCA 540  
 CCAAGGAAAG GCTTCTCTTG ACTGCGGGCG TATCTGCAGG GAGGCAATG ATTGATAACA 600  
 GCTATCAAGT TGAGAAACTG GCAAAAGATC TGGATTTCAT CAACCTCCTG TCCTTTGACT 660  
 TCCATGGGTC TTGGGAAAAG CCCCTTATCA CTGGCCACAA CAGCCCTCTG AGCAAGGGGT 720  
 GGAGGACAG AGGGCCCAAG TCCTACTACA ATGTGGAATA TGCTGTGGGG TACTGGATAC 780  
 ATAAGGGAAT GCCATCAGAG AAGGTGGTCA TGGGCATCCC CACATATGGG CACTCCTTCA 840  
 CACTGGCCTC TGAGAAACC ACCGTGGGGG CCCCTGCCTC TGGCCCTGGA GCTGCTGGAC 900  
 CCATCAGAGA GTCTTCAGGC TTCTTGGCCT ATTATGAGAT CTGCCAGTTC CTGAAAGGAG 960  
 CCAAGATCAC GCGCCTCCAG GATCAGCAGG TTCCTACGC AGTCAAGGGG AACCAAGTGG 1020  
 TGGGCTATGA TGATGTGAAG AGTATGAGA CCAAGGTTCA GTTCTTAAAG AATTTAAACC 1080  
 TGGGAGGAGC CATGATCTGG TCTATTGACA TGGATGACTT CACTGGCAAA TCCTGCAACC 1140  
 AGGGCCCTTA CCTCTTGTG CAAGCAGTCA AGAGAAGCCT TGCTCTCTTG TGAAGGATTA 1200  
 ACTTACAGAG AAGCAGGCAA GATGACCTTG CTGCTGGGG CCTGCTCTCT CCCAGGAATT 1260  
 CTCATGTGGG ATTCCCTTG CCAGGCTGGC CTTTGGATCT CTCTTCCAAG CCTTCTCTGA 1320  
 CTTCTCTTA GATCATAGAT TGGACCTGGT TTTGTTTCC TGCAGCTGTT GACTTGTGTC 1380  
 CCTGAAGTAC AATAAAAAA ATTCAATTTG CTCCAGTA

Seq ID NO: 278 Protein sequence  
 Protein Accession #: NP\_003991.1

1 11 21 31 41 51  
 MDQKSLWAGV VLLLLLQGGG AYKLVCYFTN WSQDRQEPGK FTPENIDPFL CSHLIYSFAS 60  
 IENNKVHKD KSEVMLVQTI NSLTKNPKL KILLSIGGYL FGSKGPHPMV DSSTSRLEFI 120  
 NSIILFLRNH NFDGLDVSWI YPDQKENTHF TVLIHELAE FQKDFTKSTK ERLLLTAGVS 180  
 AGRQMDNSY QVETLAKLDI FINLSFDFH GSWEKPLITG HNSPLSKGWQ DRGPSSYINV 240  
 EYAVGYWIHK GMPSEKVVVG IPTYGHSTFL ASAETTVGAP ASGPAAAGPI TESSGFLAYY 300  
 EICQFLKGAK ITRLDQQVVP YAVKGNQWVG YDDVKSMETK VQFLKNLNLG GAMIWSIDMD 360  
 DFTGKSCNQG PYPLVQAVKR SLGSL

Seq ID NO: 279 DNA sequence  
 Nucleic Acid Accession #: NM\_015166.1  
 Coding sequence: 116..1249

1 11 21 31 41 51  
 TGCTGGAAGT CCCTCACCCA GAGACCACTG CTCCCAACGG CAGAGCAGCG GGGGAGATAA 60  
 AGAACTGGTG ACACGTGGCT GTACATTAG CACAGCTGTG GTGTCCCAA GTGCCATGAC 120  
 CCAGGAGCCA TTCAGAGAGG AGCTGGCCTA TGACCGGATG CCCACGCTGG AGCGGGGCGG 180  
 GCAAGACCCC GCCAGCTATG CCCAGACGCG GAAGCCGAGC GACCTGCAGC TGTGGAAGAG 240  
 ACTGCCCCC TGCTTCAGCC ACAAGACGTG GGTCTTCTCT GTGCTGATGG GGAGCTGCCT 300  
 CCTGGTGACC TCGGGGTTTT CGCTGTACCT GGGGAACGTG TTCCCGGCTG AGATGGATTA 360  
 CTTGCGCTGT GCTGCAGGCT CTTGCATCCC CTCGCAATT GTGAGCTTCA CCGTCTCCAG 420  
 GAGGAACGCC AATGTGATTC CCAACTTTC GATATTGTT GTTTCCACGT TTGCTGTGAC 480  
 CACTACGTGT TTAATTTGGT TTGGATGCAA ACTAGTCTGT AACCCATCAG CAATAAACAT 540  
 CAACTTCAAC CTCATCCTGC TGCTCCTGCT GGAGCTGCTC ATGGCGGCCA CGGTGATCAT 600  
 CGCTGCACGG TCCAGCGAGG AGGACTGCAG GAAAAGAAG GGCTCCATGT CTGACAGCGC 660  
 CAACATTCTG GACGAAGTGC CATTTCCTGC TCGGGTCTGT AAATCTTACT CAGTCGTGCA 720  
 GGTAAATCGA GGCATCTCTG CCGTCTCGG GGGGATCATT GCCCTGAACG TGGATGACTC 780  
 AGTTTCAGCG CCACACCTCT CAGTGACGTT CTTTGGATC CTAGTGGCCT GCTTTCCAAG 840  
 TGCCATTGCC AGTCATGTGG CAGCAGAGTG TCCCAGCAAG TGTCTGGTGG AGGTCTCTGAT 900  
 TGCCATAAGC AGCCTCACGT CTCCGCTGCT GTTCAAGGCC TCTGGATATC TGTATTGAG 960  
 CATCATGAGA ATCGTGGAGA TGTTTAAGGA TTACCCGCCA GCCATAAAC CATCCTACGA 1020  
 TGTGCTGCTG CTGCTGCTGC TGCTAGTGTCT CTTGCTGAG GCCCGCTTCA ACACGGGCAC 1080  
 CGCCATCCAG TCGTGCCTCT TCAAGGTGAG TGCAAGGCTG CAGGCTGCTC CCTGGGACAC 1140  
 CCAGAACGGC CCGCAGGAGC GCCTGGCTGG GGAGGTGGCC AGGAGCCCCC TGAAGGAGTT 1200  
 CGACAGGAG AAAGCCTGGA GAGCCGCTGT GGTGCAATG GCCCAGTGA CCCCAGACGC 1260  
 GGAACCCGGG TGGCAGCGCC CAGCCTGGCC CCAAGCATGG AAACGCACAA CCCCTAATCG 1320  
 CCCTGAGCTA CTGCTTCTAA CACCTCTTTT CCCTTGTGTG AGGGCAACCC AGGTGTCAGG 1380  
 TGGGTGTTTC ACTTCTTAGG GTAGTTTAAT TTTAAATAG GCCAATGTTG GCTAGTCTGT 1440  
 GCCTCAGTGA GATCAGTCAG CTCCGAGTGG CTCCGCTGTC GTAACAGCAG GAGCATGGCC 1500

5 GCAACTTCCC AGGCCGAGGA AGGGCCCCCG GCTCGGCCTC TTGAGAGCCC CACCCCTGAA 1560  
 CTGGCCCCAG CTCTCTTCTC TGCTCTCTCT ATGGCTTGGG CTGGAGTGGG CTCTCTGGAC 1620  
 CTGACCAGAC TGTGGGTCCC TGCGTCTCCT GCCCACTCTG ACCGGGCTTC CTCCCTCCAC 1680  
 GCTTAGGGTC TGTCCCGGGT ACTCAGTCAG CCCAGTGGGA TCTTACCCAC TTCCCTGCAA 1740  
 GGTCACCTGT CCCCAGGCTC AGGCTGCCCA GCGGCTCTTC CTGGACAGTG AGAGCAGGGC 1800  
 TTGGCGCCTC TGTCTTGGCC CGGGAGCCGC AGGGGCCCTT CCTCCAGAGC CTGGGCGCAA 1860  
 CGCACACAGG CTGCCGCTGC TCTCCAGGT GAAATCCACA CCAGTCCACG CCGGGTCGCC 1920  
 TGCCCTGTCT CCCTACTTAG ACCCAGTCAT TCTAGAGGGA TCCACCGCCA CACTGGCCGG 1980  
 10 CCACAGTCCT GGGTGTCTGT ATGCCAGCT TGGAGTGCCA CGTGGCCGCT GCCCAGCTCC 2040  
 CGGGCACTGT CATGCCAGC TTGGAGTGCC ACATGGCCGC TGCCACGTC CCGGGCACTG 2100  
 TCAATGCCAG CTGGAGTGC CACGTGGCCG CTGCTGTGAC AGGCAGTGTT CTGGGGGTG 2160  
 GGGCTGCATC CAAGGCTTTG TAAACCGGCT GGACCAAGTC TCCTGGCCG CAGTGACCGG 2220  
 GGAAGCTGA GCCCTCCCT CCTGTGTTTG CTCCATTAC TCAAAATGCA GGACAGATCA 2280  
 15 GGTGAGAGCC CAGGAATCTT CACAGGTTC AAGGCCCCAG GGCAGCGGCT TTCTCCATCT CCGCTGTTTT 2340  
 TTGTCTTGT CACTCAGTGA AAGGCCCCAG GGCAGCGGCT TTCTCCATCT CCGCTGTTTT 2400  
 GGGGTCTTAG GGTACAGCCC AGGCGGTGAC TGCCACCTG CCAGGCTGCA GGGACAGTTG 2460  
 GGTGTGAGAA TAACACTGGC TTTGGGTAGT GCCATGGCCA GGAGTGGGTT TCCTGCGTTC 2520  
 TCCTCGTCCC GAGGGCGCCT GGGTCTCTCC AGCTGACGGC AGTAAATCCA CAGTGAGTTG 2580  
 20 GGGCGACTGT GAAACTGGAA TGCTGTACT TTGATAATTA CTTCACGCA GGTGTTTTCC 2640  
 TTCACAATGG TTTTGTCTT TCCCTTCTGA TCTGAGAAGA CATGAACGTT TTCTCTTCAC 2700  
 CGCCGTGGGG TGTATTGACT GGTCCCCCAT GGGCTGCTGG AAAGGCCCGG AGATGCATCT 2760  
 GTGGCCTGGG GCCATCAAGA TCAAGAACC AGGAGGCTG GGAGATGACG CTGGATGGGG 2820  
 CGGCCTGCAG ACCTCAGTGA GGGGTTGAG GACCCTCCA GGTTCCTCC TGCGGAACAG 2880  
 25 GAGTGACTCT GGCTGCCAAG ATACCTTCAT GGTGTTTCAT ACAAGTGGAA TCATTATTTT 2940  
 CAACCATTTA AGGGGGATGC AGGCAAGACA CCTTCCCAGC TGCTCCTAGA GGGGACAAGC 3000  
 CAGGCCCTCT CTCGAGTCTT CGGCAGTCTC GGAAGGACAC AGTCAGGGGC CGGGCAAACA 3060  
 CTTTGGCCAC AGCCCCAAC AAGCGCCACC GTGGGAGAGG AGAGGCTGCT GTCACTGGTA 3120  
 CCGGATGCAG ACCCCACCTC GTCTGCAGGC CACCCCCACC TCCTGTCAGC TTTGAGGCTG 3180  
 30 GCGGGGTCTG CTCTGCGGAA TGGGGTGGGA GCCACAGGGA CGACCCGGGG CGGGCTGATG 3240  
 TCTTCTGGG GGCAGACCAAG AGAGCTCAAG TTTCAGAGTC AGAATTAGGC ACTTGGAACG 3300  
 TTTTGTCTGG CTTGCACTTT CTTATTTTCT TATTTTAGAG CGCTTAAAAA ATCCGAAAAA 3360  
 ATGGGGTTTA AAAGAACTGT CTCCTTCAGT CTACATTTTT GTTTAATACG CTTGAGCAAT 3420  
 AAACGCTGAC TTGAGACGT G

Seq ID NO: 280 Protein sequence  
 Protein Accession #: NP\_055981.1

40 1 11 21 31 41 51  
 MTQEPFREEL AYDRMPTLER GRQDPASYAP DAKPSDLQLS KRLPPCFPSHK TWVFSVLMGS 60  
 CLLVTSGFSL YLGNVFPDEM DYLRCAAGSC IPSAIVSFTV SRRNANVIPN FQILFVSTFA 120  
 VTTTCLIWFG CKLVNPSAI NINFNILLLL LLELLMAATV IIAARSSEED CKKKKGSMSD 180  
 SANILDEVFP PARVLKSYSV VEVIAGISAV LGGIIALNVD DSVSGPHLSV TFFWILVACF 240  
 45 PSIAISHVAA ECPKSLKVEV LIAISSLTSP LLFTASGYLS FSIIMRIVEMF KDYPPIAIKPS 300  
 YDVLVLLLLL VLLQAGLNT GTAIQCVRFK VSARLQASW DTQNGPQERL AGEVARSLPK 360  
 EFDKEKAWRA VVVQMAQ

Seq ID NO: 281 DNA sequence  
 Nucleic Acid Accession #: NM\_004518.1  
 Coding sequence: 43..2577

55 1 11 21 31 41 51  
 GCTGAGCCTG AGCCCGACCC GGGGCGCCTC CCGCCAGGCA CCATGGTGA GAAGTCGCGC 60  
 AACCGCGCGG TATACCCCGG CCGGAGCGGG GAGAAGAAGC TGAAGGTGGG CTTCGTGGGG 120  
 CTGGAACCCG GCGCGCCCGA CTCCACCCGG GACGGGCGCG TGCTGATCGC CGGCTCCGAG 180  
 GCCCCCAAGC GCGGACGAGT CCTCAGCAA CCTCGCGCGG GCGGCGCGGG CGCCGGGAAG 240  
 CCCCACAAGC GCAACGCTTT CTACCGCAAG CTGCAGAAAT TCCTCTACAA CGTGCTGGAG 300  
 CGGCGCGCGG GCTGGGCGTT CATCTACCAC GCCTACGTGT TCCTCCTGGT TTTCTCTGTC 360  
 60 CTGCTGCTGT CTGTGTTTTT CACCATCAAG GAGTATGAGA AGAGCTCGGA GGGGGCCCTC 420  
 TACATCTCTG AAATCGTGAC TATCGTGGTG TTTGGCGTGG AGTACTTCGT GCGGATCTGG 480  
 GCCGCAAGCT GCTGTGCGG GTACCGTGGC TGGAGGGGGG GGCTCAAGTT TGCCCGGAAA 540  
 CCGTTCTGTG TGATTGACAT CATGGTGCTC ATCGCCTCCA TTGCGGTGCT GGCCGCGCGC 600  
 TCCCAAGGGA ACGTCTTTGC CACATCTGCG CTCGCGAGCC TGCGCTTCCT GCAGATTCTG 660  
 65 CGGATGATCC GCATGGACCG GCGGGGAGGC ACCTGGAAGC TGCTGGGCTC TGTGTTCTAT 720  
 GCCCACAGCA AGGAGCTGGT CACTGCTGG TACATCGGCT TCCTTTGTCT CATCCTGGCC 780  
 TCGTTCTCTG TGTACTTGGC AGAGAAGGGG GAGAAGCACC ACTTTGACAC CTACGCGGAT 840  
 GCACTCTGGT GGGGCTGAT CACGCTGACC ACCATTGGCT ACGGGGACAA GTACCCCCAG 900  
 70 ACCTGGAACG GCAGGCTCCT TGCGGCAACC TTCACCTCA TCGGTGTCTC TTCTCTCGCG 960  
 CTGCTGTCAG GCATCTGGG GTCTGGGTTT GCCCTGAAGG TTCAGGAGCA GCACAGGCG 1020  
 AAGCACTTTG AGAAGAGGGC GAACCCGGCA GCAGGCTGCA TCCAGTCGGC CTGGAGATTC 1080  
 TACGCCACCA ACCTCTCGCG CACAGACCTG CACTCCACGT GGCAGTACTA CGAGCGAAGC 1140  
 GTACCGGTGC CACTGTACAG ACTTATCCCC CCGCTGAACC AGCTGGAGCT GCTGAGGAAC 1200  
 75 CTCAAGAGTA AATCTGGACT CGCTTTCAGG AAGGACCCCC CGCCGGAGCC GTCTCCAAGC 1260  
 CAGAAGGTCA GTTTGAAAGA TCGTGTCTTC TCCAGCCCCC GAGGCGTGGC TGCCAAGGGG 1320  
 AAGGGGTCCC CGCAGGCCCA GACTGTGAGG CGGTCAACCA GCGCGGACCA GAGCCTCGAG 1380  
 GACAGCCCA GCAAGGTGCC CAAGAGCTGG AGCTTCGGGG ACCGAGCCCG GGCACGCCAG 1440  
 GCTTTCGCGA TCAAGGGTGC CGCGTCACGG CAGAAGCTAG AAGAAGCAAG CCTCCCCGGA 1500  
 80 GAGGACATTG TGGATGACAA GAGCTGCCCC TGCGAGTTTG TGACCGAGGA GTCTACCCCG 1560  
 GGCCTCAAAG TCAGCTACAG AGCCGTGTGT GTCATGCGGT TCCTGGTGTG CAAGCGGAAG 1620  
 TTCAAGGAGA CGCTGCGGCG CTACGACGTG ATGGACGTCA TCGAGCAGTA CTCAGCCGGC 1680  
 CACCTGGACA TGCTGTCCCC AATTAAGAGC CTGCAGTCCA GAGTGGACCA GATCGTGGGG 1740  
 CGGGGCCCCG CGATCACGGA CAAGGACCGC ACCAAGGGCC CGGCGGAGG GAGAGCTGCC 1800  
 GAGGACCCCA GCATGATGGA ACGGCTCGGG AAGGTGGAGA AGCAGGTCTT GTCCATGGAG 1860

	AAGAAGCTGG	ACTTCCTGGT	GAATATCTAC	ATGCAGCGGA	TGGGCATCCC	CCCGACAGAG	1920
	ACCGAGGCCCT	ACTTTGGGGC	CAAAGAGCCG	GAGCCGGGCG	CGCCGTACCA	CAGCCCGGAA	1980
	GACAGCCGGG	AGCATGTGGA	CAGGCACGGC	TGCATTGTCA	AGATCGTGGC	CTCCAGCAGC	2040
5	TCACAGGGCC	AGAAGAAGTT	CTCGGCGCCC	CCGGCCGCGC	CCCTGTCCCA	GTGTCCGCCC	2100
	TCACCTCCT	GGCAGCCACA	GAGCCACCCG	CGCCAGGGCC	ACGGCACCTC	CCCCGTGGGG	2160
	GACCACGGCT	CCCTGGTGGC	CATCCCGCCG	CCGCTGCCCC	ACGAGCGGTC	GCTGTCCGCC	2220
	TACGGCGGGG	GCAACCCGCG	CAGCATGGAG	TTCTGCGGCG	AGGAGGACAC	CCCGGGCTGC	2280
	AGGCCCCCGG	AGGGGACCTT	GCGGGACAGC	GACACGTCCA	TCTCCATCCC	GTCCGTGGAC	2340
10	CACGAGGAGC	TGAGAGCTTC	CTTCAGCGGC	TTAGCATCTT	CCAGTCCAA	GGAGAACCTG	2400
	GATGCTCTCA	ACAGCTGCTA	CGCGGCCGTG	GCGCCTTGTC	CCAAAGTCAG	GCCCTACATT	2460
	GCGGAGGGAG	AGTCAGACAC	CGACTCCGAC	CTCTGTACCC	CGTGGGGGCC	CCCGCCACGC	2520
	TCGGCCACCG	GCGAGGGTCC	CTTTGGTGAC	GTGGGCTGGG	CCGGGCCGAG	GAAGTGAGGC	2580
	GGCGCTGGGC	CAGTGGACCC	GCCCGCGGCC	CTCCTCAGCA	CGGTGCCTCC	GAGGTTTGA	2640
15	GGCGGGAACC	CTCTGGGGCC	CTTTCTTAC	AGTAAGTGA	TGTGGCGGGA	AGGGTGGGCC	2700
	CTGGAGGGGC	CCATGTGGGC	TGAAGGATGG	GGGCTCCTGG	CAGTGACCTT	TTACAAAAGT	2760
	TATTTTCCAA	CAGGCGCCTT	CAGGCCCTTG	TGCGCATGTA	GGTGCCCTCC	CTGGGCTGTC	2820
	TCCTCACCCC	TCCTGTGCT	GGAGCCTGTC	CCAAAAGGT	GCCAAGTGGG	AGGCCTCGGA	2880
	AGCCACTGTC	CAGGCTCCCA	CTGCCTGTCT	GCTCTGTTC	CAAGGCAGC	GTGTGTGGCC	2940
20	TCGGGCCCTG	CGGTGGCATG	AAGCATCCCT	TCTGGTGTGG	GCATCGCTAC	GTGTTTGGG	3000
	GGCAGCGTTT	CACGGCGGTG	CCCTTGCTGT	CTCCCTTGGG	CTGGCTCGAG	CCTGGGGTCC	3060
	ATGTCCCTTT	GCCGTCCCGT	CATGGGGCAG	GGAATCCATA	GCGGGGCCCA	CAGGCAGGGG	3120
	TATGAGTGGC	TCCACCCCAA	CGCAGCACCA	GCCCGGCCCA	CCGTCCCCCG	TGTCCCAAGT	3180
	TCCGTCTCAG	CTACTCTGGC	TCCAGGACCC	TGGAGAAGGG	AGACCTGGCA	GTGGAGGGAG	3240
25	GCTGTGCTGT	GTGTCCCTCT	GCAGGTGTGA	CCCCGCTGTC	TCTTCTCTCC	CCCGCCAGGT	3300
	GTGGCCCGGC	CTGTCTTTTC	CTCCCCCACC	AGTATGGCCC	CACCTGCTCT	TTCTNCCCC	3360
	CCCAAGGTGT	GGCCCCACCT	GTTCTTCTCT	CCCCTGCCGA	GGTGTGACCC	CACCTGCTCT	3420
	TTCTCTCCCTC	CCAGTATGGC	CCCACCTGCT	CTTCTCTCCC	CCGAGGTGAG	GGCCCGCTCT	3480
	CTCTTTCTCTC	CCATGGGAGC	CGCTGAGGCG	TGCGCACCTG	GGCACAGGTT	GGGGCTCTGC	3540
30	AGGATGAGGA	AGACAGGCCA	ATCCCTTCCC	TCCACAGAAGC	TGGCCGCCCA	CAGGAGGGGA	3600
	CTGAGGCCAG	ACTCATGTCC	AGCAAGGAAC	GTGTGGTGTG	TCCCTTGGGA	AGTCTCTGGG	3660
	CCCTGGGAGG	AGGGAAGGTG	CACGTCCTGG	GATGGTTGCG	GGGCCCTGTT	TTGGGAGACA	3720
	AAGGGGTAGA	GGGTCTGTCT	TGNGCCCCCC	CAGACTCTAG	CCCGAGCAGT	GCAGCCACCT	3780
	ACTGCCCCAC	CTCAGAGAAG	TGCAGCGGGA	AGGAGGCTGG	AGGTGGTGCG	CGCGTGCCTC	3840
35	GGGTGTCTGC	TGAATGAGC	GTGGCCAAGG	ACCAGTGCCA	CCTCATGGCA	AAGAGCTCCC	3900
	GCAGTGTTTT	TTAGAGTGCA	CATCCTACGT	GCCCACTGGC	ACACACAGCT	GCTCACATAC	3960
	ANGTCNGNCT	ACAGGNGTAC	ACATGCANGC	TTGCACACAT	GCACACAGAC	CACATAGCAC	4020
	ACATGTGCAC	TGACACACAC	TGTATAGACC	ATGCACAGTA	CACATACGTG	CATACACATG	4080
	CCTGCATACA	GGCATACACA	TGCACGCTTA	CATGTACACG	TGCACAGATC	ACACACATGC	4140
40	ACACACGTGT	AGCTCACACA	CAGTATACAC	ATACACAAGT	GCACAGACCA	CACACAGCAC	4200
	TAAACATATG	ACACACAAAG	TGCATAGGCC	ACACAGCACA	TGCACACAGG	TGCACAGACC	4260
	ACACAGCACA	CACAAGTGCA	CAGAGCACAC	TGCACACATG	CACACACACA	CGCGTGCATG	4320
	CACACTCCTC	CGACTTCCAG	CCTTGGAGCC	CTTCTGTCTC	TGGTCTTTCT	CTTTGACCCT	4380
	GCTGAGTGTA	AGCTGCCTGG	GGAGGGGCTA	CAAGGAGTAA	TTGTGGCTTT	AGGGGTCTGT	4440
45	GTGATGCTGG	AATGTCAAGC	GCCGTCTGTG	GGTATCCGAC	TGTCGGGGCT	CCTGGTCCGC	4500
	AGTGGCAGAG	CGCCAGGCAG	AGCCAAATCAG	GGTCTCGTGC	TGCCCTTCCC	CCCCACAGCC	4560
	TGGCAGCCAT	CCAGAGGAGG	GGCTCTACCA	GATGCCAAGG	TGCCCCGGTG	TCTGTATGGG	4620
	TGTCCGGTTG	GGTCTCTGT	TTGGTCTGCC	CTGGAGGTGG	CTGGGCCCTC	CTGGGATGGG	4680
	TGGCTCAGCC	TGGAATCCCA	GGCCCCAGCC	CAGGCAGGTG	CTGCTGCCTG	TTGTGGTTTC	4740
50	CTGGCCCGAG	TTCTCTCTCT	CCCTCTGCAT	AAAATCACAG	TCCGTGAGTC	TTCCAGCTGC	4800
	CACACCGGCT	GGGACAGGCT	GGGGGAGGGC	TCCTCCCATG	CCTCCTGCAC	ACAGCCGTCT	4860
	GAGCAGGGCA	GGTGCCAACA	CCCCCACCCG	GAGACACGCT	GCCCTCAGC	GATGCCCTTA	4920
	CCTTTTGGGG	GGCTCTGTCT	CAAGCCCCCC	CTTGGAGGCT	GAATACACC	CAGGCACTGT	4980
	GAGGGCTTCT	CCAGGGGGAG	ACCCTTTGAG	CTGTGGGTCT	GATCACCCCA	AGTCCCGCAC	5040
55	ACGGAGGAGA	GGCAGAGCCA	GGGCGTGTGG	TTTAATGTTT	GCCCCCTCGG	GGCTGGAGGT	5100
	CTCAGTGTTC	CTAGATTCCA	AGCCCTGCTG	CCAGAGAGAC	CTGCTGCCGG	AGAGAAGGGG	5160
	AGGAGGACTC	CAGCTGGGCT	CGGTCCCCCA	CAGTCAGGGA	CCCCCATAAA	GGACACCCCC	5220
	TTCTCTCTAG	AAAGAGCTGG	GCTCTCAGCT	ATTCTTAGTT	GCTTCCAGTA	AGCCGAGGAG	5280
	CAGAAGGAGC	TGTGAGAGCT	TTGCAGAAAC	GCCCTTGTCC	CGCCCTCCTT	GAGCTATGAA	5340
60	TGCCGTACAG	AGCAGAGGCT	GGGCGATTGG	CAAGATCACA	GGTGTATGCT	GCACAGCCCC	5400
	ATTGACACAA	ACCCTCAAAG	CAGACGTGAG	AGGGACGGTT	CACAAAGCTT	GGACCTGCCG	5460
	TGGAGGGTGC	CCCGCAGACG	TGGCGTGAGA	GGGACGGCTC	ACGAGGCTTG	GACCTGCTGT	5520
	GGAGGGTGCC	CAGCAGACGT	GGTGTGAGAG	GAACGGCTCA	CGAGACTTGG	ACCTGGTGGA	5580
	GGGTGCCCGG	CAGACGTGGT	GTGAGAGGGA	CGGCTCACAG	GGCTTGGACC	GGAGAGAGAT	5640
65	GGCTCATGAG	ACTTGGACCT	GCCGTGGAGG	GTGCCAGACA	GACGTGGTAT	GAGAGGGATG	5700
	GCTCACGAGG	CTTGGACCTG	GTGGAGGGTG	CCCGGCAGAC	GTGTGAGAGG	GACGGTTTAC	5760
	AAGGCTTGGA	CCTGCCATGG	AGGGTGCCCA	GCAGACGTGG	TGTGAGAGGG	ACAGCTCACG	5820
	AGGCTTGAGC	CTGCCGTGGA	GGGTGCCCAG	CAGGGGGCTG	AGCTCTGAGG	GGTGGGTGCT	5880
	CAGTGACCGG	GTGCCCCAG	TGTCTCTGTA	TCTGTCCCGG	TGCCCTCCCC	AACCCCCACA	5940
70	CCCATGCAGA	ACTCCAGGT	CACATGCACG	TATGTCCAGG	GCAATGGGGT	GGCGTGAAGA	6000
	GGCCTGTGTA	GGGCTTTTAG	GGGCTGCAGG	ACGGAATGGC	CACCTGGGGA	GCCTGTGTGG	6060
	CTGTGCCGGG	CAGCATCCCT	GCAITCCCA	CCAGCGCGCA	GTCTCCACCT	CGGCCCCAGC	6120
	AAAGCGCTAA	GCAGCCGGAG	AGACAGCCAG	GGCGGCTTCC	TGAAGGATGT	GGGATGGTGG	6180
	ACTCCGGGGT	CGAGGGAATA	CGCAGGTTCC	TGTCCTCCGG	GAGACCTAGA	GAAGCTGCAC	6240
75	ACCCAGGAGC	TTTCCATGAC	CCGGGAGCAT	GAGTGAATGG	GGGGTTCCAG	TTTGTGTAAC	6300
	TTTGTGTCT	TGTAAGGGTG	GGGGCTGACG	GCCGACCCCT	GGAGGAGGTG	ACACCCGAGG	6360
	GGGAGGTTGT	GGGCAACGGT	GGAGGAGGAG	AGACGGGAGG	GGACCATTTG	GGATGGAGGG	6420
	GCCTCTCAG	AGTTTAAAAA	GGCGTTTGTG	GGGTGGAGTT	GAGTGTGCTC	TGGGCTTGGG	6480
	CACFTTGCCCT	GGTGCCCCCT	GCTGGCCGAG	GAGACTGGCT	CTGGCCAGGG	CCCCGTCTCT	6540
80	AGAGGTCTCT	AGCGTCTGAC	TCTCGGCCAG	GCGCCAGCAA	GGAGGGGCCG	GTCCCCGGGG	6600
	CTACCAGGCA	GGCAGCTGCA	CATCGCCATC	GCCACAGGCC	AACTCCGCTT	GGGTTTACAA	6660
	AAGTCGTTGC	CTTAATGTCAT	GTGGACAGGA	ACTCCCTGAG	GTGCCCCCAT	GCCCCCTGGC	6720
	TGTGTCAGGT	ACGGACGCCCT	TGGACCCCTG	GAACAGGTGG	GCGCGGGCAG	GGGCCCAAGG	6780
	GACGGGCTCC	AGAGACACGC	GCAGGGCAGG	AGGGGTCTCA	CGGAGGGGTC	TGCACTGAGG	6840
	GCGCCAGAG	CTGGTGGTCC	CGCTGGACGC	CATCCCTCTG	CCCGGGATCC	ACACGGCCCA	6900

CGTGTGCCCG CCATGCCCCG GCCCAGCCG ATTGCAGTCT TCCATCCTCT GGCCGTGACG 6960  
 GTGGCTGCAG CTTCCCCATT TGCGCCGTTG CCTCTGGCTG TCTGCACTTT TGTTCATGCT 7020  
 CCAAAGAACCA TTTCATAATG CCTTCAGTAC CGACGTACAC TTCTGACCAT TTTGTATGTG 7080  
 TCCTTGTGCC GTAGTGACCA GGCCTTTTTT TGGTGGATGT GTTACCCCGC ACACTTCAAT 7140  
 CTCACCTTTG TGCACGCTCF ATTTTCTAGG GATAGACGCC CAGGGAATGA ACTCTAGTTT 7200  
 TCTAACAGAT TAGCTGAGAT ATTAACCTAC TCACACGGAC AGGTTGATGC CAGAGCCGTA 7260  
 AGAATGCGCC AGTGCGGGTT TCGGGGGGAC TTCGGGTGTG GGGTCTGTCG GCCGCGATGG 7320  
 CCGTGAAGG TTTCTGGGAT CCTGCTGCC ACGGGGACGA GTTCGAGCGC CAGGTGGACC 7380  
 TGTGCACTCA GTAAACGCA GTGATTCAAA AAAAAAAAAA

Seq ID NO: 282 Protein sequence  
 Protein Accession #: NP\_004509.1

1 11 21 31 41 51  
 MVQKSRNGGV YPGPSGEKKL KVGFLVGLDPG APDSTRDGL LIAGSEAPKR GSILSKPRAG 60  
 GAGAGKPPKR NAFYRKLQNF LYNVLERPRG WAFIYHAYVF LLVFSCLVLS VFSTIKEYEK 120  
 SSEGALYILE IVTIVVFGVE YFVRIWAAGC CCRYRGWRGR LKFARKPFCV IDIMVLIASI 180  
 AVLAAGSQGN VFATSLRSL RFLQILRMIR MDRRGGTWKL LGSVVYAHSK ELVTAWYIGF 240  
 LCLILASFLV YLAEGKENDH FDTYADALWV GLITLTITIGY GDKYPQTWNG RLLAATFTLI 300  
 GVSFFALPAG ILGSGFALKV QEQHRQKHE KRRNPAAGLI QSAWRFYATN LSRTDLHSTW 360  
 QYYERTVTVP MYRLIPPLNQ LELLRLNLSK SGLAFRKDPP PEPSPSQKVS LKDRVFSPPR 420  
 GVAAGKKGSP QAQTVRSPS ADQSLSDSPS KVPKSWSPGD RSRARQAFRI KGAASRQNSE 480  
 EASLPGEDIV DDKSCPCBEFV TEDLTPLKLV SIRAVCMVRF LVSKRKFKES LRPYDVMQVI 540  
 EQYSAGHLDM LSRIKSLQSR VDQIVGRGPA ITDKDRTKGP AEALPEDPS MMGRGLKVEK 600  
 QVLSMEKKLD FLVNIYMQRM GIPPTETEAY FGAKEPEPAP PYHSPEDSRE HVDHRHCIVK 660  
 IVRSSSTTQK KNFSAPPAAP PVQCPPSTSW QPQSHPRQGH GTSPVGDHGS LVRIPPPPAH 720  
 ERSLSAYGGG NRASMEFLRQ EDTPGCRPPE GTLRSDTSI SIPSDHEEL ERSFSGFSIS 780  
 QSKENLDALN SCYAAVAECA KVRPYIAEGE SDTDSDLCTP CGPPPRSATG EGPFPGDVGWA 840  
 GPRK

Seq ID NO: 2838 DNA sequence  
 Nucleic Acid Accession #: AF152496.1  
 Coding sequence: 1..2391

1 11 21 31 41 51  
 ATGGAGGCGG GAGGAGAGCG ATTTCTTAGA CAAAGGCAAG TCTTGCTTCT CTTTGTTTTT 60  
 CTGGGAGGGT CTCTGGCTGG GTCCGAGTCA AGACGCTATT CTGTGGCTGA GGAAGAGAG 120  
 AAGGGCTTTT TAATAGCCAA CCTAGCAAAG GATCTGGGAC TAAGGGTAGA GGAAGTGGCC 180  
 GCGAGGGGGG CCCAAGTTGT GTCCAAAGGG AACAAACAGC ATTTTCAGCT CAGTCATCAG 240  
 ACAGGTGATT TGCTCCTGAA TGAGAAATTG GACCGGGAGG AGCTATGCGG CCCCACAGAA 300  
 CCATGCATAC TACATTTTCA GATATTACTG CAAAACCTTT TGCAATTCGT TACAAACGAG 360  
 CTCCGTATCA TAGATGTAAA TGACCAATTCT CCGGTATTCT TTGAAAATGA AATGCATCTG 420  
 AAAATCTTAG AAAGCACTCT GCCAGGAACA GTAATTCCTT TGGGAAATGC TGAGGACTTG 480  
 GATGTGGGAA GAAACAGCCT CCAAAACTAC ACTATCACTC CGAATTCCTA CTTCCACGTA 540  
 CTCACCTCGA GTCTAGGGGA CGGAAGGAAG TACCCGGAAC TAGTACTGGA TAAAGCGCTC 600  
 GATCGGGAGG AGCAGCCGGA ACTCAGCTTA ACGCTCACCG CGCTGGACGG CGGCTCTCCC 660  
 CCTCGTCTG GGACAGCCCA GATAAACATC CAGGTCTTAG ATATAAACGA CAATGCACCA 720  
 GAATTTGCAC AGCCGCTCTA TGAGGTTGCA GTTCTAGAGA ATACCCCGGT TAACTCTGTC 780  
 ATTGTCACTG TCTCGGCTTC TGACTTAGAT ACAGGAAGTT TTGGGACAAT ATCATATGCA 840  
 TTTTTCATG CTCTGGAAGA AATTCGCAAA ACTTTTCAGC TAAATCCAAT TACTGGTGAT 900  
 ATGCAACTGG TCAAAATATT GAATTTTGAA GCGATTAATA GTTATGAAGT CGACATCGAG 960  
 GCCAAGGATG GCGGAGGCCT ATCCGGAAAG TCTACAGTCA TAGTCCAGGT GGTGTATGTC 1020  
 AACGACAACC CACCGGAAC TACCTTGCTC TCAGTAAACA GCCCTATTCC TGAGAACTCG 1080  
 GGAGAGACTG TACTGCTGTG TTTCAGTGTT TCTGATCTAG ACTCTGGAGA CAAACGAAGA 1140  
 GTGATGTGTT CCATTGAGAA CAATCTCCCC TTCTTCTCTG AACCATCTGT AGAGAATTTT 1200  
 TACACCTTAG TGTCAGAAAG CGCGCTGGAC AGAGAGACCA GATCCGAGTA CAACATTACC 1260  
 ATCACTATCA CTGACCTGGG GACACCCAGG CTGAAAACCA AGTACAACAT AACCGTGCTG 1320  
 GTCTCCGACG TCAATGACAA CGCCCCCGCC TTCACCCAAA TCTCTTACAC CCTGTTCTGTC 1380  
 CGCGAGAAC AAGACCCCGC CCTGCACATC GGCAGTGTCA GCGCCACAGA CAGAGACTCA 1440  
 GGCACCAAGC CCCAGGTAAC CTACTCGCTG CTGCCGCCCC AGGACCCGCA CCTGCCCTTC 1500  
 TCTTCCCTGG TCTCCATCAA CGCGGACAA GGCACCTGT TTGCCCTCAG GTCGCTGGAC 1560  
 TACGAGGCCC TGCAGGCGTT CGAGTTCCGC GTGGGCGCCA CAGACCGTGG CTCCCGGCTC 1620  
 TTGAGCAGCG AGGCGCTGGT GCGCGTGTG GTGCTGGACG CCAACGACAA CTCGCCCTTC 1680  
 GTGCTGTACC CGCTGCAGAA CGGCTCCGCG CCTGCACCG AGCTGGTGCC CCGGGCGGCT 1740  
 GAGCCGGGCT ACCTGGTGAC CAAGGTGGTG GCGGTGGACG GCGACTCGGG CCAGAACGCC 1800  
 TGCTGTGCTG ACCAGCTGCT CAAGGCCACG GAGCCCGGGC TGTTCTGCGT GTGGCGGCAC 1860  
 AATGGCGAAG TGCACACCGC CAGGCTGTCT AGCGAGCGCG ACGCGGCCAA GCACAGCTG 1920  
 GTGGTGCTGG TCAAGGACAA TGGCGAGCCT CCGCGCTCGG CCAACGCCAC GCTGCAATGT 1980  
 CTCCTGTGTG AGGCTTCTC CAGCCCTAC CTGCTCTTCC CGGAGGCGGC ACCGGCCGAC 2040  
 GCCCAGGCGC ACTTGCTCAC CGTCTACCTG GTGGTGGCAT TGGCTCGGT GTCTTCTGCTC 2100  
 TTCTCTTTT CGTGCTCCT GTTCGTGGCG GTTCGGCTGT GCAGGAGGAG CAGGGCGGCC 2160  
 TCGGTGGTGC GCTGCTCGGT GTCGAGGGG CCCTTTCCAG GGCAGATGGT GGACGTGAGC 2220  
 GGCACCGGGA CCTGTGCCA GAGCTACCAG TACGAGGTGT GTCTGACTGG AGGCTCCGGG 2280  
 ACAAATGAGT TCAAGTTCTT GAAGCCAATT ATCCCAACT TCGTTGCTCA GGTGTCAGAG 2340  
 AGGGTTAGCG AGGCAATCC CAGTTTCAGG AAGAGCTTTG AATTCACTTA A

Seq ID NO: 284 Protein sequence  
 Protein Accession #: AAD43757.1

1 11 21 31 41 51  
 MEAGGERFLR QRQVLLLFVF LGGSLAGSES RRYSAEBEKE KGFLIANLAK DLGLRVEELA 60

ARGAAQVVSQK NKQHFQLSHQ TGDLLLNEKL DREELCGPTE PCILHFQILL QNPLQFVTNE 120  
 LRIIDVNDHS PVFFENEMHL KILESTLPGT VIPLGNAEDL DVGRNSLQNY TITPNSHFHV 180  
 LTRSRDRGRK YPELVLDKAL DREEQPELSL TLTALDGGSP PRSGTAQINI QVLDINDNAP 240  
 5 EFAQPLYEVA VLENTPVNSV IIVTASASDL TGSFQITISA FFHASEEIRK TFQLNPITGD 300  
 MQLVKYLNFE AINSYFVDIE AKDGGGLSGK STVIVQVVDV NDNPPPELTL SVNSPIPENS 360  
 GETVLAVFSV SLDLSDGNGR VMCSIENMLP FFLKPSVENF YTLVSEGALD RETRSEYNIT 420  
 ITITDLGTPR LKTKYINITVL VSDVNDNAPA FTQISYTLFV REMNSPALHI GSVSATDRDS 480  
 10 GTNAQVTYSL LPPQDPHLPL SSLVSINADN GHLFALRSLD YEALQAFEFV VGATDRGSPA 540  
 LLSSEALVRVL VLDANDNSPF VLYPLQNGSA PCTELVPRAA EPGYLVTKVV AVDGDGSGQA 600  
 WLSYQLLKAT EPLFLFVWAH NGEVTRARLL SERDAAKHRL VVLVKDNGEP PRSATATLHV 660  
 LLVDGFSQPY LPLPEAAPAQ AQADLLTVYL VVALASVSSL FLFSVLLFVA VRLCRRSRAA 720  
 SVGRCSVPEG PFPQMVVDVS GTGTLQSQSYQ YEVCLTGGSG TNEFKFLKPI IPNFVAQGA 780  
 RVSEANPSFR KSFEFS

Seq ID NO: 285 DNA sequence  
 Nucleic Acid Accession #: NM\_001794.2  
 Coding sequence: 15..2765

1 11 21 31 41 51  
 CGCGCGCGGG GAAGATGACC GCGGCGCGCG GCGTGCTCCT TCTGCTGCTC TCGCTCTCCG 60  
 GCGCGCTCCG GCGCCATAAT GAGGATCTTA CAACTAGAGA GACCTGCAAG GCTGGGTCTT 120  
 CTGAAGATGA TTACACGGCA TTAATCTCCC AAAATATTCT AGAAGGGGAA AAGCTACTTC 180  
 25 AAGTCAAGTT CAGCAGCTGT GTGGGGACCA AGGGGACACA ATATGAGACC AACAGCATGG 240  
 ACTTCAAAGT TGGGGCAGAT GGGACAGTCT TCGCCACCCG GGAGCTGCAG GTCCCCCTCCG 300  
 AGCAGGTGGC GTTCACGGTG ACTGCATGGG ACAGCCAGAC AGCAGAGAAA TGGGACGCGC 360  
 TGGTGCGGTT GCTGGTGGCC CAGACCTCGT CCGCGCACTC TGGACACAAG CCGCAGAAAG 420  
 GAAAGAAGGT CGTGGCTCTG GACCCCTCTC CGCTCCGAA GGACACCTTG CTGCGCTGGC 480  
 30 CCCAGCACCA GAACGCCAAC GGGCTGAGGC GCGCAACACG GGACTGGGTC ATCCCGCCCA 540  
 TCAACGTGCC CGAGAACTCG CCGGGGCCCT TCCCGCAGCA GCTCGTAGG ATCCGGTCCG 600  
 ACAAGACAA TGACATCCCC ATCCGTGACA GCATCACGGG AGTGGGCGCC GACCAGCCCC 660  
 CCATGGAGGT CTTGAGCATT GACTCCATGT CCGGCCGGAT GTACGTCAAC AGGCCCATGG 720  
 ACCGGGAGGA GCCAGCCTCT TACCACCTCC GAGCCACGCG TGTGGACATG AATGGCAACA 780  
 35 AGGTGGAGAA CACCATCGAC CTGTACATCT ACCTCATCGA CATGAATGAC AACCCTCTG 840  
 AGTTCATCAA CCAGGTCTAC AACGGCTCCG TGGACGAGGG CTCCAAGCCA GGCACCTACG 900  
 TGATGACCGT CACGGCCAAC GATGCTGACG ACAGCACCAC GGCCAACGGG ATGGTGGCGT 960  
 ACCGGATCGT GACCCAGACC CCACAGAGCC CGTCCAGAAA TATGTTTACC ATCAACAGCG 1020  
 AGACTGGAGA TATCGTCAAC GTGGCGGCTG GCCTGGACCG AGAGAAAGTT CAGCAGTACA 1080  
 40 CAGTCATCGT TCAGGCCACC GATATGGAAG GAAATCTCAA CTATGGCCTC TCAACACAG 1140  
 CCACAGCCAT CATCACGGTG ACAGATGTGA ATGACAACCC GCCAGAAATT ACCGCCAGCA 1200  
 CGTTTGACAG TGAGGTCCCC GAAACCGCGG TGGAGACCGT GGTGCAAAAC CTCACGGTGA 1260  
 TGGACCGAGA TCAGCCCCAC TCTCCAACT GGAATGCCGT TTACCGCATC ATCAGTGGGG 1320  
 ATCCATCCGG GCATTCACG GTCCGCACAG ACCCGGTAAC CAACGAGGGC ATGGTCAACG 1380  
 TGGTGAAGG AGTCGACTAC GAGCTCAACA GAGCTTTCAT GCTGACAGTG ATGGTGTCCA 1440  
 45 ACCAGCGGCC CCTGGCCAGC GGAATCCAGA TGTCTTTCCA GTCCACGGCA GGGGTGACCA 1500  
 TCTCCATCAT GGACATCAAC GAGGCTCCCT ACTTCCCTCC AAACCAACAG CTGATCCGCC 1560  
 TGGAGGAGGG CGTGCCCGCC GGCACCGTGC TGACACGTT TTAGCTGTG GACCTGACC 1620  
 GGTTCATGCA GCAGGCTGTG AGATACTCAA AGCTGTGAGA CCCAGCGAGC TGGCTGCACA 1680  
 TCAATGCCAC CAACGGCCAG ATCACCACGG CGGCAGTGCT GGACCGTGAG TCCCTCTACA 1740  
 50 CCAAAACAA CGTCTACGAG GCCACCTTCC TGGCAGCTGA CAATGGGATA CCCCAGGCA 1800  
 GCGGCACCGG GACCTCCAG ATCTATCTCA TTGACATCAA CGACAACGCC CCTGAGCTGC 1860  
 TGCCCAAGGA GCGCGAGATC TGCGAGAAGC CCAACCTGAA CGCCATCAAC ATCAGCGCGG 1920  
 CCGAGCGTGA CGTCGACCCC AACATCGGCC CTAAGTCTTT CGAGCTGCCC TTTGTCCCGG 1980  
 CGGCGGTGCG GAAGCACTGG ACCATCAACC GCCTGAAACG TGACTATGCC CAACTCAGCT 2040  
 55 TGCGCATCCG GTACTGTGAG GCGGGATGT ATGACGTCCC CATCATCGTC ACAGACTCTG 2100  
 GAAACCTTCC CCTGTCCAAC ACGTCCATCA TCAAAGTCAA GGTGTGCCCA TGTGATGACA 2160  
 ACGGGGACTG CACCACTATT GCGCGAGTGG CAGCGGCTGG TCTGGGCACC GGTGCCATCG 2220  
 TGGCATCTCT CATCTGCACT CTATCCCTGC TGACCATGGT CCGTCTGTTT GTCATGTGGA 2280  
 60 TGAAGCGGCG AGAGAAGGAG CGCCACACGA AGCAGCTGCT CATTGACCCC GAGGACGACG 2340  
 TCCGCGACAA CATCTCAAG TATGACGAGG AAGGCGGTGG CGAGGAGGAC CAGGACTACG 2400  
 ACCTCAGCCA GCTGCAGCAG CCGGAAGCCA TGGGGCACGT GCCAAGCAAA GCCCTTGGCG 2460  
 TGCCTGCGGT GGATGAGCGG CCGGTGGCG CTGAGCCCCA GTACCCGATC AGGCCCATGG 2520  
 TGCCGCAACC AGGCGACATC GGTGACTTCA TCAATGAGGG ACTCCGCGCT GCTGACAACG 2580  
 65 ACCCCACGGC ACCCCCTAT GACTCCCTGC TGGTCTTCGA CTACGAGGGG AGCGGCTCCA 2640  
 CCGCAGGCTC CGTCAGCTCC CTGAACCTCAT CCAGTTCCCG GGACCAAGAC TACGATTACC 2700  
 TCAACGACTG GGGGCCCCAGA TTCAAGAAGC TGGCGGACAT GTATGGAGGT GGTGAAGAGG 2760  
 ATTGACTGAC CTCGATCTT CGGACCGAAG TGAGAGCCGT GCTCGGACGC CGGAGGAGCA 2820  
 GGACTGAGCA GAGGCGGCGG GTCTTCCCGA CTCCCTGCGG CTGTGTCTTT AGTGCTGTGA 2880  
 70 GGAGGCCCCC CAATCCCCAC GTTGAGCTGT CTAGCATGAG CACCCACCCC CACAGCGCCC 2940  
 TGCACCCGCG CGCTGCCAG CACCGCGCTG GCTGGCACTG AAGGACAGCA AGAGGCATCT 3000  
 TGTCTTCACT TGAATTCTCT AGAACAGAAG CACTGTTTTT AAAAAAAAAA AAAAAAAAAAAG 3060  
 AAG

Seq ID NO: 286 Protein sequence  
 Protein Accession #: NP\_001785.2

1 11 21 31 41 51  
 MTAGAGVLLL LLSLSGALRA HNEDLTRET CKAGFSEDDY TALISQNIIE GEKLLQVKFS 60  
 SCVGTGKTQY ETNSMDFKVG ADGTVFATRE LQVPSQVAF TVTAWDSQTA EKWDVAVRLL 120  
 80 VAQTSSPSPHK HKPQKGGKVV ALDPSPPPKD TLLPWPQHQN ANGLRRRKRK WVIPPINVE 180  
 NSRGPPFPQQL VRRISDKDND IPIRYITGV GADQPPMEVF SIDSMSGRMY VTRPMDREEH 240  
 ASYHLRAHAV DMNGNKVENP IDLYIYVIDM NDNRPFINQ VYNGSVDEGS KPGTYVMTVT 300  
 ANDADDSTTA NGMVRYRIVT QTPQSPSQNM FTINSETGDI VTVAAGLDRE KVQYTVIVQ 360

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60

ATDMEGNLNY GLSNTATAII TVTDVNDNPP EFTASTFAGE VPENRVETVV ANLTVMDRDO 420  
 PHSPNNAVY RIISGDPSGH FSVRTDPVTN EGMVTVVKAV DYELNRAFML TVMVSNQAPL 480  
 ASGIQMSFQS TAGVTISIMD INEAPYFPSN HKLIRLEEVG PPGTVLTTFS AVDPDRFMQQ 540  
 AVRYSKLSDP ASWLHINATN GQITTAAVLD RESLYTKNNV YEATFLAADN GIPPASGTGT 600  
 LQIYLIDIND NApELLPKEA QICEKPNLNA INITAADADV DPNIGPYVFE LPFVPAAVRK 660  
 NWTITRLNGD YQSLSLRLYL LEAGMYDVPI IVTDSGNPPL SNTSIKVKV CPCDDNGDCT 720  
 TIGAVAAAGL TGTAIVAILI CILILLTMVL LFMVMMKRRE KERHTKQLLI DPEDDVRDNI 780  
 LKYDEEGGGE EDQYDLSQL QQPEAMGHVP SKAPGVRRVD ERPVGAEPQY PIRPMVPHFG 840  
 DIGDFINEGL RAADNDFTAP PYDSLLVFDY EGSGSTAGSV SSLNSSSSGD QDYDYLNDWG 900  
 PRFKKLADMY GGGEBED

Seq ID NO: 287 DNA sequence  
 Nucleic Acid Accession #: AF152495.1  
 Coding sequence: 1..2397

1 11 21 31 41 51  
 | | | | |  
 ATGGAGGCCG GAGAGGGGAA GGAGCGCGTT CCGAAACAAA GGCAAGTCCT GATATTCTTT 60  
 GTTTTGCTGG GCATAGCTCA GGCTAGTTGC CAGCCTAGGC ACTATTCAGT GGCCGAGGAA 120  
 ACGGAGAGTG GCTCCTTTGT GGCCAATTGT TTAAGAGACC TGGGGCTGGA GATAGGAGAA 180  
 CTGCTGTGA GGGGGGCCAG GGTCTTTTCC AAAGGAAAAA AAATGCATT GCAGTTCGAT 240  
 AGGCAGACCG GGAATTGTGT GTTAAATGAG AAATTGGACC GGGAGGAGCT GTGCGGCCCC 300  
 ACAGAGCCCT GTGTCTTACC TTTCAGGTG TTAAGTAAA ATCCCTTGCA GTTTTTCAG 360  
 GCGGAGCTAC GGATTAGGGA CGTAAATGAT CATTCCCCAG TTTTCTAGA CAAAGAAATA 420  
 CTTTGTAAAA TTCCAGAAAG TATCACTCCT GGAAGTACT TCTTAATAGA ACGTGCCGAG 480  
 GACTTGGATG TAGGAACCAA CAGTCTCCAA AATTACACAA TCAGTCCCAA TTCCACTTT 540  
 CATCTTAATT TACAAGACAG TCTCGATGGC ATAATATTAC CACAGCTGGT GCTGAACAGA 600  
 GCCCTGGATC GCGAGGAGCA GCCTGAGATC AGGTAAACCC TCACAGCGCT AGATGGCGGG 660  
 AGTCACCCA GGTCCGGCAC GGCCTTGGTA CGGATTGAAG TGTGGACAT CAATGACAAC 720  
 GTCCAGAGT TTGCAAGCT GCTCTATGAG GTGCAGATCC CGGAGGACAG CCCCCTTGA 780  
 TCCCAGGTTG CCATCGTCTC TGCCAGGAT TTAGACATTG GAACTAATGG AGAAATATCT 840  
 TATGCATTTT CCCAAGCATC TGAAGACATT CGCAAAACGT TTCGATTAAG TGCAAAATCG 900  
 GGAGAACTGC TTTTAAGACA GAAACTGGAT TTCGAATCCA TCAGACATA CACAGTAAAT 960  
 ATTACGGCGA CAGATGGTGG GGCCTTATCT GGAAGTGTG TGGTATTGT CCAAGTGATG 1020  
 GATTTGAATG ACAATCTCTC GGAAGTAACT ATGTCGACAC TTATCAATCA GATCCAGAA 1080  
 AACTTGCAGG ACACCTCAT TGCTGTATTC AGCGTTTCAG ATCCTGACTC CGGAGACAAC 1140  
 GGAAGGATGG TGTGCTCCAT CCAAGATGAT CTTCCTTTT TCTTGAAACC TTCTGTGAG 1200  
 AACTTTTACA CTTCTGTGAT AAGCACGGCC CTGGACCGGG AGACCGATC CGAATACAAC 1260  
 ATCACCATCA CCCTCACCGA CTTCGGGACA CCCAGGCTGA AAACCGAGCA CAACATAACC 1320  
 GTGCTGGTCT CCGACGTCAA TGACAACGCC CCCGCTTCA CCCAAACCTC CTACACCTG 1380  
 TTGCTCGCGG AGAACAACAG CCCCGCCTG CACATCGGCA GCGTCAGCGC CACAGACAGA 1440  
 GACTCGGGCA CCAACGCCCA GGTACCTAC TCGCTGCTGC CGCCCCAGGA CCGCACCTG 1500  
 CCCCTCGCCT CCTGTGCTC CATCAACGCG GACAACGCCC ACCTGTTCGC TCTCCAGTCG 1560  
 CTGGACTACG AGGCCCTGCA GCGCTTCGAG TTCGCGTGG GCGCCGAGA CCGCGGCTCC 1620  
 CCGCGGTTGA GCAGCGAGGC GCTGGTGC GCCTGTGCTG TGGACGCCAA CGACAACCTG 1680  
 CCCTTCGTGC TGTACCGCT GCAGAACGGC TCCGCGCCT GCACCGAGCT GGTGCCCGG 1740  
 GCGGCGGAGC CCGGCTACCT GGTGACCAAG GTGGTGGCGG TGGACGGCGA CTCGGGCGAG 1800  
 AACGCCTGCG TGTCTACCA GCTGCTCAAG GCCACGGAGC CCGGCGTGTG CCGCGTGTG 1860  
 GCGCACATG GCGAGGTGCG CACCGCCAGG CTGCTGAGG AGCGCGAGCG TGCCAAGCAG 1920  
 AGGCTGGTGG TGTCTGCTCA GGAACAATGG GAGCCTCGGC GCTCGGCCAC CGCCACGCTG 1980  
 CACGTGCTCC TGGTGGACGG CTTCTCCAG CCCTACCTGC TGTCTCCGGA GCGGCGACCG 2040  
 GCCAGGCGCC AGGCCGACTT GCTCACCGTC TACCTGGTGG TGGCGTTGGC CTCGGTGTCT 2100  
 TCGCTCTTCC TCTTCTCGGT GCTCCTGTTG GTGGCGGTGC GGCTGTGCAG GAGGAGCAGG 2160  
 GCGGCGCTCG TGGGTGCTGT CTCGGTGCCC GAGGGCCCTT TTCAGGGGCA GATGGTGGAC 2220  
 GTGAGCGGCA CCGGGACCT GTCCAGAGC TACCAGTACG AGGTGTGTCT GACTGGAGGC 2280  
 TCCGGGACAA ATGAGTTCAA GTTCTGAAG CCAATTATCC CCAACTTCGT TGCTCAGGGT 2340  
 GCAGAGAGGG TTAGCGAGGC AAATCCAGT TTCAGGAAGA GCTTTGAATT CACTTAA

Seq ID NO: 288 Protein sequence  
 Protein Accession #: AAD43756.1

1 11 21 31 41 51  
 | | | | |  
 MEAGEGKERV PKQRQVLIFV VLLGIAQASC QPRHYSVAEE TESGSFVANL LKDLGLEIGE 60  
 LAVRGARVVS KGKMKHLQFD RQTGDLLENE KLDREELCGP TEPCVLPPQV LLENPLQFFQ 120  
 AELRIRDVND HSPVFLDKIE LLKIPESITP GTTFLIERAQ DLDVGTNSLQ NYTISPNIHF 180  
 HLNLDQSLDG IILPQLVLNR ALDREEQPEI RLTLTALDGG SPFRSGTALV RIEVDINDN 240  
 VPEFAKLLYE VQIPEDSPVG SQVAIVSARD LDIGTNGEIS YAFSQASEDI RKTFRLSAKS 300  
 GELLRLQKLD FESIQTYTVN IQATDGGGLS GTCVVFVQVM DLNDNPPELT MSTLINQIPE 360  
 NLQDTLIAVF SVSDPDSDGN GRMVCISIQD LPFFLKPSVE NFYTIVISTA LDRETRSEYN 420  
 ITITVDFGT PRKTEHNIT VLVSDVNDNA PAFTQTSYTL FVRENNSPAL HIGSVSATDR 480  
 DSGTNAQVTV SLLPQDPHL PLASLVISINA DNHGLFALQS LDYEAQAFE FRVGAADRG 540  
 PALSSEALVR VLVLDANDNS PFVLYPLQNG SAPCTELVPR AAEFGYLVTK VVAVDGDSGQ 600  
 NAWLSYQLLK ATEPGLFGVW AHNGEVRTAR LLRERDAAKQ RLVVLVKDNQ EPFRSATATL 660  
 HVLLVDGFSQ PYLLLEPAAP AQQAQDLTLV YLVVALASVS SLFLFSVLLF VAVRLCRRSR 720  
 AASVGRCSVV EGFPPGQMDV VSGTGTLSQS YQYEVCLTGG SGTNEFKFLK PIIPNFVAQG 780  
 AERVSEANPS FRKSFEFT

Seq ID NO: 289 DNA sequence  
 Nucleic Acid Accession #: NM\_018674.1  
 Coding sequence: 390..2009

1 11 21 31 41 51  
 | | | | |

	CGGAGCACAT	GCTGAGCGGA	GCGGCTGGGG	CTGCGCGGCG	TGGCGGAGCA	GCGCTCGCTC	60
	CCTCGCTCAC	TGCTCGCTC	GCAGGGACAC	ACGCAGGGGC	TGACAGCTGT	GCTGGTGCTG	120
	ATAAGGGAAG	CCACAAGGAG	ACGATCGAGG	AGAGAGACAA	GCGGCGAGCAG	AGGCAGCAGC	180
5	GGCAGAGGCA	GCACCAGGGC	TGCGGAGCTG	CTGGGAGTGG	GAGTGACTCC	CCCACCTCGG	240
	GCCCCACCC	TGTCCTGTG	CTCTTCCC	TGCGCTGAG	TTTAGAAGAG	CAGCCGCTGC	300
	CACCACTGCC	ACTCGGGAGG	GCACCAGGGC	TGCTGGCTAG	GGAGGGACAG	GGCAGGGAGG	360
	CTCTGCCCAG	TCCACGACG	CGGGACAGA	TGCCGATCGA	GATTGTGTGC	AAAATCAAAT	420
	TTGCTGAGGA	GGATGCGAAA	CCCAAGGAGA	AGGAGGCAGG	GGATGAGCAG	AGCCTCCTCG	480
10	GGGCTGTTGC	CCCTGGAGCA	GCCCCCGGAG	ACCTGGCCAC	CTTTGCCAGC	ACCAGCACCC	540
	TGCATGGACT	GGGCCGGGCC	TGTGGCCAG	GCCCCACGG	ACTGCGCAGA	ACCCTGTGGG	600
	CACTGGCCCT	ACTCACTCG	CTGGCTGCCT	TCCTGTACCA	GGCGCTGSC	CTGGCCCGGG	660
	GCTACCTGAC	CCGGCCTCAC	CTGGTGGCAA	TGGACCCCGC	TGCCCCAGCC	CCAGTGGCGG	720
	GCTTCCCGGC	TGTCACCCCT	TGCAATATCA	ACCGCTTCCG	GCATTCCGCA	CTCAGCGATG	780
	CCGACATCTT	CCACCTGGCC	AATCTGACAG	GGCTGCCCCC	CAAAGACCGG	GATGGGCACC	840
15	GTGCGGCTGG	CTGCGCTAC	CCAGAGCCTG	ACATGGTAGA	CATCTCAAC	CGCACTGGCC	900
	ACCAGCTCGC	CGACATGCTT	AAGAGCTGCA	ACTTCAGTGG	GCATCACTGC	TCCGCCAGCA	960
	ACTTCTCTGT	GGTCTATACT	CGCTATGGGA	AGTGTACAC	CTTCAACGCG	GACCCGCGGA	1020
	GCTCGCTGCC	CAGCCGGGCA	GGGGGCATGG	GCAGTGGCCT	GGAGATCATG	CTGGACATCC	1080
20	AGCAGGAGGA	GTACTGCCCC	ATCTGGAGGG	AGACAAATGA	GACGTCGTTT	GAGGCAGGTA	1140
	TTGCGGTGCA	GATCCACAGC	CAGGAGGAGC	CGCCCTACAT	CCACCAGCTG	GGGTTCGGGG	1200
	TGTCCCCAGG	CTTCAGAGCC	TTTGTGTCT	GCCAGGAACA	GCGGCTGACC	TACCTGCCCC	1260
	AGCCCTGGGG	CAACTGCCCG	CGAGAGAGTG	AGCTCAGGGA	GCCTGAGCTT	CAGGGCTACT	1320
	CGGCTACAG	TGTGTCTGCC	TGCCGGCTGC	GCTGTGAAAA	GGAGGCCGTG	CTTCAGCGCT	1380
25	GCCACTGCCG	GATGTGTGAC	ATGCCAGGCA	ATGAGACCAT	CTGCCACCA	AATATCTACA	1440
	TGAGTGTGTC	AGACACACAC	CTGGACTCCC	TGGGTGGGGG	CCCTGAGGGC	CCGTGCTTCT	1500
	GCCCCACCCC	CTGCACCTTG	ACACGCTATG	GGAAAGAGAT	CTCCATGGTC	AGGATCCCCA	1560
	ACAGGGGCTC	AGCCCCGGTAC	CTGGCGAGGA	AGTACAACCG	CAACGAGACC	TACATACGGG	1620
	AGAACTTCCT	GGTCTTAGAT	GTCTTCTTTG	AGGCCCTGAC	CTTGAAGCC	ATGGAGCAGC	1680
30	GAGCAGCCTA	TGGCTGTGCA	GCCCTGCTGG	GAGACCTCGG	GGGACAGATG	GGCCTGTTC	1740
	TTGGGGCCAG	CATCTCTACG	TTGCTGGAGA	TCTCTGACTA	CATCTATGAG	GTGTCTTGGG	1800
	ATCGACTGAA	GCGGGTATGG	AGGCGTCCCA	AGACCCCTTC	GCGGACCTCC	ACTGGGGGCA	1860
	TCTCCACTTT	GGGGCTTCAG	GAGCTGAAGG	AACAGAGTCC	CTGCCCGAGC	CTGGGCCGAG	1920
	CGGAGGGTGG	GGGGGTTCAG	AGTCTGCTCC	CCAATCACCA	CCACCCCCAC	GGTCCCCCAG	1980
35	GAGGTCTCTT	TGAAGATTTT	GCTTGCTAGG	ACGGTGCTGT	GACTGAAAGG	ACCCAGGAGT	2040
	CTGGGACCCC	TCTTGGGATC	CCCAGCACAT	TCTCTGCTC	CTGGGAGAGG	CCTGGGGGCG	2100
	GTGCTCACTG	GGAGGGCCAG	GACTCAGTTC	CTGCTCTCAT	CCTCCCTGTC	CCTGATGTCA	2160
	GCTGCTTTGC	ACAAAGGTCC	TTCTTGTCCA	CACCCCTTAT	CCCCAGGCTG	GTGCCCCGGG	2220
	AGGGCTGGAG	ACCCAGCCAT	GGGCCCTCAC	GGAGAGGAAG	GGAAGGAAGG	AGAGGGAGGG	2280
40	GGAGGATAGA	GCCCATCCCA	GCCGGGGAGG	GGGAGCCCTC	TGTACATTTG	TAAATATTTA	2340
	GGGAAAGCCG	GGTGGGGGGA	GGGGATACAG	ATGTAGAAGG	TGGGTAGGGC	TACAGGGGTG	2400
	GGTGATTTAG	GGACAGCCAG	GGTCCCAGCC	CCAATGTCAG	CAGGATAGGG	AGAGCCCCAG	2460
	GACTCAGGAG	TGCTGGGCTG	GTCTACTTTC	CTGCCCTCTC	CCAGGCCCGG	CTCCCTCTTT	2520
	GGCAGGGGGA	GGGATGGGCT	CAGCAGGCCT	GGCCAGCTC	CCAGTTCCCC	CTGCACCAGC	2580
45	CCCACCCCTA	GAGTCCCTTC	TATAGGGAGG	GGGCAGGAGA	CCTTCCAGAC	TTGCGGTGAG	2640
	CTTGAGGGGT	GGGAAGGGAG	CCTTCTCAGT	CCTCTCTCCC	TCCAGTCTGA	TTTTATAAAG	2700
	TGCTGACGAG						

Seq ID NO: 290 Protein sequence  
Protein Accession #: NP\_061144.1

	1	11	21	31	41	51	
	MPHIVCKIK	FAEEDAKPKE	KEAGDEQSL	GAVAPGAAPR	DLATFASTST	LHGLGRACGP	60
	GPHGLRRTLW	ALALLTSLAA	FLYQAAGLAR	GYLTRPHLVA	MDPAAAPAPVA	GFPVAVTLN	120
55	NRFRHSALSD	ADIFHLANLT	GLPPKDRDGH	RAAGLRYPEP	DMVDILNRTG	HQLADMLKSC	180
	NFSGHHCSAS	NFVVVYTRYG	KCYTFNADPR	SSLPSRAGGM	GSGLIIMLDI	QOEYLPFIWR	240
	ETNETSFPEAG	IRVQIHSQEE	PPYIHQLGFG	VSPGFQTFVS	CQEQLRTYLP	QPWGNCRAB	300
	ELRPELQGY	SAYSVSACRL	RCEKEAVLQR	CHCRMVHMPG	NETICPPNIY	IECADHTLDS	360
60	LGSGPEGPECF	CPTPCNLTRY	GKEISMVRIP	NRGSARYLAR	KYRNRETYIR	ENFLVLVDVFP	420
	EALTEAMEAG	RAAYGLSALL	GDLGGQMLF	IGASILTLE	ILDYIYEVSW	DRLEKRVWRRP	480
	KTPRLRTSTGG	ISTLGLQELK	EQSPCPSLGR	AEGGGVSSLL	PNHHHPHGGP	GGLFEDFAC	

Seq ID NO: 291 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 62..895

	1	11	21	31	41	51	
	CACTGCTCTG	AGAATTTGTG	AGCAGCCCTT	AACAGGCTGT	TACTTCACTA	CAACTGACGA	60
	TATGATCATC	TTAATTTACT	TATTTCTCTT	GCTATGGGAA	GACACTCAAG	GATGGGGATT	120
70	CAAGGATGGA	ATTTTTCATA	ACTCCATATG	GCTTGAACGA	GCAGCCGGTG	TGTACCACAG	180
	AGAAGCAGCG	TCTGGCAAT	ACAAGCTCAC	CTACGCAGAA	GCTAAGGCGG	TGTGTGAATT	240
	TGAAGGCCGC	CATCTCGCAA	CTTACAAGCA	GCTAGAGGCA	GCCAGAAAAA	TTGGATTCTA	300
	TGTCTGTGCT	GCTGGATGGA	TGGCTAAGGG	CAGAGTTGGA	TACCCCATTG	TGAAGCCAGG	360
75	GCCCAACTGT	GGATTTGAA	AAACTGGCAT	TATTGATTAT	GGAATCCGTC	TCAATAGGAG	420
	TGAAAGATGG	GATGCTTATT	GCTACAACCC	ACACGCAAG	GAGTGTGGTG	GCGTCTTAC	480
	AGATCCAAAG	CAAATTTTTA	AATCTCCAGG	CTTCCCAAT	GAGTACGAAG	ATAACCAAT	540
	CTGCTACTGG	CACATTAGAC	TCAAGTATGG	TCAGCGTATT	CACCTGAGTT	TTTATGATT	600
	TGACCTTGAA	GATGACCCAG	GTTGCTTGGC	TGATTATGTT	GAAATATATG	ACAGTTACGA	660
80	TGATGTCCAT	GGCTTTGTGG	GAAAGATCTG	TGGAGATGAG	CTTCCAGATG	ACATCATCAG	720
	TACAGGAAT	GTCATGACCT	TGAAGTTTCT	AAGTATGCT	TCAGTGACAG	CTGGAGGTTT	780
	CCAAATCAAA	TATGTTGCAA	TGGATCCTGT	ATCCAAATCC	AGTCAAGGAA	AAAATACAAG	840
	TACTACTTCT	ACTGGAATA	AAAACGTTT	AGCTGGAAGA	TTTAGCCACT	TATAAAAAA	900
	AAAAAAGGA	TGATCAAAAC	ACACAGTGTT	TATGTTGGAA	TCTTTTGAA	CTCCTTTGAT	960



CTCACTGTGA TTATTAACAT TTATTTATTA TTTTCTAAA TGTGAAAGCA ATACATAATT 1020  
 TAGGGAAAAT TGGAAAATAT AGGAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC 1080  
 ACTGCATAGA AATAACAAGC GTTAACATTT TCATATTTTT TTCTTTTCAGT CATTTTTCTA 1140  
 TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTTGCGAT TTGAAATTTT GGAATCCTGC 1200  
 TCTATGTACA GTTTTGTATT ATACTTTTA AATCTTGAAC TTTATAAACA TTTTCTGAAA 1260  
 TCATTGATTA TTCTACAAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA 1320  
 TGTTTTATGC ATTATTTAAG CTTGTCTCTA TTGTTGGAAT TTCAGGTCAT TTTTATAAAT 1380  
 ATTGTTGCAA TAAATATCCT TGAACACACA AAAAAAAAAA AA

Seq ID NO: 292 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60  
 EGGHLATYKQ LEARKIGFH VCAAGWMAKG RVGYPIVKPG PNCGFQKGTGI IDYGI RLNRS 120  
 ERWDAYCYNP HAKECGGVFT DPKQIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180  
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDDIIS TGNVMTLKF L SDASVTAGGF 240  
 QIKYVAMDPV SKSSQKNTS TTSTGNKNFL AGRFSLH

Seq ID NO: 293 DNA sequence  
 Nucleic Acid Accession #: NM\_007115.1  
 Coding sequence: 69..902

1 11 21 31 41 51  
 | | | | |  
 GAATTCGCAC TGCTCTGAGA ATTTGTGAGC AGCCCTTAAC AGGCTGTTAC TTCACTACAA 60  
 CTGACGATAT GATCATCTTA ATTTACTTAT TTCTCTTGCT ATGGGAAGAC ACTCAAGGAT 120  
 GGGGATTCAA GGATGGAATT TTTCACTAAT CCATATGGCT TGAACGAGCA GCCGGTGTGT 180  
 ACCACAGAGA AGCAGCGTCT GGCAAAATACA AGCTCACCTA CGCAGAAGCT AAGCGGTGTG 240  
 GTGAATTTGA AGGCGGCCAT CTCGCAACTT ACAAGCAGCT AGAGCCAGCC AGAAAAATTG 300  
 GATTTCATGT CTGTGCTGCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA 360  
 AGCCAGGGCC CAACGTATGA TTTGGAAAAA CTGGCATTAT TGATTATGGA ATCCGCTCTCA 420  
 ATAGGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAAGGAG TGTGGTGGCG 480  
 TCTTTACAGA TCCAAAGCGA ATTTTAAAT CTCCAGGCTT CCCAAATGAG TACGAAGATA 540  
 ACCAAATCTG CTACTGGCAC ATTAGACTCA AGTATGGTCA GCGTATTAC CTGAGTTTCT 600  
 TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA 660  
 GTTACGATGA TGTCCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA 720  
 TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTCTAAG TGATGCTTCA GTGACAGCTG 780  
 GAGGTTTCCA AATCAAAATAT GTTGCAATGG ATCTGTATC CAAATCCAGT CAAGGAAAAA 840  
 ATACAAGTAC TACTTCTACT GGAATAAATA ACTTTTATAG TGGAAGATTT AGCCACTTAT 900  
 AAAAAAAAAA AAGGATGATC AAAACACACA GTGTTTATGT TGGAATCTTT TGGAACCTCT 960  
 TTGATCTCAC TGTATTATT AACTTTATT TATTATTTT CTAATATGTA AAGAAATACA 1020  
 TAATTTAGGG AAAATTGGAA AATATAGGAA ACTTTAAACG AGAAATGAA ACCTCTCATA 1080  
 ATCCCACTGC ATAGAAATTA CAAGCGTTAA CATTTTCATA TTTTCTCTT TCAGTCATTT 1140  
 TTGTATTGT GGTATATGTA TATATGTACC TATATGTATT TGCAATTTGAA ATTTTGGAAAT 1200  
 CCTGCTCTAT GTACAGTTT GTATTATACT TTTTAAATCT TGAACCTTAT GAACATTTTC 1260  
 TGAAATCATT GATTATCTTA CAAAAACATG ATTTTAAACA GCTGTAATAAT ATTCATATGAT 1320  
 ATGAATGTTT TATGATTTAT TTAAGCCTGT CTCTATTGTT GGAATTTTCA GTCATTTTCA 1380  
 TAAATATTGT TGCAATAAAT ATCCTTCGGA ATTC

Seq ID NO: 294 Protein sequence  
 Protein Accession #: NP\_009046.1

1 11 21 31 41 51  
 | | | | |  
 MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60  
 EGGHLATYKQ LEARKIGFH VCAAGWMAKG RVGYPIVKPG PNXGFQKGTGI IDYGI RLNRS 120  
 ERWDAYCYNP HAKECGGVFT DPKRIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180  
 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDDIIS TGNVMTLKF L SDASVTAGGF 240  
 QIKYVAMDPV SKSSQKNTS TTSTGNKNFL AGRFSLH

Seq ID NO: 295 DNA sequence  
 Nucleic Acid Accession #: NM\_001218.2  
 Coding sequence: 116..1180

1 11 21 31 41 51  
 | | | | |  
 GTACTCGCCA CGGCACCCAG GCTGCGCGCA CGCGGTCCCG GTGTGCAGCT GGAGAGCGAG 60  
 CGGCAACCGG GAGCCGCCGG CACAGCCCGG GCCCGCCCCG CAGGAGCCCCG CGAAGATGCC 120  
 CCGGCGCAGC CTGCACCGCG CGGCCGTGCT CCTGCTGGTG ATCTTAAAGG AACAGCCTTC 180  
 CAGCCCGGCC CCAGTGAACG GTTCCAAGTG GACTTATTTT GGTCTCTGATG GGGAGAATAG 240  
 CTGGTCCAAG AAGTACCCGT CGTGTGGGGG CCTGCTGCAG TCCCCCATAG ACCTGCACAG 300  
 TGACATCTC CAGTATGACG CCAGCCTCAC GCCCTCGAG TTCCAAGGCT ACAATCTGTC 360  
 TGCCAACAAG CAGTTTCTCT TGACCAACAA TGGCCATTCA GTGAAGCTGA ACCTGCCCTC 420  
 GGACATGCAC ATCCAGGGCC TCCAGTCTCG CTACAGTGCC ACGCAGCTGC ACCTGCACTG 480  
 GGGGAACCCG AATGACCCGC ACGGCTCTGA GCACACCGTC AGCGGACAGC ACTTCGCCCG 540  
 CGAGCTGCAC ATTGTCCATT ATAATCAGA CCTTATCTT GACGCCAGCA CTGCCAGCAA 600  
 CAAGTCAGAA GGCTCTGCTG TCTTGGCTGT TCTCATTTGAG ATGGGCTCCT TCAATCCGTC 660  
 CTATGACAAG ATCTTCAGTC ACCTTCAACA TGTAAAGTAC AAAGGCCAGG AAGCATTCGT 720  
 CCCGGGATTC AAGATGAAG AGCTGCTTCC GGAGAGGACC GCTGAATATT ACCGCTACCG 780  
 GGGGTCCCTG ACCACACCCC CTTGCAACCC CACTGTGCTC TGGACAGTTT TCCGAAACCC 840  
 CGTGCAAATT TCCAGGAGC AGCTGCTGGC TTTGGAGACA GCCCTGTACT GCACACACAT 900

5  
10  
15  
20  
25  
30

```

GGACGACCCT TCCCCAGAG AAATGATCAA CAACTTCCGG CAGGTCCAGA AGTTCGATGA 960
GAGGCTGGTA TACACCTCCT TCCTCCCAAGT GCAAGTCTGT ACTGCGGCAG GACTGAGTCT 1020
GGGCATCATC CTCTCACTGG CCCTGGCTGG CATTCCTTGGC ATCTGTATTG TGGTGGTGGT 1080
GTCCATTGG CTTTTCAGAA GGAAGAGTAT CAAAAAAGGT GATAACAAGG GAGTCATTTA 1140
CAAGCCAGCG ACCAAGATGG AGACTGAGGC CCACGCTTGA GGTCCCCGGA GCTCCCCGGC 1200
ACATCCAGGA AGGACCTTGC TTTGGACCTT ACACACTTCG GCTCTCTGGA CACTTGCAGC 1260
ACCTCAAGGT GTTCTCTGTA GCTCAATCTG CAAACATGCC AGGCCTCAGG GATCCTCTGC 1320
TGGGTGCCTC CTGCGCTTGG GACCATGGCC ACCCCAGAGC CATCCGATCG ATGGATGGGA 1380
TGCACTCTCA GACCAAGCAG CAGGAATTCA AAGCTGCTTG CTGTAACGT GTGAGATTGT 1440
GAAAGTGGTCT GAATTCCTGA ATCACAACC AAGCCATGCT GGTGGGCCAT TAATGGTTGG 1500
AAAAACCTTT CATCCGGGGC TTTGCCAGAG CGTGCTTCA AGTGTCTGG AAAGTCTGCT 1560
GCTTCTCCAA GCTTTCAGAG AAGAATGTGC ACTCTCTGCT TAGGTTTTCG TTTGGGAACT 1620
CAACTTCTTT CCTCTGGAGA CGGGGCATCT CCCTCTGATT TCCTTCTGCT ATGACAAAAC 1680
CTTTAATCTG CACCTTACAA CTCGGGGACA AATGGGGACA GGAAGGATCA AGTTGTAGAG 1740
AGAAAAAAGA AAACAAGAGA TATACATGTG GATATATTAG GGACACTTTC ACAGTCTCTG 1800
CCTCTGGATC ACAGACACTG CACAGACCTT AGGGAATGGC AGGTTCAAGT TCCACTTCTT 1860
GGTGGGGATG AGAAGGAGAG GAGAGCTAGA GGGACAAAGA GAATGAGAAG ACATGGATGA 1920
TCTGGGAGAG TCTCACTTTG GAATCAGAAT TGGAAATCACA TTCTGTTTAT CAAGCCATAA 1980
TGTAAGGACA GAATAATACA ATATTAAGTC CAAATCCAAC CTCTGTICAG TGGAGCAGTT 2040
ATGTTTTATA CTCTACAGAT TTTACAAATA ATGAGGCTGT TCCTTGAAAA TGTGTTGTTG 2100
CTGTGTCCTG GAGGAGCATG GAGTTCGGAG ATGACCCAAT CTGCCTTTGA ATCTGGAGGA 2160
AATAGGCAGA AACAAAAATG CTGTAGAACT TATTCCTCTG AGGCCAAATT TCATTTCAAG 2220
CACTTCTGCA GGTATCCCTAC TGCCAACTGT GAATGGAGAG TTTTATCTAC TTCCTCTCT 2280
CTGAAGATGT CAAATCGTGG TTTAGATCAA ATATATTTC AGCTATAAAA GCAGGAGGTT 2340
ATCTGTGAGG GGGGCTGGCA TCATGTATTT AGGGGCAAGT AATAATGGAA TGCTACTAAG 2400
ATACTCCATA TTCTTCCCGC AATCACACAG ACAGTTTCTG ACAGGCGCAA CTCCTCCATT 2460
TTCTTCCCGC AGGTGAGAAC CCTGTGGAGA TGAGTCAGTG CCATGACTGA GAAGGAACCG 2520
ACCCCTAGTT GAGAGCACTT TGCACTTCCC CGAGAACTTT CTGATTCACA GTCTCATTTT 2580
GACAGCATGA AATGTCTCTT TGAAGCATAG CTTTAAAT ATCTTTTCC TTCTACTCCT 2640
CCCTCTGACT CTAAGAATTC TCTCTCTGGA AATCGCTTGA ACCCAGGAGG CGGAGGTTGC 2700
AGTAAGCCAA GGTCTATGCCA CTGCACTCTA GCCTGGGTGA CAGAGCGAGA CTCCATCTCA 2760
AAAAA AAAAA

```

Seq ID NO: 296 Protein sequence  
Protein Accession #: NP\_001209.1

40  
45

```

1 11 21 31 41 51
| | | | |
MPRRSLHAAA VLLLVILKEQ PSSPAPVNGS KWTYFGPDGE NSWSKYPSPC GLLQSPIDL 60
HSDILQYDAS LTPLEFQGVN LSANKQFLLT NNGHSVKLNL PSDMHIQGLQ SRYSATQLHL 120
HWGNPNDPHG SBHTVSGQHF AAEHLIVHYN SDLYPDASTA SNKSEGLAVL AVLIEMGSFN 180
PSYDKIFSHL QHVKYKGQEA FVPGFNIEEL LPERTAERYR YRGSLLTPPC NPTVLWTVFR 240
NPVQISQEQ LLALETALYCT HMDDPSPREM INNFRQVQKF DERLVITSFS QVQVCTAAGL 300
SLGIILSLAL AGILGICIVV VVSIWLFERRK SIKKGDNKG V IYKPAKMET EAHA

```

Seq ID NO: 297 DNA sequence  
Nucleic Acid Accession #: NM\_006632.1  
Coding sequence: 377..1582

50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
ACGCGTCCGC CCACGCGTCC GCCCACGCGT CCGGTGCGGG CCAGAGCGCA GGTGTACCTG 60
GCGGCGGTGC TGGAGCACCT GACCGCGGAG ATCCTGGAGC TGGCTGGCAA CCGGCGCCGC 120
GACAAGAAGA CCCGCATCAT CTGCGCCAC CTGTAGCTGG CCATTGCGAA CGGCGAGGAG 180
CTTAACAAGC TGCTGGGCGA AGTCACCATC GCGCAGGCGG GTGTCCTGCC CAACATTCAG 240
GGCGTGCTTC TGCCCCAGAA GACCAAGAGC CACCACAAGG CCAAGGGTGA AAACCATTC 300
CTAGGAGAGG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCCACAG CAAGGGAGAG 360
CAAGAAGCGA CAAGATATGC AAGTGGATGA GACACTGATC CCCAGGAAAG GTCCAAGTTT 420
ATGTTCTGCT CGCTATGGAA TAGCCCTCGT CTTACATTTT TGCAATTTCA CAACGATAGC 480
ACAAAAATGC ATCATGAACA TCACCATGGT AGCCATGGTC AACAGCACAA GCCCTCAATC 540
CCAGCTCAAT GATTCCTCTG AGGTGCTGCC TGTGACTCA TTTGGTGGCC TAAGTAAAGC 600
CCCAAAGAGT CTTCTGCAA AGTCTCAAT ACTTGGGGGT CAGTTTGCAA TTTGGGAAAA 660
GTGGGGCCCT CCACAAGAAC GAAGCAGACT CTGCAGCATT GCTTTATCAG GAATGTTACT 720
GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTTATTAGT GAAACCCCTT GGTGGCCCTT 780
TGTCTTCTAT ATCTTTGGAG GTGTTGGCTG TGTCTGTGCT CTTCTCTGGT TTGTTGTGAT 840
TTATGATGAC CCCTTTCTCT ATCCATGGAT AAGCACCTCA GAAAAAGAAT ACATCATATC 900
CTCCTTGAAA CAACAGGTCG GGTCTTCTAA GCAGCCTCTT CCCATCAAAG CTATGCTCAG 960
ATCTCTACCC ATTTGGTCCA TATGTTTAGG CTGTTTCAGC CATCAATGGT TAGTTAGCAC 1020
AATGGTTGTA TACATACCAA CTTACATCAG CTCTGTGTAC CATGTTAACA TCAGAGACAA 1080
TGGACTTCTA TCTGCCCTTC CTTTATTGTT TGCCCTGGTC ATAGGCATGG TGGGAGGCTA 1140
TCTGGCAGAT TTCCTTCTAA CCAAAAAGTT TAGACTCATC ACTGTGAGGA AAATTTGCCA 1200
AATTTTAGGA AGTCTCCCTT CTTGAGCACT CATTGTGTCT CTGCCTTACC TCAATTCGGG 1260
CTATATCACA GCAACTGCCT TGCTGACGCT CTCTTGCGGA TTAAGCACAT TGTGTAGTC 1320
AGGGATTTAT ATCAATGTCT TAGATATTGC TCCAAGGTAT TCCAGTTTTC TCATGGGAGC 1380
ATCAAGAGGA TTTTCGAGCA TAGCACTGT CATTGTACCC ACTGTGAGCG GATTCTTCT 1440
TAGTCAGGAC CCTGAGTTTG GGTGGAGGAA TGTCTTCTTC TTGCTGTTG CCGTTAACTT 1500
GTTAGGACTA CTCTTCTACC TCATATTTGG AGAAGCAGAT GTCCAAGAAT GGGCTAAAGA 1560
GAGAAACTC ACTCGTTTAT GAAGTTATCC CACCTTGGAT GGAAAAGTCA TTAGGCACCG 1620
TATGCAATAA AATAGAAGGC TTCCGTGATG AAAATACCAG TGAAAAGATT TTTTTCCT 1680
GTGGCTCTTT TCAATTATGA GATCAGTTCA TTATTTTAT CAGACTTTT TTTGAGAGAA 1740
ATGTAAGATG AATAAAAT CAAATAAAT GATAACTAAG AAAAAA AAAAA

```

Seq ID NO: 298 Protein sequence  
Protein Accession #: NP\_006623.1

1 11 21 31 41 51  
 5 MQVDETLIPR KGPSLCSARY GIALVLHFCN FTTIAQNVIM NITMVMVNS TSPQSQLNDS 60  
 SEVLVPDSFG GLSKAPKSLP AKSSILGGQF AIWEKWGPPQ ERSRLCSIAL SGMLLGCFPTA 120  
 ILIGGFISSET LGWPFVIFYF GVGVCVCCLL WFWVIYDDPF SYPWISTSEK EYIISSLKQK 180  
 VGSSKQPLPI KAMLRSLPIW SICLGCFSHQ WLVTMVVYI PTYISSVYHV NIRDNGLLSA 240  
 LPFIVAWVIG MVGGYLDLFL LTKKFRLLTV RKIATILGSL PSSALIVSLP YLNSGYITAT 300  
 10 ALLTLSCGLS TLCQSGIYIN VLDIAPRYSS FLMGASRGFS SIAPVIVPTV SGFLLSQDPE 360  
 FGWRNVFFLL FAVNLLGLLF YLIFGEADVQ EWAKERKLTR L

Seq ID NO: 299 DNA sequence  
 Nucleic Acid Accession #: NM\_003058.1  
 Coding sequence: 145..1812

1 11 21 31 41 51  
 20 GGCCCTGCCC TGAAGGCTGG TCACTTGCGAG AGGTAAACTC CCCTCTTTGA CTCTGCGCCA 60  
 GGGTTTGTGC TGAGCTGGCT GCAGCCGCTC TCAGCCTCGC TCGGGGCACG TCGGGCAGCC 120  
 TCGGGCCCTC CTGCTTGCGAG GATCATGCCC ACCACCGTGG ACGATGTCCT GGAGCATGGA 180  
 GGGGAGTTTC ACTTTTTCCTA GAAGCAAATG TTTTCTCTCT TGGCTCTGCT CTCGGCTACC 240  
 TTCGCGCCCA TCTACGTGGG CATCGTCTTC CTGGGCTTCA CCCTGACCA CCGCTGCCGG 300  
 AGCCCGGAG TGGCCGAGCT GAGTCTGCGC TCGCGCTGGA GTCTGCAGA GGAAGTGAAC 360  
 25 TACACGGTGC CGGGCCGAG ACCTGCGGGC GAAGCCTCCC CAAGACAGTG TAGGCGCTAC 420  
 GAGGTGGAGT GGAACCAAG CACCTTTGAC TCGGTGGACC CCCTGGCCAG CCTGGACACC 480  
 AACAGGAGCC GCCTGCCACT GGGCCCTGCG CGGGACGGCT GGGTGTACGA GACGCCTGGC 540  
 TCGTCCATCG TCACCGAGTT TAACCTGGTA TGTGCCAACT CTGGATGTT GGACCTATTTC 600  
 CAGTCATCAG TGAATGTAGG ATTCTTTATT GGCTCTATGA GTATCGGCTA CATAGCAGAC 660  
 30 AGGTTTGGCC GTAAGCTCTG CCTCCTAACT ACAGTCTCTA TAAATGCTGC AGCTGGAGTT 720  
 CTCATGGCCA TTTCCCAAC CTATACGTGG ATGTTAATTT TTCGCTTAAT CCAAGGACTG 780  
 GTCAGCAAAG CAGCGTGGTT AATAGGCTAC ATCCTGATTA CAGAATTGTT TGGGCGGAGA 840  
 TATCGGAGAA CAGTGGGGAT TTTTACCAA GTTGCCTATA CAGTTGGGCT CTGCTGCTCA 900  
 GCTGGGGTGG CTTACGCACT TCCTCACTGG AGGTGGTTCG AGTTCACAGT TGCTCTGCCC 960  
 35 AACTTCTTCT TCTTGCTCTA TTACTGGTGC ATACCTGAGT CTCCAGGTG GCTGATCTCC 1020  
 CAGAATAAGA ATGCTGAAGC CATGAGAATC ATTAAGCACA TCGCAAAGAA AAATGGAAAA 1080  
 TCTCTACCCG CCTCCCTTCA GCGCCTGAGA CTTGAAGAGG AAACCTGGCA GAAATTGAAC 1140  
 CCTTCATTTT TTAGCTTGGT CAGAACTCCT CAGATAAGGA AACATACTAT GATATTGATG 1200  
 TACAACGGT TCACGAGCTC TGTGCTCTAC CAGGGCCTCA TCATGCACAT GGGCCTTGCA 1260  
 40 GGTGACAATA TCTACCTGGA TTTCTTCTAC TCTGCCCTGG TTGAATTCCT AGCTGCCTTC 1320  
 ATGATCATCC TCACCATCGA CCGCATCGGA CGCGTTACC CTGGGCTGCT ATCAAATATG 1380  
 GTTGACGGG CAGCCTGTCT GGCCTCAGTT TTTATACCTG GTGATCTACA ATGGCTAAAA 1440  
 ATTATTATCT CATGCTTGGG AAGAATGGGG ATCACAATGG CCTATGAGAT AGTCTGCCTG 1500  
 GTCAATGCTG AGCTGTACCC CATATTCATT AGGAATCTTG GCGTCCACAT CTGTTCTCTCA 1560  
 45 ATGTGTGACA TTGGTGGCAT CATCACGCCA TTCCTGGTCT ACCGGCTCAC TAACATCTGG 1620  
 CTTGAGCTCC CGCTGATGGT TTTGCGCGTA CTTGGCTTGG TTGCTGGAGG TCTGGTGTCTG 1680  
 TTGCTTCCAG AAATAAAGG GAAAGCTTTG CCTGAGACCA TCGAGGAAGC CGAAAAATATG 1740  
 CAAAGACCAA GAAAAAATAA AGAAAAAGATG ATTTACCTCC AAGTTACAGAA ACTAGACATT 1800  
 CCATTGAAC TGAAGAGAG ACCGTTGCTG CTGTATGAC CTAGCTTTGA TGGCAGCAAG 1860  
 50 ACCAAAAGTA GAAATCCCTG CACTCATCAC AAAGCCCATC CAACCTCAAC AAACCTTACCC 1920  
 CTGAGCCCTA TCAACCTTAG TCTACAGCCA GTGGAGTCTA TTGTACACTG TGGAAAAATA 1980  
 CCCATGGGAC CAGATCCTGC CAAATCTTTC CAGCTCACTT TATTCTCAGC ATTCTTAGGA 2040  
 CATTGGACAT TGGTTTCTCT GAGGTTTCTT TTTCCGATCT TTGTATTTT TTAATTTGA 2100  
 55 TTCTTTTCTT TGCAATGCTA GCAACCAGAA TACATAGGGG AACTGTGGGC TAGGCAAANA 2160  
 AAATAGAAAA AGTGTGAAAA ACAGTAAAGT TGGGAGAGGA GCATCTATTT TCTTAAAGAA 2220  
 ATAAACACCC NAAACAAAAA AAAAAAANA AAAAAA

Seq ID NO: 300 Protein sequence  
 Protein Accession #: NP\_003049.1

1 11 21 31 41 51  
 60 MPTTVDDVLE HGGEFHFQK QMFFLLALLS ATFAPYVGI VFLGFTPDHR CRSPGVAELS 60  
 LRCGWSPAE E LNYTVPGPGP AGEASPRQCR RYEVDWNQST FDCVDPLASL DTNRSRLPLG 120  
 65 PCRDGWVYET PGSSIVTEFN LVCANSWMLD LFQSSVNVGF FIGSMSIGYI ADRFGRKLCL 180  
 LTTVLINAAA GVLMAISPTY TWMLIFRLIQ GLVSKAGWLI GYILITEFVG RRYRRTVGIF 240  
 YQVAYTVGLL VLAGVAYALP HWRWLQFTVA LPNFFFLYY WCIPESPRWL ISQNKNAEAM 300  
 RIIKHIKKN KSLPASLQR LRLEETGKK LNPSFLDLVR TPQIRKHTMI LMYNWFTSSV 360  
 LYQGLIMHMG LAGDNIYLDY FYSALVEFPA AFMIILTIDR IGRYPWAAS NMVAGAACLA 420  
 70 SVFIPGDLQW LKIIISCLGR MGITMAYEIV CLVNAELYPT FIRNLGVHIC SSMCDIGGII 480  
 TPFLVYRLTN IWLEPLNMVF GVLGLVAGGL VLLLPEKTKG ALPETIEEAE NMQRPRKNKE 540  
 KMILYQVQKL DIPLN

Seq ID NO: 301 DNA sequence  
 Nucleic Acid Accession #: NM\_012206.1  
 Coding sequence: 52..1131

1 11 21 31 41 51  
 80 GTTACCCAGC ATTGTGAGTG ACAGAGCCTG GATCTGAACG CTGATCCCAT AATGCATCCT 60  
 CAAGTGGTCA TCTTAAGCCT CATCTACAT CTGGCAGATT CTGTAGCTGG TTCTGTAAAG 120  
 GTTGGTGGAG AGGCAGGTCC ATCTGTACA CTACCCTGCC ACTACAGTGG AGCTGTACA 180  
 TCAATGTGCT GGAATAGAGG CTCATGTTCT CTATTACAT GCCAAATAGG CATGTCTGCT 240  
 ACCAATGGAA CCCAGCTCAC CTATCGGAAG GACACACGCT ATAAGCTATT GGGGGACCTT 300  
 TCAAGAAGGG ATGTCTCTTT GACCATAGAA AATACAGCTG TGTCTGACAG TGGCGTATAT 360

TGTGTCCTGT TTAGGACCCG TGGGTGGTTC AATGACATGA AAATCACCCT ATCATTTGGAG 420  
 ATTGTGCCAC CCAAGGTACG GACTACTCCA ATTGTACAAA CTGTTCCAAC CGTCACGACT 480  
 GTTCGAACGA GCACCACTGT TCCAACGACA ACGACTGTTC CAACGACAAC TGTTCACAAC 540  
 ACAAATGAGCA TTCCAACGAC AACGACTGTT CCGACGACAA TGACTGTTTC AACGACAACG 600  
 AGCGTTCCAA CGACAACGAG CATTCACAACA ACAACAAGTG TTCCAGTGAC AACAAACGGTC 660  
 TCTACCTTTG TTCTTCCAAT GCCTTTGCCC AGGCAGAAC ATGAACCACT AGCCACTTCA 720  
 CCATCTTCAC CTCAGCCAGC AGAAACCCAC CCTACGACAC TGCAGGAGC AATAAGGAGA 780  
 GAACCCACCA GCTCACCATT GTACTCTTAC ACAACAGATG GGAATGACAC CGTGACAGAG 840  
 TCTTCAGATG GCCTTTGGAA TAACAATCAA ACTCAACTGT TCCTAGAAC TAGTCTACTG 900  
 ACGGCCAATA CCACTAAAGG AATCTATGCT GGAGTCTGTA TTTCTGTCTT GGTGCTCTT 960  
 GCTCTTTTGG GTGTCATCAT TGCCAAAAAG TATTTCTTCA AAAAGGAGGT TCAACAACATA 1020  
 AGTGTTCAT TTAGCAGCCT TCAAATTAAG GCTTTGCAAA ATGCAGTTGA AAAGGAAGTC 1080  
 CAAGCAGAAG ACAATATCTA CATTGAGAAT AGTCTTTATG CCACGGACTA AGACCCAGTG 1140  
 GTGCTCTTTG AGAGTTTACG CCCATGACTG CAGAAGACTG AACAGGTATC AGCACATCAG 1200  
 ATGTCTTTTA GACTCCAAGA CAATTTTCTT GTTTCAGTTT CATCTGGCAT TCCAACATGT 1260  
 CAGTGATACT GGGTAGAGTA ACTCTCCAC TCCAAACTGT GTATAGTCAA CCTCATCATT 1320  
 AATGTAGTCC TAATTTGTTT TGCTAAAACT GGCTCAATCC TTCTGATCAT TGCAAGTCTT 1380  
 TCTCTCAAC ATGAACACTT TAGAATTGTA TGTCTCTTCT AGACCCCAT AATCCTGTAT

Seq ID NO: 302 Protein sequence  
 Protein Accession #: NP\_036338.1

1 11 21 31 41 51  
 | | | | |  
 MHPQVVLISL ILHLADSVAG SVKVGGEAGP SVTLPCYHSG AVTSMCWNRG SCSLFTCQNG 60  
 IVWNGTHVT YRKTRYKLL GDLRRDVSLS TIENITAVSDS GVCYCRVEHR GWFNDMKITV 120  
 SLEIVPPKVT TTPIVTTVPT VITVTRISTTV PTTTIVPTTT VPTTMSIPTT TTVPTTMTVS 180  
 TRTSVPTTTS IPTTTSVPT TTVSTFVFPF PLPRQNHPEV ATSPSSPQPA ETHPTTLQGA 240  
 IRREPTSSPL YSYTTDGNVT VTSSDGLWN NNQTLFLFLEH SLLTANTTKG IYAGVCISVL 300  
 VLLALLGVII AKKYFFKKEV QQLSVSFSSS QIKALQNAVE KEVQAEDNIY IENSLYATD

Seq ID NO: 303 DNA sequence  
 Nucleic Acid Accession #: NM\_001044.1  
 Coding sequence: 129..1991

1 11 21 31 41 51  
 | | | | |  
 ACCGCTCCGG AGCGGGAGGG GAGGCTTCGC GGAACGCTCT CGGCGCCAGG ACTCGCGTGC 60  
 AAAGCCACAG CCCGGCGCGC CAGACCAAGA GGAAGAAGC ACAGAATTCC TCAACTCCCA 120  
 GTGTGCCCCAT GAGTAAGAGC AAATGCTCCG TGGGACTCAT GTCTTCCGTG GTGGCCCCGG 180  
 CTAAGGAGCC CAATGCCGTG GCGCCGAAGG AGGTGGAGCT CATCTTGTTC AAGGAGCAGA 240  
 ACGGAGTGCA GCTCACAGC TCCACCCTCA CCAACCCGCG GCAGAGCCCC GTGGAGGGCC 300  
 AGGATCGGGA GACCTGGGGC AAGAAGATCG ACTTCTCCT GTCCGCTCAT GGCTTTGCTG 360  
 TGGACCTGGC CAACGCTCTG CGGTTCCTCT ACCTGTGCTA CAAAATGGT GCGGTGCTCT 420  
 TCGTGGTCCC CTACCTGCTC TTCATGGTCA TTGCTGGGAT GCCACTTTTC TACATGGAGC 480  
 TGGCCCTCGG CAGTTTCAAC AGGGAAGGGG CCGCTGGTGT CTGGAAGATC TGCCCCATAC 540  
 TGAAGGTGT GGGCTTACAG GTCATCTCA TCTCACTGTA TGTCCGCTTC TTCTACAACG 600  
 TCATCATCGC CTGGGCGCTG CACTATCTCT TCTCCTCCT CACCACGGAG CTCCTCTGGA 660  
 TCCACTGCAA CAACTCTGAG AACAGCCCCA ACTGCTCGGA TGCCCCATCT GGTGACTCCA 720  
 GTGGAGACAG CTCGGGCTTC AACGACACT TTGGGACCA ACCTGCTGCC GAGTACTTTG 780  
 AACGTGGCGT GCTGCACCTC CACCAGAGCC ATGGCATCGA CGACCTGGGG CCTCCGCGGT 840  
 GGCAGCTCAC AGCCTGCCTG GTGCTGGTCA TCGTGTCTGT CTAFTCAGC CTCTGGAAGG 900  
 GCGTGAAGAC CTCAGGGAAG GTGGTATGGA TCACAGCCAC CATGCCATAC GTGGTCTCTA 960  
 CTGCCCTGCT CCGCGCTGGG GTCACCTCC CTGGAGCCAT AGACGGCATC AGAGCATACC 1020  
 TGAGCGTTGA CTTCTACCGG CTCTGCGAGG CGTCTGTTTG GATTGACGCG GCCACCCAGG 1080  
 TGTGCTTCTC CTGGGCGGTG GGGTTCGGGG TGTGATCGC CTCTCCAGC TACAACAAGT 1140  
 TCACCAACAA CTGCTACAGG GACGCGATTG TCACCACCTC CATCAACTCC CTGACGAGCT 1200  
 TCTCTCTCCG GTTCGTCTGC TTCTCTTCC TGGGGTACAT GGCACAGAAG CACAGTGTGC 1260  
 CCATCGGGGA CGTGGCCAA GACGGGCCAG GGCTGATCTT CATCATCTAC CCGGAAGCCA 1320  
 TCGCCACGCT CCCTCTGTCC TCAGCTGGG CCGTGGTCTT CTTCATCATG CTGCTACCC 1380  
 TGGGTATCGA CAGCGCCATG GGTGGTATGG AGTCAGTAT CACCGGGCTC ATCGATGAGT 1440  
 TCCAGCTGCT GCACAGACAC CGTGAGCTCT TCACGCTCTT CATCGTCTCT GCGACCTTCC 1500  
 TCCTGTCCCT GTTCTGCTGC ACCAACGGTG GCATCTACGT CTTCACGCTC CTGGACCAT 1560  
 TTGACGCGG CAGTCCATC CTCTTTGGAG TGCTCATCGA AGCCATCGGA GTGGCTTGGT 1620  
 TCTATGGTGT TGGGCACTTC AGCGACGACA TCCAGCAGAT GACCGGGCAG CGGCCACGCC 1680  
 TGTACTGGCG GCTGTGCTGG AAGCTGGTCA GCCCTGTCTT TCTCCTGTTT GTGGTCTGTG 1740  
 TCAGCATGTG GACCTTCAGA CCCCCCACT ACAGGAGCTA CATCTTCCCC GACTGGGCCA 1800  
 ACGCGCTGGG TGGGCTCATC GCCACATCTT CCATGGCCAT GGTGCCCATC TATGCGGCTT 1860  
 ACAAGTTCTG CAGCTGCTT GGGTCTTTTC GAGAGAAACT GGCCTACGCC ATTGCACCCG 1920  
 AGAAGGACCG TGAGCTGGTG GACAGAGGGG AGGTGCGCCA GTTCACGCTC CGCCACTGGC 1980  
 TCAAGGTGTA GAGGGAGCAG AGACGAAGAC CCCAGGAAGT CATCCTGCAA TGGGAGAGAC 2040  
 ACGAACAAAC CAAGGAAATC TAAGTTTCGA GAGAAAGGAG GGCAACTTCT ACTCTTCAAC 2100  
 CTCTACTGAA AACACAACA ACAAGCAGA AGACTCTCTT CTCTGACTG TTTACACCTT 2160  
 TCCGTGCGCG GAGCGCACTT CGCGTGTCT TGTGTGCTG TAATAACGAC GTAGATCTGT 2220  
 GCAGCGAGGT CCACCCCGTT GTTGTCTCTG CAGGGCAGAA AAACGTCTAA CTTCATGCTG 2280  
 TCTGTGTGAG TCTCTCTCCC TCCGTGCTCC CTGCTCCCGG CTCTGAGGCT GCCCGAGGG 2340  
 CACTGTGTTT TCAGGCGGGG ATCAGCATCC TTGTAGACGC ACCTGCTGAG AATCCCGGTG 2400  
 CTCACAGTAG CTTCCTAGAC CATTTACTTT GCCCATATTA AAAAGCCAAG TGTCTCTGTT 2460  
 GGTTTAGCTG TGCAGAAAGT GAAATGGAGG AAACACACAA TTCATGCAAA GTCTTTTCCC 2520  
 GATGCGTGGC TCCAGCAGA GGCCTGAAAT TGAGCGTTCA GTTGACACAT TGACACACA 2580  
 GTCTGTTCAG AGGCATTGGA GGTATGGGGT CCTGGTATGT CTCACAGGA AATCTGTGTT 2640  
 ATGTTCTTGG AGCAGAGAGA AATAAACTC CTTGAAACCA GCTCAGGCTA CTGCCACTCA 2700  
 GGCAGCCTGT GGGTCTTGT GGTGTAGGGA ACGGCTTGG AGGAGCGTGT CCTATCCCCG 2760  
 GACGATGCA GGGCCCCAC AGGAGCGTGT CCTATCCCCG GACGATGCA GGGCCCCAC 2820

5 AGGAGCATGT CCTATCCCTG GACGCATGCA GGGCCCCCAC AGGAGCGTGT ACTACCCACG 2880  
 AACGCATGCA GGGCCCCCAC AGGAGCGTGT ACTACCCACG GACGCATGCA GGGCCCCCAC 2940  
 TGGAGCGTGT ACTACCCACG GACGCATGCA GGGCCCCCAC AGGAGCGTGT CCTATCCCTG 3000  
 GACCGGACGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC CCCAGGACGC ATGCAGGGCC 3060  
 CCCACAGGAG CGTGTACTAC CCCAGGATGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC 3120  
 CCCAGGACGC ATGCAGGGCC CCCATGCAGG CAGCCTGCAG ACCAACACTC TGCCTGGCCT 3180  
 TGAGCCGTGA CCTCCAGGAA GGGACCCAC TGAATTTTA TTTCTCTCAG GTGCGTGCCA 3240  
 CATCAATAAC AACAGTTTTT ATGTTTGCGA ATGGCTTTTT AAAATCATAT TTACCTGTGA 3300  
 10 ATCAAACAA ATTCAGAAAT GCAGTATCCG CGAGCCTGCT TGCTGATATT GCAGTTTTTG 3360  
 TTTACAAGAA TAATTAGCAA TACTGAGTGA AGGATGTTGG CCAAAAGCTG CTTTCCATGG 3420  
 CACACTGCCC TCTGCCACTG ACAGGAAAGT GGATGCCATA GTTTGAATTC ATGCCTCAAG 3480  
 TCGGTGGGCC TGCCFACGTG CTGCCCCAGG GCAGGGGCCG TGCAGGGCCA GTCATGGCTG 3540  
 TCCTCTGCAA GTGGACGTGG GCTCCAGGGA CTGGAGTGTA ATGCTCGGTG GGAGCCGTCA 3600  
 15 GCCTGTGAAC TGCCAGGCAG CTGCAGTTAG CACAGAGGAT GGCTTCCCA TTGCTTCTG 3660  
 GGGAGGGACA CAGAGGACGG CTTCCCATC GCCTTCTGGC CGCTGCAGTC AGCACAGAGA 3720  
 GCGGCTTCCC ATGTGCTTTC TGGGGAGGGA CACAGAGGAC AGTTTCCCA TCGCTTCTG 3780  
 GTTGTGAAG ACAGCACAGA GAGCGGCTTC CCCATCGCCT TCTGGGGAGG GGCTCCGTGT 3840  
 AGCAACCCAG GTGTTGTCCG TGTCTGTGA CCAATCTCTA TTCAGCATCG TGTGGGTCCC 3900  
 20 TAAGCACAAT AAAAGACATC CACAATGGAA AAAAAAAG GAATTC

Seq ID NO: 304 Protein sequence  
 Protein Accession #: NP\_001035.1

25 1 11 21 31 41 51  
 MSKSKCSVGL MSSVVAPAKE PNAVGPKEVE LILVKEONGV QLTSSSTLNP RQSPVEAQDR 60  
 ETWKKIDFL LSVIGFAVDL ANVWRFPYLC YKNGGGAFLV PYLLFMVIAG MPLFYMELAL 120  
 30 GQFNREGAAG VWKICPILKG VGFTVILISL YVGFYFNVII AWALHYLFSS FTTELPIWIC 180  
 NNSWNSPNCB DAHPGSSGD SSGLDNDFGT TPAAEYFERG VLHLHQSHGI DDLGPPRWQL 240  
 TACLVLVIVL LYFSLWKGVK TSGKVVNITA TMPYVVLTA LRGVTLPGA IDGIRAYLSV 300  
 DFYRLCEASV WIDAATQVCF SLGVGFGVLI AFSSYNKFTN NCYRDAIVTT SINSLSFS 360  
 GFVVFSFLGY MAQKHSVPIG DVAKDGPGLI FIYPEAIAT LPLSSAWAVV FFIMLLTLGI 420  
 DSAMGMESV ITGLIDEFQL LHRHRELFTL FIVLATFLLS LFCVTNGGIY VFTLLDHFAA 480  
 35 GTSILFGVLI EAGVAVFYG VGQFSDDIQ MTGQRPSLYW RLCWKLVSPC FLFVVVVS 540  
 VTRFRPHYGA YIFPDWANAL GWVIATSSMA MVPIYAYKF CSLPGSFREK LAYIAPEKD 600  
 RELVDRGEVR QFTLRHWLKV

Seq ID NO: 305 DNA sequence  
 Nucleic Acid Accession #: NM\_001216.1  
 Coding sequence: 43..1422

45 1 11 21 31 41 51  
 GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CTTGTGCCCC 60  
 AGCCCTTGGC TCCTCTGTGT GATCCCGGCC CTGCTCCAG GCCTCACTGT GCAACTGCTG 120  
 CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCAGAGGT TGCCCCGGAT GCAGGAGGAT 180  
 TCCCCCTGG GAGGAGGCTC TTCTGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCC 240  
 AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGAG AGGAGGATCT ACCTGGAGAG 300  
 GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAATCAGA AGAAGAGGCG 360  
 50 TCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCAG 420  
 AATAATGCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480  
 CCGCCCTGGC CCGGGGTGTC CCCAGCCTGC CGGGGCGCTC TCCAGTCCC GGTGGATATC 540  
 CGCCCCCAGC TCGCCGCTT CTGCCCCGCC CTGCGCCCC TGGAACTCCT GGGCTTCCAG 600  
 55 CTCCCGCGCG TCCAGAACT CGCGCTGCGC AACAATGGCC ACAGTGTGCA ACTGACCTG 660  
 CCTCTGGGG TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT CAGCTGCAT 720  
 CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC 780  
 CCTGCCAGA TCCACGTGTT TCACCTCAGC ACCGCCTTTC CCAGAGTTGA CGAGGCCCTG 840  
 GGGCGCCCGG GAGGCCCTGC CGTGTGGGCC GCCTTCTGAG AGGAGGGGCC GGAAGAAAC 900  
 60 AGTGCCCTAG AGCAGTGTCT TCTCTCGCTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960  
 CAGGTCCAG GACTGGAGAT ATCTGCACTC CTGCCCTCTG ACTCAGCCG CTACTTCCAA 1020  
 TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAA 1080  
 CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCTCT CTGACACCT GTGGGGACCT 1140  
 GGTGACTCPL GGCTACAGCT GAACTTCCGA GCGACGCAGC CTTTGAATGG CCGAGTGATT 1200  
 65 GAGGCTCCT TCCCTGTGAG AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260  
 AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCCTCCT TTTTGCTGTC 1320  
 ACCAGCGTCG CTTTCTTGT GCAGATGAGA AGGCAGACA GAAGGGGAAC CAAAGGGGT 1380  
 GTGAGCTACC GCCAGCAGA GGTAGCCGAG ACTGAGCCT AGAGGCTGGA TCTTGGAGAA 1440  
 70 TGTGAGAAAG CAGCCAGAGG CATCTGAGG GAGCCGGTA ACTGCTCTGT CTGCTCATT 1500  
 ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTATA AT

Seq ID NO: 306 Protein sequence  
 Protein Accession #: NP\_001207.1

75 1 11 21 31 41 51  
 MAPLCPSPWL PLLIPAPAFG LTVQLLSLL LMPVHPQRL PRMQEDSPLG GSSGEDDPL 60  
 GEEDLPSEED SPREDDPPGE EDLPGEEDLP GEEDLPVVKP KSEBEGSLKL EDLPVEAPG 120  
 DPQEPQNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180  
 80 ELLGQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240  
 VEGHRFPAEI HVVHLSTAFR RVDEALGRPG GLAVLAAFL EGPENSAEY QLSRLLEIA 300  
 EGGSETQVFG LDISALLPSD FSRYPQYEGS LTPPCAQGV IWTVFNQVFM LSAKQLHTLS 360  
 DTLWGPDSR LQLNFRATQP LNRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420  
 GLLFAVTSVA FLVQMRQRH RGTGKGVSYR PAEVAETGA

Seq ID NO: 307 DNA sequence  
Nucleic Acid Accession #: NM\_003039.1  
Coding sequence: 76..1581

```

5      1      11      21      31      41      51
|      |      |      |      |      |
CTTCTCTCTC CATTCACTGC ACGCGTTACT TTGGCTAAAA GGAGGTGAGC GGCACCTCTGC 60
CCTTCCAGAG CAAGCATGGA GCAACAGGAT CAGAGCATGA AGGAAGGGAG GCTGACGCTT 120
GTGCTTGCCC TGGCAACCCG GATAGCTGCC TTTGGGTCAT CCTTCCAGTA TGGGTACAAC 180
10    GTGGCTGCTG TCAACTCCCC AGCACTGCTC ATGCAACAAT TTTACAATGA GACTTACTAT 240
GGTAGGACCG GTGAATTCAT GGAAGACTTC CCCTTGACGT TGCTGTGGTC TGTAAACCGTG 300
TCCATGTTTC CATTGAGAGG GTTATTCGGA TCCTCTCTGG TCGGCCCTCT GGTGAATAAA 360
TTTGGCAGAA AAGGGGCTTT GCTGTTCAAC AACATATTTT CTATCGTGCC TGCATCTCTA 420
ATGGGATGCA GCAGAGTCGC CACATCATTT GAGCTTATCA TTATTTCCAG ACTTTTGGTG 480
15    GGAATATGTG CAGGTGTATC TTCCAACGTG GTCCCCATGT ACTTAGGGGA GCTGGCCCCCT 540
AAAAAAGCTG GGGGGGCTCT CGGGGTGGTG CCCAGCTCTT TCATCACTGT TGGCATCCTT 600
GTGGCCAGAG TCTTTGGTCT TCGGAATCTC CTGCAAAACG TAGATGGCTG GCCGATCCTG 660
CTGGGGCTGA CCGGGGCTCC CGCGGCGCTG CAGCTCCTTC TGCTGCCCTT CTCCCCGAG 720
20    AGCCCCAGGT ACCTGCTGAT TCAGAAGAAA GACGAAGCGG CCGCCAAGAA AGCCCTACAG 780
ACGCTGCGCG GCTGGGACTC TGTGGACAGG GAGGTGGCCG AGATCCGGCA GGAGGATGAG 840
GCAGAGAAGG CCGCGGGCTT CATCTCCGTG CTGAAGCTGT TCCGGATGCG CTGCTGCGCG 900
TGGCAGCTGC TGTCCATCAT CGTCTCATG GCGGCCAGC AGCTGTGGG CGTCAACGCT 960
ATCTACTACT ACGCGGACCA GATCTACCTG AGCGCCGGCG TGCCGGAGGA GCACGTGACG 1020
TAGGTGACGG CCGGACCCGG GCGCGTGAAC GTGGTCATGA CCTTCTGCGC CGTGTTCGTG 1080
25    GTGGAGCTCC TGGGTCCGAG GCTGCTGCTG CTGCTGGGCT TCTCCATCTG CCTCATAGCC 1140
TGCTGCGTGC TCACTGCAGC TCTGGCACTG CAGGACACAG TGTCTGGAT GCCATACATC 1200
AGCATCGTCT GTGTCACTC CTACGTCATA GGACATGCCC TCGGGCCAG TCCCATACCC 1260
GCCTGTCTCA TCACTGAGAT CTTCCTGCAG TCCTCTCGGC CATCTGCCTT CATGGTGGGG 1320
GGCAGTGTGC ACTGGCTCTC CAACCTCACC GTGGGCTTGA TCTTCCGTT CATCCAGGAG 1380
30    GGCCTCGGCC CGTACAGCTT CATGTCTTTC GCCGTGATCT GCCTCCCTAC CACCATCTAC 1440
ATCTTCTTGA TTGTCCCGGA GACCAAGGCC AAGACGTTCA TAGAGATCAA CCAGATTTTC 1500
ACCAAGATGA ATAAGGTGTC TGAAGTGTAC CCGGAAAGG AGGAACGTAA AGAGCTTCCA 1560
CCTGTCACTT CGGAACAGTG ACTCTGGAGA GGAAGCCAGT GGAGCTGGTC TGCCAGGGGC 1620
TTCCCACTTT GGCCTATTTT TCTGACTTCT AGCTGTCTGT GAATATCCAG AAATAAAACA 1680
35    ACTCTGATGT GGAATGCAGT CCTCATCTCC AGCCTCCCCA CCCCAGTGGG AACTGTGCAA 1740
AGGGCTGCCT TGCTGTCTT GAAGCTGGGC TGTCTCTCTC CATGTTGGCC TGTCAACAGA 1800
CCCGAGTCAA TTAACAGACT GGTCTCCAC TTTGCTGGTT CAGCCTTCGT GTGGCTCTG 1860
GTAACGTGGC TCCACCTTGA TGGGTCAACC TTTGTGTGGC TCCTGGTAAC ATAACAACA 1920
40    CAGTTACTAT AGTGGTGAGA TGAAGGAAT CAAATTTTGC CAGAGAAACT AACTCGGTGG 1980
CCCCAACAGG TCTTCCGGGG CCATGGGCAT TTGTTTAGAG CCAAAATTCAT CCTCTTACCA 2040
GATCCTTTTC CAGAAATACC TGTCTAGGAA GGTGTGATGT CAGAAACAAT GACATCCAGA 2100
AAGCTGAGGA ACAGGTTTCT GTGGAGACAC TGAGTCAGAA TTCTTCATCC AAATTTATTT 2160
GTTAGTGAA AATGGAATTG CTTCTGTGTA GTCATAAAAA TGAACCTGAT CACTTTTC

```

Seq ID NO: 308 Protein sequence  
Protein Accession #: NP\_003030.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MEQQDQSMKE GRLTLVLALA TLIAAFGSSF QYGVNVAAVN SPALLMQQFY NETYYGRTGE 60
FMEDFPLTLL WSVTVSMPPF GGFIGSLLVG PLVNKFGRRK ALLFNNIFS I VPAILMGCSR 120
VATSFELIII SRLLVGICAG VSSNVVPMYL GELAPKNLRG ALGVVPQLFI TVGILVAQIF 180
GLRNLLANVD GWPILLGLTG VPAALQLLL PFFPESPRYL LIQKDEAAA KKALQTLRGW 240
55    DSVDRVABEI RQEDBAEKAA GFISVLKFLR MRSRLRWQLLS IIVLMGGQQL SGVNAIYYA 300
DQIYLSAGVP BEHVQYVITAG TGAVNVMTF CAVFVVELLG RRLLLLLGFS ICLIAACVLT 360
AALALQDTSV WMPYISIVCV ISYVIGHALG PSPIPALLIT EIFLQSSRPS AFMVGGSVHW 420
LSNFTVGLIF PFIQGLGPHY SFIVFAVICL LTTIYIFLIV PETKAKTFIE INQIFTKMNK 480
VSEVPEKEE LKELPPVTSE Q

```

Seq ID NO: 309 DNA sequence  
Nucleic Acid Accession #: NM\_001252.1  
Coding sequence: 138..719

```

1      11      21      31      41      51
|      |      |      |      |      |
GGCTGGTCCC CTGACAGGTT GAAGCAAGTA GACGCCAGG AGCCCCGGGA GGGGGCTGCA 60
GTTTCCTTCC TTCCTTCTCG GCAGCGCTCC GCGCCCCCAT CGCCCTCTCT GCGCTAGCGG 120
AGGTGATCGC CGCGGCGATC CCGGAGGAGG GTTCGGGCTG CTCGGTGCGG CGCAGGCCCT 180
70    ATGGGTGCGT CTGCGGGGCT GCTTTGGTCC CATTGGTTCG GGGCTTGGTG ATCTGCCTCG 240
TGGTGTGACT CCAGCGCTTC GCACAGGCTC AGCAGCAGCT GCCGCTCGAG TCACTTGGGT 300
GGGACGTAGC TGAGCTGTCG CTGAATCACA CAGGACCTCA GCAGGACCCC AGGCTATACT 360
GGCAGGGGGG CCCAGCACTG GCGCGCTCCT TCCTGCATGG ACCAGAGCTG GACAAGGGGC 420
AGCTACGTAT CCATCGTGAT GGCATCTACA TGGTACACAT CCAGGTGACG CTGGCCATCT 480
GCTCCTCCAC GACGGGCTCC AGGCACCACC CCACCACCCT GGCCGTGGGA ATCTGTCTCT 540
75    CCGCCTCCCG TACGATCAGC CTGCTGCGTC TCAGCTTCCA CCAAGTTTGT ACCATTGCCT 600
CCGAGCGCCT GACGCCCCCT GCCCGAGGGG ACACACTCTG CACCAACCTC ACTGGGACAC 660
TTTTGCCTTC CCGAAACACT GATGAGACCT TCTTTGGAGT GCAGTGGGTG CGCCCTGAC 720
CACTGCTGCT GATTAGGGTT TTTTAAATTT TATTTTATTT TATTTAAGTT CAAGAGAAAA 780
80    AGGTATACCA CAGGGGCCAC CCGGGGTTGG GGTGGGAGTG TGGTGGGGGG TAGTGGTGGC 840
AGGACAAGAG AAGGCATTGA GCTTTTCTT TCATTTCTCT ATTAATAA

```

Seq ID NO: 310 Protein sequence  
Protein Accession #: NP\_001243.1

1	11	21	31	41	51	
MPEEGSGCSV	RRRPFYGCVL	AALVPLVAGL	VICLVVCIQR	FAQAQQQLPL	ESLGWDVAEL	60
QLNHTGPQQD	PRLYWQGGPA	LGRSFLHGPE	LDKGQLRIHR	DGIYMVHIQV	TLAICSSTTA	120
SRHPHTTLAV	GICSPASRSI	SLRLSLFHQ	CTIASQRLTP	LARGDTLCTN	LTGTLLPSRN	180
TDETFFGVQW	VRP					

Seq ID NO: 311 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..3978

1	11	21	31	41	51	
ATGGTGGGTG	AAGGACCCTA	CCTTATCTCA	GATCTGGACC	AGCGAGGCCG	GCGGAGATCC	60
TTTGCAGAAA	GATATGACCC	CAGCCTGAAG	ACCATGATCC	CAGTGCGACC	CTGTGCAAGG	120
TTAGCACCCA	ACCCGGTGGG	TGATGCCGGG	CTACTCTCCT	TGCCCCACAT	TTCTCTGGCT	180
ACGCCGGTGA	TGGTGAAGG	CTACCGGCAA	AGGCTGACCG	TAGACACCC	GCCCCCATTG	240
TCGACATATG	ACTCATCTGA	CACCAATGCC	AAAAGATTTC	GAGTCCTTTG	GGATGAAGAG	300
GTAGCAAGGG	TGGTCTCTGA	GAAGGCCTCT	CTGAGCCACG	TGGTGTGGAA	ATTCCAGAGG	360
ACACGCGTGT	TGATGGACAT	CGTGGCCAA	ATCCTGTGCA	TGATCATGGC	AGCCATAGGG	420
CCGACAGTTT	TCATTACCA	AATCCTCCAG	CAGACTGAGA	GGACCTCTGG	GAAAGTCTGG	480
GTGGGCGATT	GACTGTGCAT	AGCCCTTTTT	GCCACCGAGT	TTACCAAAAG	CTTCTTTTGG	540
GCCTTGCCT	GGCCCATCAA	CTACCGCACG	GCCATCCGGT	TGAAGGTGGC	GCTCTCCACC	600
TTGGTTTTTG	AAAACCTAGT	GTCTTCAAG	ACATTGACCC	ACATCTCTGT	TGGCGAGGTG	660
CTCAATATAC	TGTCAGTGA	TAGCTATTCT	TTGTTTGAAG	CTGCCCTTGT	TTGTCTTTTG	720
CCAGCCACCA	TCCCGATCCT	AATGGTCTTT	TGTGCGCGGT	ACGCCCTTTT	CATTCTGGGG	780
CCACAGCTC	TCATCGGGAT	ATCAGTGTAT	GTCTATTTCA	TACCCGTCCA	GATGTTTATG	840
GCCAAGCTCA	ATTGAGCTTT	CCGAAGGTCA	GCAATTTTGG	TGACAGACAA	GCGAGTTTCAG	900
ACAATGAATG	AGTTTCTGAC	CTGCATCAGG	CTGATCAAAA	TGTATGCCCT	GGAGAAATCT	960
TTTACCAACA	CTATCCAAGA	TATAAGAAGG	AGGGAAGAAA	AATTACTGGA	AAAAGCTGGA	1020
TTTGTCCAAA	GTGGAACACT	TGCCCTGGCC	CCCATCGTGT	CCACCATAGC	CATCGTGCTG	1080
ACATTATCCT	GCCACATCCT	CCTGAGACGC	AACTCACC	CACCCGTGGC	ATTTAGTGTG	1140
ATTGCCATGT	TTAATGTAA	GAAGTTTTC	ATTGCAATCT	TGCCCTTCTC	CATCAAAGCA	1200
ATGGCTGAAG	CGAATGTCTC	TCTAAGGAGA	ATGAAGAAAA	TTCTCATAGA	TAAAAGCCCC	1260
CCATCTTACA	TCACCCAAAC	AGAAGACCCA	GATACGTCT	TGCTTTTAGC	AAATGCCACC	1320
TTGACATGGG	AGCATGAAGC	CAGCAGGAAA	AGTACCCCAA	AGAAATTGCA	GAACCAGAAA	1380
AGGCATTTAT	CCAGAAACAA	GAGGTGAGAG	GCATACAGTG	AGAGGAGTCC	ACCAGCCAAG	1440
GGAGCCACTG	GCCGAGAGGA	GCAAGGTGAC	AGCCTCAAAT	CGGTTCTGCA	CAGCATAAGC	1500
TTTGTGGTGA	GAAAGTTATG	TGCTTATCCC	GAAGCCGAGC	TCCTGGCTTG	GAGGTGGCCA	1560
GCAGTGTGTT	TTGGGAGAAT	CATCAGAGGA	TACAGGCCCT	ATGGATTTTC	TGCTAAAGAC	1620
AAGGATGAAT	CTAGAAGGCT	TCTTACTTGG	CCCCAAGAAG	TGGATAGGAC	TCAAAGGGCA	1680
GCCAAATACC	TGGGGAAGAT	CTTGGGAATA	TGTGGGAATG	TGGGAAGTGG	AAAGAGCTCC	1740
CTCCTTGCA	CTCTCCTAGG	ACAGATGCAG	CTGCAGAAAG	GGGTGGTGGC	AGTCAATGGA	1800
ACTTTGGCCT	ACGTTTTCAC	GCAGGCATGG	ATCTTTTCAT	GAAATGTGAG	AGAAAAACATA	1860
CTCTTTGGAG	AAAAGTATGA	TCACCAAGAG	TATCAGCACA	CAGTCCGCGT	CTGTGGCCTC	1920
CAGAAGGACC	TGAGCAACCT	CCCCTATGGA	GACCTGACTG	AGATTGGGGA	GCGGGGCTCT	1980
AACCTCTCTG	GGGGGCAAGT	GCAGAGGATT	AGCCTGGCCC	GCGCTGTCTA	CTCCGACCTG	2040
CAGCTCTACC	TGCTGGACGA	CCCCCTGTCT	GCCGTGGACG	CCCACGTGGG	GAAGCACGTC	2100
TTTGAGGAGT	GCATTAAGAA	GACGCTCAGG	GGAAGACAG	TGCTCCTGGT	GACCCACACG	2160
CTACAGTTCT	TAGAGTCTTG	TGATGAAGTT	ATTTTATTAG	AAGATGGAGA	GATTTTGTGA	2220
AAGGGAACCC	ACAGAGGATT	AATGGAGGAG	AGAGGGCGCT	ATGCAAAAC	GATTCAACAAC	2280
CTGCGAGGAT	TGCAGTTCAA	GGATCTTGAA	CACCTTTACA	ATGCAGCAAT	GGTGGAGGCC	2340
TTCAAGGAGA	GCCCTGCTGA	GAGAGAGGAA	GATGCTGGTA	TAATCGGGTA	CCTCCTTTCT	2400
CTCTTCACTG	TGTTTCTCTT	CCTCCTGATG	ATTGGCAGCG	CTGCCTTCAG	CAACTGGTGG	2460
CTGGGTCTCT	GTTTGGACAA	GGGCTCACGG	ATGACCTGTG	GGCCCCAGGG	CAACAGGACC	2520
ATGTGTGAGG	TCCGCGCGGT	GCTGGCAGAC	ATCGGTGAGC	ATGTGTACCA	GTGGGTGTAC	2580
ACTGCAAGCA	TGGTGTTCAT	GCTGGTGTTC	GGCGTACCCA	AAGGCTTCGT	CTTCAACCAAG	2640
ACCACATCTG	TGGCATCTCT	CTCTCTGCAT	GACACGGTGT	TTGATAAGAT	CTTAAAGAGC	2700
CCAATGAGTT	TCTTTGACAC	GACTCCCACT	GGCAGGCTAA	TGAACCGTTT	TTCCAAGGAT	2760
ATGGACGAGC	TGGATGTGAG	GCTGCCGTTT	CACGCAGAGA	ACTTCTGCA	GCAGTTTTTT	2820
ATGGTGGTGT	TTATTCTCGT	GATCTTGGCT	GCTGTGTTTC	CTGCTGTCTT	TTTAGTCTGT	2880
GCCAGCCTTG	CTGTAGGCTT	CTTCATTCTG	TTACGCATTT	TCCACAGAGG	AGTCCAGGAG	2940
CTCAAGAAGG	TGGAGAATGT	CAGCCGGTCA	CCCTGGTTCA	CCCACATCAC	CTCCTCCATG	3000
CAGGGCCTGG	GCATCATTTA	CGCCTATGGC	AAGAAGGAGA	GCTGCATCAC	CTATACTTCA	3060
TCCAAAGGCC	TGTCATTGTC	ATACATCATC	CAGCTGAGCG	GACTGCTCCA	AGTGTGTGTG	3120
CGAACGGGAA	CAGAGACGCA	AGCCAAATTC	ACCTCCGTGG	AGCTGCTCAG	GGAATACATT	3180
TCGACCTGTG	TTCCTGAATG	CACCTATCCC	CTCAAAGTGG	GGACCTGTCC	CAAGGACTGG	3240
CCAGCTGTG	GGGAGATCAC	CTTCAGAGAC	TATCAGATGA	GATACAGAGA	CAACACCCCC	3300
CTTGTCTCG	ACAGCCTGAA	CTTGAACATA	CAAAGTGGGC	AGACAGTCGG	GATTGTTGGA	3360
AGAACAGGTT	CCGGAAGTCA	ATCGTTAGGA	ATGGCTTTGT	TTGCTCTGGT	GGAGCCAGCC	3420
AGTGGCAACA	TCTTTATTGA	TGAGGTGGAT	ATCTGCATTC	TCAGCTTGGG	AGACCTCAGA	3480
ACCAAGCTGA	CTGTGATCCC	ACAGGATCCT	GTCCTGTTTG	TAGGTACAGT	AAGGTACAAC	3540
TTGATCCCT	TTGAGATGCA	CACCGATGAG	ATGCTCTGGC	AGGTTCTGGA	GAGAACATTC	3600
ATGAGAGACA	CAATAATGAA	ACTCCCAGAA	AAATTACAGG	CAGAAGTCAC	AGAAAAATGA	3660
GAAAACTTCT	CAGTAGGGGA	ACGTGAGCTG	CTTTGTGTGG	CCCGAGCTCT	TCTCCGTAAT	3720
TCAAAGATCA	TTCTCTTTGA	TGAAGCCACC	GCCTCTATGG	ACTCCAAGAC	TGACACCTGT	3780
GTTCAAGACA	CCATCAAAGA	TGCCCTCAAG	GGCTGCACCT	TGCTGACCAT	CGCCACCCGC	3840
CTCAACACAG	TTCTCAACTG	CGATCACGTC	CTGGTTATGG	AAAATGGGAA	GGTGATTGAG	3900
TTTGACAAGC	CTGAAGTCTT	TGCAGAGAAG	CCAGATTCTG	CATTTGCGAT	GTTACTAGCA	3960
GCAGAAGTCA	GATTGTAG					

Seq ID NO: 312 Protein sequence  
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
	MVGEOPYLIS	DLQGRRRRS	FAERYDPSLK	TMIPVRPCAR	LAPNPVDDAG	LLSFATFSWL	60
5	TPVMVKGYRQ	RLTVDTLPPL	STYDSSDTNA	KRFRVLWDEE	VARVGPEKAS	LSHVVKFKQR	120
	TRVLMDIVAN	ILCIIMAAIG	PTVLIHQILQ	QTERTSGKVM	VGIGLCIALF	ATEFTKVFFW	180
	ALAWAINYRT	AIRLKVALLST	LVFENLVSPK	TLTHISVGEV	LNILSSDSYS	LFEAALFCPL	240
	PATIPILMFV	CAAYAFFILG	PTALIGISVY	VIFIPVQMFM	AKLNSAFRRS	AILVTDKRVQ	300
	TMNEFLTICR	LKIMYAWEKS	FTNTIQDIRR	RERKLEKAG	FVQSGNSALA	PIVSTIAIVL	360
10	TLSCHILLRR	KLTAPEVAFSV	IAMFNVMKFS	IAILPFSIKA	MAEANVSLRR	MKKILIDKSP	420
	PSYITQPEPD	DTVLLLANAT	LTWEHEASRK	STPKKLQNKQ	RHLCKKORSE	AYSERSPPAK	480
	GATGPEEQSD	SLKSVLHSIS	FVVRKLCRYP	EAQLLAWRWP	AVFVGRIIRG	YRPHGFSAKD	540
	KDESRLRLTW	PQEVDRTOQA	AKYLGKILGI	CGNVGSGKSS	LLAALLGQMQ	LQKGVVAVNG	600
	TLAYVSQQAW	IFHGNVRENI	LFGEKYDHQR	YQHTVRVCGI	QKDLNLNLPY	DLTEIGERGL	660
15	NLSGGQRQRI	SLARAVYSR	QLYLLDDPLS	AVDAHVGKHV	FEECIKTLR	GKTVVLVTHQ	720
	LQFLESCDEV	ILEDGEICE	KGTHKELMEE	RGRYAKLIHN	LRGLQFKDPE	HLNNAAMVEA	780
	FKESPAEREE	DAGITGYLLS	LFTVFLFLM	IGSAAFSNWW	LGLWLDKGSR	MTCGPQGNRT	840
	MCEVGAFLAD	IQGHVQVQVY	TASMVFMVLF	GVTKGFVFTK	TTLMASSSLH	DTVFDKILKS	900
	PMSEFDTTPT	GRLMNRFSDK	MDELVDRLPF	HAENFLQQFF	MVVFILVILA	AVFPAVLLVV	960
20	ASLAVGFFIL	LRIFHRGVQE	LKKVENVSRS	PWFTHITSSM	QGLGIIHAYG	KKESCITYTS	1020
	SKGLSLSYII	QLSGLLQVCV	RTGTETQAKF	TSVELLEREYI	STCVPECTHP	LKVGTCPKDW	1080
	PSCGEITFRD	YQMYRDNTPT	LVLDLSNLNI	QSGQTVGIVG	RTGSGKSSLG	MALFRLVEPA	1140
	SGTIFIDEVD	ICILSLSEDLR	TKLTVIPQDP	VLFGVTVRYN	LDPFESHTDE	MLWQVLERTF	1200
25	MRDTIMKLPE	KLQAEVTENG	ENFSVGERQL	LCVARALLRN	SKIILLDEAT	ASMDSKDTTL	1260
	VQNTIKDAFK	GCTVLTIAHR	LNTVLNCDHV	LVMENGKVIE	FDKPEVLAEK	PDSAFAMLLA	1320
	AEVRL						

Seq ID NO: 313 DNA sequence  
Nucleic Acid Accession #: Z31560  
Coding sequence: 1-966

	1	11	21	31	41	51	
	CACAGCGCCC	GCATGTACAA	CATGATGGAG	ACGGAGCTGA	AGCCGCCGGG	CCCGCAGCAA	60
35	ACTTCGGGGG	GCGCGCGCGG	CAACTCCACC	GCGCGCGCGG	CCCGCGGCAA	CCAGAAAAAC	120
	AGCCCGGACC	GCGTCAAGCG	GCCCATGAAT	GCCTTCATGG	TGTGGTCCCG	CGGGCAGCGG	180
	CGCAAGATGG	CCCAGGAGAA	CCCCAAGATG	CACAACCTCG	AGATCAGCAA	GCGCCTGGGC	240
	GCCGAGTGG	AACCTTTGTC	GGAGACGGAG	AAGCGGCCGT	TCATCGACGA	GGCTAAGCGG	300
	CTGCGAGCGC	TGCACATGAA	GGAGCACCCG	GATTATAAAT	ACCGGCCCCG	CCGGAAAACC	360
40	AAGACGCTCA	TGAAGAAGGA	TAAGTACACG	CTGCCCGCGG	GGCTGCTGGC	CCCGGCGGGC	420
	AATAGCATGG	CGAGCGGGGT	CGGGGTGGGC	GCCGGCCTGG	GCGCGGGCGT	GAACGAGCGC	480
	ATGACAGGTT	ACGCGCACAT	GAACGGCTGG	AGCAACGGCA	GCTACAGCAT	GATGCAGGAC	540
	CAGCTGGGCT	ACCCGACGCA	CCCGGGCCTC	AATGCGCACG	GCGCAGCGCA	GATGCAGCCC	600
	ATGCACCGCT	ACGACGTGAG	CGCCCTGCAG	TACAACCTCA	TGACACGCTC	CGACACCTAC	660
45	ATGAACGGCT	CGCCACCTTA	CAGCATGTCC	TACTCGCAGC	AGGGCACCCC	TGGCATGGCT	720
	CTTGGCTCCA	TGGGTTCGGT	GGTCAAGTCC	GAGGCCAGCT	CCAGCCCCCC	TGTGGTTACC	780
	TCTTCTCTCC	ACTCCAGGGC	GCCCTGCCAG	GCCGGGGACC	TCCGGGACAT	GATCAGCATG	840
	TATCTCCCGG	GCGCCGAGGT	GCCGGAACCC	GCCGCCCCCA	GCAGACTTCA	CATGTCCAG	900
	CACTACCAGA	GCGGCCCGGT	GCCCGGCACG	GCCATTAAACG	GCACACTGCC	CCTCTCACAC	960
50	ATGTGAGGGC	CGGACAGCGA	ACTGAGGGG	GGAGAAATTT	TCAAGAAAAA	ACGAGGGAAA	1020
	TGGGAGGGGT	GCAAAAGAGG	AGAGTAAGAA	ACAGCATGGA	GAAAACCCCG	TACGCTCAAA	1080
	AAAAA						

Seq ID NO: 314 Protein sequence  
Protein Accession #: CAA83435

	1	11	21	31	41	51	
	HSARMYNMME	TELKPFPGPQ	TSGGGGGNST	AAAAGGNQKN	SPDRVKRPMN	AFMVVSRGQR	60
60	RKMAQENPKM	HNSEISKRLG	AEWKLLSETE	KRPFIDEAKR	LRALHMKEHP	DYKYRPRRKT	120
	KTLMKKDKYT	LPGLLAPGG	NSMASGVGVG	AGLGAGVNQR	MDSYAHMNGW	SNGSYMMQD	180
	QLGYPPQHPL	NAHGAAQMQP	MHRYDVSAIQ	YNSMTSSQTY	MNGSPITYMS	YSQQGTPGMA	240
	LGSMGSVVKS	EASSSPVVT	SSSHSRAPCQ	AGDLRDMISM	YLPGEVPEP	AAPSRLHMSQ	300
	HYQSGVPVGT	AINGTLP LSH M					

Seq ID NO: 315 DNA sequence  
Nucleic Acid Accession #: U91618  
Coding sequence: 29..541

	1	11	21	31	41	51	
	CGGACTTGGC	TTGTTAGAAG	GCTGAAAGAT	GATGGCAGGA	ATGAAAATCC	AGCTTGTATG	60
70	CATGCTACTC	CTGGCTTTCA	GCTCCTGGAG	TCTGTGTCTCA	GATTTCAGAAG	AGGAAATGAA	120
	AGCATTAGAA	GCAGATTTCT	TGACCAATAT	GCATACATCA	AAGATTAGTA	AAGCACATGT	180
	TCCCTCTTGG	AAGATGACTC	TGCTAAATGT	TTGCAGTCTT	GTAATAAATT	TGAAACGCCC	240
75	AGCTGAGGAA	ACAGGAGAAG	TTTCATGAAGA	GGAGCTTGTT	GCAAGAAGGA	AACTTCTCTAC	300
	TGCTTTAGAT	GCCTTTAGCT	TGGAAGCAAT	GTTGACAATA	TACCAGCTCC	ACAAAATCTG	360
	TCACAGCAGG	GCTTTTCAAC	ACTGGGAGTT	AATCCAGGAA	GATATTCTTG	ATACTGGAAA	420
	TGACAAAAAT	GGAAAGGAAG	AAGTCATAAA	GAGAAAAAAT	CCTTATATTC	TGAAACGGCA	480
	GCTGTATGAG	AATAAACCCTA	GAAGACCCTA	CATACTCAAA	AGAGATTCTT	ACTATTACTG	540
80	AGAGAATAAA	TCATTTTATT	ACATGTGATT	GTGATTCATC	ATCCCTTAAT	TAAATATCAA	600
	ATTATATTTG	TGTGAAAAATG	TGACAAACAC	ACTTATCTGT	CTCTCTTACA	ATTGTGGTTT	660
	ATTGAATGTG	TTTTTCTGCA	CTAATAGAAA	TTAGACTAAG	TGTTTTCAAA	TAAATCTAAA	720
	TCTTCAAAAA	AAAAAAAATA	AAATGGGGCC	GCAATT			



Seq ID NO: 316 Protein sequence  
Protein Accession #: AAB50564

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
MMAGMKIQLV CMLLLAFSSW SLCS DSEEM KALEADFLTN MHTSKISKAH VPSWKMTLLN 60
VCSLVNNLNS PAEETGEVHE EELVARRKLP TALDGFSLTA MLTIYQLHKI CHSRAFAQHWE 120
LIQEDILD TG NDKNGKEEVI KKKIPYILKR QLYENKPRRP YILKRDSYYY

```

Seq ID NO: 317 DNA sequence  
Nucleic Acid Accession #: NM\_006536.2  
Coding sequence: 109..2940

```

15      1      11      21      31      41      51
      |      |      |      |      |      |
ACCTAAAACC TTGCAAGTTC AGGAAGAAAC CATCTGCATC CATATTGAAA ACCTGACACA 60
ATGTATGCAG CAGGCTCAGT GTGAGTGAAC TGGAGGCTTC TCTACAACAT GACCCAAAGG 120
AGCATTGCAG GTCCCTATTG CAACCTGAAG TTTGTGACTC TCCTGGTTGC CTTAAGTTCA 180
GAACTCCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
20      ATTGCAATTA ATCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAAACAT TAAGGAAATG 300
ATAACTGAAG CTTCAATTTA CCTATTTAAT GCTACCAAGA GAAGAGTATT TTTGAGAAAT 360
ATAAAGATTT TAATACCTGC CACATGGAAA GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
TCATATGAAA AGGCAAAATG CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
TACACCTCAT AATACAGAGG GTGTGGAAAA GAGGGAAAT ACATTCATTT CACACCTAAT 540
25      TTCCTACTGA ATGATAACTT AACAGCTGGC TACGGATCAC GAGGCCGAGT GTTTGTCCAT 600
GAATGGGCCC ACCTCCGTTG GGGTGTGTTC GATGAGTATA ACAATGACAA ACCTTTCTAC 660
ATAAATGGGC AAAATCAAAAT TAAAGTGACA AGGTGTTTCT CTGACATCAC AGGCATTTT 720
GTGTGTGAAA AAGGTCTTGA CCCCCAAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
30      AGTTTATCTT CTGTGTTTGA ATTTTGTAAAT GCAAGTACCC ACAACCAAGA AGCACCAAAC 900
CTACAGAAAC AGATGTGCAG CCTCAGAAGT GCATGGGATG TAATCACAGA CTCTGCTGAC 960
TTTCACCACA GCCTTCCCAT GAATGGGACT GAGCTTCCAC CTCCTCCAC ATTCTCGCTT 1020
GTACAGGCTG GTGACAAAGT GGTCTGTGTTA GTCTGGATG TGTCCAGCAA GATGGCAGAG 1080
GCTGACAGAC TCCTTCAACT ACAACAAGCC GCAGAAATTT ATTTGATGCA GATTGTGAA 1140
35      ATTCAATACC TCGTGGGCAT TGCCAGTTTC GACAGCAAAAG GAGAGATCAG AGCCAGCTA 1200
CACCAAATTA ACAGCAATGA TGATCGAAAG TTGCTGGTTT CATATCTGCC CACCACTGTA 1260
TCAGCTAAAA CAGACATCAG CATTGTGTTCA GGGCTTAAGA AAGGATTGTA GGTGGTTGAA 1320
AAACTGAATG GAAAAGCTTA TGGCTCTGTG ATGATATTAG TGACCAGCGG AGATGATAAG 1380
CTTCTTGCCA ATTGCTTACC CACTGTGCTC AGCAGTGGTT CAACAATTCAT CTCCATTGCC 1440
40      CTGGGTTTAT CTGCAGCCCC AAATCTGGAG GAATTATCAC GTCTTACAGG AGGTTTAAAG 1500
TTCTTTGTTC CAGATATATC AAATCTCAAT AGCATGATTG ATGCTTTCAG TAGAATTTC 1560
TCTGGAAGTG GAGACATTTT CCAGCAACAT ATTCACTTG AAAGTACAGG TGAAAATGTC 1620
AAACCTCACC ATCAATTGAA AAAACACAGTG ACTGTGGATA ATACTGTGGG CAACGACACT 1680
ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCTGAGA TTATATTATT TGATCTGTAT 1740
45      GGACGAAAT ACTACACAAA TAAATTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT 1800
TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCCTGAACAA TACCCATCAT 1860
TCTCTGCAAG CCCTGAAAGT GACAGTGACC TCTCGCGCCT CCAACTCAGC TGTGCCCCCA 1920
GCCACTGTGG AAGCTTTTGT GGAAAGAGAG AGCCTCCATT TTCCTCATCC TGTGATGATT 1980
TATGCCAATG TGAACAGGGG ATTTTATCCC ATTTCTAATG CCACCTGTAC TGCCACAGTT 2040
50      GAGCCAGAGA CTGGAGATCC TGTACGCTG AGACTCCTTG ATGATGGAGC AGTGTCTGAT 2100
GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTCTCT CCTTTGCTGC AAATGGTAGA 2160
TATAGCTTGA AAGTGATGT CAATCACTCT CCCAGCATAA GCACCCAGC CCACCTCTAT 2220
CCAGGGAGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280
55      GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340
AGCTCAGGAG GCTCTTTTTC AGTGTCTGGG GTTCCAGCTG GCCCCACCC TGATGTGTTT 2400
CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCTATCT 2460
TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG 2520
AGTAAAGTCT TACAGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA 2580
60      AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTCC 2640
ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTATGTT 2700
GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCAGGCG 2760
CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820
GGAGTTTTTA CAGCAATGGG TTTGATAGGA ATCATTGCCC TTATTATAGT TGTGACACAT 2880
65      CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA 2940
ATAAATATCC AAGTGTCTT CTCTCTTGA TATAAGACCC ATGGCCTTCG ACTACAAAAA 3000
CATACTAACA AAGTCAAAT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTGACA 3060
ATACAGATAA GATTTTACA TGGTAGATCA ACAATCTTT TTGGGGTAG ATTAGAAAAC 3120
CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATCTT TTAAGTAAT GTCTTTAAAG 3180
70      GCAAAGGGAA GGTAAAGTC GGACCAAGT CAAGGAAAGT TTGTTTATT GAGGTGGA 3240
AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACTGTCTG TGTGAAGCAA 3300
TCATTTAGTT ACTTTGATTA ATTTTCTTT TCTCTTATC TGTGAGTAC AGGTGTCTG 3360
TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAG CTCTTTACCT 3420
CTTGCTATTT TGTATATAT ATTTTCAGAT ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480
TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTGTCTCT TCATACCGGT 3540
75      TTTATGACAA AGGTCTATTG AATTTATTG TGTGTAAGTT TCTACTCCCA TCAAAGCAGC 3600
TTTCTAAGTT TATTGCTTGG GGTATTATG GAATGATAGT TATAGCCCN TATAATGCCT 3660
TACCTAGGAA A

```

Seq ID NO: 318 Protein sequence  
Protein Accession #: NP\_006527.1

```

80      1      11      21      31      41      51
      |      |      |      |      |      |
MTQRSIAGPI CNLKFVTLV ALSSELPLFG AGVQLQDNGY NGLLIAINPQ VPENQNLI 60

```

IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAA 120  
 GDDPYTLQYR GCGKEGKYIH FFPNFLINDN LTAGYGSRRG VVHWEWAHLR WGVFDEYNND 180  
 KPFIYINGQNK IKVTRCSSDI TGFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240  
 MFMQSLSSVV EFCNASTHNQ EAPNLQNMCM SLRSANDVIT DSADFHHSFP MNGTELPPPP 300  
 5 TFSLVQAGDK VVCLVLDVSS KMAEADRLQ LQAAEFYLM QIVEIHTFVG IASFDSKGEI 360  
 RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGF EVVEKLNKA YGSVMILVTS 420  
 GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRIT GGLKFFVPDI SNSNSMIDAF 480  
 SRISSTGTDI FQHQIQLST GENVKPHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL 540  
 10 FDPDGRKYIT NNFITNLTFR TASLWIPGTA KPGHWYITLN NTHHSLQALK VTVTSRASNS 600  
 AVPPATVEAF VERDSLHFPF PVMYANVKQ GFYPILNATV TATVEPETGD PVTLRLLDDG 660  
 AGADVIKNDG IYSRYFFSFA ANGRYSLKVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN 720  
 IQMNAPRKSV GRNEEERKWF FSRVSSGGSF SVLGVPAAPH PDVFPPCKII DLEAVKVEEE 780  
 LTLSWTAPGE DFDQGOATSY EIRMSKSLQN IQDDFNAIL VNTSKRNPQQ AGIREIFTFS 840  
 15 PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPI NSDPVPARDY 900  
 LILKGVLTAM GLIGITCLII VVTHHTLSRK KRADKKENG T KLL

Seq ID NO: 319 DNA sequence

Nucleic Acid Accession #: NM\_000228.1

Coding sequence: 82..3600

1 11 21 31 41 51  
 | | | | |  
 GCTTTCAGGC GATCTGGAGA AAGAACGGCA GAACACACAG CAAGGAAAGG TCCTTTCTGG 60  
 25 GGATCACCCC ATTGGCTGAA GATGAGACCA TTCTTCTCT TGTGTTTTC CCTGCCTGGC 120  
 CTCTGTCATG CCCAACAAAG CTGCTCCCGT GGGGCTCTCT ATCCACCTGT TGGGGACCTG 180  
 CTTGTTGGGA GGACCCGGTT TCTCCGAGCT TCATCTACCT GTGGACTGAC CAAGCCTGAG 240  
 ACCTACTGCA CCCAGTATGG CGAGTGGCAG ATGAAATGCT GCAAGTGTGA CTCCAGGCAG 300  
 CCTCACAAC TACTACAGTCA CCGAGTAGAG AATGTGGCTT CATCTCCGG CCCCATGCGC 360  
 30 TGGTGGCAGT CCCAGAACTGA TGTGAACCTT GTCTCTCTGC AGCTGGACCT GGACAGGAGA 420  
 TTCCAGCTTC AAGAAGTCAT GATGGAGTTC CAGGGGCCCA TGCCCGCCGG CATGCTGATT 480  
 GAGCGCTCCT CAGACTTCGG TAAGACCTGG CGAGTGTACC AGTACCTGGC TGCCGACTGC 540  
 ACCCTCACCT TCCCTCGGGT CCGCCAGGGT CGGCCTCAGA GCTGGCAGGA TGTTCGGTGC 600  
 CAGTCCCTGC CTCAGAGGCC TAATGCACGC TAAATGGGG GGAAGGTCCA ACTTAACCTT 660  
 35 ATGGATTAG TGTCTGGGAT TCCAGCAACT CAAAGTCAA AAATTCAAGA GGTGGGGGAG 720  
 ATCACAACCT TGAGAGTCAA TTTCCACAGG CTGGCCCTGT TGCCCAAGG GGGCTACCAC 780  
 CCTCCCAGCG CTTACTATGC TGTGTCCAG CTCCGTCTGC AGGGGAGCTG CTTCTGTGTC 840  
 GGCCATGCTG ATCGCTGCGC ACCCAAGCCT GGGGCTCTGT CAGGCCCTCT CACCGCTGTG 900  
 CAGGTCCACG ATGTCTGTGT CTGCCAGCAC AACACTGCCG GCCCAAATTG TGAGCGCTGT 960  
 40 GCACCTTCTT ACAACAACCG GCCCTGGAGA CCGGCGGAGG GCCAGGACGC CCATGAATGC 1020  
 CAAAGGTGCG ACTGCAATGG GCACCTCAGAG ACATGTCACT TTGACCCCGC TGTGTTTGCC 1080  
 GCCAGCCAGG GGGCATATGG AGGTGTGTGT GACAATTGCC GGGACACAC CGAAGGCAAG 1140  
 AACTGTGAGC GGTGTCACT GCATATTTC CGGAACCGGC GCCCGGAGC TTCCATTGAG 1200  
 GAGACCTGCA TCTCTGCGA GTGTGATCCG GATGGGGCAG TGCCAGGGGC TCCCTGTGAC 1260  
 45 CCAGTGACCG GGCAGTGTGT GTGCAAGGAG CATGTGCAGG GAGAGCGCTG TGACCTATGC 1320  
 AAGCGGGCTG TCACTGAGCT CACCTACGCC AACCCGACGG GCTGCCACCG CTGTGACTGC 1380  
 AACATCCTGG GGTCCCGGAG GGACATGCCG TGTGACGAGG AGAGTGGGCG CTGCCCTTGT 1440  
 CTGCCCAACG TGGTGGGTCC CAAATGTGAC CAGTGTGCTC CTTACCACTG GAAGCTGGCC 1500  
 AGTGGCCAGG GTGTGAACG GTGTGCTGCG GACCCGCACA ACTCCCTCA GCGCCAGTG 1560  
 50 CAACCACTG ACAGGGCAGT GCCCTGTGCG GAAGGCTTTG GTGGCTGAT GTGCAGCGCT 1620  
 GCAGCATCC CGCAGTGTCC AGACCGGACC TATGAGAGC TGCCACAGG ATGCCGAGCC 1680  
 TGTGACTGTG ATTTCCGGGG AACAGAGGGC CCGGGCTGCG ACAAGGCATC AGGCCGCTGC 1740  
 CTCTGCCCGC CTGGCTTGAC CGGGCCCCCG TGTGACCACT GCCAGCGAGG CTACTGCAAT 1800  
 CGCTACCCGG TGTGCTGGCG CTGCCACCTT TGCTTCCAGA CCTATGATGC GGACCTCCGG 1860  
 55 GAGCAGGCCC TGCGCTTTGG TAGACTCCGC AATGCCACCG CCAGCTGTG GTCCAGGCGCT 1920  
 GGGCTGGAGG ACCGTGGCCT GGCCTCCCGG ATCCTAGATG CAAAGAGTAA GATTGAGCAG 1980  
 ATCCGAGCAG TTCTCAGCAG CCGCGCAGTC ACAGAGCAGG AGGTGGCTCA GGTGGCCAGT 2040  
 GCCATCCTCT CCCTCAGCGG AACTCTCCAG GGCCTGCAGC TGGATCTGCC CTTGGAGGAG 2100  
 60 GAGACGTTGT CCCTTCCGAG AGACCTGGAG AGTCTTGACA GAAGCTTCAA TGGTCTCCTT 2160  
 ACTATGTATC AGAGGAAGAG GGAGCAGTTT GAAAAAATAA GCAGTGTGTA TCCTTCAGGA 2220  
 GCCTTCCGGA TGTCTGAGCAG AGCCTACGAG CAGTCAGCCC AGGCTGCTCA GCAGGTCTCC 2280  
 GACAGCTCGC GCCTTTTGGA CCAGCTCAGG GACAGCCGGA GAGAGGCAGA GAGGCTGGTG 2340  
 CGGCAGGCGG GAGGAGGAGG AGGCACCGGC AGCCCCAAGC TTGTGGCCCT GAGGCTGGAG 2400  
 65 ATGTCTTCGT TGCCTAGCTT GACACCCACC TTCAACAAGC TCTGTGGCAA CTCACGGCAG 2460  
 ATGGCTTGCA CCCCATAATC ATGCCCTGGT GAGCTATGTC CCCAAGACAA TGGCACAGCC 2520  
 TGTGGCTCCC GCTGCAAGGG TGTCTTCCC AGGGCCCGGT GGGCCTTCTT GATGGCGGGG 2580  
 CAGGTGGCTG AGCAGCTGCG GGGCTTCAAT GCCAGCTCC AGCGGACCA GACAGATGAT 2640  
 70 AGGGCAGCCG AGGAATCTGC CTCACAGATT CAATCCAGTG CCCAGCGCTT GGAGACCCAG 2700  
 GTGAGCGCCA GCCCTCCCA GATGGAGGAA GATGTCAGAC GCACACGGCT CCTAATCCAG 2760  
 CAGGTCCGGG ACTTCCTAAC AGACCCCGAC ACTGATGCAG CCACTATCCA GGAGGTGAGC 2820  
 GAGGCCGTGC TGGCCCTGTG GCTGCCACA GACTCAGCTA CTGTTCTGTC GAAGATGAAT 2880  
 75 GAGATCCAGG CCAITGACAG CAGGCTCCCG AACGTGGACT TGGTGTGTC CCAGACCAAG 2940  
 CAGGACATTG CGCGTGCCCG CCGGTGTCAG GCTGAGGCTG AGGAAGCCAG GAGCCGAGCC 3000  
 CATGCAGTGG AGGGCCAGGT GGAAGATGTG GTTGGGAACC TGCGGCAGGG GACAGTGGCA 3060  
 CTGCAGGAAG CTCAGGAAC CATGCAAGGC ACCAGCCGCT CCCTTCGGCT TATCCAGGAC 3120  
 AGGGTGTCTG AGGTTCAGCA GGTACTGCGG CCAGCAGAAA AGCTGGTGAC AAGCATGACC 3180  
 80 AAGCAGCTGG GTGACTTCTG GACACGGATG GAGGAGCTCC GCCACCAAGC CCGGCAGCAG 3240  
 GGGGCAGAGG CAGTCCAGGC CCAGCAGCTT GCGGAAGGTG CCAGCGAGCA GGCATTGAGT 3300  
 GCCCAAGAGG GATTTGAGAG AATAAAACAA AAGTATGCTG AGTTGAAGGA CCGGTTGGGT 3360  
 CAGAGTTCCA GTTGGGTGA GCAGGGTGCC CGGATCCAGA GTGTGAAGAC AGAGGCAGAG 3420  
 GAGCTGTTTG GGGAGACCAT GGAGATGATG GACAGGATGA AAGACATGGA GTTGGAGCTG 3480  
 CTGCGGGGCA GCCAGGCCAT CATGCTGCGC TCGGCGGACC TGACAGGACT GGAGAAGCGT 3540  
 GTGGAGCAGA TCCGTGACCA CATCAATGGG CGCGTGCTCT ACTATGCCAC GTGCAAGTGA 3600  
 TGCTACAGCT TCCAGCCCGT TGCCCCACTC ATCTGCCGCC TTTGCTTTTG GTTGGGGGCA 3660  
 GATTGGGTG GAATGCTTTC CATCTCCAGG AGACTTTCAT GCAGCCTAAA GTACAGCCTG 3720

GACCACCCCT GGTGTGTAGC TAGTAAGATT ACCCTGAGCT GCAGCTGAGC CTGAGCCAAT 3780  
 GGGACAGTTA CACTTGACAG ACAAGATGG TGGAGATTGG CATGCCATTG AAACCTAAGAG 3840  
 CTCTCAAGTC AAGGAAGCTG GGCTGGGCAG TATCCCCCGC CTTTAGTTCT CCACTGGGGA 3900  
 GGAATCTCG ACCAAGCACA AAAACTTAAC AAAAGTGATG TAAAAATGAA AAGCCAAATA 3960  
 AAAATCTTTG G

Seq ID NO: 320 Protein sequence  
 Protein Accession #: NP\_000219.1

1 11 21 31 41 51  
 | | | | |  
 MRPFLLCFA LPGLLHAQQA CSRGACYPPV GDLLVGRTRF LRASSTCGLT KPETYCTQYG 60  
 EWQMKCKCD SRQPHNYSH RVENVASSSG PMRWQSQND VNPVSLQLDL DRRFQLQEVN 120  
 MEFGPMPAG MLIERSSDFG KTWRYVQYLA ADCTSTFPRV RQGRPQSQWD VRCQSLPQRP 180  
 15 NARLNGGKVQ LNLMDLVSGI PATQSQKIQE VGEITNLRVN FTRLAPVPQR GYHPPSAYYA 240  
 VSQRLQSGC FCHGHADRC PKPGASAGPS TAVQVHDCV CQHNTAGPNC ERCAPFYNNR 300  
 PWRPAEGQDA HECGRDCNCG HSETCHFDPA VFAASQGAYG GVCNDCRDHT EGNKNCERCQL 360  
 HYFRNRRPGA SIQETCISCE CDPDGA VPGA PCDPVTGCVC KEHVQGERC DLCKPGFTGL 420  
 20 TYANPQGGCHR CDCNILGSR DMPCDEESGR CLCLPNVVGK KCDQCAPYHW KLASGQCEP 480  
 CACDPHNSPQ PTVPVHRAV PCREGFGGLM CSAAAIRQCP DRTYGDVATG CRACDCDFRG 540  
 TEGPGCDKAS GRCLCRPGLT GPRCDQCGRG YCNRYPCVA CHPCFQTYDA DLREQALRFG 600  
 RLRNATASLW SGPGLERGL ASRILDAKSK IEQIRAVLSS PAVTEQEVAG VASAILSLRR 660  
 TLQGLQLDLP LEEETLSLPR DLESIDRSFN GLLTMYQRKR EQFEKISSAD PSGAFRMLST 720  
 25 AYEQSAQAAQ QVSDSSRLLD QLRDSRREAE RLVRQAGGGG GTGSPKLVAL RLEMSSLPDL 780  
 TPTFNKLCGN SRQMACTPIS CPGELCPQDN GTACGSRCRG VLPRAGGAFI MAGQVABQLR 840  
 GFNAQLQRT SRMIRAAEESA SIQSSAQRL ETQVSASRSQ MEEDVRRTRL LIQQVRDFLT 900  
 DPTDAATIQ EVSEAVLALW LPTDSATVLQ KMNEIQAIWA RLPNVLDVLS QTKQDIARAR 960  
 RLQAEAEAR SRHAEVGEVQ EDVVGNLRQG TVALQEAQDT MQGTSRSLRL IQDRVAEVQQ 1020  
 30 VLRPAEKLVV SMTKQLGDFW TRMEELRHQA RQQGAEAQQA QQLAEGASEQ ALSAQEGFER 1080  
 IKQKYAELKD RLGGSSMLGE QGARIQSVKT EAEELFGETM EMDRMKDMDE LELLRGSQAI 1140  
 MLRSADLTGL EKRVBQIRDH INGRVLYAT CK

Seq ID NO: 321 DNA sequence  
 Nucleic Acid Accession #: NM\_001944.1  
 Coding sequence: 84..3083

1 11 21 31 41 51  
 | | | | |  
 TTTTCTTAGA CATTAACTGC AGACGGCTGG CAGGATAGAA GCAGCGGCTC ACTTGGA CTT 60  
 40 TTTCACCAGG GAAATCAGAG ACAATGATGG GGCTCTTCCC CAGAACTACA GGGGCTCTGG 120  
 CCATCTTCCT GGTGTGTATA TTGGTTCATG GAGAATTGCG AATAGAGACT AAAGGTCAAT 180  
 ATGATGAAGA AGAGATGACT ATGCAACAAG CTAAAAGAG GCAAAAACGT GAATGGGTGA 240  
 AATTTCGCAA ACCCTGCAGA GAAGGAGAAG ATAACCTCAA AAGAAACCCA ATTGCCAAGA 300  
 45 TTACTTCAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG 360  
 ATCAGCCGCC TTTTGGAATC TTTGTGTGGT ACAAAAACAC TGGAGATATT AACATAACAG 420  
 CTATAGTCGA CCGGGAGGAA ACTCCAAGCT TCCTGATCAC ATGTGCGGCT CTAATGCCCC 480  
 AAGGACTAGA TGTAGAGAAA CCACTTATAC TAACGGTTAA AATTTTGGAT ATTAATGATA 540  
 ATCCTCCAGT ATTTTCACAA CAAATTTTCA TGGGTGAAAT TGAAGAAAAT AGTGCCTCAA 600  
 ACTCACTGGT GATGATACTA AATGCCACAG ATGCAGATGA ACCAAACAC TGAATTTCTA 660  
 50 AAATTCGCTT CAAAAATGTC TCTCAGGAAC CAGCAGGCAC ACCCATGTTT CTCCTAAGCA 720  
 GAAACACTGG GGAAGTCCGT ACTTTGACCA ATCTCTTGA CCGAGAGCAA GCTAGCAGCT 780  
 ATCGTCTGGT TGTGAGTGGT GCAGACAAAG ATGGAGAAG ACTATCACT CAATGTGAAT 840  
 GTAATATTAA AGTGAAAGAT GTCAACGATA ACTTCCCAAT GTTTAGAGAC TCTCAGTATT 900  
 CAGCACGTA TGAAGAAAT ATTTTAAGTT CTGAATTACT TCGATTTCAG GTAACAGATT 960  
 55 TGGATGAAGA GTACACAGAT AATTGGCTTG CAGTATATTT CTTTACCTCT GGAATGAAG 1020  
 GAAATTTGTT TGAATACAA ACTGATCCTA GAACTAATGA AGGCATCCTG AAAGTGGTGA 1080  
 AGGCTCTAGA TTAATGAACA CTACAAGCG TGAACCTTAG TATTGCTGTC AAAAAACAG 1140  
 CTGAATTTCA CCAATCAGT ATCTCTCGAT ACCGAGTTCA GTCAACCCCA GTCACAATTC 1200  
 60 AGGTAATAAA TGTAAAGAGAA GGAATTCAT TCCGTCTGTC TTCCAAGACA TTACTGTGTC 1260  
 AAAAAGGCAT AAGTAGCAAA AAATTTGGTG ATTATATCCT GGGAAACAT CAAGCCATCG 1320  
 ATGAGGACAC TAACAAGCT GCCTCAATG TCAATATGT CATGGGACGT AACGATGGTG 1380  
 GATACCTAAT GATTGATTCA AAAACTGCTG AAATCAAAAT TGTCAAAAAT ATGAACCGAG 1440  
 ATTCTACTTT CATAGTTAAC AAAACAATCA CAGCTGAGGT TCTGGCCATA GATGAATACA 1500  
 65 CGGGTAAAC TTCTACAGGC ACGGTATATG TTAGAGTACC CGATTTCAT GACAATGTGTC 1560  
 CAACAGCTGT CCTCGAAAAA GATGCAGTTT GCAGTTCTTC ACCTTCCGTG GTTGTCTCCG 1620  
 CTAGAACACT GAATAATAGA TACACTGGCC CCTATACATT TGCACTGGAA GATCAACCTG 1680  
 TAAAGTTGCC TGCCGTATGG AGTATACAA CCCTCAATGC TACCTCGGCC CTCTCAGAG 1740  
 70 CCCAGGAACA GATACCTCTT GGAGTATACC ACATCTCCCT GGTACTTACA GACAGTCAGA 1800  
 ACAATCGGTG TGAGATGCCA CGCAGCTTGA CACTGGAAGT CTGTCACTGT GACAACAGGG 1860  
 GCATCTGTGG AACTTCTTAC CCAACACAA GCCTTGGGAC CAGGTATGGC AGGCCGCACT 1920  
 CAGGAGGCT GGGGCTGCTC GCCATCGGCC TGCTGCTCCT TGGTCTCTGT CTGCTCTGCT 1980  
 TGGCCCCCTT TCTGCTGTTG ACCTGTGACT GTGGGGCAGG TTCTACTGGG GGAGTGACAG 2040  
 GTGGTTTTAT CCCAGTTCTT GATGGCTCAG AAGGAACAAT TCATCAGTGG GGAATTGAAG 2100  
 75 GAGCCATCC TGAAGACAAG GAAATCACAA ATATTTGTGT GCCTCCTGTA ACAGCCAATG 2160  
 GAGCCGATTT CATGGAAGT TCTGAAGTT GTACAAATAC GTATGCCAGA GGCACAGCGG 2220  
 TGAAGGCAC TTCAGGATG GAAATGACCA CTAAGCTTGG AGCAGCCACT GAATCTGGAG 2280  
 GTGCTGCAGG CTTTGCAACA GGGACAGTGT CAGGAGCTGC TTCAGGATTC GGAGCAGCCA 2340  
 CTGGAGTTGG CATCTGTTCC TCAGGGCAGT CTGGAAACAT GAGAACAAGG CATTCCTACT 2400  
 80 GAGGAACCAA TAAGCACTAC GCTGATGGGG CGATAAGCAT GAATTTTCTG GACTCCTACT 2460  
 TTTCTCAGAA AGCATTTGCC TGTGCGGAGG AAGACGATGG CCAGGAAGCA AATGACTGCT 2520  
 TGTGATCTA TGATAATGAA GGCAGATG CCACTGGTTC TCCTGTGGGC TCCGTGGGTT 2580  
 GTTGCACTTT TATTGCTGAT GACCTGGATG ACAGCTTCTT GGACTCACTT GGACCCAAAT 2640  
 TTAACAACT TGCAGAGATA AGCCTTGGTG TTGATGGTGA AGGCAAGAA GTTCAGCCAC 2700  
 CCTCTAAGA CAGCGTTAT GGGATTGAAT CCTGTGGCCA TCCCATAGAA GTCCAGCAGA 2760

CAGGATTTGT TAAGTGCCAG ACTTTGTCAG GAAGTCAAGG AGCTTCTGCT TTGTCCGCCT 2820  
 CTGGGTCTCT CCAGCCAGCT GTTTCACATCC CTGACCCTCT GCAGCATGGT AACTATTTAG 2880  
 TAACGGAGAC TTACTCGGCT TCTGGTTCCT TCGTGCAACC TTCCACTGCA GGCTTTGATC 2940  
 CACTTCTCAC ACAAATGTG ATAGTGACAG AAAGGGTGAT CTGTCCCAT TCCAGTGTTC 3000  
 5 CTGGCAACCT AGCTGGCCCA ACGCAGCTAC GAGGGTCACA TACTATGCTC TGTACAGAGG 3060  
 ATCCTTGTCT CCGTCTAATA TGACCAGAAT GAGCTGGAAT ACCACACTGA CCAAACTCGG 3120  
 ATCTTTGGAC TAAAGTATTC AAAATAGCAT AGCAAAGCTC ACTGTATTGG GCTAATAATT 3180  
 TGGCACTTAT TAGCTTCTCT CATAAACTGA TCACGATTAT AAATTAAATG TTTGGGTTCA 3240  
 10 TACCCCAAAA GCAATATGTT GTCACTCCTA ATTCTCAAGT ACTATTCAAA TTGTAGTAAA 3300  
 TCTTAAAGTT TTTCAAAACC CTAAAATCAT ATTCGC

Seq ID NO: 322 Protein sequence  
 Protein Accession #: NP\_001935.1

15 1 11 21 31 41 51  
 MMGLFPRTTG ALAIFVVVIL VHGELEIETK GQYDEEEMTM QQAKRRQKRE WVKFAKPCRE 60  
 GEDNSKRNP I AKITSDYQAT QKITYRISGV GIDQPPFGIF VVDKNTGDI IN ITAIVDREET 120  
 20 PSFLITCRAL NAQGLDVEKP LILTVKILDI NDNPVFSQQ IFMGEIEENS ASNSLVMILN 180  
 ATDADEPNHL NSKIAFKIVS QEPAGTPMFL LSRNTGEVRT LTNSLDREQA SSYRLVVSQA 240  
 DKDGEGLSTQ CECNIKVKDV NDNFPMFRDS QYSARIEENI LSSELLRFQV TDLDEEYTDN 300  
 WLAVYFFTSQ NEGNWFIEQT DPRTNIEGILK VVKALDYEQL QSVKLSIAVK NKAEFHQSVI 360  
 SRYRVQSTPV TIQVINVREG IAFRPASKTF TVQKGISSKK LVDYILGTQY AIDEDTNKAA 420  
 25 SNVKYVMGRN DGGYLMIDSK TAEIKFVKNM NRSTFIVNK TITAEVLAI D EYTGKTSTGT 480  
 VYVRVPDFND NCPTAVLEKD AVCSSSPSVV VSARTLNNRY TGPYTFAL ED QPVKLPVWS 540  
 ITTLNATSAL LRAQEQIPPG VYHISLVLT D SQNNRCEMPR SLTLEVCQCD NRGICGTSYP 600  
 TTSFGTRYGR PHSGRLGPAA IGLLLGLLLL LLLAPLLLLT CDCGAGSTGG VTGGFIPVPD 660  
 GSEGTIHQWG IEGAHPEDEK ITNICVPPVT ANGADFMESS EVCTNTYARG TAVEGTSGME 720  
 30 MTTKLGAATE SGGAGFATG TVSGAASGFG AATGVGICSS GQSGTMRTRH STGGTNKDYA 780  
 DGAISMNFDL SYFSQKAFAC AEEDDGQEAN DCLLIYDNEG ADATGSPVGS VGCCSFIADD 840  
 LDDSFPLDSL PKFKKLAEIS LGVDGEGKEV QPPSKDSGYG IESCGHPIEV QQTGFVKCQT 900  
 LSGSQGASAL SASGSVQPAV SIPDPLQHGN YLVTETYSAS GSLVQPS TAG FDPILLTQNV I 960  
 VTERVICPIS SVPGNLAGPT QLRGSHTMLC TEDPCSRLI

35 Seq ID NO: 323 DNA sequence  
 Nucleic Acid Accession #: XM\_058069.2  
 Coding sequence: 1..1413

40 1 11 21 31 41 51  
 ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCTGAAC 60  
 AGCTCTACAA GCCTGGAAAA AATAATGTG CTATTGGTG AAAGATACTT AGAAAAATT 120  
 TATGGCCTTG AGATAAACAA ACTTCCAGTG ACAAATGA AATATAGTGG AAACCTAATG 180  
 45 AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240  
 ACATCTACCC TGGAGATGAT GCACGCACCT CGATGTGGAG TCCCGCATGT CCATCATTTT 300  
 AGGGAAATGC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT 360  
 TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCCGGAAGC TTTCCAAGTA 420  
 TGGAGTAATG TTACCCCTT GAAATTACAG AAGATTAACA CAGGCATGGC TGACATTTTG 480  
 50 GTGGTTTTTG CCGGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540  
 CTAGCCCATG CTTTGGACC TGGATCTGGC ATTGGAGGGG ATGCACATT CGATGAGGAC 600  
 GAATTCTGGA CTACACATTC AGGAGGCACA AACTTGTTC TCACTGCTGT TCACGAGATT 660  
 GGCCATTCCT TAGGTCTTGG CCATCTAGT GATCCAAAGG CCGTAATGTT CCCCACCTAC 720  
 AATATGTGT ACATCAACAC ATTTCGCCTC TCTGCTGATG ACATACGTGG CATTCAGTCC 780  
 55 CTGTATGGAG ACCCAAAGA GAACCAACGC TTGCCAAATC CTGACATTC AGAACCAGCT 840  
 CTCTGTGACC CCAATTGAG TTTTGTATGCT GTCACTACCG TGGGAAATAA GATCTTTTTC 900  
 TTCAAAGACA GGTCTCTCTG GCTGAAGGT TCTGAGAGAC CAAAGACCAG TGTTAATTTA 960  
 ATTTCTTCCT TATGGCCAAC CTTGCCATCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020  
 AGAAATCAAG TTTTCTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080  
 60 GAGCCAAATT ATCCCAAGAG CATACATTCT TTTGGTTTTC CTAACCTTGT GAAAAAATT 1140  
 GATGCAGCTG TTTTAAACCC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAACCAATAT 1200  
 TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCCTGGTT ATCCCAAACT GATTACCAAG 1260  
 AACTTCCAAG GAATCGGGCC TAAATTTGAT GCAGTCTTCT ACTCTAAAA CAAATACTAC 1320  
 TATTTCTTCC AAGGATCTAA CCAATTTGAA TATGACTTCC TACTCCAACG TATCACCAAA 1380  
 65 ACACCTGAAA GCAATAGCTG GTTTGGTTGT TGA

Seq ID NO: 324 Protein sequence  
 Protein Accession #: P39900

70 1 11 21 31 41 51  
 MKFLILLILQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60  
 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHVF REMPGGPVWR KHYITYRINN 120  
 YTPDMNR EDV DYAIRKAFQV WSNVTPFKFS KINTGMADIL VVFARGAHGD PHAFDGGKGI 180  
 75 LAHAFPGSG IGGDAHFDEB EFWTTHSGGT NLFLTAVHEI GHSGLGLHSS DPKAVMFPTY 240  
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LNPDPNSEPA LCDPNLSFDA VTTVGNKIFF 300  
 FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360  
 EPNYPKSHS FGFNPNFKKI DAAVFNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420  
 NFQIGIPKID AVFYSKNKYY YFFQGSNQFE YDFLLQRIK TLKSNWFGC

80 Seq ID NO: 325 DNA sequence  
 Nucleic Acid Accession #: NM\_024423.1  
 Coding sequence: 64..2590

1 11 21 31 41 51

	GGCAGGTCTC	GCTCTCGGCA	CCCTCCCGGC	GCCC CGCTTC	TCCTGGCCCT	GCCCGGCATC	60
	CCGATGGCCG	CCGCTGGGCC	CCGGCGCTCC	GTGCGCGGAG	CCGTCTGCCT	GCATCTGCTG	120
	CTGACCCCTG	TGATCTTCAG	TCGTGATGGT	GAAGCCTGCA	AAAAGGTGAT	ACTTAATGTA	180
5	CCTTCTAAAC	TAGAGGCAGA	CAAAATAATT	GGCAGAGTTA	ATTTGGGAAG	GTGCTTCAGG	240
	TCTGCAGACC	TAGTCCGGTC	AAGTGATCCT	GATTTTCAGAG	TTCTAAATGA	TGGGTTCAGT	300
	TACACAGCCA	GGGCTGTTGC	GCTGTCTGAT	AAGAAAAGAT	CATTTACCAT	ATGGCTTTCT	360
	GACAAAAGGA	AACAGACACA	GAAAGAGGTT	ACTGTGCTGC	TAGAACATCA	GAAGAAGGTA	420
10	TCGAAGACAA	GACACACTAG	AGAACTGTGT	CTCAGGCGTG	CCAAGAGGAG	ATGGGCACCT	480
	ATTCCTTGCT	CTATGCAAGA	GAATTCCTTG	GGCCCTTTCC	CATTGTTTCT	TCAACAAGTT	540
	GAATCTGATG	CAGCACAGAA	CTATACTGTC	TTCTACTCAA	TAAGTGGACG	TGGAGTTGAT	600
	AAAGAACCCT	TAAATTTGTT	TTATATAGAA	AGAGACACTG	GAAATCTATT	TTGCACTCGG	660
	CCTGTGGATC	GTGAAGAATA	TGATGTTTTT	GATTTGATTG	CTTATGCGTC	AACTGCAGAT	720
15	GGATATTCAG	CAGATCTGCC	CCTCCCACTA	CCCATCAGGG	TAGAGGATGA	AAATGACAAC	780
	ACCCCTGTTT	TCACAGAAGC	AATTTATAAT	TTTGAAGTTT	TGGAAAGTAG	TAGACCTGGT	840
	ACTACAGTGG	GGGTGTTTGG	TGCCACAGAC	AGAGATGAAC	CGGACACAAT	GCATACGCGC	900
	CTGAAATACA	GCATTTTGCA	GCAGACACCA	AGGTCACCTG	GGCTCTTTTC	TGTGCATCCC	960
	AGCACAGGCG	TAATCACCAC	AGTCTCTCAT	TATTTGGACA	GAGAGGTTGT	AGACAAGTAC	1020
20	TCATTGATAA	TGAAGTACA	AGACATGGAT	GGCCAGTTTT	TTGGATTGAT	AGGCACATCA	1080
	ACTTGTATCA	TAACAGTAAC	AGATTCAAAT	GATAATGCAC	CCACTTTCAG	ACAAAATGCT	1140
	TATGAAGCAT	TTGTAGAGGA	AAATGCATTC	AATGTGGAAA	TCTTACGAAT	ACCTATAGAA	1200
	GATAAGGATT	TAATTAACAC	TGCCAATTGG	AGAGTCAATT	TTACCATTTT	AAAGGGAAAT	1260
	GAATAATGGC	ATTTCAAAT	CAGCACAGAC	AAAGAACTA	ATGAAGGTGT	TCCTTCTGTT	1320
25	GTAAGGCCAC	TGAATTATGA	AGAAAACCGT	CAAGTGAACC	TGGAAATGG	AGTAAACAAT	1380
	GAAGCGCCAT	TTGCTAGAGA	TATTCACAGA	GTGACAGCCT	TGAACAGAGC	CTTGGTTACA	1440
	GTTCATGTGA	GGGATCTGGA	TGAGGGGCCCT	GAATGCACTC	CTGCAGCCCA	ATATGTGCGG	1500
	ATTAAAGAAA	ACTTAGCAGT	GGGGTCAAAG	ATCAACGGCT	ATAAGGCATA	TGACCCCGAA	1560
	AATAGAAATG	GCAATGGTTT	AAGGTACAAA	AAATTGTCATG	ATCCTAAAGG	TTGGATCACC	1620
	ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GGTGAAACT	1680
30	CCCAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
	ACTGGAACAC	TTGCTGTGAA	CATTGAAGAT	GTAAATGATA	ATCCACCAGA	AATACTTCAA	1800
	GAATATGTAG	TCATTTGCAA	ACCAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTTCAGTTTC	CCAATACCTC	TCCAGAAATC	1920
35	AGTAGACTGT	GGAGCCTCAC	CAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGAATA	TACCATTCTT	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
	GCAACAAAAT	TATTTAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACCTA	GTGTGCTGCG	2100
	ACTTCAAGGA	GTACAGGAGT	AATACCTTGA	AAATGGGCAG	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCTTTTCTGT	ATTGCTAACT	TTAGTATGTG	GAGTTTTTGG	TGCAACTAAA	2220
40	GGGAAACGTT	TTCTGGAAGA	TTTAGCACAG	CAAACTTAA	TTATATCAAA	CACAGAAGCA	2280
	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTATGTA	CCCAAACTAC	CAACAACTCT	2340
	AGCCAAGGTT	TTTGTGGTAC	TATGGGATCA	GGATGAAAA	ATGGAGGGCA	GGAAACCAT	2400
	GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCCTGGACT	CCTGCAGGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACTTACTCG	2520
45	GAGTGGCACA	GTTTTACTCA	ACCCCGTCTC	GGTGAAGAA	CCATTAGAGG	ACACACTGGT	2580
	TAAAAATTA	ACATAAAGCA	AATTGCTATG	ATGTAATCAG	AATGAAGACC	GCATGCCATC	2640
	CCAAGATTAT	GTCTCTCACT	ATAACTATGA	GGGAAGAGGA	TCTCCAGCTG	GTCTGTGGGG	2700
	CTGCTGCAGT	GAAAAGCAGG	AAGAAGATGG	CCTTGACTTT	TTAAATAATT	TGGAACCCAA	2760
	ATTATTATCA	TTAGCAGAAG	CATGCACAAA	GAGATAATGT	CACAGTGCTA	CAATTAGGTC	2820
50	TTTGTGAGAC	ATTCTGGAGG	TTTCCAAAAA	TAATATTGTA	AAGTTCAATT	TCAACATGTA	2880
	TGTATATGAT	GATTTTTTTT	TCAATTTTGA	ATTATGCTAC	TACCAATTTT	ATATTTTTAA	2940
	AGCCAGTTGT	TGCTTATCTT	TTCCAAAAAG	TGAAAAATGT	TAAAAACAGC	AACTGGTAAA	3000
	TCTCAAACCT	CAGCACTGGA	ATTAAGGTCT	CTAAAGCATC	TGCTCTTTTT	TTTTTTTACG	3060
	GATATTTTAG	TAAATAAATA	GCTGGATAAA	TATTAGTCCA	ACAATAGCTA	AGTTATGCTA	3120
55	ATATCACATT	ATTATGTATT	CACCTTAAAGT	GATAGTTTAA	AAAATAAACA	AGAAATATTG	3180
	AGTATCACTA	TGTGAAGAAA	GTTTTGAAAA	AGAAACAATG	AAGACTGAAT	TAAATTAATA	3240
	ATGTTGCAGC	TCATAAAGAA	TTGGGACTCA	CCCCTACTGC	ACTACCAAA	TCATTTGACT	3300
	TTGGAGGCAA	AATGTGTTGA	AGTGCCCTAT	GAAGTAGCAA	TTTCTTATAG	GAATATAGTT	3360
	GGAAATAAAT	GTGTGTGTGT	ATATTATTAT	TAATCAATGC	AATATTAAAA	ATGAATAGAG	3420
60	AACAAAGAGG	AAAATGGTAA	AACTTGAAAA	TGAGGCTGGG	GTATAGTTTG	TCCTACAATA	3480
	GAAAAAAGAG	AGAGCTTCCT	AGGCCTGGGC	TCTTAAATGC	TGCATTATAA	CTGAGTCTAT	3540
	GAGGAAATAG	TTCTGTGCCA	ATTGTGTAA	TTTGTTTAAA	ATTGTAAATA	AATTAACCTT	3600
	TTCTGGTTTC	TGTGGGAAGG	AAATAGGGAA	TCCAATGGAA	CAGTAGCTTT	GCTTTGCAGT	3660
	CTGTTTCAAG	ATTCTTCGAT	CCACAAGTTA	GTAGCAAATC	GGGGAATACT	CGCTGCAGCT	3720
65	GGGGTTCCCT	GCTTTTTGGT	AGCAAGGGTC	CAGAGATGAG	GTGTTTTTTT	CGGGGAGCTA	3780
	ATAACAAAAA	CATTTTAAAA	CTTACCTTTA	CTGAAGTTAA	ATCCTCTATT	GCTGTTTCTA	3840
	TTCTCTCTTA	TAGTGACCAA	CATCTTTTAA	ATTAGATGCC	AAATAACCAT	GTCTCTCTAG	3900
	AGTTTAGAGG	CTAGAGGGAG	CTGAGGGGAG	GATCTTACTG	AAAGCACCTT	GGGGAGATTG	3960
	ATTGTCTCTA	AACCTAAGCC	CCACAAACTT	GACACCTGAT	CAGGTCTGGG	AGCTACAAAA	4020
70	TTTCATTTT	CTCTCACTG	CCCTTCTTCT	GAGTGGCATT	GGCCTGAATC	AAGGAAAGCC	4080
	AGGCCTTGTG	GGCCCCCTTT	TTTCGGCTTT	CTGCTAAAGC	AACACCTCCA	GCAGAGATTC	4140
	CCTTAAGTGA	CTCCAGGTTT	TCCACCATCC	TTCAAGCTGA	ATTAATTTTT	AATCAGTTTG	4200
	CTTTCTCCAG	AGAAATTTTA	AAATAATAGA	AGAAATAGAA	ATTTTGAART	TATAAAGAAA	4260
	AAAGATCAAG	TTGTCAATTT	AGAACAGAGG	GAACCTTTGG	AGAAAGCAGC	CCAAGTAGGT	4320
75	TATTTGTACA	GTCAGAGGGC	AACAGGAAGA	TGCAGGCCCT	CAAGGGCAAG	GAGAGGCCAC	4380
	AAGGAATATG	GGTGGGAGTA	AAAGCAACAT	CGTCTGCTTC	ATACTTTTTT	CTAGGCTTGG	4440
	CACGTGCTTT	TCCTTTCTCA	GGCCAATGGC	AACTGCCATT	TGAGTCCGGT	GAGGGATCAG	4500
	CCAACCTCTT	CTCTATGGCT	CACCTTATTT	GGAGTGAGAA	ATCAAGGAGA	CAGAGCTGAC	4560
	TGCATGATGA	GTCTGAAGGC	ATTTGCAGGA	TGAGCCTGAA	CTGTTTGTGC	AGAACAAACA	4620
80	AGGCATTCTAT	GGGAATTTGT	GTATTCCTTC	TGCAGCCCTC	CTTCTGGGCA	CTAAGAAGGT	4680
	CTATGAATTA	AATGCCTATC	TAAAATTCCT	ATTTATTCCT	ACATTTTCTG	TTTTCTAATT	4740
	TGACCCTAAA	ATCTATGTGT	TTTAGACTTA	GACTTTTTAT	TGCCCCCCCC	CCCTTTTTTT	4800
	TTGAGACGGA	GTCTCGCTCT	GACGCACAGG	CTGGAGTGCA	GTGGCTCCGA	TCTCTGCTCA	4860
	CTGAAAGCTC	CGCCTCCCGG	GTTCTATGCC	TTCTCCTGCC	TCAGCCTCCT	GAGTAGCTGG	4920
	GACTACAGGC	GCCCACCACC	ACGCCCGGCT	AATTTTTTGT	ATTTTAAATA	GAGACGGGGT	4980

5 T T C A C T G T G T T A G C C A G G A T G G T C T C G A T C T C C T G A C C T C G T G A T C C G C C T G C C T C G G C C 5040  
 T C C C A A A G T G C T G G G A T T A C A G G C A T G A C C C A C C G C T C C C G G C C T T G T T T T C C G T T A A A 5100  
 G T C G T C T T C T T T A A T G T A A T C A T T T T T G A A C A T G T G T G A A A G T T G A T C A T A C G A A T T G G A 5160  
 T C A A T C T T G A A A T A C T C A A C C A A A A G A C A G T C G A G A A G C C A G G G G G A G A A A G A A C T C A G G 5220  
 G C A C A A A A T A T T G G T C T G A G A A T G G A A T T C T C T G T A A G C C T A G T T G C T G A A A T T C C T C G 5280  
 T G T A A C C A G A A G C C A G T T T T A T C T A A C G G C T A C T G A A A C A C C A C T G T G T T T G C T C A C T 5340  
 C C C A C T C A C C G A T C A A A A C C T G C T A C C T C C C A A G A C T T T A C T A G T G C C G A T A A A C T T T C 5400  
 T C A A A G A G C A A C C A G T A T C A C T T C C C T G T T T A T A A A A C C T A A C C A T C T C T T G T T C T T 5460  
 10 T G A A C A T G C T G A A A A C C A C C T G G T C T G C A T G T A T G C C C G A A T T T G T A A T T C T T T C T C T C 5520  
 A A A T G A A A A T T A A T T T T A G G A T T C A T T T C A T T T C T A T A T T T T C A C A T A T G T A G T A T T A T T A T 5580  
 T C C T T A T A T G T G T A A G G T G A A A T T T A T G G T A T T T G A G T G T G C A A G A A A A T A T A T T T T T A A 5640  
 A G C T T T C A T T T T C C C C A G T A A T G A T T A G A A T T T T T A T G T A A A T A T A C A G A A T G T T 5700  
 T T T T C T T A C T T T T A A G G A A G C A G C T G T C T A A A T G C A G T G G G G T T T G T T T T G C A A T G T 5760  
 15 T T T A A C A G A G T T T T A G T A T T G C T A T T A A A A A G A T T A C T T T G C T T T T A A A G A A A C T T G G 5820  
 C T G C T T A A A A T A A G C A A A A A T T G G A T G C A T A A A G T A A T A T T A C A G A T G T G G G G A G A T G T 5880  
 A A T A A A A C A A T A T T A A C T T G C T G C T T A A A A T A A G C A A A A A T T G G A T G C A T A A A G T A A A 5940  
 T T T C A G A T G T G G G G A G A T G T A A T A A A A C A A T A T T A A C T T G G T T C T T G T T T T G C T G T A 6000  
 T T T A G A G A T T A A T A A T T C T A A G A T G A T C A C T T G C A A A A T T A T G C T T A T G G C T G G C A T G 6060  
 20 G A A A T A G A A A T A C T C A A T T A T G T C T T T G T T G T A T T A A T G G G A A T A T T T T G G A C A A T G T T 6120  
 T C A T T A T C A A A T T G T C G A C A T C A T T A A T A T A T A T T G T A A T G T T G G G A A G A G A T C A C T A T T 6180  
 T T G A A G C A C A G C T T T A C A G A T G A T A G A T A C T A T G A T A A T A A A S T T T G A T C G G 6240  
 G T A T T A A A A G T A T T A G A A G G T G T T A A T T G C A G A T A T T C C A T G A A T A G T A C A C T G A C 6300  
 A C A G G G G T T T T A C T T T G A G G A C C A G T G T A G T C A A G G G A A A C A T G A G T T A A A A G A A A A G 6360  
 25 C A G G C A A T A T T G C A G T C T T G A T T C T G C C A C T T A C A G G A T A G A T A A T G C C T G A A C T T T A A T 6420  
 G A C A A G A T G A T C C A A C C A A A A G G T G C T C T G T G C T T C A C A G T A A T C T T T C C C C A T G C A 6480  
 G G A G T G T G C T C C C T A C A A A C G T T A A G A C T G A T C A T T T C A A A A A T C T A T T A G C T A T A T C A 6540  
 A A A G C C T T A C A T T T A A T A T A G G T T G A A C C A A A A T T T C A A T T C C A G T A A C T T C T A T T G T A 6600  
 A C C A T T A T T T T T G T A T G T C T T C A A G A A T G T T C A T T G G A T T T T G T T G T A A T A G T A A A 6660  
 30 A T A C C G A T A C A T T C A C G T G T C C T T C A G T A T T G A T T T G G T T G A A T A T G G G T C A T A A T G 6720  
 G T T G A G A A G C A T G G A C A C T A G A G C C A A A T G C T T G G A T A T G A A T C C T G G A T C T G T C A C T T 6780  
 A C T T C T G T G T G A C C T T T G A A A G G C T A C T T A T T C C T C T C T A G C T T T C T C A T T A A A A T C A 6840  
 A T G A A C A A T G C C A G C C T C A T G G G G T T G T T G A A T G A T T A A A T T A G T T A A T A T A C C T A A A G T 6900  
 A C A T A G A A C A C T G C C T G C A C A T A G T A A A A G A A T T A T A A G T G T A G G T A G T T G G T A A A A T T 6960  
 35 A T G T A G T T G G A T A T A C T A C C G A C A A T A T C T A A T C T C T T T T A G G G A A A T A A A G T T T G T G 7020  
 C A T A T A T A T A T C C C G A A A C A T G

Seq ID NO: 326 Protein sequence  
 Protein Accession #: NP\_077741.1

40 1 11 21 31 41 51  
 M A A A G P R R S V R G A V C L H L L L T L V I F S R D G E A C K K V I L N V P S K L E A D K I I G R V N L E E C F R S 60  
 A D L I R S S D P D F R V L N D G S V Y T A R A V A L S D K K R S F T I W L S D K R K Q T Q K E V T V L L E H Q K K V S 120  
 45 K T R H T R E T V L R R A K R R W A P I P C S M Q E N S L G P P P L F L Q Q V E S D A A Q N Y T V F Y S I S G R G V D K 180  
 E P L N L F Y I E R D Y G N L F C T R P V D R E E Y D V F D L I A Y A S T A D G Y S A D L P L P L P I R V E D E N D N H 240  
 P V F T E A I Y N F E V L E S R R P G T T V G V V C A T D R D E P D T M H T R L K Y S I L Q Q T P R S P G L F S V H P S 300  
 T G V I T T V S H Y L D R E V V D K Y S L I M K V Q D M D G Q F F L I G T S T C I I T V T D S N D N A P T F R Q N A Y 360  
 E A F V E N A F N V E I L R I P I E D K D L I N T A N W R V N F T I L K G N E N G H F K I S T D K E T N E G V L S V V 420  
 50 K P L N Y E E N R Q V N L E I G V N N E A P F A R D I P R V T A L N R A L V T V H V R D L D E G P E C T P A A Q Y V R I 480  
 K E N L A V G S K I N G Y K A Y D P E N R N G N G L R Y K K L H D P K G W I T I D E I S G S I I T S K I L D R E V E T P 540  
 K N E L Y N I T V L A I D K D R S C T G T L A V N I E D V N D N P P E I L Q E Y V V I C K P K M G Y T D I L A V D P D 600  
 E P V H G A P F Y F S L P N T S P E I S R L W S L T K V N D T A A R L S Y Q K N A G F Q E Y T I P I T V K D R A G Q A A 660  
 T K L L R V N L C E C T H P T Q C R A T S R S T G V I L G K W A I L A I L L G I A L L F S V L L T L V C G V F G A T K G 720  
 55 K R F P E D L A Q Q N L I I S N T E A P G D D R V C S A N G F M T Q T T N N S S Q G F C G T M G S G M K N G G Q E T I E 780  
 M M K G G N Q T L E S C R G A G H H H T L D S C R G G H T E V D N C R Y T Y S E W H S F T Q P R L G E S I R G H T G

Seq ID NO: 327 DNA sequence  
 Nucleic Acid Accession #: NM\_001941.2  
 Coding sequence: 64..2754

60 1 11 21 31 41 51  
 G G C A G G T C T C G C T C T G G C A C C C T C C C G G C G C C G C G T T C T C T G G C C C T G C C C G G C A T C 60  
 C C G A T G G C C G C C G C T G G C C C G G C G C T C C G T G C G G A G C C G T C T G C C T G C A T C T G C T G 120  
 65 C T G A C C C T C G T G A T C T T C A G T C G T G A T G G T G A A G C C T G C A A A A G G T G A T A C T T A A T G T A 180  
 C C T T C T A A A C T A G A G G C A G A C A A A A T A A T T G G C A G A G T T A A T T G G A A G A G T G C T T C A G G 240  
 T C T G C A G A C C T C A T C C G G T C A A G T G A T C C T G A T T C A G A G T T C T A A T A T G A T G G G T C A G T G 300  
 T A C A C A G C C A G G C T G T T G C G C T G C T G A T A A G A A A G A T C A T T A C C A T A T G G C T T T C T 360  
 70 G A C A A A A G G A A A C A G A C A C A G A A A G A G G T T A C T G T G C T G C T A G A A C A T C A G A A G A A G G T A 420  
 T C G A A G A C A A G A C A C A T A G A A A A C T G T T C T C A G G C G T G C C A A G A G G A G A T G G G C A C C T 480  
 A T T C C T T G C T C T A T G C A A G A G A A T T C C T G G C C T T T C C C A T T G T T T C T T C A C A A A G T T 540  
 G A A T C T G A T G C A G C A C A G A A C T A T A C T G T C T T C T A C T C A A T A A G T G G A C G T G G A G T T G A T 600  
 A A A G A A C C T T T A A A T T G T T T A T A T A G A A A G A G A C A C T G G A A T C T A T T T T G C A C T C G G 660  
 75 C C T G T G G A T C G T G A A G A A T A T G A T G T T T T G A T T G A T T G C T T A T G C G T C A A C T G C A G A T 720  
 G G A T A T T C A G C A G A T C T G C C C T C C A C C A T C A G G G T A G A G G A T G A A A T G A C A A C 780  
 C A C C C T G T T T C A C A G A A G C A A T T A T A A T T T T G A A G T T T T G G A A A G T A G T A G A C C T G G T 840  
 A C T A C A G T G G G G T G G T T T G T G C C A C A G A C A G A G A T G A A C C G G A C A C A A T G C A T A C G C G C 900  
 C T G A A A T A C A G A T T T T G C A G C A G A C C C A A G G T C A C C T G G G C T T T T C T G T G A T C C C 960  
 80 A G C A C A G G C T A A T C A C C A C A G T C T C T C A T T A T T T G G A C A G A G A G G T T G T A G A C A A G T A 1020  
 T C A T T G A T A A T G A A A G T A C A G A C A T G G A T G G C C A G T T T T T G A T T G A T A G G C A C A T C A 1080  
 A C T T G T A T C A T A C A G T A A C A G A T T C A A A T G A T A A T G C A C C A C T T T C A G A C A A A A T G C T 1140  
 T A T G A A G C A T T T G T A G A G A A A A T G C A T T C A A T G T G G A A A T C T T A C G A A T A C C T A T A G A A 1200  
 G A T A A G G A T T A A T T A A C A C T G C C A A T T G G A G A T C A A T T T A C C A T T T T A A G G G A A A T 1260  
 G A A A A T G G A C A T T T C A A A A T C A G C A C A G A C A A A G A A A C T A T G A A G G T G T T C T T T C T G T T 1320

	GTAAGCCAC	TGAATTATGA	AGAAAACCGT	CAAGTGAACC	TGGAAATTGG	AGTAAACAAT	1380
	GAAGCGCCAT	TTGCTAGAGA	TATTTCCAGA	GTGACAGCCT	TGAACAGAGC	CTTGTTTACA	1440
	GTTCAATGTA	GGGATCTGGA	TGAGGGGCTT	GAATGCACCT	CTGCAGCCCA	ATATGTGCGG	1500
5	ATTAAGAAA	ACTTAGCAGT	GGGGTCAAAG	ATCAACGGCT	ATAAGGCATA	TGACCCCGAA	1560
	AATAGAAATG	GCAATGGTTT	AAGGTACAAA	AAATTGCATG	ATCCTAAAGG	TTGGATCACC	1620
	ATTGATGAAA	TTTCAGGGTC	AATCATAACT	TCCAAAATCC	TGGATAGGGA	GTTTGAAACT	1680
	CCCAAAAATG	AGTTGTATAA	TATTACAGTC	CTGGCAATAG	ACAAAGATGA	TAGATCATGT	1740
	ACTGGAACAC	TTGCTGTGAA	CATTGAAGAT	GTAAATGATA	ATCCACCAGA	AATACTTCAA	1800
10	GAATATGTAG	TCATTTGCAA	ACCAAAAATG	GGGTATACCG	ACATTTTAGC	TGTTGATCCT	1860
	GATGAACCTG	TCCATGGAGC	TCCATTTTAT	TTCAGTTTGC	CCAATACTTC	TCCAGAAATC	1920
	AGTAGACTGT	GGAGCCTCAC	CAAAGTTAAT	GATACAGCTG	CCCGTCTTTC	ATATCAGAAA	1980
	AATGCTGGAT	TTCAAGAATA	TACCATTCCCT	ATTACTGTAA	AAGACAGGGC	CGGCCAAGCT	2040
	GCAACAAAAT	TATTGAGAGT	TAATCTGTGT	GAATGTACTC	ATCCAACTCA	GTGTCGTGCG	2100
15	ACTTCAAGGA	GTACAGGAGT	AATACTTGGG	AAATGGGCAA	TCCTTGCAAT	ATTACTGGGT	2160
	ATAGCACTGC	TCTTTTCTGT	ATTGCTAATC	TTAGTATGTG	GAGTTTTTGG	TGCAACTAAA	2220
	GGGAAACGTT	TTCTTGAAGA	TTTAGCACAG	CAAACTTAA	TTATATCAAA	CACAGAAAGCA	2280
	CCTGGAGACG	ATAGAGTGTG	CTCTGCCAAT	GGATTATGA	CCCAAACTAC	CAACAACTCT	2340
	AGCCAAGGTT	TTTGTGGTAC	TATGGGATCA	GGAATGAAAA	ATGGAGGGCA	GGAAACCAAT	2400
20	GAAATGATGA	AAGGAGGAAA	CCAGACCTTG	GAATCCTGCC	GGGGGGCTGG	GCATCATCAT	2460
	ACCCCTGGAT	CCTGACAGGG	AGGACACACG	GAGGTGGACA	ACTGCAGATA	CACCTACTCG	2520
	GAGTGGCACA	GTTTACTACA	ACCCGCTCTC	GGTGA AAAAT	TGCATCGATG	TAATCAGAAT	2580
	GAAGACCGCA	TGCCATCCCA	AGATTATGTC	CTCACTTATA	ACTATGAGGG	AAGAGGATCT	2640
	CCAGCTGGTT	CTGTGGGCTG	CTGCAGTGAA	AAGCAGGAAG	AAGATGGCCT	TGACTTTTTTA	2700
25	AATAAATTGG	AACCCAAAAT	TATTACATTA	GCAGAAAGCAT	GCACAAAGAG	ATAATGTCAC	2760
	AGTGCTACAA	TTAGGTCCTT	GTGACACATT	CTGGAGGTTT	CCAAAAATAA	TATTGTAAAG	2820
	TTCAATTTC	ACATGTATGT	ATATGATGAT	TTTTTTCTCA	ATTTTGAATT	ATGCTACTCA	2880
	CCAATTTATA	TTTTTAAAGC	CAGTTGTTGC	TTATCTTTTC	CAAAAAGTGA	AAAATGTTAA	2940
	AACAGACAAC	TGGTAAATCT	CAAACCTCCAG	CACCTGGAATT	AAGGTCTCTA	AAGCATCTGC	3000
30	TCTTTTTTTT	TTTTACGAGT	ATTTTAGTAA	TAAATATGCT	GGATAAATAT	TAGTCCAAAC	3060
	ATAGCTAAGT	TATGCTAATA	TCACATTATT	ATGTATTAC	TTTAAGTGAT	AGTTTAAAAA	3120
	ATAAACAAAG	AATATTGAGT	ATCACTATGT	GAAGAAAGTT	TTGGAAAGAG	AACAATGAAG	3180
	ACTGAATTA	ATTAAAAATG	TTGCAGCTCA	TAAAGAATTG	GGACTCACCC	CTACTGCAC	3240
	ACCAAAATTC	TTTGACTTTG	GAGGCAAAAT	GTGTTGAAGT	GCCTATGAA	GTAGCAATTT	3300
35	TCTATAGTAA	TATAGTTTGA	AATAATGTG	TGTGTGTATA	TTATTATTA	TCAATGCAAT	3360
	ATTTAAAAAT	AAATGAGAAC	AAAGAGGAAA	ATGGTAAAA	CTTGAATGA	GGCTGGGGTA	3420
	TAGTTTGTCC	TACAATAGAA	AAAAGAGAGA	GCTTCCTAGG	CCTGGGCTCT	TAAATGCTGC	3480
	ATTATAACTG	AGTCTATGAG	GAATAGTTTC	CTGTCCAATT	TGTGTAATTT	GTTTAAATTT	3540
	GTAAATAAAT	TAAACTTTTC	TGGTTTCTGT	GGGAAGGAAA	TAGGGAATCC	AATGGAACAG	3600
40	TAGCTTTGCT	TTGCAGTCTG	TTTCAAGATT	TCTGCATCCA	CAAGTTAGTA	GCAAACTGGG	3660
	GAATACTGCT	TGCAGCTGGG	GTTCCCTGCT	TTTTGGTAGC	AAGGGTCCAG	AGATGAGGTG	3720
	TTTTTTTTCG	GGAGCTAATA	ACAAAAACAT	TTTTAAACTT	ACCTTTACTG	AAGTTAAATC	3780
	CTCTATTGCT	TTCTCTATTC	TCTCTTATAG	TGACCAACAT	CTTTTAAAT	TAGATCCAAA	3840
	TAACCATGTC	CTCCTAGAGT	TTAGAGGCTA	GAGGGAGCTG	AGGGGAGGAT	CTTACTGAAA	3900
45	GCACCTGGG	GAGATTGATT	GTCCCTTAAAC	CTAAGCCCCA	CAAACTTGAC	ACCTGATCAG	3960
	GTCTGGGAG	TACAAAATTT	CATTTTTCTC	CTCACTGCCC	TTCTTCTGAG	TGGCATTGGC	4020
	CTGAATCAAG	GAAAGCCAGG	CCTTGTGGGC	CCCCTTCTTT	CGGCTTCTG	CTAAAGCAAC	4080
	ACCTCCAGCA	GAGATTCCTT	TAAGTGACTC	CAGGTTTTCC	ACCATCCTTC	AGCGTGAATT	4140
	AATTTTTAAT	CAGTTTGCTT	TCTCCAGAGA	AATTTTTAAA	TAATAGAAGA	AATAGAAATT	4200
50	TTGAATGTAT	AAAAGAAAAA	GATCAAGTTG	TCAATTTAGA	ACAGAGGGAA	CTTTGGGAGA	4260
	AAGCAGCCCA	AGTAGGTTAT	TTGTACAGTC	AGAGGGCAAC	AGGAAGATGC	AGGCCTTCAA	4320
	GGGCAAGGAG	AGGCCACAAG	GAATATGGGT	GGGAGTAAAA	GCAACATCGT	CTGCTTCATA	4380
	CTTTTTCCTA	GGCTTGGCAC	TGCCTTTTCC	TTTCTCAGGC	CAATGGCAAC	TGCCATTGGA	4440
	GTCCGGTAG	GGATCAGCCA	ACCTCTTCTC	TATGGCTCAC	CTTATTTGGA	GTGAGAAATC	4500
55	AAGGAGACAG	AGCTGACTGC	ATGATGAGTC	TGAAGGCATT	TGCAGGATGA	GCCTGAACTG	4560
	GTTGTGCAGA	ACAAACAAGG	CATTCAATGG	AATTGTTGTA	TTCTTCTGTC	AGCCCTCCTT	4620
	CTGGGCCTA	AGAAGGCTTA	TGAATTAAT	GCCTATCTAA	AATTCTGATT	TATTCCTACA	4680
	TTTTCTGTTT	TCTAATTTTG	CCCTAAAAATC	TATGTGTTTT	AGACTTAGAC	TTTTTATTGC	4740
	CCCCCCCCC	TTTTTTTTTG	AGACGGAGTC	TCGCTCTGAC	GCACAGGCTG	GAGTGCAGTG	4800
60	GCTCCGATCT	CTGCTCACTG	AAAGCTCCGC	CTCCCGGTTT	CATGCCATTC	TCCTGCCTCA	4860
	GCCTCCTGAG	TAGCTGGGAC	TACAGGCGCC	CACCACCACG	CCCGGCTAAT	TTTTTGTATT	4920
	TTTAATAGAG	ACGGGGTTTC	ACTGTGTTAG	CCAGGATGGT	CTCGATCTCC	TGACCTCGTG	4980
	ATCCGCTGTC	CTCGGCTTCC	CAAAGTGCTG	GGATTACAGG	CATGACCCAC	CGCTCCCGGC	5040
	CTTGTTTTCG	GTCTTAAAGT	GTCTTCTTTT	AATGTAATCA	TTTTGAACAT	GTGTGAAAGT	5100
65	TGATCATACG	AATTGGATCA	ATCTTGAAT	ACTCAACCAA	AAGACAGTCG	AGAAGCCAGG	5160
	GGGAGAAAGA	ACTCAGGGCA	CAAAATATTG	GTCTGAGAA	GGAAATCTCT	GTAAGCCTAG	5220
	TTGCTGAAAT	TTCTGCTGT	AACCAGAAAG	CAGTTTATAT	TAACGGCTAC	TGAAACACCC	5280
	ACTGTGTTTT	GCTCACTCCC	TCACTCACCG	ATCAAAACCT	GCTACCTCCC	CAAGACTTTA	5340
	CTAGTGCCGA	TAAACTTTCT	CAAAGAGCAA	CCAGTATCAC	TTCCCTGTTT	ATAAAACCTC	5400
70	TAACCATCTC	TTTGTCTTTT	GAACATGCTG	AAAACCACTT	GGTCTGCATG	TATGCCCGAA	5460
	TTTGTAATCT	TTTTCTCTCA	AATGAAAAAT	TAATTTTAGG	GATTCAATTC	TATATTTTCA	5520
	CATATGTAGT	ATTATTTATT	CCTTATATGT	GTAAGGTGAA	ATTATGGTGA	TTTGAGTGTG	5580
	CAAGAAAATA	TATTTTAAAA	GCTTTTCAAT	TTCCCCAGT	GAATGATTGA	GAATTTTTTA	5640
	TGTAAATATA	CAGAATGTTT	TTTCTTACTT	TTATAAGGAA	GCAGCTGTCT	AAAAATGCAGT	5700
75	GGGGTTTGT	TTGCAATGTT	TTAAACAGAG	TTTTAGTATT	GCTATTAAAA	GAAGTTACTT	5760
	TGCTTTTAAA	GAAACTTGGC	TGCTTAAAA	AAGCAAAAAT	TGGATGCATA	AAGTAATATT	5820
	TACAGATGTG	GGGAGATGTA	ATAAAACAAT	ATTAACCTGG	TTTCTTGTGT	TTGCTGTATT	5880
	TAGAGATTAA	ATAATTCTAA	GATGATCACT	TTGCAAAAAT	ATGCTTATGG	CTGGCATGGA	5940
	AATAGAAATA	CTCAATTATG	TCTTTGTTGT	ATTAATGGGG	AATATTTTGG	ACAATGTTTC	6000
80	ATTATCAAA	TGTCGACATC	ATTAATATAT	ATTGTAATGT	TGGGAAGAGA	TCACTATTTT	6060
	GAAGCACAGC	TTTACAGATG	AGTATCTATG	ATACATATGT	ATAATAAAT	TTGATCGGGT	6120
	ATTTAAAGTA	TTAGAAGGGT	GTTATAATTG	CAGAGTATTC	CATGAATAGT	ACACTGACAC	6180
	AGGGGTTTTA	TCTTGAAGTC	CAGTGATGTC	AAGGGAAAA	ATGAGTTAAA	AAGAAAAGCA	6240
	GGCAATATTG	CAGTCTTGAT	TCTGCCACTT	ACAGGATAGA	TAATGCCTGA	ACTTTAATGA	6300
	CAAGATGATC	CAACCATAAA	GGTGCTCTGT	GCTTCACAGT	GAATCTTTTC	CCCATGCAGG	6360

AGTGTGCTCC CCTACAAACG TTAAGACTGA TCATTTCAAA AATCTATTAG CTATATCAAA 6420  
 AGCCTTACAT TTTAATATAG GTTGAACCAA AATTTCAATT CCAGTAACTT CTATTGTAAC 6480  
 CATTATTTTT GTGTATGTCT TCAAGAATGT TCATTGGATT TTTGTTTGTA ATAGTAAAT 6540  
 ACCGGATACA TTTCACGTGT CCTTCAGTAT TGATTGGGT GAATATTGGG TCATAATGGT 6600  
 TGAGAAGCAT GGACACTAGA GCCAGAATGC TTGGATATGA ATCCTGGATC TGTCACTTAC 6660  
 TTCTGTGTGA CCTTTGAAAG GCTACTTATT TCCTCTCTTA GCTTCTCAT TAAAAATCAAT 6720  
 GAACAATGCC AGCCTCATGG GGTGTGTGAA TGATTAAAT AGTTAATATA CCTAAAGTAC 6780  
 ATAGAACACT GCCTGCACAT AGTAAAAGAA TTATAAGTGT GAGGTAGTTG GTAAAATTAT 6840  
 GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTTT AGGGAATAA AGTTTGTGCA 6900  
 TATATATAAT CCCGAAACAT G

Seq ID NO: 328 Protein sequence  
 Protein Accession #: NP\_001932.1

1 11 21 31 41 51  
 | | | | |  
 MAAAGPRRSV RGAVCLHLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS 60  
 ADLIRSDPD FRVLNDGSVY TARAVALSDK KRSFTIWLSD KKKQTQKEVT VLEHQKKVS 120  
 KTRHRTRETV RRAKRRWAPI PCSMQENSLG PFFLFLQQVE SDAAQNYTVF YSISGRGVDK 180  
 EPLNLFYIER DTGNLFCRTP VDREYDVFD LIAYASTADG YSADLPLPLP IRVEDENDNH 240  
 PVFTEAIYNF EVLESSRPGT TVGVVCATDR DEPDTHMTRL KYSILQOTPR SPGLFSVHPS 300  
 TGVITTVSHY LDREVVDKYS LIMKVQDMDG QFFGLIGTST CIITVTDSND NAPTFRQNAV 360  
 EAFVEENAFN VEILRIPIED KDLINTANWR VNFTILKNE NGHFKISTDK ETNEGVLSVV 420  
 KPLNYEENRQ VNLEIGVNEE APPARDIPRV TALNRALVTV HVRDLDEGPE CTAAQYVRI 480  
 KENLAVGSKI NGYKAYDPEN RGNGLRYKK LHDPKGWITI DEISGSITS KILDREVETP 540  
 KNELYNITVL AIDKDDRSCT GTLAVNIEDV NDNPPAILQE YVICKPKMG YTDILAVDPD 600  
 EPVHGAPFYF SLPNTSPEIS RLWSLTKVND TAARLSYQKN AGFQEYTIPI TVKDRAGQAA 660  
 TKLLRVNLCE CTHPTQCRAT SRSTGVILKG WAILAILGI ALLFSVLLTL VCGVFGATKG 720  
 KRFPEDLAQQ NLIISNTPEAP GDDRVCSANG FMTQTTNNS QGFCGTMSGG MNNGGQETIE 780  
 MMKGQNQILE SCRAGHHHT LDSCRGGHTE VDNCRITYSE WHSFTQPRLG EKLHRCNQNE 840  
 DRMPSQDYVL TYNYEGRGSP AGSVGCCSEK QEEDGLDFLN NLEPKFITLA EACTKR

Seq ID NO: 329 DNA sequence  
 Nucleic Acid Accession #: NM\_016583.2  
 Coding sequence: 72..842

1 11 21 31 41 51  
 | | | | |  
 GGAGTGGGGG AGAGAGAGGA GACCAGGACA GCTGCTGAGA CCTCTAAGAA GTCCAGATAC 60  
 TAAGAGCAA GATGTTTCAA ACTGGGGGCC TCATTGTCTT CTACGGGCTG TTAGCCCGAGA 120  
 CCATGGCCCA GTTTGGAGGC CTGCCGTGTC CCCTGGACCA GACCCGTGCC TTGAATGTGA 180  
 ATCCAGCCCT GCCCTTGAGT CCCACAGGTC TTGCAGGAAG CTTGACAAAT GCCCTCAGCA 240  
 ATGGCCTGCT GTCTGGGGGC CTGTTGGGCA TTCTGGAAAA CCTTCCGCTC CTGGACATCC 300  
 TGAAGCCTGG AGGAGGTACT TCTGTTGGCC TCCTTGGGGG ACTGCTTGGA AAAGTGACGT 360  
 CAGTGATTCC TGGCCTGAAC AACATCATTG ACATAAAGGT CACTGACCCC CAGCTGCTGG 420  
 AACTTGGCCT TGTGCAGAGC CCTGATGGCC ACCGTCTCTA TGTACCATC CCTCTCGGCA 480  
 TAAAGCTCCA AGTGAATACG CCCCTGGTCG GTGCAAGTCT GTTGAGGCTG GCTGTGAAGC 540  
 TGGACATCAC TGCAGAAATC TTAGCTGTGA GAGATAAGCA GGAGAGGATC CACCTGGTCC 600  
 TTGTTGACTG CACCCATTCC CTGGAAGGCC TGCAAATTTT TCTGCTTGAT GGAATTGGCC 660  
 CCTCCCCAT TCAAGTCTCT CTGACAGGCC TCACAGGGAT CTGAATAAA GTCCCTGCCTG 720  
 AGTTGGTTCA GGGCAACGTG TGCCCTCTGG TCAATGAGGT TCTCAGAGGC TTGGACATCA 780  
 CCTCTGTGCA TGACATTGTT AACATGCTGA TCCACGGACT ACAGTTTGTC ATCAAGGTCT 840  
 AAGCCTTCCA GGAAGGGGCT GGCCTCTGCT GAGCTGCTTC CCAGTGCTCA CAGATGGCTG 900  
 GCCCATGTGC TGAAGATGA CACAGTTGCC TTCTCTCCGA GGAACCTGCC CCTCTCCTT 960  
 TCCACCAGG CGTGTGTAAC ATCCCATGTG CCTCACCTAA TAAATGGCT CTCTCTCTGC 1020  
 AAAAAAAAA AAAAAAAAA AAAAAAAAA

Seq ID NO: 330 Protein sequence  
 Protein Accession #: NP\_057667.1

1 11 21 31 41 51  
 | | | | |  
 MFQTGGLIVF YGLLAQTMAG FGGFLVPLDQ TLPLNVNPAL PLSFTGLAGS LTNALSNGLL 60  
 SGGLLGILEN LPLLDILKPG GGTSGGLLGG LLGKVTSVIP GLNNIIDIKV TDPQLLELGL 120  
 VQSPDGHRLY VTIPGLIKLQ VNTPLVGASL LRLAVKLDIT AEILAVRDQ ERIHLVLGDC 180  
 THSPGSLQIS LLDGLPLPI QGLLDLSLTGI LNKVLPVLVQ GNVCPVNEV LRGLDITLVH 240  
 DIVNMLIHGL QFVIKV

Seq ID NO: 331 DNA sequence  
 Nucleic Acid Accession #: NM\_004363.1  
 Coding sequence: 115..2223

1 11 21 31 41 51  
 | | | | |  
 CTCAGGGCAG AGGGAGGAAG GACAGCAGAC CAGACAGTCA CAGCAGCCTT GACAAAACGT 60  
 TCCTGGAAC CAAGCTCTTC TCCACAGAGG AGGACAGAGC AGACAGCAGA GACCATGGAG 120  
 TCTCCCTAGT CCCCTCCCCA CAGATGCTGC ATCCCTGGC AGAGGCTCCT GCTCACAGCC 180  
 TCACTTCTAA CCTTCTGAA CCCGCCACC ACTGCCAAGC TCACTATTGA ATCCACGCCG 240  
 TTCAATGTCG CAGAGGGGAA GGAGGTGCTT CTACTTGTC ACAATCTGCC CCAGCATCTT 300  
 TTTGGTACA GCTGTACAA AGGTGAAAGA GTGGATGGCA ACCGTCAAAT TATAGGATAT 360  
 GTAATAGGAA CTAACAAGC TACCCAGGG CCCGCATACA GTGGTCGAGA GATAATATAC 420  
 CCCAATGCAT CCTGCTGAT CCAGAATATC ATCCAGAATG ACACAGGATT CTACACCTTA 480



CACGTCTATAA AGTCAGATCT TGTGAATGAA GAAGCAACTG GCCAGTTCGG GGTATACCCG 540  
 GAGCTGCCCCA AGCCCTCCAT CTCCAGCAAC AACTCCAAAC CCGTGGAGGA CAAGGATGCT 600  
 GTGGCCCTTCA CCTGTGAACC TGAGACTCAG GACGCAACCT ACCTGTGGTG GGTAAACAAT 660  
 CAGAGCCTCC CGGTAGTCC CAGGCTGCAG CTGTCCAATG GCAACAGGAC CCTCACTCTA 720  
 5 TTCAATGTCA CAAGAAATGA CACAGCAAGC TACAAATGTG AAACCCAGAA CCCAGTGAGT 780  
 GCCAGGGCGCA GTGATTCACT CATCCTGAAT GTCTCTATG GCCCGGATGC CCCACCCATT 840  
 TCCCTCTTAA ACACATCTTA CAGATCAGGG GAAAATCTGA ACCTCTCTCT CCACGCAGCC 900  
 TCTAACCCAC CTGCACAGTA CTCTTGGTTT GTCAATGGGA CTTTCCAGCA ATCCACCCAA 960  
 10 GAGCTCTTTA TCCCCAACAT CACTGTGAAT AATAGTGGAT CCTATACGTG CCAAGCCCAT 1020  
 AACTCAGACA CTGGCCTCAA TAGGACCACA GTCCAGCAGA TCACAGTCTA TGCAGAGCCA 1080  
 CCCAAACCCCT TCATCACCAG CAACAACCTC AACCCTGTGG AGGATGAGGA TGCTGTAGCC 1140  
 TTAACCTGTG AACCTGAGAT TCAGAACACA ACCTACCTGT GGTGGGTAAA TAATCAGAGC 1200  
 CTCCCGGTCA GTCCAGGCT GCAGCTGTCC AATGACAACA GGACCTCAC TCTACTCAGT 1260  
 15 GTCACAAGGA ATGATGTAGG ACCCTATGAG TGTGGAATCC AGAACGAATT AAGTGTGAC 1320  
 CACAGCGACC CAGTCACTCT GAATGTCTCT TATGGCCAG ACGACCCAC CAATTCCCCC 1380  
 TCATACACCT ATTACCTCC AGGGGTGAAC CTCAGCCTCT CCTGCCATGC AGCCTCTAAC 1440  
 CCACCTGCAC AGTATTCTTG GCTGATTGAT GGGAACTACC AGCAACACAC ACAAGAGCTC 1500  
 TTTATCTCCA ACATCACTGA GAAGAACAGC GGACTCTATA CCTGCCAGGC CAATAACTCA 1560  
 20 GCCAGTGGCC ACAGCAGGAC TACAGTCAAG ACAATCAGAG TCTCTGCGGA GCTGCCCCAAG 1620  
 CCCTCCATCT CCAGCAACAA CTCCAAACCC GTGGAGGACA AGGATGTCTGT GGCCTTCACC 1680  
 TGTGAACCTG AGGCTCAGAA CACAACCTAC CTGTGGTGGG TAAATGGTCA GAGCCTCCCA 1740  
 GTCAGTCCCA GGCTGCAGCT GTCCAATGGC AACAGGACCC TCACTCTATT CAATGTCA 1800  
 AGAAATGAGC CAAGAGCCTA TGTATGTGGA ATCCAGAACT CAGTGAGTGC AAACCGCAGT 1860  
 25 GACCCAGTCA CCCTGGATGT CCTCTATGGG CCGGACACCC CCATCATTTT CCCCCCAGAC 1920  
 TCGTCTTACC TTTCCGGAGC GAACCTCAAC CTCTCCTGCC ACTCGGCCCTC TAACCCATCC 1980  
 CCGCAGTATT CTTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTTATC 2040  
 GCCAAATCA CGCCAAATAA TAACGGGACC TATGCCTGTT TTGCTCTTAA CTTGGCTACT 2100  
 GGCCGCAATA ATTCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCCTGGT 2160  
 30 CTCTCAGCTG GGGCCACTGT CGGCATCATG ATTGGAGTGC TGGTTGGGGT TGCTCTGATA 2220  
 TAGCAGCCCT GGTGTAGTTT CTTCAATTTCA GGAAGACTGA CAGTTGTTT GCTTCTCTCT 2280  
 TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTTCTTT ACCAAGGATA TTTACAGAAA 2340  
 AGACTCTGAC CAGAGATCGA GACCATCTTA GCCAACATCG TGAAACCCCA TCTCTACTAA 2400  
 AAATACAAA ATGAGCTGGG CTGTGTGGCG CGCACTCTGA GTCCAGTTA CTCGGGAGGC 2460  
 35 TGAGGCAGGA GAATCGCTTG AACCGGGAG GTGGAGATTG CAGTGAGCCC AGATCGCACC 2520  
 ACTGCACTCC AGTCTGGCAA CAGAGCAAGA CTCATCTCA AAAAGAAAAG AAAAGAAGAC 2580  
 TCTGACCTGT ACTCTGAAT ACAAGTTTCT GATACCACTG CACTGTCTGA GAATTTCCAA 2640  
 AACTTTAATG AACTAACTGA CAGCTTCATG AAAGTGTCCA CCAAGATCAA GCAGAGAAAA 2700  
 TAATTAATTT CATGGGACTA AATGAAGTAA TGAGGATTGC TGATTTCTTA AATGTCTTGT 2760  
 40 TTCCAGATT TCAGGAAACT TTTTCTTTT TAAGCTATCC ACTCTTACAG CAATTGATA 2820  
 AAATATACCT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTCGCTCC 2880  
 AGACTTGGGA AACTATTCTA GAATATTTAT ATTGTATGTT AATATAGTTA TTGCACAAGT 2940  
 TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

Seq ID NO: 332 Protein sequence  
 Protein Accession #: NP\_004354.1

1 11 21 31 41 51  
 | | | | |  
 50 MESPSAPPHR WCIPIWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLVHNLPO 60  
 HLEFGYSWKY ERVDGNRQII GYVIGTQOAT PGPAYSGREI IYPNASLLIQ NIIQNDTGFY 120  
 TLHVIKSDLV NEEATGQFRV YPELPKPSIS SNNSKPVEDK DAVAFTECEPE TQDATYLWVW 180  
 NNQSLVPSPR LQLSNGNRTL TLFNVTRNDT ASYKCEQNP VSARRSDSVI LNVLYGPDAP 240  
 TISPLNTSYR SGENLNLSC AASNPPAQYS WFNVTGQQS TQELFIPNIT VNNSSGYTCQ 300  
 55 AHNSDTGLNR TTVTTITVYA EPPKPFITSN NSNPVEDEDA VALTCEPEIQ NTYLVWVNN 360  
 QSLFVSPRLQ LSNDRNLTL LSVTRNDVGP YECGIONELS VDHSDPVILN VLYGPDPTI 420  
 SPSYTYRPG VNLSSLCHAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480  
 NSASGHSRTT VKTITVSAEL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLVWVNGQS 540  
 LPVSPRLQLS NGNRTLLEN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPTIISP 600  
 60 PDSSYLSGAN LNLSCSASN PSPQYSWRIN GIPQHTQVL FIAKITPNMN GTYACFVSNL 660  
 ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

Seq ID NO: 333 DNA sequence  
 Nucleic Acid Accession #: NM\_006952.1  
 Coding sequence: 11..793

1 11 21 31 41 51  
 | | | | |  
 65 AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTTGC TTCCAGGGCC TGCTGATTTT 60  
 TGGAAATGTG ATTATTTGTT GTTGCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120  
 70 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACACAGATG ACATCTATGG 180  
 GGCTGCCCTGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCCTGTCTG TTCTAGGCAT 240  
 TGTAGGCATC ATGAAGTCCA GCAGGAAAAA TCTTCTGGCG TATTTTCATC TGATGTTTAT 300  
 AGTATATGCC TTTGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360  
 75 ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACACACGCC CTCCAAACAA 420  
 TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480  
 CAATTGCTGT GGCCTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540  
 TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600  
 AGAACCTCTC AACCTGGAGG CTGTGAAACT AGGCGTGCCT GGTTTTATAT ACAATCAGGG 660  
 80 CTGCTATGAA CAGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CTGGTTTGG 720  
 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTGGGT ACCATGTTCT ACTGAGCAG 780  
 AATTGAATAT TAAGAA

Seq ID NO: 334 Protein sequence  
 Protein Accession #: NP\_008883.1

1 11 21 31 41 51  
 5 MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60  
 IGIFVGICLF CLSVLGIIVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTPNL 120  
 FLKQMLERYQ NNSPPNNDQ WKNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAFRTENN 180  
 DADYPWPRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAVFGFAI 240  
 LCWTFWVLLG TMFYWSRIEY

10 Seq ID NO: 335 DNA sequence  
 Nucleic Acid Accession #: NM\_002638.1  
 Coding sequence: 120..473

1 11 21 31 41 51  
 15 CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CCGCCCTGGA GCCAGGCCAA 60  
 GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120  
 TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCCTCAT CGCTGGGACG CTGGTTCTAG 180  
 20 AGGCAGCTGT CACGGGAGTT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCCTAT 240  
 TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300  
 CGCAAGAGCC AGTCAAAGGT CCACTCTCCA CTAAGCCTGG CTCTGCCCC ATTATCTTGA 360  
 TCCGGTGCAG CATGTTGAAT CCCCCTAACC GCTGCTTGAA AGATACTGAC TGCCACGGAA 420  
 TCAAGAAAGT CTGTGAAGGC TCTTGCCGGA TGGCCTGTTT CGTTCCCCAG TGAAGGGAGC 480  
 25 CGGTCTCTGC TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCATCTGGT CCTAAGTCCC 540  
 TGCTGCCCTT CCCTTCCCA CACTGTCCAT TCTTCTCCC ATTCAAGATG CCCACGGCTG 600  
 GAGCTGCCTC TCTCATCCAC TTTCATAATA A

30 Seq ID NO: 336 Protein sequence  
 Protein Accession #: NP\_002629.1

1 11 21 31 41 51  
 35 MRASSFLIVV VFLLIAGTLVL EAAVTGVFVK GQDITVKGRVP FNGQDPVKGQ VSVKGQDKVK 60  
 AQEPVKGPVS TKPGSCPIIL IRCAMLNPPN RCLKDITDCPG IKKCEGSCG MACFVVPQ

Seq ID NO: 337 DNA sequence  
 Nucleic Acid Accession #: NM\_001793.2  
 Coding sequence: 71..2560

40 1 11 21 31 41 51  
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCGTGC CCGCAGCTGCT TCACCCCTCT 60  
 CTCTGCAGCC ATGGGGCTCC CTCGTGGACC TCTCGCGTCT CTCCTCCTTC TCCAGGTTTG 120  
 45 CTGGCTGCAG TGCGCGGCTC CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180  
 CTGGAGGCGG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG 240  
 CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300  
 TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360  
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420  
 TGAAAATGGC AAGGTCCTCT TCCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480  
 50 AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540  
 CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600  
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGAG AATGGTGCTT CAGTGGAGGA 660  
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720  
 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAGGT 780  
 55 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840  
 CCATAGCCAA GAACCAAGAG ACCCACACGA CCTCATGTTT ACCATTACCC GGAGCACAGG 900  
 CACCATCAGC GTCACTCTCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960  
 CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020  
 60 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080  
 GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140  
 CAACTCACCA CGGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200  
 TACCATCACC ACCCACCTTG AGAGCAACCA GGGCATCTCT ACAACCAGGA AGGGTTTGGA 1260  
 TTTTGAGGCC AAAAACCAGC ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320  
 65 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380  
 ACCTGTGTTT GTCCCCACCT CCAAGATCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440  
 GCCTGTGTGT GTCTACACTG CAGAAAGACC TGACAAGGAG AATCAAAAAGA TCAGCTACCG 1500  
 CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTCAACGC 1560  
 70 TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTGTGAGG AACACATCT ATGAAGTCTAT 1620  
 GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680  
 ACTGATTGAT GTCAATGACC ATGGCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740  
 75 CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800  
 CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860  
 GGAAGGTGAC ACAGTGTGCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920  
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980  
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCCT 2040  
 80 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGTTGCTGC TTTTGTGGT 2100  
 GAGAAAGAAG CGGAAGATCA AGGAGCCCTT CCTACTCCCA GAAGATGACA CCGTGACAA 2160  
 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220  
 GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGACG TGGCACCAAC 2280  
 CATCATCCCG ACACCCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCACTT 2340  
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCAAC GCCCGGCCCT ACGACACCTT 2400  
 CTTGGTGTTC GACTGTGAGG GCAGCGGCTC CGACGCGCGT TCCTGTAGCT CCCTCACCTC 2460  
 CTCGCGCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTCAA 2520  
 GAAGCTGGCA GACATGTACG GTGCGGGGGA GGACGACTAG GCGGCCCTGC TGCAGGGCTG 2580

GGGACCAAAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTCAGCTGAG 2640  
 GACTTCGGAG CTTGTGACAG AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700  
 ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760  
 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCTCAG AGGCCAAGTT TCCAGAAGCC 2820  
 TCTTACCTGC CGTAAATGC TCAACCCTGT GTCCTGGGCC TGGGCTGCT GTGACTGACC 2880  
 TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940  
 TTTTTTAAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000  
 GCTGGGCCCA CTGGCCGTCC TGCATTCTG GTTCCAGAC CCAATGCCT CCCATTCGGA 3060  
 TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTGACC CCTTATTTT TATTTTCCCT 3120  
 GTTGCGTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTATTTAT 3180  
 TAAAGAAACT TTTCCAGAA AAAAA

Seq ID NO: 338 Protein sequence  
 Protein Accession #: NP\_001784.2

1 11 21 31 41 51  
 | | | | |  
 MGLPRGPLAS LLLQLVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120  
 KGFFPQRLNQ LKSNKORDTK IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREEIAK 180  
 YELFHGAHVE NGASVEDPMN ISIIITDQND HKPKFTQDTF RGSVLEGLVP GTSVMQVTAT 240  
 DEDDAIYTYN GVVAYSISHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TDMGDGSGTT TAVAVVEILD ANDNAPMFDP QKYEAVHPEN AVGHEVQRLT VTDLDAPNSP 360  
 AWRATYLMIG GDDGDHFTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDDPKE NQKISYRILR 480  
 DPAGWLAMD PDSQVTVAGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLD 540  
 VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPHTSPPQ AQLTDDSDIY WTAEVNEEGD 600  
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL 660  
 GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFF YGEEGGGEED QDYDITQLHR 720  
 GLEARPEVVL RNDVAPTII TPMPYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
 DYEAGSGDAA SLSSLTSSAS DQDQDYDLYN EWGSRFKKLA DMYGGGEDD

Seq ID NO: 339 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..672

1 11 21 31 41 51  
 | | | | |  
 ATGAGGCTCC AAAGACCCCG ACAGGCCCCG GCGGGTGGGA GGCGCGCGCC CCGGGGCGGG 60  
 CGGGGCTCCC CCTACCGGCG AGACCCGCGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG 120  
 AAGGGCGGGG AGGGGGCGCC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GACGATGGCG 180  
 CTGCTCGCCT TGCTGCTGGT CGTGCCCTTA CCGCGGTGT GGACAGACGC CAACCTGACT 240  
 GCGAGACAA CAGATCCAGA GGACTCCCGA CGAACGACG AGGGTGACAA TAGAGTGTGG 300  
 TGTCATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAAAATGG 360  
 ACAGAGCCAT ACTGGCTTAT AGCGGCCGTG AAAATATTTC CACGTTTTTT CATGGTTGCG 420  
 AAGCAGTGCT CCGCTGGTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480  
 CTCCTGGAAG AGCCCATGCC CTTCTTTTAC CTCAGTGTGT GTAAATTCG CTAAGTCAAT 540  
 TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAA ATGCTGGGAG CATGGGTGAG 600  
 AGCTGTGGTG GGCTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGCGCTC 660  
 AGCCTGTCTT GA

Seq ID NO: 340 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 MRLQRPRQAP AGRRRAPRGG RGSFYRPDPG RGARRLRRFQ KGGEGAPRAD PPWAPLGTMA 60  
 LLALLLVVAL PRVWTDANLT ARQRPEDSQ RTDEGDNRVW CHVCERENTF ECQNP RRCKW 120  
 TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKPEEKRF LLEPMPPFFY LKCKKIRYCN 180  
 LRGPPINSSV FKEYAGSMGE SCGGLNLAIL LLLASIAAGL SLS

Seq ID NO: 341 DNA sequence  
 Nucleic Acid Accession #: XM\_035292.2  
 Coding sequence: 53..1576

1 11 21 31 41 51  
 | | | | |  
 GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60  
 TGCGGGGCCC AAGCGGCGCG CGCTAGCGGC GCCGCGCGCC GAGGAGAAGG AAGAGGCGCG 120  
 GGAGAAGATG CTGGCCGCCA AGAGCGCGGA CGGCTCGGCG CCGGCGAGCG AGGGCGAGGG 180  
 CGTGACCTCG CAGCGGAACA TCACGCTGCT CAACGCGGTG GCCATCATCG TGGGGACCAT 240  
 TATCGGCTCG GGCATCTTCG TGACGCCCAC GGGCGTGCTC AAGGAGGCAG GCTCGCGGGG 300  
 GCTGGCGCTG GTGGTGTGGG CCGCGTGCGG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360  
 CGCGGAGCTC GGCACCAACA TCTCAAATC GGGCGGCGAC TACGCTTACA TGCTGGAGGT 420  
 CTACGGCTCG CTGCCCGCTC TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGCGCTTC 480  
 ATCGCAGTAC ATCGTGGGCC TGGTCTTCGC CACCTACCTG CTCAGCCGCG TCTTCCCCAC 540  
 CTGCCCGGTG CCCGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600  
 GGCCGTGAAC TGCTACAGCG TGAAGGCCGC CACCGGGTGC CAGGATGCCT TTGCCGCCGC 660  
 CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720  
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACCTGATG TGGGGAACAT 780  
 TGTGCTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGGAAATFACT TGAATTTCTG 840  
 CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTCG GCCATCATCA TCTCCCTGCC 900  
 CATCGTGACG CTGTTGTAGC TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCACCCGA 960  
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGAATTCGGG AACTATCACC TGGCGCTCAT 1020

5  
10

```

GTCCTGGATC ATCCCCGTCT TCGTGGGCCT GTCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
GTTACATACC TCAGGGTCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
CTCCATGATC CACCCACAGC TCCTCACCCC CGTGGCGTCC CTCTGTGTCA CGTGTGTGAT 1200
GACGCTGCTC TAGCCTTCTT CCAAGGACAT CTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TCGGTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCTGCCT GTGTTCTTCA TCCTGGCCTG 1380
CCTCTTCTG ATCGCGTCT CCTTCTGGAA GACACCGTG GAGTGTGGCA TCGGCTTCAC 1440
CATCATCCTC AGCGGGCTGC CCGTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA 1500
GTGGCTCCTC CAGGGCATCT TCTCCAGCAC CGTCTGTGT CAGAAGCTCA TGCAGGTGGT 1560
CCCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC

```

Seq ID NO: 342 Protein sequence  
Protein Accession #: XP\_035292.2

15  
20  
25

```

1      11      21      31      41      51
|      |      |      |      |      |
MAGAGPKRRA LAAPAAEKEE BAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYABLGTTI SKSGGDYAYM 120
LEVVGSLPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVEEEA AKLVACLCLVL 180
LLTAVNCYSV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV 240
GNIVLALYSG LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
STEMLSSEA VAVDFGNYHL GVMSWIIIPV VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360
SILSMIHQPL LTPVPSLVFT CVMTLLYAFS KDIFSVINFF SFFNWLCLVAL AIIIGMIWLRH 420
RKPELERPIK VNLALPVFFI LACLELIAVS FWKTPVECGI GFTIILSGLP VYFFGVWVWKN 480
KPKWLLQGIF STTVLCQKLM QVVPQET

```

Seq ID NO: 343 DNA sequence  
Nucleic Acid Accession #: NM\_005268.1  
Coding sequence: 168..989

30  
35  
40  
45  
50  
55

```

1      11      21      31      41      51
|      |      |      |      |      |
TAAAAAGCAA AAGAATTCGC GGCCGCGTCG ACACGGGCTT CCCCAGAAAC CTTCCCCGCT 60
TCTGGATATG AAATTCAGAG TGCTTGCTGA GTCCTATTGC CGGCTGCTGG GAGCCAGGAG 120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGCGTGG GTCCACCATG AACTGGAGTA 180
TCTTTGAGGG ACTCCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGCTCTCGGT CTTCATCTTC CGCGTGCTGG TGTACCTGGT GACGGCCGAG CGTGTGTGGA 300
GTGATGACCA CAAGGACTTC GACTGCAATA CTCGCCAGCC CGGCTGCTCC AACGCTGTCT 360
TTGATGAGTT CTTCCCTGTG TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420
CATGCCCTC ACTGCTCGTG GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTTACCT GAACCCCGGC AAGAAGCGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAG GGCGAGCGTG GACATCGCCT 600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCCTCCTGTG GTCAAGTGCC 660
ACGCAGATCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAACA 720
TTTTACCCCT CTTATGGTG GCCACAGCTG CCATCTGCAT CTGCTCAAC CTCGTGGAGC 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCTGGC AGCAAGGAAA GCTCAAGCCA 840
TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTTCTTG CAAACAAGAC GACCTCCTTT 900
CGGGTGACCT CATCTTCTG GGTCTAGACA GTCATCTCTC TCTCTTACCA GACCGCCCCC 960
GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCCTG GACTGGTCTG GCAGGTTGGG 1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGGTAG GGGCAGGCAA GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCTAGTCC 1140
TCAACTCCAG CCACCTGCC CAGCTCGACG GCACTGGGCC AGTTCCTCCCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTTCTAGA ATGGAATAG TGAGGGCCAA TGC

```

Seq ID NO: 344 Protein sequence  
Protein Accession #: NP\_005259.1

60  
65

```

1      11      21      31      41      51
|      |      |      |      |      |
MNWSIFEGLL SGVNYSTAF GRIWLSLVI FRVLVYLVA ERVWSDHDKD FDCNTRQPGC 60
SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRHREAHG ENSGRLYLNP 120
GKKRGGWLWT YVCSLVFKAS VDIAPLYVFH SFYPKYLPP VVKCHADPCP NIVDCFISKP 180
SEKNIFTLFM VATAAICILL NLVELIYLV KRCHECLAAR KQAMCTGHH PHGTTSSCKQ 240
DDLSSGLDIF LGSDSHPLLL PDRPRDHVKK TIL

```

Seq ID NO: 345 DNA sequence  
Nucleic Acid Accession #: NM\_002391.1  
Coding sequence: 26..457

70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCCTCTCTC TCACCCCTCCT 60
CGCCCTGCTG GCGCTCACCT CCGCGGTGCG CAAAAGAGAA GATAAGGTGA AGAAGGGCGG 120
CCCGGGGAGC GAGTGCGCTG AGTGGGCTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GGGCCAGACC CAGCGCATCC GGTGCAGGGT 240
GCCCTGCAAC TGGAGAAGG AGTTTGAGC CGACTGCAAG TACAAGTTTG AGAACTGGGG 300
TGCGTGTGAT GGGGGCACAG GCACCAAGT CCGCCAAGGC ACCCTGAAGA AGGCGCGCTA 360
CAATGCTCAG TGCCAGGAGA CCATCCGCGT CACCAAGCCC TGCACCCCA AGACCAAGC 420
AAAGGCCAAA GCCAAGAAAG GGAAGGGAAA GGACTAGACG CCAAGCCTGG ATGCCAAGGA 480
GCCCTGTGTG TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540
CACCAGTGCC TCTGTCTGCG TCGTTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
ACTCCCCAGC CCCACCCCTA AGTGGCCAAA GTGGGGAGGG ACAAGGGATT CTGGGAAGCT 660
TGAGCCTCCC CCAAGCAAT GTGAGTCCA GAGCCCGCTT TTGTTCTTCC CCACAATTCC 720
ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCCC CAATAAAGC TCTTCTTTT 780

```

TAATAT

Seq ID NO: 346 Protein sequence  
 Protein Accession #: NP\_002382.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MQHRGFLLLT LLALLALTSA VAKKKDKVKK GPGSECAEW AWGPCTPSSK DCGVGFREGT 60
CGAQTQRI RC RVPCNWKKEF GADCKYKFEN WGACDGGTGT KVRQGTLLKKA RYNAQCQETI 120
RVTKPCTPKT KAKAKAKGK GKD

```

Seq ID NO: 347 DNA sequence  
 Nucleic Acid Accession #: NM\_006783.1  
 Coding sequence: 1..786

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGATTGGG GGACGCTGCA CACTTTCATC GGGGGTGTCA ACAAACACTC CACCAGCATC 60
GGGAAGGTGT GGATCAGAGT CATCTTTATT TTCCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTCGTCTGCA ACACACTGCA ACCGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTCCTCC GTGTCCACAC TCCGGCTGTG GGCCTCTCCAG 240
CTGATCTTCG TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTTCAG GCGAGGAGAG AAGAGGAATG ATTTCAAAGA CATAGAGGAC 360
ATTAAAAAGC ACAAGGTTTCG GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGCATC 420
TTTTTCCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCTT TTACAATGGG 480
TACCACCTGC CCTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCTT TGTGACTGTC 540
TTTATTTCTA GGCCAAACAGA GAAGACCGTG TTTACCATTT TTATGATTTC TCGCTCTGTG 600
ATTTGCATGC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTATAG 660
AGATCAAAGA GAGCACAGAC GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAAATGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA

```

Seq ID NO: 348 Protein sequence  
 Protein Accession #: NP\_006774.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MDWGTLHTFI GGVNKHSTSI GKVWITVIFI FRVMILVVAA QEVWGDEQED FVCNTLQPGC 60
KNVCYDHFEP VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKFRRGE KRNDFKDIED 120
IKKHVRIEGR SLWWTYTSSI FRIIFEAFAF MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC 180
FISRPEKTV FTIFMISASV ICMLLNVAEL CYLLLVKVCFR RSKRAQTQKN HPNHALKESK 240
QNMNELISD SQQNAITGFP S

```

Seq ID NO: 349 DNA sequence  
 Nucleic Acid Accession #: NM\_002571.1  
 Coding sequence: 99..587

```

1      11      21      31      41      51
|      |      |      |      |      |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60
TCACCCCTGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCCC CTCTGAGGGT CCACATCACC TCACTGTTGC 240
CCACCCCCGA GGACAACTTG GAGATCGTTC TGCACAGATG GGAGAACAAC AGCTGTGTTG 300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCAACGGA GGCCACGCTG CTCGATACTG ACTACGACAA TTTCTGTGTT CTCTGCCTAC 420
AGGACACCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCCTGGTGG 480
AGGACGATGA GATCATGCA GATTTCATCA GGGCTTTCAG GCCCTTGCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAA CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCCT 600
CCAGGAAGAG GAGACTCCCA CCCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCCCC 660
TTTCAAAGAA TAACCACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCCT 720
TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTTGGAGCAT G

```

Seq ID NO: 350 Protein sequence  
 Protein Accession #: NP\_002562.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MDIPQTKQDL ELPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPPT EDNLEIVLHR 60
WENNSCVEKK VLGEKTNPK KFKINYTVAN EATLLD TDYD NFLFLCLQDT TTPIQSMCMQ 120
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLQMEEP C RF

```

Seq ID NO: 351 DNA sequence  
 Nucleic Acid Accession #: NM\_006500.1  
 Coding sequence: 27..1967

```

1      11      21      31      41      51
|      |      |      |      |      |
ACTTGCCTCT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60
TCGCGCCTCG CTGCTGCTGT CCTCGCTGCG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG 120
CGCCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240
TCATCTTCCG TGATCGCCAG GGCCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC 300

```

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55

TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCCTGACTCA AGTCACCCCC CAAGACGAGC 360  
GCATCTTCTT GTGCCAGGGC AAGGCCCTC GGTCCCAGGA GTACCGCATC CAGCTCCGCG 420  
TCTACAAAGC TCCGGAGGAG CCAAACATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA 480  
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCTAAG 540  
TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCAAGT 600  
CGTCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660  
TGGTTAAAGA AGACAAAGAT GCCCAGTTT ACTGTGAGCT CAACTACCGG CTGCCCAGTG 720  
GGAACCATCAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCGG ACAGAAAAAG 780  
TGTGGCTCGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT 840  
GTTTGGCTGA TGGCAACCTT CCACCACACT TCAGCATCAG CAAGCAGAAC CCCAGCACCA 900  
GGGAGGCAGA GGAAGAGACA ACCAACGACA ACGGGGTCTT GGTGTGGAG CCTGCCCGGA 960  
AGGAACACAG TGGGCGCTAT GAATGTCAGG CCTGGAACCTT GGACACCATG ATATCGCTGC 1020  
TGAGTGAACC ACAGGAACCTA CTGGTGAAC ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG 1080  
CCCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140  
ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAGG GGGCCTGTGC 1200  
TTCAGTTGCA TGACCTGAAA CGGGAGGCAG GAGGCGGCTA TCGTGCCTG GCGTCTGTGC 1260  
CCAGCATACC CGGCCTGAA CGCACACAGC TGGTCAAGCT GGCCATTTT GGCCCCCTT 1320  
GGATGGCATT CAAGGAGAGG AAGGTGTGGG TGAAAGAGAA TATGGTGTG AATCTGTCTT 1380  
GTGAAGCGTC AGGGCACCCC CGGCCACCA TCTCCTGGA CGTCAACGGC ACGGCAAGTG 1440  
AACAAGACCA AGATCCACAG CGAGTCTGA GCACCTGAA TGTCTCTGT ACCCCGGAGC 1500  
TGTGGAGAC AGGTGTGAA TGCACGGCCT CCAACGACCT GGGCAAAAAC ACCAGCATCC 1560  
TCTTCTGGA GCTGTCAAT TTAACACCCC TCACACCAGA CTCCAACACA ACCACTGGCC 1620  
TCAGCACTTC CACTGCCAGT CCTCATACCA GAGCCAACAG CACCTCCACA GAGAGAAAAG 1680  
TGCCGGAGCC GGAGAGCCGG GCGTGGTCA TCGTGGCTGT GATTGTGTGC ATCTGGTCC 1740  
TGGCGGTGCT GGGCGCTGT CTCTATTTC TCTATAAGAA GGGCAAGCTG CCGTGCAGGC 1800  
GCTCAGGGA GAGGAGATC ACGCTGCCCC CGTCTCGTAA GACCGAAGCT GTAGTTGAAG 1860  
TTAAGTCAGA TAAGCTCCCA GAAGAGATGG GCCTCCTGCA GGGCAGCAGC GGTGACAAGA 1920  
GGGCTCCGG AGACAGGGA GAGAAATACA TCGATCTGAG GCATTAGCCC CGAATCACTT 1980  
CAGCTCCCTT CCCTGCTGG ACCATTCCCA GCTCCCTGCT CACTCTTCTC TCAGCCAAAG 2040  
CCTCCAAAG GACTAGAGAG AAGCCTCCTG CTCCCCCTAC CTGCACACC CCTTTCAGAG 2100  
GGCCACTGGG TTAGGACTG AGGACCTCAC TTGGCCCTGC AAGCCGCTTT TCAGGGACCA 2160  
GTCACACCAC ATCTCTCCA CGTTGAGTGA AGCTCATCCC AAGCAAGGAG CCCAGTCTC 2220  
CCGAGCGGGT AGGAGAGTTT TTTGCAGAAC GTGTTTTTC TTTACACACA TTATGGCTGT 2280  
AAATACCTGG CTCTGCCCAG CAGCTGAGCT GGGTAGCCTC TCTGAGCTGG TTTCTGCCC 2340  
CAAAGGCTGG CTTCACCAT CCAGGTGCAC CACTGAAGTG AGGACACACC GGAGCCAGGC 2400  
GCCTGCTCAT GTTGAAGTGC GCTGTTTACA CCCGCTCCGG AGAGCACCCC AGCGGCATCC 2460  
AGAAGCAGCT GCAGTGTGTC TGCCACCACC CTCTGCTCG CCTCTTCAA GTCTCTGTG 2520  
ACATTTTTTC TTTGGTCAGA AGCCAGGAAC TGGTGTCTAT CCTTAAAGA TACGTGCCGG 2580  
GGCCAGGTGT GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA GGCGGGCGGA 2640  
TCACAAAGTC AGGACGAGAC CATCTGGCT AACACGGTGA AACCTGTCT CACTAAAAA 2700  
TACAAAAAAA AATTAGCTAG GCGTAGTGGT TGGCACCTAT AGTCCCAGCT ACTCGGAAGG 2760  
CTGAAGCAGG AGAATGGTAT GAATCCAGGA GGTGGAGCTT GCAGTGAGCC GAGACCGTGC 2820  
CACTGCATCT CAGCCTGGGC AACACAGCGA GACTCCGTCT CGAGGAAAAA AAAAGAAAAA 2880  
ACGCGTACCT CGCGTGAGGA AGCTGGGCGC TGTTTTCGAG TTCAGGTGAA TTAGCCTCAA 2940  
TCCCGTGTGT CACTGTCTCC CATAGCCCTC TTGATGGATC ACGTAAACT GAAAGGCAGC 3000  
GGGAGCAGA CAAAGATGAG GTCTACACTG TCCTTCATGG GGATTAAGC TATGGTTATA 3060  
TTAGCACCAA ACTTCTACAA ACCAAGCTCA GGGCCCCAAC CCTAGAAGGG CCCAAATGAG 3120  
AGAATGGTAC TTAGGGATGG AAAACGGGGC CTGGCTAGAG CTTGGGTGT GTGTGTCTGT 3180  
CTGTGTGTAT GCATACATAT GTGTGTATAT ATGGTTTTGT CAGGTGTGTA AATTTGCAAA 3240  
TTGTTTCTT TATATATGTA TGTATATATA TATATGAAAA TATATATATA TATGAAAAAT 3300  
AAAGCTTAAT TGTCCAGAA AATCATACAT TGCTTTTTTA TTCTACATGG GTACCAACAGG 3360  
AACCTGGGGG CCTGTGAAAC TACAACCAA AGGCACACAA AACCGTTTCC AGTTGGCAGC 3420  
AGAGATCAGG GGTACCTCT GCTTCTGAGC AAATGGCTCA AGCTCTACCA GAGCAGACAG 3480  
CTACCTACT TTTACGAGC AAAACGTCCC GTATGACGCA GCACGAAGGG CCTGGCAGGC 3540  
TGTTAGCAGG AGCTATGTCC CTTCTATCG TTTCCTGCTCA CT

Seq ID NO: 352 Protein sequence  
Protein Accession #: NP\_006491.1

60  
65  
70  
75

1 11 21 31 41 51  
GLPRLVCAFL LAACCCPRV AGVPGEAEQ APPELVEVEVG STALLKCGLS QSQGNLSHVD 60  
WFSVHKEKRT LIFRVRQGG QSEFGEYEQ LSLQDRGATL ALTQVTPQDE RIFLCQKRP 120  
RSQEIYIQLR VYKAPPEPNI QVNPLGIPVN SKEPEEVATC VGRNGYPIQ VIWYKNGRPL 180  
KEEKNRVHIQ SSQTVBSSGL YTLQSLKAQ LVKEDKDAQF YCELNYRLPS GNHMKESREV 240  
TVPVFYPTKE VWLEVEPVGM LKEGDRVEIR CLADGNPPPH FSISKQNPST REAEEETTND 300  
NGVLVLEPAR KEHSGRYECQ AWNLDTMISL LSEPQELLVN YVSDVRVSPA APERQEGSSL 360  
TLTCEBESSQ DLEFQNLREE TDQVLERGPV LQLHDLKREA GGGYRCVASV PSIPGLNRTQ 420  
LVKLAIFGPP WMAFKERKVV VKENMVLNLS CEASGHRPT ISWNVNGTAS EQDQDPQRLV 480  
STLNLVLTPE LLETGVECTA SNDLGKNTSI LFLELVNLT LTPDSNTTGT LSTSTASPH 540  
RANSTSTERK LPPEPSRGVV IVAVIVCILV LAVLGAVLYF LYKKGKLPKR RSGKQBITLP 600  
PSRKTIELVVE VKSDKLPPEM GLLQSSGSDK RAPGDQGEKY IDLRH

Seq ID NO: 353 DNA sequence  
Nucleic Acid Accession #: NM\_003183.3  
Coding sequence: 165..2639

80

1 11 21 31 41 51  
TCGAGCCTGG CGGTAGAATC TTCCCACTAG GCGGCGCGGG AGGGAAAAGA GGATTGAGGG 60  
GCTAGGCCGG GCGGATCCCG TCCTCCCCCG ATGTGAGCAG TTTTCCGAAA CCCGCTCAGG 120  
CGAAGGCTGC CCAGAGAGGT GGAGTCGGTA GCGGGGCCGG GAACATGAGG CAGTCTCTCC 180  
TATTCTGAC CAGCGTGGTT CCTTCTGTG TGGCGCCGCG ACCTCCGAT GACCCGGGCT 240  
TCGGCCCCCA CCAGAGACTC GAGAAGCTTG ATTCCTTGCT CTCAGACTAC GATATTCTCT 300

CTTTATCTAA TATCCAGCAG CATTCCGGTAA GAAAAAGAGA TCTACAGACT TCAACACATG 360  
 TAGAAACACT ACTAATTTT TCAGCTTTGA AAAGGCATTT TAAATTATAC CTGACATCAA 420  
 GTACTGAACG TTTTTCACAA AATTTCAAGG TCGTGGTGGT GGATGGTAAA AACGAAAGCG 480  
 AGTACACTGC AAAATGGCAG GACTTCTTCA CTGGACACGT GGTGGTGGAG CCTGACTCTA 540  
 GGGTTCTAGC CCACATAAGA GATGATGATG TTATAATCAG AATCAACACA GATGGGGCCG 600  
 AATATAACAT AGAGCCACTT TGGAGATTG TTAATGATAC CAAAGACAAA AGAATGTTAG 660  
 TTTATAAATC TGAAGATATC AAGAATGTTT CACGTTTGCA GTCTCCAAA GTGTGTGGTT 720  
 ATTTAAAAGT GGATAATGAA GAGTTGCTCC CAAAAGGGTT AGTAGACAGA GAACCACTG 780  
 AAGAGCTTGT TCATCGATG AAAAGAAGAG CTGACCCAGA TCCCATGAAG AACACGTGTA 840  
 AATTATTGGT GGTAGCAGAT CATCGCTTCT ACAGATACAT GGGCAGAGGG GAAGAGAGTA 900  
 CAACTACAAA TTAATTAATA GAGCTAATTG ACAGAGTTGA TGACATCTAT CGGAACACTT 960  
 CATGGGATAA TGCAGGTTT AAAGGCTATG GAATACAGAT AGAGCAGATT CGCATTTCTA 1020  
 AGTCTCCACA AGAGGTAAAA CCTGGTGAAA AGCACTACAA CATGGCAAAA AGTTACCCAA 1080  
 ATGAAGAAAA GGATGCTTGG GATGTGAAGA TGTGCTAGA GCAATTTAGC TTTGATATAG 1140  
 CTGAGGAAGC ATCTAAAGTT TGCTTGGCAC ACCTTTTCAC ATACCAAGAT TTTGATATGG 1200  
 GAACCTCTGG ATTAGCTTAT GTTGGCTCTC CCAGAGCAAA CAGCCATGGA GGTGTTTGTG 1260  
 CAAAGGCTTA TTATAGCCCA GTTGGGAAGA AAAATATCTA TTTGAATAGT GGTTTGACGA 1320  
 GCACAAAGAA TTATGGTAAA ACCATCCTTA CAAAGGAAGC TGACCTGGTT ACAACTCATG 1380  
 AATTGGGACA TAATTTTGA GCAGAACATG ATCCGGATGG TCTAGCAGAA TGTGCCCCGA 1440  
 ATGAGGACCA GGGAGGGAAA TATGTCATGT ATCCCATAGC TGTGAGTGGC GATCAGGAGA 1500  
 ACAATAAGAT GTTTTCAAA CAGCAGTAAA AATCAATCTA TAAGACCATT GAAAGTAAGG 1560  
 CCCAGGAGTG TTTTCAAGAA CGCAGCAATA AAGTTTGTGG GAACTCGAGG GTGGATGAAG 1620  
 GAGAAGAGTG TGATCCTGGC ATCATGTATC TGAACAACGA CACCTGCTGC AACAGCGACT 1680  
 GCACGTTGAA GGAAGGTGTC CAGTGCAGTG ACAGGAACAG TCCTTGCTGT AAAAAGTGTG 1740  
 AGTTTGGAGC TGCCCAAGAG AAGTGCCAGG AGGCGATTAA TGCTACTTGC AAAGGCGTGT 1800  
 CCTACTGCAC AGGTAATAGC AGTGAGTGCC CGCCTCCAGG AAATGCTGAA AATGACACTG 1860  
 TTTGCTTGA TCTTGCAAG TGTAAAGATG GGAATGTCAT CCCTTTCTGC GAGAGGGAAC 1920  
 AGCAGCTGGA GTCCCTGTGC TGTAAATGAA CTGACAACTC CTGCAAGGTG TGCTGCAAGG 1980  
 ACCTTTCTGG CCGCTGTGTG CCTATGTGCG ATGCTGAACA AAAGAACTTA TTTTGGAGGA 2040  
 AAGGAAAGCC CTGTACAGTA GGTATTTGTG ACATGAATGG CAAATGTGAG AAACGAGTAC 2100  
 AGATGTAAT TGAACGATT TGGGATTCTA TTGACCAGCT GAGCATCAAT ACTTTTGGAA 2160  
 AGTTTTTAGC AGACAACATC GTTGGGTCTG TCCTGGTCTT CTCTTGATA TTTTGGATTC 2220  
 CTTTCAGCAT TCTTGTCCAT TGTGTGGATA AGAAATTGGA TAAACAGTAT GAATCTCTGT 2280  
 CTCTGTTTCA CCCAGTAAC GTCGAAATGC TGAGCAGCAT GGATCTGTCA TCCGTTCTGCA 2340  
 TTATCAAACC CTTTCCCTGC CCCAGACTC CAGGCCCGCT GCAGCCTGCC CCTGTGATCC 2400  
 CTTGCGGCC AGCAGCTCCA AAAGTGGACC ACCAGAGAAT GGACACCATC CAGGAAGACC 2460  
 CCAGCACAGA CTCCTATATG GACGAGGATG GGTGTGAGAA GGACCCCTTC CCAATAGCA 2520  
 GCACAGCTGC CAAGTCATT GAGGATCTCA CGGACCATCC GGTGCGCAGA AGTGAAGAGG 2580  
 CTGCTCTCT TAAACTGCAG CGTCAGAAATC GTGTTAACAG CAAAGAAACA GAGTGCTAAT 2640  
 TTAGTCTTCA GCTCTTCTGA CTTAAGTGTG CAAATATTTT TTATAGATTT GACCTACAAA 2700  
 TCAATCAGAG CTTGTATTTT GTGAAGACTG GGAAGTGACT TAGCAGATGC TGGTCATGTG 2760  
 TTTGAACCTT CCTGAGGTAA ACAGTTCTTG TGTGTTTGG CCCTTCTCCT TTTGAAAGG 2820  
 TAAGGTGAAA GTGAATCTAC TTATTTTGTG GCTTTCAGGT TTTAGTTTTC AAAATATCTT 2880  
 TTGACCTGTG GTGCAAAAGC AGAAATACA GCTGGATTGG GTTATGAATA TTTACGTTT 2940  
 TGTAAATTAA TCTTTTATAT TGATAACAGC ACTGACTAGG GAAATGATCA GTTTTTTTTT 3000  
 ATACACTGTA ATGAACCGCT GAATATGAAG CATTTGGCAT TTATTTGTGA GAAAGTGGGA 3060  
 ATAGTTTTTT TTTTTTTTTT TTTTTTTTTG CTTCAACTAA AAACAAAGGA GATAAATTTA 3120  
 GTATACATTG TATCTAAATT GTGGGTCTAT TTCTAGTTAT TACCAGAGT TTTTATGTAG 3180  
 CAGGAAAAAT ATATATCTAA ATTTAGAAAT CATTTGGGTT AATATGGCTC TTCATAATTC 3240  
 TAAGACTAAT GCTCAGAAC TAACCACTAC CTTACAGTGA GGGCTATACA TGGTAGCCAG 3300  
 TTGAATTTAT GGAATCTACC AACTGTTTAG GGCCCTGATT TGCTGGGCAG TTTTCTGTGA 3360  
 TTTTATAAGT ATCTTCATGT ATCCCTGTTA CTGATAGGGA TACATGTCTT AGAAAATTCA 3420  
 CTATTGGCTG GGAGTGGTGG CTCATGCCTG TAATCCAGC ACTTGGAGAG GCTGAGGTTG 3480  
 CGCCACTACA CTCACGCTG GGTGACAGAG TGAGATCTGC CTC

Seq ID NO: 354 Protein sequence  
 Protein Accession #: NP\_003174.2

1 11 21 31 41 51  
 | | | | |  
 MRQSLFLFTS VVPFVLAPRP PDDPGFGPHQ RLEKLDLSLLS DYDILSLSNI QHESVVRKRD 60  
 QSTHVTETLL TFSALKRHF LYLTSSTERF SQNFKVVVD GKNESEYTAQ WQDFFTGHVV 120  
 GEPDSRVLAH IRDDVLIIRI NTDGAENYIE PLWRFVNDTK DKRMLVYKSE DIKNVSRLLQ 180  
 PKVCGYLKVD NEELLKGLV DREPPPELVH RVKRRADPD MKNTCKLLV ADHRFYRYMG 240  
 RGEESTTNY LIELIDRVDD IYRNTSWDNA GFKGYGQIE QIRILKSPQE VKPGEKHYNM 300  
 AKSYPNEEKD AWDVKMLLEQ FSPDIAEEAS KVCLAHIFTY QDFDMGTLGL AYVGSPPRNS 360  
 HGGVCPKAYI SPVGKKNYIL NSGLTSTKNY GKTILTKEAD LVTTHLGHN FGAEHDPDGL 420  
 AECAPNEDQG GKVVMYPIAV SGDHEHNKMF SNCSKQSIYK TIESKAQECF QERSNKVCGN 480  
 SRVDEGEED PGIMYLNNDT CCNSDCTLKE GVQCSDRNSP CCKNCQFETA QKKCQEAINE 540  
 TCKGVSYCTG NSSECPPPGN AENDTVCLDL GKCKDGKICP FCEREQQLS CACNETDNNS 600  
 KVCCRDLSGR CVPYVDAEQK NLFRLKGP KC TVGFCDMNGK CEKRVQDVIE RFWDFIDQLS 660  
 INTFGKFLAD NIVGSLVLFV LIFWIPFSIL VHCVDKLDK QYESLSLFHP SNVEMLSMMD 720  
 SASVRIIKPF PAPQTPGRLQ PAPVIPSAPA APKLDHQRM TQIEDPSTDS HMEDEGFEKD 780  
 PFPNSSTAAR SFEDLTDHPV ARSEKAASF LQRQNRVNSK ETEC

Seq ID NO: 355 DNA sequence  
 Nucleic Acid Accession #: NM\_021832.1  
 Coding sequence: 164..2248

1 11 21 31 41 51  
 | | | | |  
 TCGAGCCTGG CGGTAGAATC TTCCCACTAG GCGGCGCGGG AGGAAAAGAG GATTGAGGGG 60  
 CTAGGCCGGG CGGATCCCGT CCTCCCCGA TGTGAGCAGT TTTCCGAAAC CCCGTGAGGC 120  
 GAAGGCTGCC CAGAGAGGTG GAGTCGGTAG CGGGGCCGGG AACATGAGGC AGTCTCTCCT 180

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55

ATTCCTGACC AGCGTGGTTC CTTTCGTGCT GGCGCCGCGA CCTCCGGATG ACCCGGGCTT 240  
 CGGCCCCCAG CAGAGACTCG AGAAGCTTGA TTCTTTGCTC TCAGACTACG ATATTCTCTC 300  
 TTTATCTAAT ATCCAGCAGC ATTCGGTAAG AAAAAGAGAT CTACAGACTT CAACACATGT 360  
 AGAAACACTA CTAACCTTTT CAGCTTTGAA AAGGCATTTT AAATTATACC TGACATCAAG 420  
 TACTGAACGT TTTTCACAAA ATTTCAAGGT CGTGGTGGTG GATGGTAAAA ACGAAAGCGA 480  
 GTACACTGTA AAATGGCAGG ACTTCTTAC TGGACACGTG GTTGGTGAGC CTGACTCTAG 540  
 GGTTCAGCC CACATAAGAG ATGATGATGT TATAATCAGA ATCAACACAG ATGGGGCCGA 600  
 ATATAACATA GAGCCACTTT GGAGATTGT TAATGATACC AAAGACAAA GAATGTTAGT 660  
 TTATAAATCT GAAGATATCA AGAATGTTTC ACGTTTGCAG TCTCCAAAAG TGTGTGGTTA 720  
 TTTAAAAGTG GATAATGAAG AGTTGCTCCC AAAAGGGTTA GTAGACAGAG AACCACTGTA 780  
 AGAGCTTGT CATCGAGTGA AAAGAAGAGC TGACCCAGAT CCCATGAAGA ACACGTGTAA 840  
 ATTATTGGTG GTAGCAGATC ATCGCTTCTA CAGATACATG GGCAGAGGGG AAGAGAGTAC 900  
 AACTACAAAT TACTTAATAG AGCTAATTGA CAGAGTTGAT GACATCTATC GGAACACTTC 960  
 ATGGGATAAT GCAGGTTTTA AAGGCTATGG AATACAGATA GAGCAGATTG GCATTCTCAA 1020  
 GTCTCCACAA TTTTCAAACT CTGGTGAAAA GCACTACAAC ATGGCAAAAA GTTACCCAAA 1080  
 TGAAGAAAAG GATGCTTGGG ATGTGAAGAT GTTGTAGAG CAATTTAGCT TTGATATAGC 1140  
 TGAGGAAGCA TCTAAAGTTT GCTTGGCACA CCTTTTCACA TACCAAGATT TTGATATGGG 1200  
 AACTCTTGGA TTAGCTTATG TTGGCTCTCC CAGAGCAAAAC AGCCATGGAG GTGTTTGTCC 1260  
 AAAGGCTTAT TATAGCCGAG TTGGGAAGAA AAATATCTAT TTGAATAGTG GTTTGACGAG 1320  
 CACAAAGAAT TATGTTAAAA CCATCCTTAC AAAGGAAGCT GACCTGGTTA CAATCATGA 1380  
 ATTGGGACAT AATTTTGGAG CAGAATATGA TCCGGATGGT CTAGCAGAA GTGCCCGGAA 1440  
 TGAGGACCAAG GGAGGGAAT ATGTCATGTA TCCCATAGCT GTGAGTGGCG ATCAGCAGAA 1500  
 CAATAAGATG TTTTCAAACT GCAGTAAACA ATCAATCTAT AAGACCATG AAAGTAAGGC 1560  
 CCAGGAGTGT TTTCAAGAAC GCAGCAATAA AGTTTGTGGG AACTCGAGGG TGGATGAAGG 1620  
 AGAAGAGTGT GATCCTGGCA TCATGTATCT GAACAACGAC ACCTGCTGCA ACAGCGACTG 1680  
 CACGTTGAAG GAAGGTGTCC AGTGCACTGA CAGGAACAGT CCTGTCTGTA AAAACTGTCA 1740  
 GTTTGAGACT GCGCCAGAAG AGTGCCAGGA GCGGATTAAT GCTACTTGCA AAGGCGTGTG 1800  
 CTACTGCACA GGTAAATAGCA GTGAGTGCCC GCCTCCAGGA AATGCTGAAG ATGACACTGT 1860  
 TTGCTTGGAT CTTGGCAAGT GTAAGGATGG GAAATGCATC CCTTCTGCG AGAGGGAACA 1920  
 GCAGCTGGAG TCCTGTGTCAT GTAATGAAAC TGACAACTCC TGCAAGTGTG GCTGCAGGGA 1980  
 CCTTTCGGGC CGCTGTGTGC CCTATGTCGA TGCTGAACAA AAGAATTAT TTTTGAGGAA 2040  
 AGGAAAGCCC TGACAGTAG GATTTTGTGA CATGAATGGC AAATGTGAGA AACGAGTACA 2100  
 GGATGTAATT GAACGATTTT GGGATTTTAT TGACAGCTG AGCATCAATA CTTTGGGAAA 2160  
 GTTTTGTAGCA GACAACATCG TTGGGTCTGT CCTGGTTTTC TCCTTGATAT TTTGGATTCC 2220  
 TTTTCAAGT CTTGTCCATT GTGTGTAACG TCGAAATGCT GAGCAGCATG GATTCTGCAT 2280  
 CGGTTGCGAT TATCAAAACC TTTCTGCGC CCCAGACTCC AGGCCGCTG CAGCCTGCC 2340  
 CTGTGATCCC TTCGGCGCCA GCAGCTCCAA AACTGGACCA CCAGAGAATG GACACCATCC 2400  
 AGGAAGACCC CAGCAGACG TCACATATGG ACAGGATGG GTTTGAGAAG GACCCCTTCC 2460  
 CAAATAGCAG CACAGCTGCC AAGTCATTG AGGATCTCAC GGACCATCCG GTCACCAGAA 2520  
 GTGAAAAGGC TGCTCTCTTT AAATGCGAGC GTCAGAAATG TGTGACAGC AAAGAAACAG 2580  
 AGTGCTAATT TAGTTCTCAG CTCTTCTGAC TTAAGTGTGC AAAATATTTT TATAGATTG 2640  
 ACCTACAATC AATCAGACT TATATTTTGT GAAGACTGGG AAGTGACTTA GCAGATGCTG 2700  
 GTCATGTGTT TGAATCTCCT GCAGGTAAC AGTCTCTGTG TGGTTTGGCC CTTCTCCTTT 2760  
 TGAAAAGGTA AGGTGAAGGT GAATCTAGCT TATTTTGAGG CTTTCAGTT TTAGTTTTTA 2820  
 AAATATCTTT TGACCTGTGG TGCAAAAGCA GAAATACAG CTGGATTGGG TTATGAGTAT 2880  
 TTACGTTTTT GTAAATTAAT CTTTATATAT GATAACAGGC ACTGACTAGG GAAATGATCA 2940  
 GTTTTTTTTT ATACACTGTA ATGAACCGCT GAATATGAAG CATTGGGCAT TTATTGTGTA 3000  
 GAAAAGTGGTA ATAGTTTTTT TTTTTTTTTT TTTTTTTTGC CTTCAACTAA AAACAAAGGA 3060  
 GATAAATTTA GTATACATTG TATCTAAATT GTGGGTCTAT TTCTAGTTAT TACCCAGAGT 3120  
 TTTTATGTAG CAGGAAAAAT ATATATCTAA ATTTAGAAAT CATTGGGGIT AATATGGCTC 3180  
 TTCATAATC TAAGACTAAT GCTCAGAAC TAACCACTAC CTTACAGTA GGGCTATACA 3240  
 TGGTAGCCAG TTGAATTTAT GGAATCTACC AACTGTTTAG GGCCCTGATT TGCTGGGCG 3300  
 TTTTCTGTA TTTTATAAGT ATCTTCATGT ATCCCTGTTA CTGATAGGGA TACATGTCTT 3360  
 AGAAAATTTA CTATTGGCTG GGAGTGGTGG CTCATGCCCTG TAATCCCAGC ACTTGGAGAG 3420  
 3421 GCTGAGGTTG CGCCACTACA CTCAGCCTG GGTGACAGAG TGAGATCTGC CTC

Seq ID NO: 356 Protein sequence  
 Protein Accession #: NP\_068604.1

60  
 65  
 70

1 11 21 31 41 51  
 MRQSLFLTS VVPFVLAPRP PDDPGFGPHQ RLEKLSLLS DYDILSLSNI QQHSVRKRDL 60  
 QSTHVELL TFSALKRHF LYLTSSTERF SQNFVVVVD GKNESEYTVK WQDFFTHGVV 120  
 GEPDSRVLAH IRDDVDIIRI NTDGAENYIE PLWRFVNDTK DKRMLVYKSE DIKNVSRLOS 180  
 PKVCGYLKVD NEELLPKGLV DREPPPELVH RVKRRADPD MKNTCKLLV ADHRFYRYMG 240  
 RGEESTTNY LIELIDRVDD IYRNTSWDNA GFKGYGIQIE QIRILKSPQE VKPGEKHYNM 300  
 AKSYPNEEKD AWDVKMLLEQ FSDIABEAS KVCLAHLFTY QDFDMGTGLL AYVGSPRANS 360  
 HGGVCPKAYY SPVGKNIYV NSGLTSTKNY GKTILTKEAD LVTTHLGHN FGAEHDPDGL 420  
 AECAPNEDQG GKYVMYPIAV SGDHENNKMF SNCSKQSIYK TIESKAQECF QERSNKVCGN 480  
 SRVDEGEED PGIMYLNNDT CCNSDCTLKE GVQCSDRNSP CCKNCQFETA QKKQAEAINA 540  
 TCKGVSYCTG NSSECPPPGN AEDDTVCLDL GKCKDGKICP FCEREQQLS CACNETDNNSC 600  
 KVCCRDLGR CVFYVDAEQK NLFLRKGP KC TVGFCDMNGK CEKRVQDVIE RFWDFIDQLS 660  
 INTFGKFLAD NIVGSLVFS LIFWIPFSIL VHCV

Seq ID NO: 357 DNA sequence  
 Nucleic Acid Accession #: NM\_004994.1  
 Coding sequence: 20..2143

80

1 11 21 31 41 51  
 AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCCTG GTCCTGGTGC TCCTGGTGCT 60  
 GGGCTGCTGC TTTGCTGCCC CCAGACAGCG CCAGTCCACC CTTGTGCTCT TCCCTGGAGA 120  
 CCTGAGAAC AATCTCACCG ACAGGCAGCT GGCAGAGGAA TACGTGTACC GCTATGGTTA 180  
 CACTCGGGTG CAGAGAGATG GTGAGAGATC GAAATCTCTG GGGCTGCGC TGCTGCTTCT 240



5 CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT 300  
 GCGAACCCEA CGGTGCGGGG TCCCAGACCT GGGCAGATT CAAACCTTTG AGGGGCGACCT 360  
 CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGGAAG ACTTGGCCGC 420  
 GGCCTGATT GACGACGCTT TGGCCGCGC CTTCGCACTG TGGAGCGCGG TGACGCCGCT 480  
 CACCTTCACT CGCGTGTACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTGCGGGA 540  
 GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTTCCTCC 600  
 TGGCCCCGGC ATTCAGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA 660  
 GGGCCTCGTG GTTCCAATC GGTTTGAAA CGCAGATGGC GCGGCTGCC ACTTCCCCTT 720  
 10 CATCTTCGAG GGCCGCTCCT ACTCTGCCTG CACCACCGAC GGTCTGCTCCG ACGGCTTGCC 780  
 CTGGTGCACT ACCACGGCCA ACTACGACAC CGACGACCGG TTGGCTTCT GCCCAGCGA 840  
 GAGACTCTAC ACCCGGGAGC GCAATGCTGA TGGGAAACCC TGCCAGTTTC CATTCACTCT 900  
 CCAAGGCCAA TCCTACTCCG CTGCAACCAC GGACGGTCGC TCCGACGGCT ACCGCTGGTG 960  
 CGCCACCAAC GCCAACTACG ACCGGGACAA GCTCTTCCGC TTCTGCCCGA CCGAGCTGA 1020  
 CTCGACGGTG ATGGGGGGCA ACTCGGCGGG GGAGCTGTGC GTCTTCCCCT TCACTTTCCT 1080  
 15 GGGTAAGGAG TACTCGACCT GTACCAAGCA GGGCCGCGGA GATGGGCGCC TCTGGTGCGC 1140  
 TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG 1200  
 TTTGTTCTCT GTGGCGGCGC ATGAGTTCGG CCACGCGCTG GGCTTAGATC ATTCCTCAGT 1260  
 GCGGAGGGCG CTCATGTACC CTATGTACCG GTTCACTGAG GGGCCCCCTT TGCATAAGGA 1320  
 CGACGTGAAT GGCATCCGGC ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCTCC 1380  
 20 AACCAACCAC ACACCCGAGC CCACGGCTCC CCGGACGGTC TGCCCCACCG GACCCCCCAC 1440  
 TGTCCACCCC TCAGAGCGCC CCACAGCTGG CCCCACAGGT CCCCCTCAG CTGGCCCCAC 1500  
 AGGTCCCCC ACTGTGGGCC CTCTACGGC CACTACTGTG CCTTTGAGTC CGGTGGACGA 1560  
 TGCTTCAAC TGGAACATCT TCGACGCCAT CGCGGAGATT GGGAAACAGC TGTATTGTG 1620  
 CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGG AGCCGGCCGC AGGGCCCTT 1680  
 25 CCTATCGCC GACAAGTGGC CCGCGCTGCC CCGCAAGCTG GACTCGTCT TTGAGGAGCC 1740  
 GCTCTCCAAG AAGCTTTCT TCTTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCGTC 1800  
 GTGTGCTGGC CCGAGGCGTC TGGACAAGCT GGGCCTGGGA GCCGACGTGG CCCAGGTGAC 1860  
 CGGGGCCCTC CGGAGTGCCA GGGGAAGAT GCTGCTGTT AGCGGGCGGC GCCTCTGGAG 1920  
 GTTCGACGTG AAGGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGATGTT 1980  
 30 CCCCCGGGTG CCTTTGGACA CGCACGACGT CTTCAGTAC CGAGAGAAAG CCTATTTCTG 2040  
 CCAAGGACCG TTTCTACTGG CCGTGAGTTC CCGGAGTGAG TTGAACCAAG TGGACCAAGT 2100  
 GGGCTAGCTG ACCTATGACA TCCTGCAGTG CCCTGAGGAC TAGGGCTCCC GTCTGCTTT 2160  
 GCAGTGCCAT GTAAATCCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA 2220  
 35 CAAACTGGTA TTCTGTTCTG GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC 2280  
 TCACCTTGT TTTTGTGG AGTGTCTTA ATAACTTGG ATTCTCTAAC CTTT

Seq ID NO: 358 Protein sequence  
 Protein Accession #: NP\_004985.1

40 1 11 21 31 41 51  
 MSLWQPLVLV LVLGCCFAA PRQRSTLVL FPGDLRTNLT DRQLAEELY RYGYTRVAEM 60  
 RGSKSLGPA LLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLRFRQTF EGDWKWHHN 120  
 ITYWIQNYSE DLPRAVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDBGYP 180  
 45 FDGDKGLLAH AFPPGPGTQG DAHFDDDELW SLKGVVVPT RFGNADGAAC HFPFIFEGRS 240  
 YSACTTDGRS DGLPWCSTTA NYDITDRFGF CPSERLYTRD GNADGKPCQF PFIFQGQSYS 300  
 ACTIDGRSDG YRWCAATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFLGKEYST 360  
 CTSEGRGDGR LWCATTSNFD SDKKWGFCDP QGYSLFLVAA HEFGHALGLD HSSVPEALMY 420  
 50 PMYRTEGEPF LHKDDVNGFR HLYGRPEPE PRPPTTTTPQ PTAPPTVCP PTGPTVHPSE 480  
 PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFDKGKYW 540  
 RFSEGRGSRP QGPFLIADKW PALPRKLDV FEEPLSKLKF FFSGRQVWVY TGASVLGPRR 600  
 LDKLGLGADV AQVTGALRSR RGMMLLFSGR RLWRFVKAQ MVDPRSASEV DRMFPGVPLD 660  
 THDVQYREK AYFCQDRFYW RVSSRSELNQ VDQVGVVTVYD ILQCPED

Seq ID NO: 359 DNA sequence  
 Nucleic Acid Accession #: NM\_000213.1  
 Coding sequence: 127..5385

60 1 11 21 31 41 51  
 CGCCCGCGCG CTGCAGCCCC ATCTCCTAGC GGCAGCCAG GCGCGGAGGG AGCGAGTCCG 60  
 CCCCAGAGTA GGTCCAGGAC GGGCGCACAG CAGCAGCCGA GGCTGGCCGG GAGAGGGAGG 120  
 AAGAGGATGG CAGGGCCACG CCCAGGCCCA TGGGCCAGGC TGCTCTGTGC AGCCTTGATC 180  
 65 AGCGTCAGCC TCTCTGGGAC CTTCGCAAAAC CGCTGCAAGA AGGCCCCAGT GAAGAGCTGC 240  
 ACGGAGTGTG TCCGTGTGGA TAAGGACTGC GCCTACTGCA CAGACGAGAT GTTCAGGGAC 300  
 CGGCGCTGCA ACACCCAGGC GGAGCTGCTG GCCCGGGCT GCCAGCGGGA GAGCATCGTG 360  
 GTCATGGAGA GCAGCTTCCA AATCACAGAG GAGACCCAGA TTGACACCAC CTTGCGGCGC 420  
 AGCCAGATGT CCCCCAAGG CCTGCGGGTC CGTCTGCGGC CCGGTGAGGA GCGGCATTTT 480  
 70 GAGCTGGAGG TGTTTGAGCC ACTGGAGAGC CCCGTGGACC TGTACATCCT CATGGACTTC 540  
 TCCAATCCA TGTCCGATGA TCTGGACAAC CTCAGAAGA TGGGGCAGAA CCTGGCTCGG 600  
 GTCTTGAGCC AGCTACACAG CAGCTACACT ATTGGATTG GCAAGTTTGT GGACAAAGTC 660  
 AGCGTCCCGC AGACGGACAT GAGGCCTGAG AAGCTGAAGG AGCCCTGGCC CAACAGTGAC 720  
 CCCCCTTCT CTTCAAGAA CGTCATCAGC CTGACAGAAG ATGTGGATGA GTTCCGGAAT 780  
 75 AAAGTGCAGG GAGAGCGGAT CTCAGGCAAC CTGGATGCTC CTGAGGGCGG CTTGATGCC 840  
 ATCTCTCAGA CAGCTGTGTG CACGAGGGAC ATTTGGCTGGC GCCCGGACAG CACCCACCTG 900  
 CTGGTCTTCT CCACCGAGTC AGCCTTCCAC TATGAGGCTG ATGGCGCCAA CGTCTGGCT 960  
 GGCATCATGA GCCGCAACGA TGAACGGTGC CACCTGGACA CCACGGGCAC CTACACCCAG 1020  
 80 TACAGGACAC AGGACTACCC CTCGGTGCCC ACCCTGGTGC GCCTGCTGCG CAAGCAACA 1080  
 ATCATCCCCA TCTTGTCTGT CACCAACTAC TCCTATAGCT ACTACGAGAA GCTTCACACC 1140  
 TATTTCCCTG TCTCTCACT GGGGTGTCTG CAGGAGGACT CGTCCAACAT CGTGGAGCTG 1200  
 CTGGAGGAGG CCTTCAATCG GATCCGCTCC AACCTGGACA TCCGGGCCCT AGACAGCCCC 1260  
 CGAGGCCCTT GGACAGAGGT CACCTCCAAG ATGTTCCAGA AGACGAGGAC TGGGTCTCTT 1320  
 CACATCCGGC GGGGGGAAGT GGGTATATAC CAGGTGCAGC TGCGGGCCCT TGAGCACGTG 1380  
 GATGGGACGC ACGTGTGCCA GCTGCCGGAG GACCAGAAGG GCAACATCCA TCTGAAACCT 1440

	TCCTTCTCCG	ACGGCCTCAA	GATGGACGCG	GGCATCATCT	GTGATGTGTG	CACCTGCGAG	1500
	CTGCAAAAAG	AGGTGCGGTC	AGCTCGCTGC	AGCTTCAACG	GAGACTTCGT	GTGCGGACAG	1560
	TGTGTGTGCA	GCGAGGGCTG	GAGTGCCAG	ACCTGCAACT	GCTCCACCGG	CTCTCTGAGT	1620
5	GACATTTCAGC	CCTGCGCTGC	GGAGGGCGAG	GACAAGCCGT	GCTCCGGCCG	TGGGGAGTGC	1680
	CAGTGCGGGC	ACTGTGTGTG	CTACGGCGAA	GGCCGCTACG	AGGGTCAGTT	CTGCGAGTAT	1740
	GACAACTTCC	AGTGTCCCGG	CACCTCCGGG	TTCTCTGTGA	ATGACCGAGG	ACGCTGCTCC	1800
	ATGGGCCAGT	GTGTGTGTGA	GCCTGGTTGG	ACAGGCCCAA	GCTGTGACTG	TCCCTCAGC	1860
	AATGCCACCT	GCATCGACAG	CAATGGGGGC	ATCTGTAATG	GACGTGGCCA	CTGTGAGTGT	1920
10	GGCCGCTGCC	ACTGCCACCA	GCAGTCGCTC	TACACGGACA	CCATCTGCGA	GATCAACTAC	1980
	TCGGCGATCC	ACCCGGGCTT	CTGCGAGGAC	CTACGCTCCT	GCCTGCAAGT	CCAGGCGTGG	2040
	GGCACCGCGC	AGAAGAAGGG	GCGCACGTGT	GAGGAATGCA	ACTTCAAGGT	CAAGATGGTG	2100
	GACGAGCTTA	AGAGAGCCGA	GGAGGTGGTG	GTGCGCTGCT	CCTTCCGGGA	CGAGGATGAC	2160
	GACTGCACCT	ACAGCTACAC	CATGGAAGGT	GACGGCGCCC	CTGGGCCCCA	CAGCACTGTC	2220
	CTGGTGCACA	AGAAGAAGGA	CTGCCCTCCG	GGCTCCTTCT	GGTGGCTCAT	CCCCCTGCTC	2280
15	CTCCTCCTCC	TGCCGCTCCT	GGCCCTGCTA	CTGCTGCTAT	GCTGGAAGTA	CTGTGCTCTG	2340
	TGCAAGGCCT	GCCTGGCACT	TCTCCCTGTC	TGCAACCGAG	GTCAATGGT	GGGCTTTAAG	2400
	GAAGACCACT	ACATGCTGCG	GGAGAACCTG	ATGGCCTCTG	ACCACTTGGA	CACGCCCATG	2460
	CTGCGCAGCG	GGAACTTCAA	GGGCCGTGAC	GTGGTCCGCT	GGAAGGTAC	CAACAACATG	2520
20	CAGCGGCGCT	GCCTTGGCCAC	TGATGCCGCC	AGCATCAACC	CCACAGAGCT	GGTGCCCTAC	2580
	GGGCTGTCTT	TGCGCCTGGC	CCGCCTTTTC	ACCGAGAACC	TGCTGAAGCC	TGACACTCGG	2640
	GAGTGCGCCC	AGCTGCCGCC	GGAGGTGGAG	GAGAACCTGA	ACGAGGTCTA	CAGGCAGATC	2700
	TCCGGTGTAC	ACAAGCTCCA	GACAGCAAG	TTCCGGCAGC	AGCCCAATGC	CGGGAAGAAAG	2760
	CAAGACCACA	CCATTGTGGA	CACAGTGCTG	ATGGCGCCCC	GCTCGGCCAA	CCCGGCCCTG	2820
25	CTGAAGCTTA	CAGAGAAGCA	GGTGAACAG	AGGGCCTTCC	ACGACCTCAA	GGTGGCCCCC	2880
	GGCTACTACA	CCCTCACTGC	AGACCAGGAC	GCCCGGGGCA	TGGTGGAGTT	CCAGGAGGGC	2940
	GTGGAGCTGG	TGGAGGTACG	GGTGCCCTCC	TTTATCCGGC	CTGAGGATGA	CGACGAGAAG	3000
	CAGCTGTCTG	TGGAGGCCAT	CGACGTGCC	CGAGGCAGTG	CCACCCCTCG	CCGCGCCCTG	3060
	GTAACATCA	CCATCATCAA	GGAGCAAGCC	AGAGACGTGG	TGCTCTTTGA	GCAGCCTGAG	3120
30	TTCTCGGTCA	GCCCGGGGGA	CCAGGTGGCC	CGCATCCCTG	TCATCCGGCG	TGCTCTGGAC	3180
	GGCGGGAGT	CCCAGGTCTC	CTACCGCACA	CAGGATGGCA	CCGCGCAGGG	CAACCGGGAC	3240
	TACATCCCG	TGGAGGGTGA	GCTGCTGTTC	CAGCCTGGGG	AGGCCTGGAA	AGAGCTGCAG	3300
	GTGAAGCTCC	TGGAGCTGCA	AGAAGTTGAC	TCCCTCCTGC	GGGCGCCGCA	GGTCCGCGCT	3360
	TTCCACGTCC	AGCTCAGCAA	CCCTAAGTTT	GGGGCCACCC	TGGGCCAGCC	CCACTCCACC	3420
35	ACCATCATCA	TCAGGGACCC	AGATGAAGTG	GACCGGAGCT	TCACGAGTCA	GATGTTGTCA	3480
	TCACAGCCAC	CCCCTCAGCG	CGACCTGGGC	GCCCCGACGA	ACCCCAATGC	TAAGGCCCGT	3540
	GGGTCCAGGA	AGATCCATTT	CAACTGGCTG	CCCCCTTCTG	GCAAGCCAAT	GGGGTACAGG	3600
	GTAAAGTACT	GGATTACGGG	TGACTCCGAA	TCCGAAGCCC	ACCTGCTCGA	CAGCAAGGTG	3660
	CCCTCAGTGG	AGCTCACCAA	CCTGTACCCG	TATTTGCGACT	ATGAGATGAA	GGTGTGCGCC	3720
40	TACGGGGCTC	AGGGCGAGGG	ACCTTACAGC	TCCCTGGTGT	CCTGCGGCAC	CCACCAAGAA	3780
	GTGCCAGCG	AGCCAGGGCG	TCTGGCCTTC	AATGTGCTCT	CCTCCACGGT	GACCCAGCTG	3840
	AGCTGGGCTG	AGCCGGCTGA	GACCAACGGT	GAGATCACAG	CCTACGAGGT	CTGCTATGGC	3900
	CTGGTCAAG	ATGACAACCG	ACCTATTGGG	CCCATGAAGA	AAGTGTCTGG	TGACAACCCCT	3960
	AAGAACCAGG	TGCTGCTTAT	TGAGAACCTT	CGGGAGTCCC	AGCCCTACCG	CTACACGGTG	4020
45	AAGGCGCGCA	ACGGGGCCGG	CTGGGGCCCT	GAGCGGGAGG	CCATCATCAA	CCTGGCCACC	4080
	CAGCCCAAGA	GGCCCATGTC	CATCCCATC	ATCCCTGACA	TCCCTATCGT	GGACGCCACG	4140
	AGCGGGGAGG	ACTACGACAG	CTTCTTATG	TACAGCGATG	ACGTTCTACG	CTCTCCATCG	4200
	GGCAGCCAGA	GGCCGACGCT	CTCCGATGAC	ACTGAGCACC	TGGTGAATGG	CCGGATGGAC	4260
	TTTGCCTTCC	CGGGCAGCAC	CAACTCCCTG	CACAGGATGA	CCACGACCAG	TGCTGCTGCC	4320
50	TATGGCACCC	ACCTGAGCCC	ACACGTGCCC	CACCGCGTGC	TAAGCACATC	CTCCACCCTC	4380
	ACACGGGACT	ACAACCTACT	GACCCGCTCA	GAACACTCAC	ACTCGACCAC	ACTGCCGAGG	4440
	GACTACTCCA	CCCTCACTTC	CGTCTCCTCC	CACGACTCTC	GCCTGACTGC	TGGTGTGCC	4500
	GACACGCCCA	CCCGCTTGGT	GTTCTCTGCC	CTGGGGCCCA	CATCTCTCAG	AGTGAGCTGG	4560
	CAGGAGCCGC	GGTGCAGGCG	GCCGCTGCAG	GGCTACAGTG	TGGAGTACCA	GCTGCTGAAC	4620
55	GGCGGTGAGC	TGCATCGGCT	CAACATCCCC	AACCCCTGCCC	AGACCTCGGT	GGTGGTGGAA	4680
	GACCTCCTGC	CCAACCACTC	CTACGTGTTT	CGCGTGCGGG	CCCAGAGCCA	GGAAGGCTGG	4740
	GGCCGAGAGC	GTGAGGGTGT	CATCACCATT	GAATCCAGG	TGCACCCGCA	GAGCCCACTG	4800
	TGTCCCTGTC	CAGGCTCCGC	CTTCACTTTG	AGCACTCCCA	GTGCCCCAGG	CCCGCTGGTG	4860
	TTCACTGCCC	TGAGCCGAGA	CTCGCTGCAG	CTGAGCTGGG	AGCGGCCACG	GAGGCCCAAT	4920
60	GGGATATATG	TCCAGTACCT	GGTGACCTGT	GAGATGGCCC	AAGGAGGAGG	GCCAGCCACC	4980
	GCATTCCGGG	TGGATGGAGA	CAGCCCGGAG	AGCCGGCTGA	CCGTGCCGGG	CCTCAGCGAG	5040
	AACGTGCCCT	ACAAGTTCAA	GGTGCAGGCC	AGGACCACTG	AGGGCTTCGG	GCCAGAGCGC	5100
	GAGGGCATCA	TCAACATAGA	GTCCGAGGAT	GGAGGACCCT	TCCCGCAGCT	GGGCAGCCGT	5160
	GCCGGGCTCT	TCCAGCACCC	GCTGCAAGAG	GAGTACAGCA	GCATCACACC	CACCCACACC	5220
65	AGCGCCACCG	AGCCCTTCTT	AGTGGATGGG	CCGACCCCTG	GGGCCCAGCA	CCTGGAGGCA	5280
	GGCGGCTCCC	TCACCCGGCA	TGTGACCCAG	GAGTTTGTGA	GCCGGACACT	GACCACAGGC	5340
	GGAAACCTTA	GCACCCACAT	GGACCAACAG	TTCTTCCAAA	CTTGACCGCA	CCCTGCCCCA	5400
	CCCCCGCCAT	GTCCCACTAG	GCGTCTCTCC	GACTCCTCTC	CCGGAGCCTC	CTCAGTACT	5460
	CCATCTCTTC	ATCCCTGGGG	GCCAGGCCCA	CCCGCATGCA	CAGAGCAGGG	GCTAGGTGTC	5520
70	TCCTGGGAGG	CATGAAGGGG	GCAAGGTCGG	TCCTCTGTGG	GCCCAAACCT	ATTGTAAACC	5580
	AAAGAGCTGG	GAGCAGCACA	AGGACCCAGC	CTTTGTTCTG	CACCTAATAA	ATGTTTGTGC	5640
	TACTG						

Seq ID NO: 360 Protein sequence  
 Protein Accession #: NP\_000204.1

75	1	11	21	31	41	51	
	MAGPRPSPWA	RLLLAALISV	SLSGTIANRC	KKAPVKSCTE	CVRVDKDCAY	CTDEMFRDRR	60
	CNTQAELLAA	GQRESIVVM	ESSFQITEET	QIDTTLRRSQ	MSPQGLRVRL	RPGEERHFEL	120
80	EVFEPLSEPV	DLYILMDFSN	SMSDDLNLK	KMGQNLARVL	SQLTSDYTIG	FGKFVDFKVS	180
	PQTDMRPEKL	KFPWNSDPP	FSFKNVISLT	EDVDEFRNKL	QGERISGNLD	APEGGFDAIL	240
	QTAVCTRDIG	WRPDSTHLLV	FSTESAFHYE	ADGANVLAGI	MSRNDERCHL	DTTGTYYTQR	300
	TQDYPSPVPTL	VRLLAKHNNI	PIFAVTNYSY	SYEKLHTYF	PVSSLGLVLQE	DSSNIVELLE	360
	EAFNRIRSNL	DIRALDSPRG	LRTEVTSKMF	QKTRTGSFHI	RRGEVGIYQV	QLRALEHVDG	420

THVCQLPEDQ KGNHLKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480  
 CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEGQFCEYDN 540  
 FQCPRTSGLF CNDGRGRCSMG QCVCEPFGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR 600  
 CHCHQQSLYT DTICEINYS A IHPGLCEDLR SCVQCQAWGT GEKKGRCTCE CNFKVKMVDE 660  
 LKRAEEVVVR CSFRDEDDDC TYSYTMEDDG APGPNSTVLV HKKKDCPPGS FWLWLIPLLLL 720  
 LLPLLLALLL LCWKYCACK ACLALLPCCN RGHMVGFKEG HYMLRENMA SDHLDTPLMR 780  
 SGNLKGDRDV RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTRC 840  
 AQLRQEVEEN LNEVYRQISG VHKLQQTFR QQPNAKGKQD HTIVDTVLMA PRSAKPALLK 900  
 LTKQVEQRA FHDLVKAPGY YTLTADQDAR GMVEFQEGVE LVDVVRVPLFI RPEDDDEKQL 960  
 LVEAIDVPAG TATLGRRLLVN ITIIEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020  
 KQSVSYRTQD GTAQGNRDIYI PVEGELLFQF GEAWKELQVK LLELQEVDLS LRGRQVRRFH 1080  
 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGLDGLAP QNPNKAAGS 1140  
 RKIHFNLWLP SGKPMGYRVK YWIQDSESE AHLDSKVPS VELTNLYPYC DYEMKVCAYG 1200  
 AQEGEPYSSL VSCRTHQEV SEPGRILAFNV VSSTVTQLSW AEPATNGEI TAYEVCYGLV 1260  
 NDDNRPIGPM KVLVDNPKN RMLLIENLRE SQPYRYTVKA RAGAGWGPGR EAIINLATQP 1320  
 KRPMISIPII DIPIVDAQSG EDYDSLMY S DVLRSFSGS QRPVSDDTE HLVNGRMDFA 1380  
 FPGSTNSLHR MTTTSAAYG THLSPHVPHR VLSTSSILTR DYNLSLTRSEH SHSTTLPRDY 1440  
 STLTSSVSHD SRLTAGVPDT PTRLVFSALG PTLRLVSWQE PRCEPLQGY SVEYQLLNGG 1500  
 ELHRLNIPNP AGTSVVVEDL LPNHSYVFRV RAQSQEGWGR EREGVITIES QVHPQSPLCP 1560  
 LPGAFTLST PSAPGLFVSE LTVPLGSENV PYKFKVQART TEGFGPEREG IITIESQDGG PFPQLGSRAG 1620  
 RVDGDSPESE LTVPLGSENV PYKFKVQART TEGFGPEREG IITIESQDGG PFPQLGSRAG 1680  
 LFQHPQLQSEY SSITTTHTSA TEPFLVDGPT LGAQHLEAGG SLTRHVITQEF VSRTLTTSSTG 1740  
 LSHMDQQFF QT

Seq ID NO: 361 DNA sequence  
 Nucleic Acid Accession #: NM\_013332.1  
 Coding sequence: 1..63

1 11 21 31 41 51  
 GCACGAGGGC GCTTTTGCTCT CCGGTGAGTT TTGTGGCGGG AAGCTTCTGC GCTGGTGCTT 60  
 AGTAACCGAC TTTCCTCCGG ACTCCTGCAC GACCTGCTCC TACAGCCGGC GATCCACTCC 120  
 CGGCTGTTC CCCGAGGGT CCAGAGGCC T TCAGAAAGGA GAAGGCAGCT CTGTTTCTCT 180  
 GCAGAGGAGT AGGCTCCTTT CAGCCATGAA GCATGTGTG AACCTCTACC TGTAGGTGT 240  
 GGTACTGACC CTACTCTCCA TCTTCGTAG AGTGATGGAG TCCCTAGAA GCTTACTAGA 300  
 GAGCCATCG CCTGGGACCT CCGGACCA CAGAAGCCAA CTAGCCACA CAGAGCCAC 360  
 CAAGGCCCTT CCAGACCATC CATCCAGAAG CATGTGATAA GACCTCCTTC CATACTGGCC 420  
 ATATTTTGA ACACCTGACCT AGACATGTCC AGATGGGAGT CCCATTCTTA GCAGACAAGC 480  
 TGAGCACCGT TGTAAACAGA GAACCTATTAC TAGGCCTTGA AGAACCTGTC TAACTGGATG 540  
 CTCATTGCTT GGGCAAGGCC TGTTAGGCC GGTTCGGTG GCTCATGCTT GTAATCCTAG 600  
 CACTTTGGGA GGCTGAGGTG GGTGGATCAC CTGAGGTCAG GAGTTCGAGA CCAGCCTCGC 660  
 CAACATGGCG AAACCCCATC TCTACTAAAA ATACAAAAGT TAGCTGGGTG TGGTGGCAGA 720  
 GGCCTGTAAT CCGATCTCTT TGGGAGGCTG AGGCGGGAGA ATTGCTTGAA CCCGGGGACG 780  
 GAGGTTCGAG TGAACCGAGA TCGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC 840  
 CATCTCAAAA AAAAAAAGAA AAAAAAAGC CTGTTTAATG CACAGGTGTG AGTGGATTGC 900  
 TTATGGCTAT GAGATAGGTT GATCTCGCCC TTACCCCGGG GTCTGGTGTG TGCTGTGCTT 960  
 TCCTCAGCAG TTGGGCTCTG ACATCTCTTA GATGTCCCAA CTTCAGCTGT TGGGAGATGG 1020  
 TGATATTTTC AACCTACTT CTAACATC TGTCTGGGGT TCCTTTAGTC TTGAATGTCT 1080  
 TAGCTCAAT TATTTGGTGT TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTTGGATAG 1140  
 CAGTTGAAGA GGTGTGTGG GTGGGCTGTT GGGAGTGAGG ATGGAGTGTI CAGTGCCCAT 1200  
 TTCTCATTTT ACATTTTAAA GTCGTCTCTC CAACATAGTG TGTATTGGTC TGAAGGGGGT 1260  
 GTGGGGATGC CAAAGCCTGC TCAAGTTATG GACATTGTGG CCACCATGTG GCTTAAATGA 1320  
 TTTTCTCTAA CTAATAAAGT GGAATATATA TTTCAAAAA AAAAAA AA

Seq ID NO: 362 Protein sequence  
 Protein Accession #: NP\_037464.1

1 11 21 31 41 51  
 MKHVLNLYLL GVVLTLISIF VRVMSLEGL LESPSPGTSW TTRSQLANTE PTKGLPDHPS 60  
 RSM

Seq ID NO: 363 DNA sequence  
 Nucleic Acid Accession #: NM\_023915.1  
 Coding sequence: 250..1326

1 11 21 31 41 51  
 GGCACGAGGG TTTCTGTTTC ATGCTTTACC AGAAAAATCCA CTTCCCTGCC GACCTTAGTT 60  
 TCAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120  
 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180  
 CCCACGCCCT AATCGTCCCC AAGTGTCTTC TGACACGCAT CTTTGCTTAC AGTGCATCAC 240  
 AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300  
 CAAGAGAGTC ACAATTTCAG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCTTCAC 360  
 AATGAATTG ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTTGT GGCAAGCATC 420  
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480  
 TTCTATCTCA AAAACATAGT GGTTCGAGAC CTCATAATGA CGCTGACATT TCCATTTCGA 540  
 ATAGTCCATG ATGCAGGATT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600  
 TCAGTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660  
 GATCGCTATC TGAAGGTGGT CAAGCCATTT GGGGACTCTC GGATGTACAG CATAACCTTC 720  
 ACGAAGGTTT TATCTGTTTG TGTGTGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC 780  
 ATCCTGACAA ATGCTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAA ACTTAAAGT 840  
 CCTTTGGGG TCAATAGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900  
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960

AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTGTGT 1020  
 GTGGCTGTGT TTTTACCTG CTTTCTACCA TATCACTGTG GCAGAATTCC TTTTACTTTT 1080  
 AGTCACTTAG ACAGGCTTTT AGATGAATCT GCACAAAAA TCCTATATTA CTGCAAAGAA 1140  
 ATTACACTTT TCTTGTCTGC GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTTCATG 1200  
 TGTAGGTCAT TTTCAAGAAG GCTGTTCAAA AAATCAAATA TCAGAACCAG GAGTGAAGAG 1260  
 ATCAGATCAC TGCAAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320  
 GTGTAGGCCT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAATA AATGTTTCTT 1380  
 TTCATTATCC TTAATAAAAA AA

Seq ID NO: 364 Protein sequence  
 Protein Accession #: NP\_076404

1 11 21 31 41 51  
 MGFNLTAKL PNNELHQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60  
 GLAVWIFFHI RNKTSFIFYL KNIVVADLIM TLTFPPRIVH DAGFGPWYFK FILCRYTSVL 120  
 FYANMYTSIV FLGLISIDRY LKVVKPFGDS RMYSTITPKV LSVCVWVIMA VLSLPNILLT 180  
 NGQPTEDNIH DCSLKSPGLG VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240  
 ISQSSRRKRKH NQSIRVVAVV FFTCFLPYHL CRIPFTFSLH DRLLDESAQK ILYYCKEITL 300  
 FLSACNVCLD PIIFYFMCRS FSRLLFKSN ITRSESIRS LQSVRRSEVR IYYDYTDV

Seq ID NO: 365 DNA sequence  
 Nucleic Acid Accession #: NM\_005365.1  
 Coding sequence: 1..948

1 11 21 31 41 51  
 ATGTCTCTCG AGCAGAGGAG TCCGCACTGC AAGCCTGATG AAGACCTTGA AGCCCAAGGA 60  
 GAGGACTTGG CCGTGTATGGG TGCACAGGAA CCCACAGGCG AGGAGGAGGA GACTACCTCC 120  
 TCCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCAGAGT 180  
 CCTCAGGAG GCGCTTCTCT CTCCATTTCG GTCTACTACA CTTTATGGAG CCAATTTCGAT 240  
 GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTGCGACC AGCTCAGCTG 300  
 GAGTTCAFTG TCCAAGAAGC ACTGAAATG AAGGTGGCTG AGTTGGTTCA TTTCTGTCTC 360  
 CACAAATATC GAGTCAAGGA GCCGGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAAA 420  
 AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAAGGCCT CCGAGTTTCA GCAGGTGATC 480  
 TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CTACATCCT TGTCACTGCT 540  
 CTTGGCCTCT CGTGGGATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCCGCCCTC 600  
 CTGATCATTG TCCTGGGTGT GATCCTAACC AAAGACAACG GCGCCCTTGA AGAGGTTATC 660  
 TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAGG AGCAGATGTT CTACGGGGAG 720  
 CCCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAAACT ACCTGGAGTA CCGGCAGGTG 780  
 CCCGGCAGTG ATCCTGCGCA CTACGAGTTC CTGTGGGGTT CCAAGGCCCA CGCTGAAACC 840  
 AGCTATGAGA AGGTCATAAA TTATTTGGTC ATGCTCAATG CAAGAGAGCC CATCTGCTAC 900  
 CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

Seq ID NO: 366 Protein sequence  
 Protein Accession #: NP\_005356.1

1 11 21 31 41 51  
 MSLEQRSPHC KPDEDLEAQQ EDLGLMGAQE PTGEEEEETS SSDSKEEEVS AAGSSSPPOS 60  
 PQGGASSSIS VYITLWSQFD EGSSSQEEEE PSSSVDPQAL EPMFQEALKL KVAELVHFL 120  
 HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKASEFMQVI FGTDVKEVDP AGHSYILVTA 180  
 LGLSCDSMLG DGHSMFPAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKEHMFYGE 240  
 PRKLLTDQDW QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYL 300  
 PSLYEEVLGE EQEGV

Seq ID NO: 367 DNA sequence  
 Nucleic Acid Accession #: NM\_014400  
 Coding sequence: 86..1126

1 11 21 31 41 51  
 GGTACTCAT CCTGGGCTCA GGTAAAGAGG CCCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60  
 GACGCCAAGG GAGCAGGACG GAGCCATGGA CCCCGCCAGG AAAGCAGGTG CCCAGGCCAT 120  
 GATCTGGACT CAGGGCTGGC TGCTGCTGCT GCTGCTTCG GAGGAGCGC AGGCCCTGGA 180  
 GTGTACAGC TGCGTGCAGA AAGCAGATGA CGGATGCTCC CCGAACAGA TGAAGACAGT 240  
 GAAGTGCAGC CCGGGCGTGG ACCTCTGCAC CGAGGCGGTG GGGGCGGTGG AGACCATCA 300  
 CGGACAATTC TCGCTGGCAG TGCSGGGTTG CGGTTCGGGA CTCCCCGGCA AGAATGACCG 360  
 CGGCCTGGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420  
 CTGCAACGCC AAGCTCAACC TCACCTCGCG GGCGCTCGAC CCGGCAGGTA ATGAGAGTGC 480  
 ATACCCGCCC AACGGCGTGG AGTGCTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA 540  
 GGGTACATCG CCGCGGGTGG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600  
 CTTGACGGC AACGTCACTT TGACGGCAGC TAATGTGACT GTGTCTTTC CTGTCCGGGG 660  
 CTGTGTCCAG GATGAATCTT GCACTCGGGA TGGAGTAACA GGCCAGGGT TCACGCTCAG 720  
 TGGCTCCTGT TGCCAGGGGT CCCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780  
 CCCTCGAATC CCACCCCTTG TCCGGCTGCC CCCTCCAGAG CCCACGACTG TGGCTCAAC 840  
 CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAACCCAT 900  
 GCCAGCGCCA ACCAGTCAGA CTCCGAGACA GGGAGTAGAA CACGAGGCCT CCCGGGATGA 960  
 GGAGCCCAGG TTAGCTGGAG GCGCCGCTGG CCACGAGGAC CGCAGCAATT CAGGGCAGTA 1020  
 TCCTGCAAAA GGGGGGGCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080  
 ATTGGCAGCC CTTCTGTGG CCGTGGCTGC TGGTGTCTTA CTGTGAGCTT CTCACCTGG 1140  
 AAATTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTCTGT 1200  
 CCCACACTG GACTGGGCTG GCCCAGCCCC TGTTTTCCA ACATCCCCA GTATCCCCAG 1260  
 CTTCTGCTGC GCTGGTTTGC GGCTTTGGGA AATAAATAC CGTTGTATAT ATTCTGGCAG 1320

GGGTGTTCTA GCTTTTGTAG GACAGCTCCT GTATCCTTCT CATCCTTGTC TCTCCGCTTG 1380  
 TCCTCTTGTG ATGTTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440  
 AGGATGCTAA GCTTCTACT CACTTCTCCT TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500  
 GGTGGGACAA TGGTCCCCA CTCTAAGCAC TGCCTCCCCT ACTCCCCGCA TCTTTGGGGA 1560  
 ATCGGTTCCC CATATGCTCT CTTACTAGA CTGTGAGCTC CTCGAGGGCA GGGACCGTGC 1620  
 CTTATGCTCT TGTGTGATCA GTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680  
 TTGTATAGTG AAAAAAA

Seq ID NO: 368 Protein sequence  
 Protein Accession #: NP\_055215

1 11 21 31 41 51  
 | | | | |  
 MDPARKAGAQ AMIWTAGWLL LLLLRRGAQA LECYSCVQKA DDGCSNPKMK TVKCAPGV DV 60  
 CTEAVGAVET IHQFSLAVX GCGSLPGKN DRGLDLHGLL AFQLQQAQ DRCNAKLNLT 120  
 SRALDPAGNE SAYPPNGVEC YSCVGLSREA CQGTSPPVVS CYNASDHVYK GCFDGNVTLT 180  
 AANVTVSLPV RGCVDQEFCT RDGVTGPFT LSGSCCQGSR CNSDLRNKTY FSPRIPLVR 240  
 LPPPEPTTVA STTSVTSTTS APVRPTSTTK PMPAPTSQTP RQGVHEHARS DEEPRLTGGA 300  
 AGHQDRSNSG QYPAKGGFQQ PHNKGCVAPT AGLAALLLAV AAGVLL

Seq ID NO: 369 DNA sequence  
 Nucleic Acid Accession #: NM\_005329.1  
 Coding sequence: 1..1662

1 11 21 31 41 51  
 | | | | |  
 ATGCCGGTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCCTGGCA 60  
 GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTCATCCA CACGGAAG 120  
 CACTACCTGT CTTTCGGGCT GTACGGCGCC ATCCTGGGCC TGACCTGCTT CATTAGAGC 180  
 CTTTTCGCTT TCCTGGAGCA CCGCGCATG CGACGTGCGC GCCAGGCCCT GAAGCTGCCC 240  
 TCCCGCGGCG GGGGCTCGGT GGCACGTGTC ATTGCCGCAT ACCAGGAGGA CCCTGACTAC 300  
 TTGGCGAAGT GCCTGCGCTC GGCACGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCATG 360  
 GTGGTGGATG GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420  
 GGCGGCACCG AGCAGGCCGG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480  
 GGTGAGACGG AGGCAGCCT CGAGGAGGCG ATGGACCGTG TCGGGATGT GGTGCGGGCC 540  
 AGCACCTTCT CGTGATCAT GCAGAAGTGG GGAGGCAAGC GCGAGGTCT GTACACGGCC 600  
 TTCAAGGCC TCGGCGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660  
 GATCCAGCCT GCACCATCGA GATGCTTCGA GTCTGGAGG AGGATCCCA AGTAGGGGA 720  
 GTCCGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCCTT CCTGAGCAGC 780  
 GTGCGGTACT GGATGCGCTT CAACGTGGAG CGGGCTGCGC AGTCTACTT TGGCTGTGTG 840  
 CAGTGATATA GTGGGCGCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTGGAG 900  
 GACTGGTACC ATCAGAAGTT CCTAGGCAGC AAGTGCAGCT TCGGGATGA CCGGCACCTC 960  
 ACCAACCAGG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCTC 1020  
 ACAGAGACCC CCACATAGTA CCTCGGTGG CTCAACCAGC AAACCCGCTG GAGCAAGTCT 1080  
 TACTTCCGGG AGTGGCTCTA CAACTCTCTG TGGTTCCATA AGCACCACCT CTGGATGACC 1140  
 TACGAGTCAG TGGTCACGGG TTTCTTCCCC TTCTTCTCTA TTGCCACGGT TATACAGCTT 1200  
 TTCTACCGGG GCCGATCTG GAACATCTC CTCTTCTGCG TGACGGTGCA GCTGGTGGGC 1260  
 ATTATCAAG CCACCTACGC CTGCTTCTCT CGGGGCAATG CAGAGATGAT CTTATGTGCC 1320  
 CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCCGGCCA AGATCTTTGC CATTGTATCC 1380  
 ATCAACAAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGAA CTTCTATTGGC 1440  
 CTCTATCTCT GTCTCATCTG GGTGGCAGTT CTCTGGAGG GGCTGGCCTA CACAGCTTAT 1500  
 TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCTCTG TCTCTGGGCG TATACTGTAT 1560  
 GGCTGCTACT GGGTGGCCCT CCTCATGCTA TATCTGGCCA TCATCGCCCC GCGATGTGGG 1620  
 AAGAAGCCCG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA

Seq ID NO: 370 Protein sequence  
 Protein Accession #: NP\_005320.1

1 11 21 31 41 51  
 | | | | |  
 MPVQLTTALR VVGTSLFALA VLGGILAAVY TGYQFIHTEK HYLSEFLYGA ILGLHLLIQS 60  
 LFAFLEHRRM RRAGQALKLP SPRRGSVLAL IAAVQEDPDY LRKCLRSAQR ISFPDLKVV 120  
 VVDGNRQEDA YMLDIFHEVL GGTQAGFFV WRSNFHEAGE GETEASLQEG MDRVRDVVRA 180  
 STFSCIMQKW GKGREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240  
 VGGDVQILNK YDSWISFLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMY RNSLLQGFLE 300  
 DWYHQRFLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLRL LNQTTRWSKS 360  
 YFREWLNSL WFKHHLWMT YESVVTGFFP FFLIATVIQL FYRGRIWNIL LFLLTQVLVG 420  
 IIKATYACFL RGNAMIFMS LYSLLYMSSL LPAKIFAIAT INKSGWGTSG RKTIVVNF 480  
 LIPVSIWVAV LLEGLAYTAY QDLFSETEL AFLVSGAILY GCVWVALLML YLAIARRCG 540  
 KKPEQYSLAF AEV

Seq ID NO: 371 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 148-7095

1 11 21 31 41 51  
 | | | | |  
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60  
 CAAAAAAGAC ATTTCTCTCG CTCCCTCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120  
 CGGCGAGGGG CCGCAGACCG TCTGGAAATG CGAATCCTAA AGCGTTTCTT CGCTTGCAAT 180  
 CAGCTCTCTT GTGTTTCCCG CTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTTGTTGAAG AGATTGGCTG GTCCTATACA GGAGCACTGA ATCAAAAAA TTGGGGAAAG 300  
 AAATATCCAA CATGTAATAG CCCAAACAA TCTCTATCA ATATTGATGA AGATCTTACA 360  
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA 420

	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCAGA	AATGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTGTAGGA	AGCAGTCAAA	660
5	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTGTGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTTCCTAC	AATGCAACAA	960
10	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAAAT	TTGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTT	CTCATACT	GGAAGGAAG	AGATTTCATGA	AGCAGTTTGT	1080
	AGTTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTACAA	1140
	TGGGAAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
15	GGTGCTATT	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACCTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGTACAA	1500
20	AACCAATCA	GGAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TCGCATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAAGTCA	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCCT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
	GAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCTG	TTCTTAGATC	TCCACATATG	1800
25	AACCTTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAAACAGAATA	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATCTTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAAACCCAG	AGACAATAAT	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAT	2100
30	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACCTGAGATA	CGTGTGATG	AATCTGAGAA	GACAACCAAG	2220
	TCCTTTTCTG	CAGGCCCGCT	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTTCTA	CTTTTGCTTA	CTTCCCAACT	GAGGTAAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTTGGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAACCG	2400
35	GTATACAATG	GTGAGACACC	TCTTCAACCT	TCCTACAGTA	GTGAAGTCTT	TCCTCTAGTC	2460
	ACCCCTTTGT	TGCTTGACAA	TCAGATCCTC	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
	TCCGCCCTGC	ATGCTACGCC	TGTATTTCCC	AGTGTGATG	TGTCATTGTA	ATCCATCCTG	2580
	TCTTCTATG	ATGGTGACCC	TTTGCTTCCA	TTTCTCTCTG	CTTCCCTCAG	TAGTGAATTG	2640
	TTTCCGCATC	TGCTATCAGT	TTCTCAAATC	CTTCCACAAG	TTACTTCAGC	TACCGAGAGT	2700
40	GATAAGGTGC	CCTTGCATGC	TTCTCTGCCA	GTGGCTGGGG	GTGATTGCT	ATTAGAGCCC	2760
	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCTGA	GACGCTGGAA	2820
	TTTGGTAGTG	AATCTGGTGT	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2880
	AGCAGTGATG	CCATGATGCA	TGCACGTTCT	TCAGGGCCTG	AACCTTCTTA	TGCCTTGTCT	2940
	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTTCTTACA	GTTCTGCAAT	ACCTGTGCAT	3000
45	GATTCTGTGG	GTGTAACCTTA	TCAGGGTTCC	TTATTTAGCG	GCCCTAGCCA	TATACCAATA	3060
	CCTAAGTCTT	CGTTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCTCTCT	3120
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3180
	GGGCTGACAG	CCCTTAACAT	TTCTTCACCT	GTTTCTGTAG	CTGAATTAC	ATATACAACA	3240
50	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAAATGAG	3300
	ACTGAACATG	AAATTCCTTC	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCATG	3360
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTCCT	3420
	ATTTCTAGCA	CCAAGGGCAT	GTTTCCAGGG	TCCCTTGCTC	ATACCACCAC	TAAGGTTTTT	3480
	GATCATGAGA	TTAGTCAGAT	TCCAGAAAT	AACTTTTCAG	TTCAACCTAC	ACATACTGTC	3540
	TCTCAAGCAT	CTGGTGACAC	TTGCTTAAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3600
55	TCCTCTGACC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3660
	ACCTCAGCTT	CTTTTAGTAC	TGAAGTATG	CTACAACCTT	CCTTTCAGGC	TTCTGATGTT	3720
	GACACCTTGC	TTAAAACCTG	TCTTCCAGCT	GTGCCACAGT	ATCCAATATT	GGTTGAAACC	3780
	CCCAAGTTG	ATAAAATTAG	TTCTACAATG	TGTCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
	AGTGAAAACA	TGCTGCACCT	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
60	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCTATG	CAAGTGAGAA	ATATGAACCA	3960
	GTTTTGTTAA	AAAGTGAAAG	TCCCAACCAA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAAC	CAGGCCCATC	CCCCAAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTTATC	AATTGATGAA	CCATTAAATA	CACTAATAAA	TAAGCTTATA	4140
	CATTCCGATG	AAATTTTAA	CTCCACCAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
65	ATTCCAACAG	TTGCTTCTGA	TACATTGTGA	TCTACTGATC	ATTCTGTTC	TATAGGAAAT	4260
	GGGCAATGTT	GCATTACAGC	TGTTTCTCCC	CACAGAGATG	GTCTGTAAAC	CTCAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACCTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAAAG	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4440
	AGAGGTAGTG	ATGGCTTATC	CATTTCATAAG	TGTATGTCAT	GCTCATCCTA	TAGAGAATCA	4500
70	CAGGAAAAGG	TAATGAATGA	TTCAAGACAC	CACGAAAACA	GTCTTATGGA	TCAGAAATAAT	4560
	CCAATCTCAT	ACTCACTATC	TGAGAATTCT	GAAGAAGATA	ATAGAGTCAC	AAGTGTATCC	4620
	TCAGACAGTC	AAACTGGTAT	GGACAGAAGT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4680
	TCCCAAAAGC	ACAATGATGG	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4740
	CCTCTCAGCC	CTGAATCTAA	AGCATGGGCA	GTCTGACAA	GTGATGAAGA	AAGTGGATCA	4800
75	GGGCAAGGTA	CCTCAGATAG	CCTTAATGAG	AATGAGACTT	CCACAGATTT	CAGTTTGTCA	4860
	GACACTAATG	AAAAAGATGC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATACTCCTT	4920
	GGATTCCCAC	AGTCCCCAAC	ATCATCTGTT	ACTAGCGAGA	ACTCAGAAGT	GTTCCACGTT	4980
	TCAGAGGCAG	AGGCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	5040
	GAATCCGAGA	AGAAGGCGAT	TATACCCCTT	GTGATCGTGT	CAGCCCTGAC	TTTTATCTGT	5100
80	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	5160
	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	ATATCCACAC	CTCCAACACC	TATCTTTCCA	5220
	ATTTCAGATG	ATGTCGAGC	AATFCCAATA	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	5280
	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG	5340
	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	GCAGACAGCT	CCAACCAACC	AGACAACAAG	5400
	CACAGAATC	GATACATAAA	TATGTTGCC	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	5460

5 CTTGCTGAAA AGGATGGCAA ACTGACTGAT TATATCAATG CCAATTATGT TGATGGCTAC 5520  
 AACAGACCAA AAGCTTATAT TGCTGCCCAA GGCCCACTGA AATCCACAGC TGAAGATTTC 5580  
 TGGAGAATGA TATGGGAACA TAATGTGGAA GTTATGTGCA TGATAACAAA CCTCGTGGAG 5640  
 AAAGGAAGGA GAAATATGTA TCAGTACTGG CCTGCCGATG GGAGTGAGGA GTACGGGAAC 5700  
 TTTCTGGTCA CTCAGAAGAG TGTGCAAGTG CTGCGCTATT ATACTGTGAG GAATTTTACT 5760  
 CTAAGAAACA CAAAAATAAA AAAGGGCTCC CAGAAAGGAA GACCCAGTGG ACGTGTGGTC 5820  
 ACACAGTATC ACTACACGCA GTGGCCTGAC ATGGGAGTAC CAGAGTACTC CCTGCCAGTG 5880  
 CTGACCTTTG TGAGAAAGGC AGCCTATGCC AAGCGCCATG CAGTGGGGCC TGTGTCTGTC 5940  
 10 CACTGCAGTG CTGGAGTTGG AAGAACAGGC ACATATATTG TGCTAGACAG TATGTTGCAG 6000  
 CAGATTCAAC ACGAAGGAAC TGTCAACATA TTTGGCTTCT TAAAAACAT CCGTTTCAAA 6060  
 AGAAATTATT TGGTACAAAC TGAGGAGCAA TATGCTTCA TTCATGATAC ACTGGTTGAG 6120  
 GCCATACTTA GTAAAGAAAC TGAGGTGCTG GACAGTCATA TTCATGCCTA TGTTAATGCA 6180  
 CTCCTCATTC CTGGACCAGC AGGCAAAACA AAGCTAGAGA AACAAATCCA GCTCCTGAGC 6240  
 CAGTCAAAAT TACAGCAGAG TGACTATTCT GCAGCCCTAA AGCAATGCAA CAGGGAAAAG 6300  
 15 AATCGAACTT TCTCTATCAT CCTCTGGGAA AGATCAAGGG TTGGCATTTC ATCCCTGAGT 6360  
 GGAGAAGGCA CAGACTACAT CAATGCCTCC TATATCATGG GCTATTACCA GAGCAATGAA 6420  
 TTCATCATTA CCCAGCACCC TCTCCTTCAT ACCATCAAGG ATTTCTGGAG GATGATATGG 6480  
 GACCATAATG CCCAAGTGGT GGTATGATT CCTGATGGCC AAAACATGGC AGAAGATGAA 6540  
 TTTGTTTACT GGCCAAATAA AGATGAGCCT ATAAATGTGT AGAGCTTTAA GGTCACTCTT 6600  
 20 ATGGCTGAAG AACACAAATG TCTATCTAAT GAGGAAAAAC TTATAATTCA GGACTTTATC 6660  
 TTAGAAGCTA CACAGGATGA TTAGTGACTT GAAGTGAGGC ACTTTCAGTG TCCTAAATGG 6720  
 CCAAAATCCAG ATAGCCCCAT TAGTAAAACT TTTGAACCTA TAAGTGTTAT AAAAGAAGAA 6780  
 CGTGCCAAAT GGGATGGGCC TATGATTGTT CATGATGAGC ATGGAGGAGT GACGGCAGGA 6840  
 25 ACTTCTGTG CTCTGACAAC CCTTATGCAC CAACTAGAAA AAGAAAATTC CGTGGATGTT 6900  
 TACCAGGTAG CCAAGATGAT CAATCTGATG AGGCCAGGAG TCTTTGCTGA CATTGAGCAG 6960  
 TATCAGTTTC TCTACAAAGT GATCCTCAGC CTTGTGAGCA CAAGGCAGGA AGAGAATCCA 7020  
 TCCACCTCTC TGACAGTAA TGGTGCAGCA TTGCCTGATG GAAATATAGC TGAGAGCTTA 7080  
 GAGTCTTTAG TTTAACACAG AAAGGGGTGG GGGGACTCAC ATCTGAGCAT TGTTCCTC 7140  
 30 TTCTAAAAAT TAGGCAGGAA AATCAGTCTA GTTCTGTTAT CTGTTGATT CCCTACACCT 7200  
 GACAGTAATC TTTATGATAT AGGATTCTGC CGCCAAATTT ATATCATTA CAATGTGTGC 7260  
 CTTTTTGCAG GACTTGTAA TTTACTTATTA TGTTTGAAGT AAAATGATTG AATTTTACAG 7320  
 TATTTCTAAG AATGGAATTG TGGTATTTT TTCTGTATTG ATTTTAACAG AAAATTTCAA 7380  
 TTTATAGAGG TTAGGAATTC CAAACTACAG AAAATGTTT TTTTATGTT CAAATTTTAA 7440  
 35 GCTGTATTG TAGCAATTAT CAGGTTTGTG AGAAATATAA CTTTAAATAC AGTAGCCGTG 7500  
 AAATAAAACA CTCTTCCATA TGATATTCAA CATTTTACAA CTGCAGTATT CACCTAAAGT 7560  
 AGAAATAATC TGTFACTTAT TGTAAATACT GCCCTAGTGT CTCCATGGAC CAAATTTATA 7620  
 TTTATAATTG TAGATTTTTA TATTTTACTA CTGAGTCAAG TTTTCTAGTT CTGTGTAATT 7680  
 GTTTAGTTTA ATGACGTAGT TCATTAGCTG GTCTTACTCT ACCAGTTTTC TGACATTGTA 7740  
 40 TTGTGTTTAC TAAGTCAATA ACTTTGTTTC AGCATGTAAT TTTAACTTTT GTGGAAAATA 7800  
 GAAATACCTT CATTTTGAAG GAAGTTTTTA TGAGAATAAC ACCTTACCAA ACATGTGTCA 7860  
 AATGGTTTTT ATCCAAGGAA TTGCAAAAAA AAATATAAAT ATTGCCATTA AAAAAAAA 7920  
 AAAAAAAA AAAAAAAA AAAA

Seq ID NO: 372 Protein sequence:  
 Protein Accession #: built from XP\_031379

45 1 11 21 31 41 51  
 50 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNLLKL KFGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITFFW GKCINMSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KKGKGLRLS 180  
 ILFEVGTEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LNPNSTDKYYI YNGSLTSPPC 240  
 IDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300  
 55 TGKEEIEHAV CSSEPEVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360  
 HEFLTDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPEDLDFPE 420  
 LIGTEELIKE EEEKGIDIEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480  
 RSPTRGSEFS GKODVPNTSL NSTSQPVTKL ATEKDISLTS QVTLELPHT VEGTSASLND 540  
 60 GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESSLTSFKLD TGAEDSSGSS PATSAIPFIS 600  
 ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSEMG NVWFPSSTDI 660  
 TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAEPVMS QGPSVTDLEM PHYSTFAYFP 720  
 TEVTPHAFTP SSRQQLVST VNVVYSQTTQ PVYNGETPLQ PSYSSEVFPL VTPLLLDNQI 780  
 LNTTPAASSS DSALHATPVF PSVDVSFESI LSSYDGAPLL PFSSASFSSE LFRHLHTVSQ 840  
 65 ILPQVTSATE SDKVPLHASL PVAGDILLE PSLAQYSDVL STTHAASETL EFGSESGVLY 900  
 KTLMFQVPEP PSSDAMMHAR SSGPEPSYAL SDNEGSQHIF TVSYSSAIPV HDSVGVITYQG 960  
 SLFSGSPSHIP IPKSSLTPT ASLLQPTHAL SGDGEWSGAS SDSEFLLPDT DGLTALNISS 1020  
 PVSVAEFTYT TSVFGDDNKA LSKSEIIYGN ETELQIPSFN EMVYPSESTV MPNMYDNVKN 1080  
 70 LNASLQETSV SISSTKGMFP GSLAHTTKV FDHEISQVPE NNFVSQPTH VSQASGDTSL 1140  
 KPVLSANSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP 1200  
 AVPSDPILVE TPKVDKISST MLHLIVNSA SSENMLHSTS VPVFDVSPTS HMHSASLQGL 1260  
 TISYASEKYE PVLLKSESSH QVVPSTLYND ELFQTANLEI NQAHPPKGRH VFATFVLSID 1320  
 EPINTLINKL IHSDEILTST KSSVTGKVFV GIPTVASDTF VSTDHVSFVIG NGHVAITAVS 1380  
 PHRDGVSST KLFEPKSKATS ELSHSAKSDA GLVGGGEDGD TDDDDDDDDD DRGSDGLSIH 1440  
 75 KCMSCSSYRE SQEKVMDSD THENSMDQN NPISYLSSEN SEEDNRVTSV SSDSQTGMDR 1500  
 SPGKSPSANG LSQKHNDGKE ENDIQTGSAL LPLSPESKAW AVLTSDDESG SGQGTSDSLN 1560  
 ENETSTDFSF ADTNEKDADG ILAAGDSEIT PGFPQSPSTSS VTSENSEVFH VSEAEASNSP 1620  
 HESRIGLAEG LESEKKAVIP LVIVSALTFI CLVVLVGILI YWRKCFQTAH FYLEDSTSPR 1680  
 VISTPPTPIF PISDDVGAIP IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCVDLGI 1740  
 80 TADSSNHPDN KHKNRYINIV AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA 1800  
 QGPLKSTAEF FWRMIWEHNV EVIVMITNLV EKGRRKCDQY WPDAGSSEYQ NFLVTQKSVQ 1860  
 VLAYYTVRNF TLRNKKIKKG SQKGRPSGRV VTQYHYTQWP DMGVPESYSLP VLTFRVKAAY 1920  
 AKRHAVGPVV VHTCSAGVGT GTYIVLDSML QQIQHEGTVN IFGFLKHRS QRNYLVQTEE 1980  
 QYVFIHDTLV BAILSKEDEV LDSDHIAHYVN ALLIPGPAGK TKLEKQFQLL SQSNIQSDY 2040  
 SAALKQCNRE KNRSTSIIPV ERSRVGISSL SGEGTDYINA SYIMGYQSN EFIITQHPLL 2100  
 HTIKDFWRMI WDHNAQLVVM IPDGNMAED EFVYVWNKDE PINCESFKVT LMAEEHKCLS 2160

NEEKLIQDF ILEATQDDYV LEVRHFQCPK WPNPDSPISK TFE LISVIKE EAANRDGPMI 2220  
 VHDEHGGVTA GTFCALTTLM HQLEKENSVD VYQVAKMINL MRPGVFADIE QYQFLYKVIL 2280  
 SLVSTRQEEN PSTSLDSNGA ALPDGNIAES LESLV

Seq ID NO: 373 DNA sequence  
 Nucleic Acid Accession #: built from NM\_002851  
 Coding sequence: 148-4518

10	1	11	21	31	41	51	
	CACACATACG	CACGCACGAT	CTCACCTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAAC	ATTTCTCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	CGGCGAGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGTCTCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
15	CTGTGTTGAAG	AGATTGGCTG	GTCCATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATAAAC	TGGGAAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTGAGCGGAG	GAGTTTCAGA	AATGTTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
20	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
	GGAAAAAGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAAATTTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACRAGTA	TTACATTAC	840
25	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTGTG	AAGTTCTTAC	AATGCAACAA	960
	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGACA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTCT	CTCATACACT	GGAAAGGAAG	AGATTCATGA	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCCTGTTACA	1140
30	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGAGT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTAATC	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTCGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACCT	AAGAAATAAT	CAAGGAGGAG	1440
35	GAAGAGGGAA	AAGACATGTA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAAAATCA	GGAAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TGCGATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
40	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCTG	TTCTTAGATC	TCCACATATG	1800
	AACTTGTGCG	GGACTGCAGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCATT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAAACCCAG	AGACATAAAT	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
45	GAAGATTCAA	CTTCATCAGG	TTGAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTGATG	AATCTGAGAA	GACAAACCAAG	2220
	TCCTTTTCTG	CAGGCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCTTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
50	TCCAGACAAAC	AGGATTGTTG	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAACCG	2400
	GTATACAATG	CAGAGGCCAG	TAAATAGTAGC	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGAAGAAGGC	AGTTTATACC	CTTGTGATCG	TGTGAGCCCT	GACTTTTATC	2520
	TGTCTAGTGG	TTCTTGTGGG	TATTCTCATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
	TTTTACTTAG	AGGACAGTAC	ATCCCCCTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
55	CCAAATTTAG	ATGATGTCGG	AGCAATTCCA	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACAGGAA	2760
	GTGCAGAGCT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	AAGCACAAGA	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGCTAGCA	2880
	CAGCTTGCTG	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
60	TACAACAGAG	CAAAAGCTTA	TATTGCTGCC	CAAGGCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	GAAGTTATTG	TCATGATAAC	AAACCTCGTG	3060
	GAGAAAGGAA	GGAGAAAATG	TGATCAGTAC	TGGCCTGCCG	ATGGGAGTGA	GGAGTACGGG	3120
	AACCTTCTGG	TCATCAGAA	GAGTGTGCAA	GTGCTTGCTT	ATTATACTGT	GAGGAATTTT	3180
	ACTCTAAGAA	ACACAAAAAT	AAAAAAGGGC	TCCCAGAAAG	GAAGACCCAG	TGGACGCTGTG	3240
65	GTCAACAGT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTTGTC	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAACA	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
	CAGCAGATTG	AACACGAAGG	AACGTCAAC	ATATTGGGCT	TCTTAAACAA	CATCCGTTCA	3480
	CAAAGAAATT	ATTTGGTACA	AACGTAGGAG	CAATATGTCT	TCATTATGTA	TACACTGGTT	3540
70	GAGGCCATAC	TTAGTAAAGA	AACGTAGGAG	CTGGACAGTC	ATATTATGTC	CTATGTTAAT	3600
	GCACCTCTCA	TTCTTGAGCC	AGCAGGCAAA	ACAAAGCTAG	AGAAACAATT	CCAGCTCCTG	3660
	AGCCAGTCAA	ATTATACGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	3720
	AAGAATCGAA	CTTCTTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTGCGCAT	TTTATCCCTG	3780
	AGTGGAGAAG	GCACAGACTA	CATCAATGCC	TCCTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
75	GAATTCATCA	TTATCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTTCCTG	GAGGATGATA	3900
	TGGGACCATTA	ATGCCCAACT	GGTGGTTATG	ATTCTGTATG	GCCAAAACAT	GGCAGAGATG	3960
	GAATTTGTTT	ACTGGCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGGCTG	AAGAACACAA	ATGCTATCT	AATGAGGAAA	AACTTATAAT	TCAGGACTTT	4080
	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCACTTTCA	GTGTCCTAAA	4140
	TGGCCAAATC	CAGATAGCCC	CATTAGTAAA	ACTTTTGAAC	TTATAAGTGT	TATAAAGAA	4200
80	GAAGCTGCCA	ATGGGATGGG	GCCTATGATT	GTTTATGATG	AGCATGGAGG	AGTGAAGGCA	4260
	GGAACCTTCT	GTGCTCTGAC	AACCTTATG	CACCAACTAG	AAAAAGAAAA	TTCCGTGGAT	4320
	GTTTACCAGG	TAGCCAAGAT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
	CAGTATCAGT	TTCTCTACAA	AGTGATCCTC	AGCCTTGTTG	GCACAAGGCA	GGAAGAGAAT	4440



5  
10  
15

```

CCATCCACCT CTCTGGACAG TAATGGTGCA GCATTGCCTG ATGGAAATAT AGCTGAGAGC 4500
TTAGAGTCTT TAGTTTAAAC CAGAAAGGGG TGGGGGGGACT CACATCTGAG CATTGTTTTC 4560
CTCTTCTCTAA AATTAGGCAG GAAAATCAGT CTAGTTCTGT TATCTGTGTA TTTCCCATCA 4620
CCTGACAGTA ACTTTCATGA CATAGGATTC TGCCGCCAAA TTATATCAT TAACAAATGTG 4680
TGCCCTTTTG CAAGACTTGT AATTTACTTA TTATGTTTGA ACTAAATGA TTGAATTTTA 4740
CAGTATTTCT AAGAAATGAA TTGTGGTATT TTTTCTGTGA TTGATTTTAA CAGAAAAATT 4800
CAATTATAG AGGTTAGGAA TTCCAACTA CAGAAAATGT TTGTTTGTAG TGTCAAATTT 4860
TTAGCTGTAT TTGTAGCAAT TATCAGGTTT GCTAGAAATA TAACTTTTAA TACAGTAGCC 4920
TGTAATAAAA ACACCTCTTC ATATGATATT CAACATTTTA CAACTGCAGT ATTCACCTAA 4980
AGTAGAAAAA ATCTGTACT TATTGTAAAT ACTGCCCTAG TGTCTCCATG GACCAAATTT 5040
ATATTATATA TTGTAGATTT TTATATTTTA CTAAGTGTGTC AAGTTTCTTA GTTCTGTGTA 5100
ATTGTTTAGT TTAATGACGT AGTTCATTAG CTGGTCTTAC TCTACCAGT TTCTGACATT 5160
GTATTGTGTT ACCTAAGTCA TTAACITTTG TTCAGCATGT AATTTTAACT TTTGTGGAAA 5220
ATAGAAATAC CTTCAATTTG AAAGAAGTTT TTATGAGAAT AACACCTTAC CAAACATTGT 5280
TCAATGGTT TTTATCCAAG GAATTGCAAA AATAAATATA AATATTGCCA TTAATAAAAA 5340
AAAAAATAAA AAAAAATAAA AAAAAATA

```

20 Seq ID NO: 374 Protein sequence:  
Protein Accession #: built from XP\_031379

25  
30  
35  
40  
45

```

1 11 21 31 41 51
| | | | |
MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALEQKNWG KKYPTCNSPK 60
QSPINIDEDL TQNVNVLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
FKASKITFWH GKCNMSSDGS EHSLEGGKFP LEMQIYCFDA DRFSSFEBAV KGKGLRALS 180
ILFEVGTENN LDFKAIIDGV ESVSRRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300
TGKEEIHFAV CSSEPENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLV QQLDGEDQTK 360
HEPLTDGYQD LGAILNLLPL NMSYVLQIVA ICTINGLYGKY SDQLIVDMPT DNPDLDFPE 420
LIGTEEIIKE EEEGKIDIEG AIVNPGRDSA TNQIRKKEPQ ISTTHYNRI GTKYNEAKTN 480
RSPTRGSEFS GKGDPVNTSL NSTSQPVTKL ATEKDILSTL QTVTELPPT VEGTSASLND 540
GSKTVLRSFH MNLSGTAESL NTVSITEYEE ESLTSFKLD TGAEDSSGSS PATSAIPFIS 600
ENISQGYIFS SENPETITDY VLIPEASRNA SEDSTSSGSE ESLKDPSEMG NVWFPSTDI 660
TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLPM PHYSTFAYFP 720
TEVTPHATFP SSRQDLVST VNVVYSQTTQ PVYNAEASNS SHESRIGLAE GLESEKKAVI 780
PLVIVSALTF ICLVVLVGLI IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840
PIKHFPKHVA DLHASSGFTE EFETLKEFYQ EVQSTCTVDLG ITADSSNHPD NKHKNNRYINI 900
VAYDHSRVKL ALAEKDKGL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMWIEHN 960
VEVIVMINTL VEKGRKKCDQ YWPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020
GSQKGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFFVRKAA YAKRHAVGPV VVHCSAGVGR 1080
TGTYIVLDSM LQQQHEGTV NIFGFLKHIR SQRYNLVQTE EQYVFHDTL VEAILSKETE 1140
VLDSDIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIIQSD YSAALKQCNR EKNRTSSIIIP 1200
VERSRVGISS LSSEGTDYIN ASYIMGYQGS NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
MIPDQGNMAE DEFVWPKNK EPINCESFKV TLMABEHKCL SNEEKLIQD FILEATQDDY 1320
VLEVRHFQCP KWPNDPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL 1380
MHQLEKENSF DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
AALPDGNIAE SLESIV

```

50 Seq ID NO: 375 DNA sequence  
Nucleic Acid Accession #: EOS sequence  
Coding sequence: 148-4494

55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
CACACATACG CACGCACGAT CTCACITCGA TCTATACACT GGAGGATTAA AACAAACAAA 60
CAAAAAAAC ATTTCTCTTC CTCCCTCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120
CGGCGAGGGG CGCGAGACCG TCTGGAATG CGAATCCTAA AGCGTTTCCT CGCTTGCATT 180
CAGCTCCTCT GTGTTTGCCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
CTGTTTGAAG AGATTGGCTG GTCTATACA GGAGCACTGA ATCAAAAAA TTGGGGAAAG 300
AAATATCCAA CATGTAATAG CCCAAACAA TCTCCTATCA ATATTGATGA AGATCTTACA 360
CAAGTAAATG TGAATCTTAA GAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGA 420
AACACATTCA TTCATAACAC TGGGAAATTA ATCTCACTAA TGACTACCGT 480
GTCAGCGGAG GAGTTTTCAG AATGGTGTTC AAAGCAAGCA AGATAACTTT TCACTGGGGA 540
AAATGCAATA TGTCTCTGTA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600
GAGATGCAAA TCTACTGCTT TGATGCAGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAAA 660
GGAAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAAATTG 720
GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGGGAA GCAGGCTGCT 780
TTAGATCCAT TCATCTGTTT GAACCTTCTG CCAAACTCAA CTGACAGTA TTACATTTAC 840
AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900
ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTGTGAG AAGTTCTTAC AATGCAACAA 960
TCTGGTTATG TCATGCTGAT GGACTACTTA CAAACAATTT TCCAGAGACA ACAGTACAAG 1020
TTCTCTAGAC AGGTGTTTTC CTCATACACT GGAAGGAAG AGATTCTAGA AGCAGTTTGT 1080
AGTTTCAAGC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTACAA 1140
TGGGAAAGAG CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCAGT TTTGTACCAG 1200
CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260
GGTGCTATTC TCAATAATTT GCTACCCAA ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320
TGCATAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT 1380
AATCTGAAAC TTGATCTTTT CCCTGAATTA ATTGGAACAG AAGAAATAAT CAAGGAGGAG 1440
GAAGAGGGAA AAGACATTGA AGAAGGCGCT ATTTGTAATC CTGGTAGAGA CAGTGCTACA 1500
AACCAATACA GGAAAAGGA ACCCCAGATT TCTACCACAA CACACTACAA CAGCATAGGG 1560
ACGAAATACA ATGAAGCCAA GACTAACCGA TCCCAACAA GAGGAAGTGA ATTCTCTGGA 1620
AAGGGTGATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCACTCAC TAAATTAGCC 1680
ACAGAAAAAG ATATTTCCTT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740

```

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60

GAAGGTACTT CAGCCTCTTT AAATGATGGC TCTAAAAC TG TCTTAGATC TCCACATATG 1800  
 AACTTGTGCG GGACTGCAGA ATCCTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860  
 AGTTTATTGA CCAGTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC 1920  
 GCAACTTCTG CTATCCCATT CATCTCTGAG AACATATCCC AAGGGTATAT ATTTTCCTCC 1980  
 GAAAACCCAG AGACAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC 2040  
 GAAGATTCAG CTTTCATCAGG TTCAGAAAGG TCACTAAAGG ATCCTTCTAT GGAGGGAAAT 2100  
 GTGTGGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160  
 AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTGATG AATCTGAGAA GACAACCAAG 2220  
 TCCTTTTCTG CAGGCCAGT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAATGCCA 2280  
 CATTATTCTA CCTTTGCCCTA CTTCCCACT GAGGTAACAC CTCATGCTTT TACCCCATCC 2340  
 TCCAGACAAC AGGATTGGT CTCCACGGTC AACGTGGTAT ACTCGCAGAC AACCCAACCG 2400  
 GTATACAATG AGCCAGTAA TAGTAGCCAT GAGTCTCGTA TTGGTCTAGC TGAGGGGTG 2460  
 GAATCCGAGA AGAAGGCAGT TATACCCCTT GTGATCGTGT CAGCCCTGAC TTTTATCTGT 2520  
 CTAGTGGTTC TTGTGGGTAT TCTCATCTAC TGGAGGAAAT GCTTCCAGAC TGCACACTTT 2580  
 TACTTAGAGG ACAGTACATC CCTTAGAGTT ATATCCACAC CTCCAACACC TATCTTTCCA 2640  
 ATTTGAGATG ATGTGCGAGC AATTTCCAATA AAGCACTTTC CAAAGCATGT TGCAGATTTA 2700  
 CATGCAAGTA GTGGGTTTAC TGAAGAATTG GAGGAAGTGC AGAGCTGTAC TGTGACTTA 2760  
 GGTATTACAG CAGACAGCTC CAACCAACCA GACAACAAGC ACAAGAATCG ATACATAAAT 2820  
 ATCGTGTGCT ATGATCATAG CAGGGTTAAG CTAGCACAGC TTGCTGAAAA GGATGGCAAA 2880  
 CTGACTGATT ATATCAATGC CAATTATGTT GATGGCTACA ACAGACCAAA AGCTTATATT 2940  
 GCTGCCCAAG GCCCACTGAA ATCCACAGCT GAAGATTCTT GGAGAATGAT ATGGGAACAT 3000  
 AATGTGGAAG TTATTGTCTAT GATAACAAAC CTCGTGGAGA AAGGAAGGAG AAAATGTGAT 3060  
 CAGTACTGGC CTGCCGATGG GAGTGAGGAG TACGGGAAC TTTCTGTCAC TCAGAAGAGT 3120  
 GTGCAAGTGC TTGCTTATTA TACTGTGAGG AATTTTACTC TAAGAAACAC AAAAAATAAA 3180  
 AAGGGCTCCC AGAAAGGAAG ACCCAGTGGG CGTGTGCTCA CACAGTATCA CTACACGCAG 3240  
 TGGCCTGACA TGGGAGTACC AGAGTACTCC CTGCCAGTGC TGACCTTTGT GAGAAAGGCA 3300  
 GGCTATGCCA AGCGCATATG AGTGGGGCCT GTTGTCTGTC ACTGCACTGC TGGAGTTGGA 3360  
 AGAACAGGCA CATATATTGT GCTAGACAGT ATGTTGCAGC AGATTCAACA CGAAGGAACT 3420  
 GTCAACATAT TTGGCTTCTT AAAACACATC CGTTCACAAA GAAATTATTT GGTACAAACT 3480  
 GAGGAGCAAT ATGTCTTCAT TCATGATACA CTGGTTGAGG CCATACCTTAG TAAAGAACT 3540  
 GAGGTGCTGC ACAGTCATAT TCATGCTCAT GTTAATGCAC TCCTCATTTCC TGGACCAGCA 3600  
 GGCAAAACAA AGCTAGAGAA ACAATTCAGC CTCTGAGCC AGTCAAATAT ACAGCAGAGT 3660  
 CACTATTCTG CAGCCCTAAA GCAATGCAAC AGGAAAAAGA ATCGAACTTC TTCTATCATC 3720  
 CCTGTGGAAG GATCAAGGGT TGGCATTTC TCCCTGAGTG GAGAAGGCAC AGACTACATC 3780  
 AATGCCCTCT ATATCATGGG CTATTACCAG AGCAATGAAT TCATCATTAC CCAGCACCCCT 3840  
 CTCTTTCATA CCATCAAGGA TTTCTGGAGG ATGATATGGG ACCATAATGC CCAACTGGTG 3900  
 GTTATGATTC CTGATGGCCA AAACATGGCA GAAGATGAAT TTGTTTACTG GCCAAATAAA 3960  
 GATGAGCCTA TAAATTGTGA GAGCTTTAAG GTCACCTCTA TGGCTGAAGA ACACAAATGT 4020  
 CTATCTAATG AGGAAAAACT TATAATTACG GACTTTATCT TAGAAGCTAC ACAGGATGAT 4080  
 TATGTACTTG AAGTGAGGCA CTTTCAGTGT CCTAAATGGC CAAATCCAGA TAGCCCCATT 4140  
 AGTAAACTTT TTGAACCTAT AAGTGTATA AAAGAAGAAG CTGCCAATAG GGATGGGCCT 4200  
 ATGATTGTTC ATGATGAGCA TGGAGGAGTG ACGGCAGGAA CTTTCTGTGC TCTGCAACC 4260  
 CTTATGCACC AACTAGAAAA AGAAAAATCC GTGATGTTT ACCAGGTAGC CAAGATGATC 4320  
 AATCTGATGA GGCAGGAGT CTTTGTGAC ATTGAGCAGT ATCAGTTTCT CTACAAAGTG 4380  
 ATCCTCAGCC TTGTGAGCAC AAGGCAGGAA GAGAATCCAT CCACCTCTCT GGACAGTAAT 4440  
 GGTGCGACAT TGCCGTATGG AAATATAGCT GAGAGCTTAG AGTCTTTAGT TTAACACAGA 4500  
 AAGGGGTGGG GGGACTCACA TCTGAGCATT GTTTTCCTCT TCCTAAAAAT AGGCAGGAAA 4560  
 ATCAGTCTAG TTCTGTTATC TGTTGATTTC CCATCACCTG ACAGTAACCT TCATGACATA 4620  
 GGATTCTGCC GCCAAATTA TATCATTAAC AATGTGTGCC TTTTGTGAAG ACTTGTAATT 4680  
 TACTTATTAT GTTTGAACATA AAATGATTGA ATTTTACAGT ATTTCTAAGA ATGGAATTGT 4740  
 GGTATTTTTT TCTGTATTGA TTTTAACAGA AAATTTCAAT TTATAGAGGT TAGGAATTCC 4800  
 AAACACAGA AAATGTTTGT TTTTAGTGT AAATTTTAG CTGTATTGT AGCAATTATC 4860  
 AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCCTGTA AATAAACAC TCTTCCATAT 4920  
 GATATTCAAC ATTTTACAAC TGCAGTATTC ACCTAAAGTA GAAATAATCT GTTACTTATT 4980  
 GTAAATACTG CCTAGTGTC TCCATGGACC AAATTTATAT TTATAATTGT AGATTTTTAT 5040  
 ATTTTACTAC TGAGTCAAGT TTTCTAGTTC TGTGTAATG TTTAGTTTAA TGACGTAGTT 5100  
 CATTAGCTGG TCTTACTCTA CCAGTTTCTT GACATTGTAT TGTGTACCT AAGTCATTAA 5160  
 CTTTGTTCAT GCATGTAAAT TTAACCTTTG TGGAAAATAG AAATACCTTC ATTTTGAAAG 5220  
 AAGTTTTTAT GAGAATAACA CCTTACCAA CATTGTTCAA ATGGTTTTTA TCCAAGGAAT 5280  
 TGCAAAAAATA AATATAAATA TGGCCATTAA AAAAAAATA AAAAAAATA AAAAAAATA 5340  
 AAA

Seq ID NO: 376 Protein sequence:  
 Protein Accession #: EOS sequence

65  
70  
75  
80

1 11 21 31 41 51  
 | | | | |  
 MRILKRFLAC IQLLCVRLD WANGYYRQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITFFH GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRSSFEAEV KKGKGLRLS 180  
 ILFEVGTENN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240  
 TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGVYMLMDY LQNNFREQQY KFSRQVFSSY 300  
 TGKEEIEHAV CSSEPNVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360  
 HEPLTDGYQD LGAILNLLP NMSYVLQIVA ICTNGLYKGY SDQLIVDMPT DNPDLDFPE 420  
 LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTHYNNRI GTKYNEAKTN 480  
 RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540  
 GSKTVLRSPH MNLSGTAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600  
 ENISQGYIFS SENPETTYD VLIPESARNA SEDSTSSGSE ESKLDPSMEG NVWFPSSTDI 660  
 TAQPDVSGSR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720  
 TEVTPHAFPT SSRQQLDVST VNVVYSQTTQ PVYNEASNSS HESRIGLAEG LESEKKAVIP 780  
 LVLVSALTFFI KLVVLVGLI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840  
 IKHFPKHVAD LHASSGFTEE FEEVQSCITVD LGITADSSNH PDNKHKNRYI NIVAYDHSRV 900  
 KLAQLAEKDG KLTDYINANY VDGYNRPKAY IAAQGPLKST AEDFWRMIWE HNVFVIMIT 960  
 NLVEKGRKDC DQYWPADGSE EYGNFLVTQK SVQVLAYTYV RNFTLRNTKI KKSQKGRPS 1020

GRVVVTQYHYT QWPDMDGVPEY SLPVLTFVVRK AAYAKRHAVG PVVVHCSAGV GRTGTYYIVLD 1080  
 SMLQQIQHEG TVNIFGFLKH IRSQRNYLVQ TEEQYVFIHD TLVEAIIKSKE TEVLDSHIHA 1140  
 YVNAILIPGF AGKTKLEKQF QLLSQSNIQ SDYSAALKQC NREKNRTSSI IPVERSRVGI 1200  
 5 SLSGEGTDY INASYIMGY QSNEFIITQH PLLHTIKDFW RMIWDHNAQL VVMIPDQNM 1260  
 AEDEFVYWFN KDEPINCESF KVTLMABEHK CLSNEEKLI QDFILEATQD DYVLEVRHFQ 1320  
 CPKWPNDPSP ISKTFELISV IKBEAANRDG PMIVHDEHGG VTAGTFCAIT TLMHQLKEKN 1380  
 SVDVYQVAKM INLMRPGVFA DIEQYQFLYK VILSLVSTRQ EENPSTSLDS NGAAALPDGNI 1440  
 AESLESLELV

Seq ID NO: 377 DNA sequence  
 Nucleic Acid Accession #: EOS sequence  
 Coding sequence: 501-4514

15 1 11 21 31 41 51  
 | | | | |  
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60  
 CAAAAAAAAC ATTTCTCTCG CTCCTCCCTC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120  
 CGGCGAGGGG CCGCAGACCG TCTGGAAATG CGAATCCTAA AGCGTTTCCT CGCTTGCAAT 180  
 20 CAGCTCCTCT GTGTTTGCCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTTGTTGAAG AGATTGGCTG GTCCATATACA GGAGCACTGA ATCAAAAAAT TGGGGAAGA 300  
 AATATCCAAC ATGTAATAGC CCAAAACAAT CTCCTATCAA TATTGATGAA GATCTTACAC 360  
 AAGTAAATGT GAATCTTAAG AAACCTAAAT TTCAGGGTTG GGATAAAACA TCATTGGAAA 420  
 25 ACACATTCAT TCATAACACT GGGAAAAACG TGGAAATTAA TCTCACTAAT GACTACCGTG 480  
 TCAGCGGAGG AGTTTCAGAA ATGGTGTGTA AAGCAAGCAA GATAACTTT CACTGGGGAA 540  
 AATGCAATAT GTCATCTGAT GGATCAGAGC ATAGTTTAGA AGGACAAAAA TTTCCACTTG 600  
 AGATGCAAAAT CTACTGCTTT GATGCGGACC GATTTCAGG TTTTGAGGAA GCAGTCAAAG 660  
 GAAAAGGGAA GTTAAGAGCT TTATCCATT TGTGAGGT TGGGACAGAA GAAAATTGG 720  
 30 ATTTCAAAGC GATTATTGAT GGAGTCGAAA GTGTTAGTCG TTTTGGGAAG CAGGCTGCTT 780  
 TAGATCCATT CATACTGTG AACCTTCTGC CAAACTCAAC TGACAAGTAT TACATTTACA 840  
 ATGGCTCATT GACATCTCCT CCCTGCACAG ACACAGTTGA CTGGATTGTT TTTAAAGATA 900  
 CAGTTAGCAT CTCGAAAGC CAGTTGGCTG TTTTGTGTA AGTTCTTACA ATGCAACAAT 960  
 CTGCTTATGT CATGCTGATG GACTACTTAC AAAACAATTT TCGAGAGCAA CAGTACAAGT 1020  
 35 TCTCTAGACA GGTGTTTTCC TCATACACTG GAAAGGAAGA GATTTCATGAA GCAGTTTGTG 1080  
 GTTCAGAAAC AGAAATGTT CAGGCTGACC CAGAGAATTA TACCAGCCTT CTTGTTACAT 1140  
 GGGAAAGACC TCGAGTCGTT TATGATACCA TGATTGAGAA GTTTGCAGTT TTGTACCAGC 1200  
 AGTTGGATGG AGAGGACCAA ACCAAGCATG AATTTTTGAC AGATGGCTAT CAAGACTTGG 1260  
 GTGCTATTCT CAATAATTG CTACCCAATA TGAGTTATGT TCTTCAGATA GTAGCCATAT 1320  
 40 GCATTAATGG CTTTATATGA AAATACAGCG ACCAAGTATG TGTCGACATG CCTACTGATA 1380  
 ATCTGAACT TGATCTTTTC CCTGAATTAA TTGGAACCTGA AGAAATAATC AAGGAGGAGG 1440  
 AAGAGGGAAA AGACATTGAA GAAGGCGCTA TTGTGAATCC TGGTAGAGAC AGTGCTACAA 1500  
 ACCAAATCAG GAAAAGGAAA CCCCAGATTT CTACCACAAC ACACATCAAT CGCATAGGGA 1560  
 CGAAATACAA TGAAGCCCAAG ACTAACCGAT CCCCACAAG AGGAAAGTGA TTTCTCTGGA 1620  
 45 AGGTGATGT TCCCAATACA TCTTTAAATT CCACTTCCCA ACCAGTCACT AAATTAGCCA 1680  
 CAGAAAAAGA TATTTCTCTG ACTTCTCAGA CTGTGACTGA ACTGCCACCT CACACTGTGG 1740  
 AAGGTACTTC AGCCTCTTTA AATGATGGCT CTAAAAGTGT TCTTAGATCT CCACATATGA 1800  
 ACTTGTGCGG GACTCAGAAA TCCTTAAATA CAGTTTCTAT AACAGAATAT GAGGAGGAGA 1860  
 GTTTATTGAC CAGTTTCAAG CTTGATACTG GAGCTGAAGA TTTCTCAGGC TCCAGTCCCG 1920  
 50 CAACTTCTGC TATCCCATTC ATCTCTGAGA ACATATCCCA AGGATATATA TTTCTCTCG 1980  
 AAAACCCAGA GACAATAACA TATGATGTCC TTATACCAGA ATCTGCTAGA AATGCTTCCG 2040  
 AAGATTCAAC TTCACTCAGT TCAGAGAAT CACTAAAGGA TCCTTCTATG GAGGGAATG 2100  
 TGTGTTTCC TAGCTCTACA GACATAACAG CACAGCCCGA TGTGATGATG GGCAGAGAGA 2160  
 GCTTTCTCCA GACTAATTAC ACTGAGATAC GTGTTGATGA ATCTGAGAAG ACAACCAAGT 2220  
 CCTTTCTGC AGGCCAGTG ATGTACAGG GTCCCTCAGT TACAGATCTG GAAATGCCAC 2280  
 55 ATTATTCTAC CTTTGCTTAC TTCCCACTG AGGTAACACC TCATGCTTTT ACCCATCTCT 2340  
 CCAGACAACA GGATTTGGTC TCCACGGTCA ACGTGGTATA CTGCGAGACA ACCCAACCGG 2400  
 TATACAATGA GGCCAGTAAT AGTAGCCATG AGTCTCGTAT TGGTCTAGCT GAGGGTTGG 2460  
 AATCCGAGAA GAAGGCAGTT ATACCCCTTG TGATCGTGTC AGCCCTGACT TTTATCTGTC 2520  
 TAGTGGTTCT TGTGGGTATT CTCATCTACT GGAGGAAATG CTTCCAGACT GCACACTTTT 2580  
 60 ACTTAGAGGA CATTGCTATC CCTAGAGTTA TATCCACACC TCCAACACCT ATCTTTCCAA 2640  
 TTTCAAGATG TGTCGAGCA ATTCCAATAA AGCACTTCC AAAGCATGTT GCAGATTTAC 2700  
 ATGCAAGTAG TGGGTTTACT GAAGAATTG AGACACTGAA AGAGTTTAC CAGGAAGTGC 2760  
 AGAGCTGTAC TGTGACTTA GGTATTACAG CAGACAGCTC CAACCAACCA GACAACAAGC 2820  
 65 ACAAGAAATG ATACATAAAT ATCGTTGCCT ATGATCATAG CAGGGTTAAG CTAGCACAGC 2880  
 TTGCTGAAAA GGATGGCAAA CTGACTGATT ATATCAATGC CAATTATGTT GATGGCTACA 2940  
 ACAGACCAAA AGCTTATATT GCTGCCCAAG GCCCACTGAA ATCCACAGCT GAAGATTCT 3000  
 GGAGAAATGAT ATGGGAACAT AATGTGGAAG TTATTGTCAT GATAACAAAC CTCGTGGAGA 3060  
 AAGGAAGGAG AAAATGTGAT CAGTACTGGC CTGCCGATGG GAGTGAGGAG TACGGGAAC 3120  
 70 TTCGTGTCAC TCAGAAAGAT GTGCAAGTGC TTGCCTATTA TACTGTGAGG AATTTTACTC 3180  
 TAAGAAACAC AAAAATAAAA AAGGGCTCCC AGAAAGGAAG ACCCAGTGGG CGTGTGGTCA 3240  
 CACAGTATCA CTACACGCAG TGGCCTGACA TGGGAGTACC AGAGTACTCC CTGCCAGTGC 3300  
 TGACCTTTGT GAGAAAGGCA GCCTATGCCA AGCGCCATGC AGTGGGCGCT GTTGTCTGTC 3360  
 75 ACTGCAGTGC TGGAGTTGGA AGAACAGGCA CATATATTGT GCTAGACAGT ATGTTGCAGC 3420  
 AGATTCAACA CGAAGGAACT GTCAACATAT TTGGCTTCTT AAAACACATC CGTTCACAAA 3480  
 GAAATTATTT GGTACAACCT GAGGAGCAAT ATGCTTTCAT TCATGATACA CTGGTTGAGG 3540  
 CCATACCTAG TAAAGAAACT GAGGTGCTGG ACAGTCATAT TCATGCCATAT GTTAATGCAC 3600  
 80 TCCTCATTTCC TGGACCAGCA GGCAAAACAA AGCTAGAGAA ACAATTCCAG CTCCTGAGCC 3660  
 AGTCAAAATAT ACAGCAGAGT GACTATTCTG CAGCCCTAAA GCAATGCAAC AGGGAAGA 3720  
 ATCGAACTTC TTCTATCATC CCTGTGGAAA GATCAAGGGT TGGCATTTCA TCCCTGAGTG 3780  
 GAGAAAGCAC AGACTACATC AATGCTCTCT ATATCATGGG CTATTACCAG AGCAATGAAT 3840  
 TCATCATTAC CCAGCACCTC CTCCTTCATA CCATCAAGGA TTTCTGGAGG ATGATATGGG 3900  
 ACCATAATGC CCACTGGTG GTTATGATTC CTGATGGCCA AAACATGGCA GAAGATGAAT 3960  
 TTGTTTACTG GCCAAATAAA GATGAGCCTA TAAATTGTGA GAGCTTTAAG GTCACCTTAA 4020  
 TGGCTGAAGA ACACAAATGT CTATCTAATG AGGAAAAACT TATAATTACAG GACTTTATCT 4080

TAGAAGCTAC ACAGGATGAT TATGTACTTG AAGTGAGGCA CTTTCAGTGT CCTAAATGGC 4140  
 CAAATCCAGA TAGCCCCATT AGTAAACTT TTGAACCTAT AAGTGTATTA AAAGAAGAAG 4200  
 CTGCCAATAG GGATGGGCTT ATGATTGTTC ATGATGAGCA TGGAGGAGTG ACGGCAGGAA 4260  
 CTTTCTGTGC TCTGACAAAC CTTATGCACC AACTAGAAAA AGAAAATTCC GTGGATGTTT 4320  
 ACCAGGTAGC CAAGATGATC AATCTGATGA GGCCAGGAGT CTTTGTCTGAC ATTGAGCAGT 4380  
 ATCAGTTTCT CTACAAGTG ATCCTCAGCC TTGTGAGCAC AAGGCAGGAA GAGAAATCCAT 4440  
 CCACCTCTCT GGACAGTAAT GGTGCAGCAT TGCCTGATGG AAATATAGCT GAGAGCTTAG 4500  
 AGTCTTTAGT TTAACACAGA AAGGGGTGGG GGGACTCACA TCTGAGCATT GTTTCTCTCT 4560  
 TCCTAAAAAT AGGCAGGAAA ATCAGTCTAG TTCTGTTATC TGTGATTTC CCATCACCTG 4620  
 ACAGTAACCT TCATGACATA GGATTCTGCC GCCAAATTTA TATCATTAAAC AATGTGTGCC 4680  
 TTTTGTGAAG ACTTGTAATT TACTTATTAT GTTTGAACCT AAATGATTGA ATTTTACAGT 4740  
 ATTTCTAAGA ATGGAATTGT GGTATTTTTC TCTGTATTGA TTTTAACAGA AAATTTCAT 4800  
 TTATAGAGGT TAGGAATTCC AACTACAGA AAATGTTTGT TTTTAGTGTC AAATTTTTCAG 4860  
 CTGTATTGTG AGCAATTATC AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCCTGTA 4920  
 AATAAACAC TCTTCCATAT GATATTCAAC ATTTTACAAC TGCAGTATTC ACCTAAAGTA 4980  
 GAAATAATCT GTTACTTATT GTAAATACCT CCCTAGTGTC TCCATGGACC AAATTTATAT 5040  
 TTATAATTGT AGATTTTATC ATTTTACTAC TGAGTCAAGT TTTCTAGTTC TGTGTAATTG 5100  
 TTTAGTTTAA TGACGTAGTT CATTAGCTGG TCTTACTCTA CCAGTTTCTT GACATTGTAT 5160  
 TGTGTTACCT AAGTCATTAA CTTTGTTCCT GCATGTAATT TTAACTTTTC TGGAAAATAG 5220  
 AAATACCTTC ATTTTGAAAG AAGTTTTTAT GAGAATAACA CCTTACCAA CATGTGTTCAA 5280  
 ATGGTTTTTA TCCAAGGAAT TGCAAAAATA AATATAAATA TTGCCATTAA AAAAAAATAA 5340  
 AAAAAAATAA AAAAAAATAA AAA

Seq ID NO: 378 Protein sequence:  
 Protein Accession #: EOS sequence

1 11 21 31 41 51  
 | | | | |  
 MVFKASKITF HWGKCNMSSD GSEHSLEGQK FPLEMQIYCF DADRFSSEFEE AVKKGKGLRA 60  
 LSILFEVGTG ENLDFKATID GVESVSRFGK QAALDPFILL NLLPNSTDYK YIYNGSLTSP 120  
 PCTDTVDWIV FKDTVSISES QLAVFCEVLT MQQSGYVMLM DYLNQNFREQ QYKFSRQVFS 180  
 SYTGKEEIHG AVCSSEPENV QADPENYTSI LVTWERPRV YDTMIEKFAV LYQQLDGEDQ 240  
 TKHEFLTDGY QDLGAILNML LPNMSYVLQI VAITCNGLYG KYSDQLIVDM PTDNPELDF 300  
 PELIGTEBII KEEBEGKID EGAIVNPGRD SATNQIRKKE PQISTTTHYN RIGTKYNEAK 360  
 TNRSPTRGSE PSGKGDVPNT SLNSTSQPVT KLATEKDIDL TSQVTLELPP HTVEGTSASL 420  
 NDGSKTVLRS PHMNLSTGAE SLNVTISITEE EESLLTSFK LDTGAEDSSG SSPATSAIPF 480  
 ISENISQGYI FSSNPETIT YDVLIPESAR NASEDSTSSG SEESLKDPSM BGNVWFPSST 540  
 DITAGPDVGS GRESFLQNTY THIRVDESEK TTKSFSAGPV MSQGPSVTDL EMPHYSTFAY 600  
 FPEVTTPHAF TPSSRQQLV STVNVVYSQT TQPVYNEASN SSHESTRIGLA BGLESEKKAV 660  
 IPLVIVSALT FICLVVLVGI LIYWRKCFQT AHFYLEDSTS PRVISTPPTP IFPIISDDVGA 720  
 IPIKHPFKHV ADLHASSGFT EEFETLKEFY QEVQSCVTDL GITADSSNHP DNKHKRYIN 780  
 JVAYDHSRVK LAQLAEKDGK LTDYINANYV DGYNRPKAYI AAQGPLKSTA EDFWRMIWEH 840  
 NVEVIVMTIN LVEKGRKCD QYWPADGSEE YGNFLVTQKS VQVFLAYYTVR NFTLRNTKIK 900  
 KGSQKGRPSG RVVTQYHYTQ WPDMGVPEYS LPVLTFVRKA AYAKRHAVGP VVVHCSAGVG 960  
 RTGTIYVLDS MLQQIQHEGT VNIFGFLKHI RSQRNYLVQT EEEQYVFIHDT LVEAILSKET 1020  
 EYLDSHIHAY VNALLIPGPA GKTLEKQFQ LLSQSNIQQS DYSALKQCN REKNRTSSII 1080  
 PVERSRRVGS SLSGEGTDYI NASYIMGYQ SNEFIIIOHP LHHTIKDFWR MIWDHNAQLV 1140  
 VMIPDQNMMA EDEFVYWPNK DEPINCESFK VTLMAEBHKC LSNEEKLIIO DFILEATQDD 1200  
 YVLEVRHFQC PKWPNPDSPI SKTFELISVI KEEAANRDGP MIVHDEHGGV TAGTFCALTT 1260  
 LMHOLEKENS VDVYQVAKMI NLMRPGVFAD IEQYQFLYKV ILSLVSTRQE ENPSTSLDSN 1320  
 GAALPDGNIA ESLESIV

Seq ID NO: 379 DNA sequence  
 Nucleic Acid Accession #: EOS sequence  
 Coding sequence: 148-4632

1 11 21 31 41 51  
 | | | | |  
 CACACATACG CAGCAGCAGT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60  
 CAAAAAAAC ATTTCCCTTCG CTCCCTCCCTC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120  
 CGGCGAGGGG CCGCAGACCG TCTGGAAATG CGAATCCTAA AACGTTTCCT CGCTTGCAAT 180  
 CAGCTCCTCT GTGTTTGCCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTTGTTGAAG AGATTGGCTG GTCTATACA GGAGCACTGA ATCAAAAAA TTGGGGAAG 300  
 AAATATCCAA CATGTAATAG CCCAAACAA TCTCCTATCA ATATTGATGA AGATCTTACA 360  
 CAAGTAAATG TGAATCTTAA GAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA 420  
 AACACATCA TTCATAACAC TGGGAAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT 480  
 GTCAGCGGAG GAGTTTCAGA AATGGTGTTC AAAGCAAGCA AGATAACTTT TCACTGGGGA 540  
 AAATGCAATA TGTCACTGTA TGGATCAGAG CATAGTTTAG AAGGACAAA ATTTCCACTT 600  
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTCCTA GTTTTGAGGA AGCAGTCAAA 660  
 GGAAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAATTG 720  
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGGGAA GCAGGCTGCT 780  
 TTAGATCCAT TCATACTGTT GAACCTCTG CCAAACCTCA CTGACAAGTA TTACATTTAC 840  
 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900  
 ACAGTTAGCA TCTCTGAAG CCAGTTGGCT GTTTTGTGAG AAGTCTTAC AATGCAACAA 960  
 TCTGGTTATG TCATGCTGAT GGACTACTTA CAAAACAATT TTCGAGAGCA ACAGTACAAG 1020  
 TTCTCTAGAC AGGTGTTTTC CTCATACACT GGAAAGGAAG AGATTCAATGA AGCAGTTTGT 1080  
 AGTTCAGAAC CAGAAAATGT TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTTCAC 1140  
 TGGGAAAGAC CTCGAGTCGT TTATGATACC ATGATTGAGA AGTTTGCAGT TTTGTACCAG 1200  
 CAGTTGATG GAGAGGACCA AACCAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260  
 GGTGCTATTG TCAATTAATT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320  
 TGCATAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT 1380  
 AATCCTGAAC TTGATCTTTT CCTGAATTA ATTGGAACCT AAGAAATAAT CAAGGAGGAG 1440  
 GAAGAGGGAA AAGACATTGA AGAAGSCGCT ATTGTGAATC CTGGTAGAGA CAGTGCTACA 1500  
 AACCANAATCA GGAAGGAAGG ACCCCAGATT TCTACCACAA CACACTACAA TCGCATAGGG 1560

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65

```

ACGAAATACA ATGAAGCCAA GACTAACCGA TCCCCAACAA GAGGAAGTGA ATTCTCTGGA 1620
AAGGGTGATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCAGTCAC TAAATTAGCC 1680
ACAGAAAAAG ATATTTCCTT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740
GAAGGTACTT CAGCCTCTTT AAATGATGGC TCTAAACTG TTCTTAGATC TCCACATATG 1800
AACTTGTCCG GGACTGCAGA ATCCTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860
AGTTTATTGA CCAGTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC 1920
GCAACTTCTG CTATCCCATT CATCTCTGAG AACATATCCC AAGGGTATAT ATTTTCTCTC 1980
GAAAACCCAG AGACAAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AATGCTTCCC 2040
GAAGATTCAA CTTCATCAGG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAAT 2100
GTGTGGTTTC TAGTCTCTC AGACATAACA GCACAGCCCC ATGTTGGATC AGGCAGAGAG 2160
AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTGATG AATCTGAGAA GACAACCAAG 2220
TCCTTTTCTG CAGGCCCAGT GATGTCCACG GGTCCCTCAG TTACAGATCT GGAAATGCCA 2280
CATTATTCTA CCTTTGCCCTA CTCCCAACT GAGGTAACAC CTCATGCTTT TACCCCATCC 2340
TCCAGACAAC AGGATTGTGT CTCCACGGTC AACGTGGTAT ACTCGCAGAC AACCCAACCG 2400
GTATACAATG AGGCCAGTAA TAGTAGCCAT GAGTCTCGTA TTGGTCTAGC TGAGGGGTTG 2460
GAATCCGAGA AGAAGGCAGT TATACCCCTT GTGATCGTGT CAGCCCTGAC TTTTATCTGT 2520
CTAGTGGTTC TTGTGGGTAT TCTCATCTAC TGGAGGAAAT GCTTCCAGAC TGCACACTTT 2580
TACTTAGAGG ACAGATGATC CCTAGAGTT ATATCCACAC CTCCAACACC TATCTTTCCA 2640
ATTTTCAGATG ATGTCGGAGC AATTCCAATA AAGCACTTTC CAAAGCATGT TGCAGATTTA 2700
CATGCAAGTA GTGGGTTTAC TGAAGAAATT GAGACACTGA AAGAGTTTTA CCAGGAAGTG 2760
CAGAGCTGTA CTGTTGACTT AGGTATTACA GCAGACAGCT CCAACCACCC AGACAACAAG 2820
CACAAGAATC GATACATAAA TATCGTTGCC TATGATCATA GCAGGGTTAA GCTAGCACAG 2880
CTTGCTGAAA AGGATGGCAA ACTGACTGAT TATATCAATG CCAATTATGT TGATGGCTAC 2940
AACAGACCAA AAGCTTATAT TGCTGCCCAA GGCCCACTGA AATCCACAGC TGAAGATTTT 3000
TGGAGAAATG TATGGGAACA TAATGTGGAA GTTATTGTCA TGATAACAAA CCTCGTGGAG 3060
AAGGAAAGGA GAAATGTGTA TCAGTACTGG CCTGCCGATG GGAGTGAGGA GTACGGGAAC 3120
TTTCTGTTCA CTAGAAGAG TGTCGAAGTG CTTGCCCTATT ATACTGTGAG GAATTTTACT 3180
CTAAGAAACA CAAAAATAAA AAAGGGCTCC CAGAAAGGAA GACCCAGTGG ACGTGTGGTC 3240
ACACAGTATC ACTACACGCA GTGGCCTGAC ATGGGAGTAC CAGAGTACTC CCTGCCAGTG 3300
CTGACCTTTG TGAGAAAGGC AGCCTATGCC AAGCGCCATG CAGTGGGGCC TGTGTGCTG 3360
CACTGCAGTG CTGAGGTTGG AAGAACAGGC ACATATATTG TGCTAGACAG TATGTTGCAG 3420
CAGATTC AACGAGGAAC TGTCACATA TTTGGCTTCT TAAACACAT CCGTTCACAA 3480
AGAAATTATT TGGTACAAAC TGAGGAGCAA TATGTCCTCA TTCATGATAC ACTGGTTGAG 3540
GCCATACCTA GTAAAGAAAC TGAGGTGCTG GACAGTCATA TTCATGCTTA TGTTAATGCA 3600
CTCCTCATTC CTGACACAGC AGGCAAAACA AAGCTAGAGA AACAATTCCA GGGTCTCACT 3660
CTGTCAACCA GGCTGGAGTG CAGAGGCACA ATCTCGGCTC ACTGCAACCT TCCTCTCCCT 3720
GGCTTAACCTG ATCCTCTTAC CTCAGCCTCC CGAGTGGCTG GACTATACT CCTGAGCCAG 3780
TCAAAATATC AGCAGATGTA CTATTCTGCA GCCCTAAAGC AATGCAACAG GGAAGAAGAT 3840
CGAACTTCTT CTATCATCCC TGTGGAAGA TCAAGGGTTG GCATTTCATC CCTGAGTGA 3900
GAAGGCACAG ACTACATCAA TGCCTCCTAT ATCATGGGCT ATTACCAGAG CAATGAATTC 3960
ATCATTACCC AGCACCTCTC CCTTCATACC ATCAAGGATT TCTGGAGGAT GATATGGGAC 4020
CATAATGCCC AACTGGTGGT TATGATTCCCT GATGGCCAAA ACATGGCAGA AGATGAATTT 4080
GTTTACTGGC CAAATAAAGA TGAGCCTATA AATTGTGAGA GCTTTAAGGT CACTCTTATG 4140
GCTGAAGAAC ACAAATGTCT ATCTAATGAG GAAAAACTTA TAATTCAGGA CTTTATCTTA 4200
GAAGCTACAC AGGATGATTA TGTACTTGAA GTGAGGCACT TTCAGTGTCC TAAATGGCCA 4260
AATCCAGATA GCCCATTAG TAAACTTTT GAACTTATA GTGTTATAAA AGAAGAAGCT 4320
GCCAATAGGG ATGGGCCCTT GATTGTTTCA TATGAGCATG GAGGAGTGAC GGCAGGAAC 4380
TTCTGTGCTC TGACAAACCT TATGCACCAA CTAGAAAAAG AAAATTCCTG GATGTTTAC 4440
CAGGTAGCCA AGATGATCAA TCTGATGAGG CCAGGAGTCT TTGCTGACAT TGAGCAGTAT 4500
CAGTTTCTCT ACAAAGTGAT CCTCAGCCTT GTGGGCACAA GGCAGGAAGA GAATCCATCC 4560
ACCTCTCTGG ACAGTAATGG TGCAGCATTE CCTGATGGAA ATATAGCTGA GAGCTTAGAG 4620
TCTTTAGTTT AACACAGAAA GGGGTGGGG GACTCACATC TGAGCATTTG TTTCTCTCTC 4680
CTAAATTAG GCAGGAAAAT CAGTCTAGTT CTGTTATCTG TTGATTTCCT ATCACTGAC 4740
AGTAACTTTC ATGACATAGG ATTCTGCCGC CAAATTTATA TCATTAACAA TGTGTGCCCT 4800
TTTGCAAGAC TTGTAATTGA CTTATTATGT TTGAACATAA ATGATTGAAT TTTACAGTAT 4860
TTCTAAGAAT GGAATTGTGG TATTTTTTTC TGTATTGATT TTAACAGAAA ATTTCAATTT 4920
ATAGAGGTTA GGAATTTCAA ACTACAGAAA ATGTTTGTGT TTAGTGTCAA ATTTTAGCT 4980
GTATTTGTAG CAATTATCAG GTTTGCTAGA AATATAACTT TTAATACAGT AGCCTGTAAA 5040
TAAACACTC TTCCATATGA TATTCAACAT TTACAACCTG CAGTATTCAC CTAAGTAGA 5100
AATAATCTGT TACTTATTTG AAATACTGCC CTAGTGTCTC CATGGACCAA ATTTATATTT 5160
ATAATTGTAG ATTTTTATAT TTTACTACTG AGTCAAGTTT TCTAGTCTG TGTAAATGTT 5220
TAGTTTAAAT ACGTAGTTCA TTAGCTGGTC TTACTCTACC AGTTTTCTGA CATTGTATTG 5280
TGTTACCTAA GTCAATTAAC TTGTTTCAGC ATGTAATTTT AACTTTTGTG GAAAATAGAA 5340
ATACCTTCAT TTTGAAAGAA GTTTTTATGA GAATAACACC TTACCAACAA TTGTTCAAAT 5400
GGTTTTTATC CAAGGAATTG CAAAAATAAA TATAAATATT GCCATTAAAA AAAAAAATAA 5460
AAAAAATAAA AAAAAAATAA A

```

Seq ID NO: 380 Protein sequence:  
Protein Accession #: EOS sequence

70  
75  
80

```

1      11      21      31      41      51
|      |      |      |      |      |
MRILKRFAC IQLLCVCRID WANGYYRQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60
QSPINIDEDL TQVNVNLKKL KFGQWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
FKASKITHFW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFBFAV KKGKGLRALS 180
ILFEVGTEN LDFKAILDVG ESVSRFGKQA ALDPFILLNL LPNSTDKYII YNGSLTSPPC 240
TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300
TGKEEIEHAV CSSEPENVQA DPENYTSLLV TWERPRVVYD TMIEKFAVLX QQLDGEDQTK 360
HEFLTDGYQD LGAILNNLLP NMSVVLQIVA ICTNGLYGY SDQLIVDMPT DNPDLDFPE 420
LIGTEBIIKE BEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNRI GTKYNEAKTN 480
RSPTRGSEFS KGKDVNTSLG NSTSQPVTKL ATEKDISLTS QTVTELPHT VEGTSASLND 540
GSKTVLRSFH MNLSTGAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600
ENISQGYIFS SENPETITYD VLIPE SARNA SEDSTSSGSE ESKDPSMEG NVWFPSSTDI 660
TAQPDVGSGR ESFLQNTYNE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAFFP 720

```

TEVTPHAFPT SSRQDLVST VNVVYSQTTQ PVYNEASNSS HESRIGLAEG LESEKKAVIP 780  
 LVIVSALTFI CLVVLVGLI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840  
 IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCVTDLGI TADSSNHPDN KHKNRYINIV 900  
 AYDHSRVKLA QLAEKDGKLT DYINANYVDG YNRPKAYIAA QGPLKSTAED FWRMIWEHNV 960  
 EVIVMITNLV EKGRRKCDQY WPADGSEBYG NFLVTQKSVQ VLAYYTVRNF TLRNTKIKKG 1020  
 SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFFVRKAAY AKRHAVGPVV VHCAGVGRVT 1080  
 GTYIVLDSML QQIQHEGTVN IFGLKHIRS QRNYLVQTEE QYVFIHDTLV EAILSKEDEV 1140  
 LDSHIHAYVN ALLIPGPAGK TKLEKQFQGL TSPRLRCRG TISAHCNLPL PGLTDPPTS 1200  
 SRVAGTILLS QSNIQSDYS AALKQCNREK NRTSSIIPE RSRVGISSLS GEGTDYINAS 1260  
 YIMGYQSNL FIITQHPLLH TIKDFWRMIW DHNAQLVMI PDGQNAEDE FVYWPKNDEP 1320  
 INCESFKVTL MABEHKCLSN EEKLIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPIST 1380  
 FELISVKEE AANRDGPMIV HDEHGGVTAG TFCALTILMH QLEKENSVDV YQVAKMINLM 1440  
 RGPVFADIEQ YQFLYKVLS LVGTRQENP STSLDSNGAA LPDGNIAESL ESLV

Seq ID NO: 381 DNA sequence  
 Nucleic Acid Accession #: NM\_002851.1  
 Coding sequence: 148..7092

1 11 21 31 41 51  
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60  
 CAAAAAAAAC ATTTCCCTTCG CTCGCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120  
 CGGCGAGGGG CCGCAGACCG TCTGGAATG CGAATCCTAA AGCGTTTCCT CGCTTGCAAT 180  
 CAGCTCCTCT GTGTTTGCCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTTGTGGAAG AGATTGGCTG GTCCTATACA GGAGCACTGA ATCAAAAAAA TTGGGGAAAG 300  
 AAATATCCAA CATGTAATAG CCAAAACAA TCTCCTATCA ATATTGATGA AGATCTTACA 360  
 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA 420  
 AACACATTCA TTCATAACAC TGGGAAAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT 480  
 GTCAGCGGAG GAGTTTCAGA AATGGTGTIT AAAGCAAGCA AGATAACTTT TCACCTGGGA 540  
 AAATGCAATA TGTACCTTGA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600  
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAAA 660  
 GGAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAATTTTG 720  
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGGGAA GCAGGCTGCT 780  
 TTAGATCCAT TCATCTGTG GAACTTCTG CCAAACTCAA CTGACAAGTA TTACATTTAC 840  
 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900  
 ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTTGTG AAGTTCTTAC AATGCAACAA 960  
 TCTGTTATG TCATCTGTG GCACTACTTA CAAAACAAAT TTCGAGAGCA ACAGTACAAAG 1020  
 TTCTCTAGAG AGGTGTTTTT CTCATACACT GGAAAGGAAG AGATTATGA AGCAGTTTGT 1080  
 AGTTCAGAAC CAGAAATGT TCAGGCTGAC CCAGAGAAAT ATACCAGCCT TCTTGTACA 1140  
 TGGGAAAGAC CTCGAGTCGT TTAGTATACC ATGATTGAGA AGTTTGCAGT TTTGTACCAG 1200  
 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260  
 GGTGCTATTC TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320  
 TGCACATATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT 1380  
 AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAAC TGAAATAAT CAAGGAGGAG 1440  
 GAAGAGGGAA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGGTAGAGA CAGTGTCTAC 1500  
 AACCAATACA GGAAGGAGGA ACCCCAGATT TCTACCACAA CACACTACAA TCAGATAGGG 1560  
 ACGAAATACA ATGAAGCCAA GACTAACCGA TCCCCAACAA GAGGAAGTGA ATTCTCTGGA 1620  
 AAGGGTGATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCAGTCAC TAAATTAGCC 1680  
 ACAGAAAAAG ATATTTCCCT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740  
 GAAGGTACTT GACCCCTCTT AAATGATGGC TCTAAAAC TGCTTAGATC TCACATATG 1800  
 AACTTGTGCG GGACTGCAGA ATCCTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860  
 AGTTTATTGA CCAGTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCAGTCCC 1920  
 GCAACTCTG CTATCCCAT CTCTCTGAG AACATATCCC AAGGGTATAT ATTTTCTCTC 1980  
 GAAACCCAG AGACAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC 2040  
 GAAGATTCAA CTTATCAGG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT GAGGAGGAAAT 2100  
 GTGTGTTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160  
 AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTGATG AATCTGAGAA GACAACCAAG 2220  
 TCCTTTCTG CAGGCCAGT GATGTCCAG GGTCCCTCAG TTACAGATCT GGAATGCCA 2280  
 CATATTCTGA CCTTTGCCA CTTCCTAACT GAGGTAACAC CTCATGCTTT TACCCCATCC 2340  
 TCCAGACAAC AGGATTTGGT CTCCACGTC AACGTGGTAT ACTCGCAGAC AACCCAACCG 2400  
 GTATACATG TGAGAGACCC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC 2460  
 ACCCTTTGT GTCTTGACAA TCAGATCCTC AACACTACCC CTGCTGCTTC AAGTAGTGAT 2520  
 TCGGCTTGC ATGTACGCC TGTATTTCCC AGTGTGATG TGTCAATTGA ATCCATCTG 2580  
 TCTTCTATG ATGCTGCACC TTTGCTTCCA TTTTCTCTG CTTCCTTCAG TAGTGAATTG 2640  
 TTTGCGCATC TGCATACAGT TTCTCAAATC CTTCCACAAG TTAATTCAGC TACCAGAGAT 2700  
 GATAAGGTGC CCTTGATGC TTCTCTGCCA GTGGCTGGGG GTGATTTGCT ATTAGAGCCC 2760  
 AGCTTGTCT AGTATCTGA TGTGCTGTCC ACTACTCATG CTGCTTCAGA GACGCTGGAA 2820  
 TTTGGTAGTG AATCTGGTGT TCTTTATAAA ACGCTTATGT TTTCTCAAGT TGAACCAACC 2880  
 AGCAGTGATG CCATGATGCA TGCAGTTCT TCAGGGCCTG AACCTTCTTA TGCCTTGTCT 2940  
 GATAATGAGG GCTCCCAACA CATCTTCACT GTTTCTTACA GTTCTGCAAT ACCTGTGCAT 3000  
 GATTCTGTGG GTGTAACCTA TCAGGGTTC TATTTAGCG GCCCTAGCCA TATACCAATA 3060  
 CCTAAGTCTT CGTTAATAAG CCAACTGCA TCATTACTGC AGCCTACTCA TGCCCTCTCT 3120  
 GGTGATGGGG AATGGTCTGG AGCCTCTTCT GATAGTGAAT TTCTTTTACC TGACACAGAT 3180  
 GGGCTGACAG CCCTTAACAT TTCTTCACT GTTCTGTAG CTGAATTTAC ATATACAACA 3240  
 TCTGTGTTTG GTGATGATA TAAGGCGCT TCTAAAAGT AAATAATATA TGGAAATGAG 3300  
 ACTGAAGTGC AATTCCTTTC TTCAATGAG ATGGTTTACC CTCTGAAAG CACAGTCATG 3360  
 CCCAACATGT ATGATAATGT AAATAAGTTG AATGCGTCTT TACAAGAAAC CTCTGTTTCC 3420  
 ATTTCTAGCA CCAAGGGCAT GTTCCAGGG TCCCTTGTCT ATACCACCAC TAAGGTTTTT 3480  
 GATCATGAGA TTAGTCAAGT TCCAGAAAAT AACTTTTCAG TTCAACCTAC ACATACTGTC 3540  
 TCTCAAGCAT CTGGTGACAC TTCGCTTAAA CCGTGTCTTA GTGCAAACTC AGAGCCAGCA 3600  
 TCCTCTGACC CTGCTTCTAG TGAAATGTTA TCTCCTTCAA CTCAGTCTT ATTTTATGAG 3660  
 ACCTCAGCTT CTTTATGATC TGAAGTATTG CTACAACCTT CCTTTCAGGC TTCTGATGTT 3720  
 GACACCTTGC TTAAAACGT TCTTCCAGCT GTGCCAGTG ATCCAATAT GTTGAAGAAC 3780

	CCCCAAGTTG	ATAAAATTAG	TTCTACAATG	TTGCATCTCA	TTGTATCAAA	TTCTGCTTCA	3840
	AGTGAAAAACA	TGCTGCACTC	TACATCTGTA	CCAGTTTTTG	ATGTGTCGCC	TACTTCTCAT	3900
	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCTCTATG	CAAGTGAGAA	ATATGAACCA	3960
5	GTTTTGTATA	AAAGTGAAAG	TTCCCAACCA	GTGGTACCTT	CTTTGTACAG	TAATGATGAG	4020
	TTGTTCCAAA	CGGCCAATTT	GGAGATTAA	CAGGCCCATC	CCCCAAAAGG	AAGGCATGTA	4080
	TTTGCTACAC	CTGTTTTATC	AATTGATGAA	CCATTAAATA	CACATAATAA	TAAGCTTATA	4140
	CATTCCGATG	AAATTTTAA	CTCCACCAAA	AGTTCTGTTA	CTGGTAAGGT	ATTTGCTGGT	4200
	ATTCCAACAG	TTGCTTCTGA	TACATTTGTA	TCTACTGATC	ATTCTGTTCC	TATAGGAAAT	4260
10	GGGCATGTTT	CCATTACAGC	TGTTTTCTCC	CACAGAGATG	GTTCTGTAA	CTCAACAAAG	4320
	TTGCTGTTTC	CTTCTAAGGC	AACCTTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCCGGT	4380
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGACAGA	4440
	GATAGTGATG	GCTTATCCAT	TCATAAGTGT	ATGTCATGCT	CATCTATAG	AGAATCACAG	4500
	GAAAAGGTAA	TGAATGATT	AGACACCCAC	GAAAACAGTC	TTATGGATCA	GAATAATCCA	4560
	ATCTCATACT	CACATCTGTA	GAATCTGAA	GAAGATAATA	GAGTCACAAG	TGTATCCTCA	4620
15	GACAGTCAAA	CTGGTATGGA	CAGAAGTCTT	GGTAAATCAC	CATCAGCAAA	TGGGCTATCC	4680
	CAAAAGCACA	ATGATGGAAA	AGAGGAAAT	GACATTGAGA	CTGGTAGTGC	TCTGCTTCTT	4740
	CTCAGCCCTG	AATCTAAAGC	ATGGGCAGTT	CTGACAAGTG	ATGAAGAAAG	TGGATCAGGG	4800
	CAAGGTACTT	CAGATAGCCT	TAATGAGAA	GAGACTTCCA	CAGATTTCAG	TTTTGCAGAC	4860
	ACTAATGAAA	AAGATGCTGA	TGGGATCCTG	GCAGCAGGTG	ACTCAGAAAT	AACTCCTGGA	4920
20	TTCCCAACAGT	CCCCAACATC	ATCTGTTACT	AGCGAGAAGT	CAGAAGTGT	CCACGTTTCA	4980
	GAGGCAGAGG	CCAGTAATAG	TAGCCATGAG	TCTCGTATTG	GTCTAGCTGA	GGGGTTGGAA	5040
	TCCGAGAAGA	AGGCAGTTAT	ACCCCTTGTG	ATCGTGTCAG	CCCTGACTTT	TATCTGTCTA	5100
	GTGGTTCTTG	TGGGTATTCT	CATCTACTGG	AGGAAATGCT	TCCAGACTGC	ACACTTTTAC	5160
25	TTAGAGGACA	GTACATCCCC	TAGAGTTATA	TCCACACCTC	CAACACCTAT	CTTTCCAATT	5220
	TCAGATGATG	TGGGAGCAAT	TCCAATAAAG	CACTTTCCAA	AGCATGTTGC	AGATTTACAT	5280
	GCAAGTAGTG	GGTTTACTGA	AGAATTGAG	ACACTGAAAG	AGTTTACCAC	GGAAGTGCAG	5340
	AGCTGTACTG	TTGACTTAGG	TATTACAGCA	GACAGCTCCA	ACCACCCAGA	CAACAAGCAC	5400
	AAGAATCGAT	ACATAAATAT	CGTTGCTTAT	GATCATAGCA	GGGTTAAGCT	AGCACAGCTT	5460
30	GCTGAAAAGG	ATGGCAAACT	GACTGATTAT	ATCAATGCCA	ATTATGTTGA	TGGCTACAAC	5520
	AGACCAAAAG	CTTATATATG	TGCCCAAGGC	CCACTGAAAT	CCACAGCTGA	AGATTTCCTG	5580
	AGAATGATAT	GGGAACATAA	TGTGGAAGTT	ATTGTCATGA	TAACAAACCT	CGTGGAGAAA	5640
	GGAAAGGAGA	AATGTGATCA	GTACTGGCCT	GCCGATGGGA	GTGAGGAGTA	CGGGAACCTT	5700
	CTGGTCACTC	AGAAGAGTGT	GCAAGTGCTT	GCCTATTATA	CTGTGAGGAA	TTTTACTCTA	5760
35	AGAAACACAA	AAATAAAAAA	GGGCTCCAG	AAAGGAAGAC	CCAGTGGAGC	TGTGGTCACA	5820
	CAGTATCACT	ACACGCACTG	GCCTGACATG	GGAGTACCAG	AGTACTCCCT	GCCAGTGCTG	5880
	ACCTTTGTGA	GAAAGGCAGC	CTATGCCAAG	CGCCATGCAG	TGGGGCCTGT	TGTCGTCAC	5940
	TGCAGTGTCT	GAGTTGGAAG	AACAGGCACA	TATATTGTGC	TAGACAGTAT	GTTGCAGCAG	6000
	ATTCAACACG	AAGGAACATG	CAACATATTT	GGCTTCTTAA	AACACATCCG	TTCAACAAGA	6060
40	AATTATTTGG	TACAAACTGA	GGAGCAATAT	GTCTTCATTC	ATGATACACT	GGTTGAGGCC	6120
	ATACTTAGTA	AAGAACTGTA	GGTGCTGGAC	AGTCATATTC	ATGCCATATG	TAATGCACCT	6180
	CTCATTCCTG	GACCAGCAGG	CAAAACAAAG	CTAGAGAAAC	AATTCAGCT	CCTGAGCCAG	6240
	TCAAATATAC	AGCAGAGTGA	CTATTCTGCA	GCCCTAAAGC	AATGCAACAG	GGAARAGAAT	6300
	CGAATCTCTT	CTATCATCCC	TGTGGAAGA	TCAAGGGTTG	GCATTTTCATC	CCTGAGTGGA	6360
45	GAAGGCACAG	ACTACATCAA	TGCCTCCTAT	ATCATGGGCT	ATTACCAGAG	CAATGAATTC	6420
	ATCATTACCC	AGCACCTCT	CCTTCATACC	ATCAAGGATT	TCTGGAGGAT	GATATGGGAC	6480
	CATAATGCC	AACTGGTGGT	TATGATTCCT	GATGGCCAAA	ACATGGCAGA	AGATGAATTT	6540
	GTTTACTGGC	CAAAATAAGA	TGAGCCTATA	AATTGTGAGA	GCTTTAAGGT	CACCTCTATG	6600
	GCTGAAGAAC	ACAAATGTCT	ATCTAATGAG	GAAAACTTA	TAATTCAGGA	CTTTATCTTA	6660
50	GAAGCTACAC	AGGATGATTA	TGTACTTGAA	GTGAGGCACT	TTCAAGTGCC	TAAATGGCCA	6720
	AATCCAGATA	GCCCCATTAG	TAAAACTTTT	GAACTTATAA	GTGTTATAAA	AGAAGAAGCT	6780
	GCCAATAGGG	ATGGGCCCTAT	GATTGTTTCT	GATGAGCATG	GAGGAGTGAC	GGCAGGAAC	6840
	TTCTGTGCTC	TGACAAACCT	TATGCACCAA	CTAGAAAAAG	AAAAATCCGT	GGATGTTTAC	6900
	CAGGTAGCCA	AGATGATCAA	TCTGATGAGG	CCAGGAGTCT	TTGCTGACAT	TGAGCAGTAT	6960
55	CAGTTTCTCT	ACAAAGTGAT	CCTCAGCCTT	GTGAGCACAA	GGCAGGAAGA	GAATCCATCC	7020
	ACCTCTCTGG	ACAGTAATGG	TGCAGCATTG	CCTGATGGAA	ATATAGCTGA	GAGCTTAGAG	7080
	TCCTTAGTTT	AACACAGAAA	GGGGTGGGGG	GACTCACATC	TGAGCATTGT	TTCTCTCTTC	7140
	CTAAAATTAG	GCAGGAAAA	CAGTCTAGTT	CTGTTATCTG	TTGATTTCCT	ATCACCTGAC	7200
	AGTAACCTTC	ATGACATAGG	ATTCTGCCGC	CAAATTTATA	TCATTAACAA	TGTTGTCCCT	7260
60	TTTGCAAGAC	TTGTAATTTA	CTTATTATGT	TTGAACATAA	ATGATTGAAT	TTTACAGTAT	7320
	TTCTAAGAAT	GGAATTGTGG	TATTTTTTTC	TGTATTGATT	TTAACAAGAA	ATTTCAATTT	7380
	ATAGAGGTTA	GGAATTCCAA	ACTACAGAAA	ATGTTTGTGT	TTAGTGTCAA	ATTTTGTAGT	7440
	GTATTTGTAG	CAATTATCAG	GTTTGTCTAG	AAATAAATCT	TTAATACAGT	AGCCTGTAAA	7500
65	TAAACACATC	TTCCATATGA	TATTCAACAT	TTTACAACCTG	CAGTATTCAC	CTAAAGTAGA	7560
	AATAATCTGT	TACTTATTTG	AAATACTGCC	CTAGTGTCTC	CATGGACCAA	ATTTATATTT	7620
	ATAATTGTAT	ATTTTATAT	TTTACTACTG	AGTCAAGTTT	TCTAGTTCTG	TGTAATTGTT	7680
	TAGTTTAATG	ACGTAGTTCA	TTAGCTGGTC	TTACTCTACC	AGTTTCTCTG	CATGTGATTG	7740
	TGTTACCTAA	GTCATTAAC	TTGTTTCAGC	ATGTAATTTT	AACTTTTGTG	GAAAAAGAA	7800
	ATACCTTCAT	TTTGAAGAAA	GTTTTTATGA	GAATAACACC	TTACCAACAA	TTGTTCAAAT	7860
70	GGTTTTTATC	CAAGGAATTG	CAAAAATAAA	TATAAATATT	GCCATTAAAA	AAAAAATAAA	7920
	AAAAAATAAA	AAAAAATAAA	A				

Seq ID NO: 382 Protein sequence  
Protein Accession #: NP\_002842.1

75	1	11	21	31	41	51	
	MRILKRFLAC	IQLLCVCRLD	WANGYYRQOR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNKKL	KFGQWDKTS	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
	FKASKITFW	GKCNMSSDGS	BHSLGQKFP	LEMQIYCFDA	DRFSSFEAV	KGKGLRLALS	180
80	ILFVEGTEN	LDFAKIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPFC	240
	TDVTDWVFK	TDVTSISEQL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIEHAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLFE	420
	LIGTEEIIKE	EEEGKDIEEG	AIVNFGRDSA	TNQIRKKEPO	ISTTTHYNRI	GTKYNEAKTN	480

RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPTH VEGTSASLND 540  
 GSKTVLRSPH MNLSTGAESL NTVSITEYEE ESLLTSFKLD TGAEDSSGSS PATSAIPFIS 600  
 ENISQGYIFS SENPETITYD VLIPIESARNA SEDSTSSGSE ESLKDPMSMEG NVWFPSTDI 660  
 TAQPDVGSGR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720  
 TEVTPHAFPT SSRQQLDVST VNVVYSQTTQ PVYNGETPLQ PSYSSEVFPL VTPLLLDNQI 780  
 LNTTPAASSS DSALHATPVF PSVDVSFESI LSSYDGAPLL PFSSASFSSSE LFRHLHTVSQ 840  
 ILPQVTSATE SDKVPLHASL PVAGDDLLE PSLAQYSDVL STTHAASETL EFGSESGVLY 900  
 KTLMFSSQVEP PSSDAMMHAR SSGPEPSYAL SDNEGSQHIF TVSYSSAIPV HDSVGVITYQG 960  
 SLFSGPSHIP IPKSSLITPT ASLLQPTHAL SGDGEWSGAS SDSEFLLPDT DGLTALNISS 1020  
 PVSVAEFTYT TSVFGDDNKA LSKSEIYGN ETELQIPSFN EMVYPSESTV MPNMYDNVNK 1080  
 LNASLQETSV SISSTKGMFP GSLAHTTTKV FDHEISQVPE NNFSVQPTH VSQASGDTSL 1140  
 KPVLSEANSEP ASSDPASSEM LSPSTQLLFY ETSASFSTEV LLQPSFQASD VDTLLKTVLP 1200  
 AVPSDPILVE TPKVDKISST MLHLIVNSA SSENMLHSTS VPVFDVSPTS HMHSASLQGL 1260  
 TISYASEKYE PVLLKSESSH QVVPSLYSND ELFQTANLEI NQAHPPKGRH VFATPVLSID 1320  
 EPLNTLINKL IHSDEILTST KSSVTGKVFA GIPTVASDTF VSTDHSPVIG NGHVAITAVS 1380  
 PHRDGSVST KLLFPFSKATS ELSHSAKSDA GLVGGGEDGD TDDGDGDDDD RDSGDLGSIHK 1440  
 CMSCSSYRES QEKVMNDSST HENSMLDQNN PISYSLSENS EEDNRVTSVS SDSQTGMDRS 1500  
 PGKSPSANGS SQKNDGKEE NDIQTGSALL PLSPESKAWA VLTSDEESGS GQGTSDSLNE 1560  
 NETSTDFSFA DTNEKTDADGI LAAGDSEITP GFQPSPTSSV TSENSEVFHV SEAEASNSSH 1620  
 BSRIGLAEBL ESEKKAVIPL VIVSALTFC LVLVGLIYI WRKCFQTAHF YLEDSTSPRV 1680  
 ISTPPTPIFP ISDDVGAIPK KHFPKHVADL HASSGFTEEF ETLKEFYQEV QSCSTVDLGIT 1740  
 ADSSNHPDNK HKNRYINIVA YDHSRVKLAQ LAEKDGKLYD YINANYVDGY NRPKAYIAAQ 1800  
 GPLKSTAEFD WRMWIEHNVE VIVMITNLVE KRRKCDQYW PADGSEEGYN FLVTQKSVQV 1860  
 LAYTVTRNFT LRNKIKKKS QKGRPSGRV TQYHYTQWPD MGVPEYSLPV LTFVRKAAYA 1920  
 KRHAVGPVVV HCSAGVGRGT TYIVLDSMLQ QIQHEGTVNI FGFLKHRSQ RNYLVQTEEQ 1980  
 YVFIHDTLVE AILSKETEVL DSHIHAYVNA LLIPGPAGKT KLEKQFQLLS QSNIQQSDYS 2040  
 AALKQCNEK NRTSSIIPEV RSRVGISLS GEGTDYINAS YIMGYQYQNE FIITQHPLH 2100  
 TIKDFWRMIV DHNAQLVVM PDGQNMABED FVYWPNDKDEP INCSEFKVTL MAEEHKCLSN 2160  
 BEKLIQDFI LEATQDDYVL EVRHFQCPKW PNPDSPIST FELISVKEE AANRDGPMIV 2220  
 HDEHGGVTAG TFCALTTLMH QLEKENSVDV YQVAKMINLM RPFVADIEQ YQFLYKVLIS 2280  
 LVSTRQEENP STSLDSNGAA LPDGNIAESL ESLV

Seq ID NO: 383 DNA sequence

Nucleic Acid Accession #: NM\_005688.1

Coding sequence: 126..4439

1 11 21 31 41 51  
 CCGGGCAGGT GGCTCATGCT CGGGAGCGTG GTTGAGCGGC TGGCGCGGTT GTCTTGAGC 60  
 AGGGGCGCAG GAATTCCTGAT GTGAAACTAA CAGTCTGTGA GCCCTGGAAC CTCCGCTCAG 120  
 AGAAGATGAA GGATATCGAC ATAGGAAAG AGTATATCAT CCCAGTCTCT GGGTATAGAA 180  
 GTGTGAGGGA GAGAACACAGC ACTTCTGGGA CGCACAGAGA CCGTGAAGAT TCCAAGTTCA 240  
 GGAGAACTCG ACCGTTGGAA TGCCAAGATG CCTTGGAAAC AGCAGCCCGA GCCGAGGGCC 300  
 TCTCTCTTGA TGCTTCCATG CATCTCTCAG TCAGAACTCT GGATGAGGAG CATCCCAAGG 360  
 GAAAGTACCA TCATGCGCTG AGTGCTCTGA AGCCCATCCG GACTACTTCC AAACACACAGC 420  
 ACCCAGTGGG CAATGCTGGG CTTTTTTCCT GTATGACTTT TTCGTGGCTT TCTTCTCTGG 480  
 CCCGTGTGGC CCACAAGAAG GGGGAGCTCT CAATGGAAGA CGTGTGGTCT CTGTCCCAAGC 540  
 ACGAGTCTTC TGACGTGAAC TGCAGAAGAC TAGAGAGACT GTGGCAAGAA GAGCTGAATG 600  
 AAGTTGGGCC AGACGCTGCT TCCTGCGGAA GGGTTGTGTG GATCTTCTGC CGCACACAGG 660  
 TCATCTGTGC CATCGTGTGC CTGATGATCA CGCAGCTGGC TGGCTTCAGT GGACCAAGCT 720  
 TCATGGTGAA ACACCTCTTG GAGTATACCC AGGCAACAGA GTCTAACCTG CAGTACAGCT 780  
 TGTGTGTAGT GCTGGGCTCT CTCTGACGCG AAATCGTGCG GTCTTGGTCG CTGTGCACTG 840  
 CTTGGGCATT GAATTACCGA ACCGGTGTCC GCTTGGCGGG GGCATCCTA ACCATGGCAT 900  
 TTAAGAAGAT CCTTAAGTTA AAGAACATTA AAGAGAAATC CCTGGGTGAG CTCATCAACA 960  
 TTTGCTCCAA CGATGGGCAG AGAATGTTTG AGGCAGCAGC CGTGGGCAGC CTGCTGGCTG 1020  
 GAGGACCCGT TGTGGCCATG TTAGGCATGA TTTATAATGT AATATTCTG GGACCAACAG 1080  
 GCTTCTGGG ATCAGCTGTT TTTATCCTCT TTTACCCAGC AATGATGTTT GCATCACGGC 1140  
 TCACAGCATA TTTACAGGAG AAATGCGTGG CCGCCACGGA TGAACGTGTC CAGAAGATGA 1200  
 ATGAAGTTCT TACTTACATT AAATTTATCA AAATGTATGC CTGGGTCAAA GCATTTTCTC 1260  
 AGAGTGTTC AAAAAACCGC GAGGAGGAGC GTCGGATATT GGAATAAGCC GGGTACTTCC 1320  
 AGGGTATCAC TGTGGGTGTG GCTCCCATTT TGGTGGTGAT TGCCAGCGTG GTGACCTTCT 1380  
 CTGTTTCATAT GACCCTGGGC TTCGATCTGA CAGCAGCACA GGCTTTCACA GTGGTGACAG 1440  
 TCTTCAATTC CATGACTTTT GCTTTGAAAG TAACACCGTT TTCAGTAAAG TCCCTCTCAG 1500  
 AAGCCTCAGT GGCTGTTGAC AGATTTAAGA GTTTGTTTCT AATGGAAGAG GTTCACATGA 1560  
 TAAAGAACAA ACCAGCCAGT CCTCACATCA AGATAGAGAT GAAAAATGCC ACCTTGGCAT 1620  
 GGGACTCCTC CCACTCCAGT ATCCAGAACT CGCCCAAGCT GACCCCAAAA ATGAAAAAAG 1680  
 ACAAGAGGGC TTCCAGGGGC AAGAAAGAGA AGGTGAGGCA GCTGCAGCGC ACTGAGCATC 1740  
 AGGCGGTGCT GGCAGAGCAG AAAGGCCACC TCCTCCTGGA CAGTGACGAG CGGCCAGTGC 1800  
 CCGAAGAGGA AGAAGGCAAG CACATCCACC TGGGCCACCT GCGCTTACAG AGGACACTGC 1860  
 ACAGCATCGA TCTGGAGATC TCAGCCATTT TAGGCCAGAT GACGCTTCTA GAGGGCAGCA 1920  
 GTGGAAAAAC CTCTCTCATT TCAGCCATTT TAGGCCAGAT GACGCTTCTA GAGGGCAGCA 1980  
 TTGCAATCAG TGGAACTTTC GCTTATGTGG CCCAGCAGGC CTGGATCCTC AATGCTACTC 2040  
 TGAGAGACAA CATCTGTTT GGGAAAGGAA ATGATGAAGA AAGATAACAAC TCTGTGCTGA 2100  
 ACAGCTGCTG CCTGAGGCCT GACCTGGCCA TTCTTCCAG CAGCGACCTG ACGGAGATTG 2160  
 GAGAGCGAGG AGCCAACTTG AGCGGTGGGC AGCGCCAGAG GATCAGCCTT GCCCGGGCCT 2220  
 TGTATAGTGA CAGGAGCATC TACATCCTGG ACGACCCCTC CAGTGCCTTA GATGCCCCAT 2280  
 TGGGCAACCA CATCTTCAAT AGTGCTATCC GGAAACATCT CAAGTCCAAG ACAGTTCTGT 2340  
 TTGTTACCCA CAGTATACAG TACCTGTTG ACTGTGATGA AGTGATCTTC ATGAAAGAGG 2400  
 GCTGTATTAC GGAAAGAGGC ACCCATGAGG AACTGATGAA TTTAAATGGT GACTATGCTA 2460  
 CCATTTTAA TACCTGTTTG CTGGGAGAGA CACCGCCAGT TGAGATCAAT TCAAAAAAGG 2520  
 AAACCAAGTG TTACACAGAG AAGTCACAAG ACAAGGGTCC TAAAAACAGGA TCAGTAAAGA 2580  
 AGGAAAAAGC AGTAAAGCCA GAGGAAGGGC AGCTTGTGCA GCTGGAAGAG AAAGGGCAGG 2640  
 GTTCAGTGCC CTGGTCAAGT TATGGTGTCT ACATCCAGGC TGCTGGGGGC CCCTTGGCAT 2700  
 TCCTGTTTAT TATGCCCTTT TATCATGCTGA ATGTAGGCAG CACCCGCTTC AGCACCTGGT 2760



5 GGTGTGAGTTA CTGGATCAAG CAAGGAAGCG GGAACACCAC TGTGACTCGA GGGAAACGAGA 2820  
 CCTCGGTGAG TGACAGCATG AAGGACAATC CTCATATGCA GTACTATGCC AGCATCTACG 2880  
 CCCTCTCCAT GGCAGTCAATG CTGATCCTGA AAGCCATTTC AGGAGTTGTC TTTGTCAAGG 2940  
 GCACGCTGCG AGCTTCTCTCC CGGCTGCATG ACGAGCTTTT CCGAAGGATC CTTGGAAGCC 3000  
 CTATGAAGTT TTTTGACACG ACCCCACAG GGAGGATTCT CAACAGGTTT TCCAAAGACA 3060  
 TGGATGAAGT TGACGTGCGG CTGCCGTTCC AGGCCGAGAT GTTCATCCAG AACGTTATCC 3120  
 TGGTGTCTT CTGTGTGGGA ATGATCGCAG GAGTCTTCCC GTGGTTCCTT GTGGCAGTGG 3180  
 GGCCCTTGT CATCTCTTTT TCAGTCTGCG ACATTGTCTC CAGGGTCTG ATTCCGGAGC 3240  
 10 TGAAGCGTCT GGACAATATC ACGCAGTCAC CTTTCTCTC CCACATCACG TCCAGCATAC 3300  
 AGGGCCTTGC CACCATCCAC GCCTACAATA AAGGGCAGGA GTTCTGCGAC AGATACCAGG 3360  
 AGCTGCTGGA TGACAACCA GCTCTTTTTT TTTGTGTTAC GTGTGCGATG CGGTGGCTGG 3420  
 CTGTGCGGCT GGACCTCATC AGCATCGCCC TCATCACAC CACGGGCTG ATGATCGTTC 3480  
 TTATGACAGG GCAGATTCCC CCAGCCTATG CGGTCTCTCG CATCTCTTAT GCTGTCCAGT 3540  
 15 TAACGGGGCT GTTCCAGTTT ACGGTGAGC TGGCATCTGA GACAGAAGCT CGATTACACT 3600  
 CGGTGGAGAG GATCAATCAC TACATTAAGA CTCTGTCTT GGAAGCACCT GCCAGAATTA 3660  
 AGAACAAGGC TCCCTCCCCT GACTGGCCCC AGGAGGGAGA GGTGACCTTT GAGAACGCGAG 3720  
 AGATGAGGTA CCGAGAAAAC CTCCTCTCTG TCCTAAAGAA AGTATCCTTC ACGATCAAAC 3780  
 CTAAAGAGAA GATTGGCATT GTGGGGCGGA CAGGATCAGG GAAGTCTCTG CTGGGGATGG 3840  
 CCCTCTTCCG TCTGTGGGAG TTATCTGGAG GCTGCATCAA GATTGATGGA GTGAGAATCA 3900  
 20 GTGATATTGG CCTTGGCCAG CTCCGAAGCA AACTCTCTAT CATTCTCTCA GAGCCGGTGC 3960  
 TGTTCAGTGG CACTGTGAGA TCAAATTTGG ACCCTTCTCA CCAGTACACT GAAGACCAGA 4020  
 TTTGGGATGC CCTGGAGAGG ACACACATGA AAGAAATGTAT TGCTCAGCTA CCTCTGAAAC 4080  
 TTTGAATCTGA AGTGATGGAG AATGGGGATA ACTTCTCAGT GGGGGAAACG CAGCTCTTGT 4140  
 GCATAGCTAG AGCCCTGCTC CGCCACTGTA AGATTCTGAT TTTAGATGAA GCCACAGCTG 4200  
 25 CCATGGACAC AGAGACAGAC TTATTGATTG AAGAGACCAT CCGAGAAGCA TTTGCAGACT 4260  
 GTACCATGCT GACCATTGCC CATCGCCTCG ACACGGTTCT AGGCTCCGAT AGGATTATGG 4320  
 TGCTGGCCCA GGGACAGGTG GTGGAGTTTG ACACCCCATC GGTCTCTCTG TCCAAACGACA 4380  
 GTTCCCGATT CTATGCCATG TTTGCTGCTG CAGAGAACAA GGTCTGCTGC AAGGGCTGAC 4440  
 30 TCTCTCCGTG TGACGAAGTC TCTTTTCTTT AGAGCATTGC CATTCCCTGC CTGGGGCGGG 4500  
 CCCCTCATCG CGTCTCTCTA CCGAAACCTT GCCTTTCTCG ATTTTATCTT TCGCAGACGA 4560  
 GTTCCGGATT GGCCTTGTGT TTTCACTTTT AGGGAGAGTC ATATTTTGTAT TATTGTATTT 4620  
 ATTCATATT CATGTAAACA AAATTTAGTT TTTGTTCTTA ATTGCATCT AAAAGGTTCA 4680  
 35 GGGAAACCGTT ATTATAATTG TATCAGAGGC CTATAATGAA GCTTTATACG TGTAGCTATA 4740  
 TCTATATATA ATTCTGTACA TAGCCTATAT TTACAGTGAA AATGTAAGCT GTTTATTTTA 4800  
 TATTAATAATA AGCACTGTGC TAATAACAGT GCATATTCTT TTCTATCATT TTTGTACAGT 4860  
 TTGCTGTACT AGAGATCTGG TTTTGTCTAT AGACTGTAGG AAGAGTAGCA TTTTCTCTT 4920  
 CTCTAGCTGG TGGTTTCACG GTGCCAGGTT TTCTGGGTGT CCAAAGGAAG ACGTGTGGCA 4980  
 ATAGTGGGCC CTCCGACAGC CCCCTCTGCC GCCTCCCCAC AGCCGCTCCA GGGGTGGCTG 5040  
 40 GAGACGGGTG GGGCGGTGGA GACCATGCAG AGCGCCGTGA GTTCTCAGGG CTCTCGCTT 5100  
 CTGTCTGGT GTCACCTACT GTTCTGTGTA GGAGAGCAGC GGGGCGAAGC CCAGGCCCTT 5160  
 TTTCACTCCC TCCATCAAGA ATGGGGATCA CAGAGACATT CCTCCGAGCC GGGGAGTTTC 5220  
 TTTCTGCTCT TCTTCTTTT GCTGTGTGTT CTAAACAAGA ATCAGTCTAT CCACAGAGAG 5280  
 TCCCACTGCC TCAGGTTCTT ATGGCTGGCC ACTGCACAGA GCTCTCCAGC TCCAAGACCT 5340  
 45 GTTGGTTCCA AGCCCTGGAG CCAACTGCTG CTTTGTGAGG TGGCACTTTT TCATTGCTT 5400  
 ATTCACACAC CTCCACAGTT CAGTGGCAGG GCTCAGGATT TCGTGGGTCT GTTTTCTT 5460  
 CTCACCGCAG TCGTGCACCA GTCTCTCTCT CTCTCTCCCC TCAAAGTCTG CAACTTTAAG 5520  
 CAGCTCTTGC TAATCAGTGT CTCACACTGG CGTAGAAGTT TTTGTACTGT AAAGAGACCT 5580  
 ACCTCAGGTT GCTGTTGCT GTGTGGTTTG GTGTGTTCCC GCAAACCCCC TTTGTGCTGT 5640  
 50 GGGGCTGGTA GCTCAGGTGG GCGTGGTCAC TGCTGTCTAT AGTTGAATGG TCAGCGTTGC 5700  
 ATGTCGTGAC CAACTAGACA TTCTGTCGCC TTAGCATGTT TGCTGAACAC CTTGTGGAAG 5760  
 CAAAATCTG AAAATGTGAA TAAATATTAT TTGGATTTTG TAAAAAATAA AAAAAAATAA 5820  
 AAAAAAATAA AAAAAAATAA

Seq ID NO: 384 Protein sequence

Protein Accession #: NP\_005679.1

55  
 60  
 65  
 70  
 75  
 80

1	11	21	31	41	51	
MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFRR	TRPLECQDAL	ETAARAEGLS	60
LDASMHSQLR	ILDEEHPKKG	YHHGLSALKP	IRTTSKHQHP	VDNAGLFSCM	TFSWLSSSLAR	120
VAHKKGELSM	EDVWSLSKHE	SSDVNCRRLE	RLWQBELNEV	GPDAASLRV	VWIFCRTRLI	180
LSIVCLMITQ	LAFSGPAPFM	VKHLLLEYTQA	TESNLQYSLL	LVLGLLLTET	VRWSLALTW	240
ALNYRTGVRL	RGAILTMAFK	KILKLKNIKE	KSLGELINIC	SNDGQRMFEA	AAVGSLLAGG	300
PVVAILGMIY	NVILGPTGF	LGSVFIIFY	PAMMFASRLT	AYFRRCVAA	TDERVQKMNE	360
VLTYIKFIKM	YAVVKAQS	VQKIREBERR	ILEKAGYFQG	ITVGVAPIV	VIASVVTFSV	420
HMTLGFDLTA	AQFTVTVTF	NSMTFALKVT	PFSVKSLSEA	SVAVDRFKSL	FLMEEVHMIK	480
NKPASPHIKI	EMKNATLAWD	SSHSSIQNSP	KLTPMKMKDK	RASRGKKEKV	RQLQRTEHQA	540
VLAEQKGHL	LDSDERSPE	EEBKGHIHLG	HLRLQRTLHS	IDLEIQEGL	VGICGSVSGG	600
KTSLISAILG	QMTLLEGSIA	ISGTFAYVAQ	QAWILNATLR	DNILFGKEYD	EERYNSVLNS	660
CCLRPDLAIL	PSSDLTEIGE	RGANLSGGQR	QRISLARALY	SDRSIYLDD	PLSALDAHVG	720
NHIFNSAIRK	HLKSKTVLFV	THQLQYLVD	DEVIFMKEGC	ITERGTHEEL	MNLNGDYATI	780
FNLLLLGETP	PVEINSKET	SGSQKKSQDK	GPKTGSVKKE	KAVKPEGQL	VQLEEKQGG	840
VPWSVYGVYI	QAAGGFLAFL	VIMALFMLNV	GSTAFSTWWL	SYWIKQSGN	TTVTRGNETS	900
VSDSMKDNPH	MQYYASIALY	SMAMVLLILKA	IRGVVFKVGT	LRASSRLHDE	LFRRILRSPM	960
KFPDTPPTGR	ILNRFSKDM	EVDVRLPFQA	EMFIQNVILV	FFCVGMIAGV	FPWFLVAVGP	1020
LVILFVLHII	VSRVLIRELK	RLDNITQSPF	LSHITSSIQG	LATHIAYNKG	QEFLLHRYQEL	1080
LDDNQAPFPL	FTCAMRWLAV	RLDLISIALI	TTTGLMIVLM	HGQIPPAYAG	LAISYAVQLT	1140
GLFOFTVRLA	SETEARFTSV	ERINHYIKTL	SLEAPARIKN	KAPSPDPQPE	GEVTFENAEM	1200
RYRENLPVLV	KKVSFTIKPK	EKIGIVGRTG	SGKSSLMGMA	FRVLSGGC	IKIDGVRISD	1260
IGLADLRSKL	SIIQPEVPLF	SGTVRSNLD	FNQYTEDQIW	DALERTHME	CIAQLPLKLE	1320
SEVMENGDNF	SVGERQLLCI	ARALLRHCKI	LILDEATAAM	DTETDLIQE	TIREAFADCT	1380
MLTIAHRLHT	VLGSDRIMVL	AQQQVVEFDT	PSVLLSNDSS	RFYAMFAAAE	NKVAVKG	

Seq ID NO: 385 DNA sequence  
Nucleic Acid Accession #: NM\_001327.1  
Coding sequence: 89..631

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
      CTGAGAGCCG GGCAGAGGCT CCGGAGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTTC 120
      GACGGGCCAT GCTGATGGCC CAGGAGGCCC TGGCATTCTT GATGGCCCG GGGGCAATGC 180
10     TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCCCAGGGCG CAGGGGCAGC 240
      AAGGGCCTCG GGGCCGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGGCG CGGCTTCAGG 300
      GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCGGAG AGCCGCCTGC TTGAGTTCTA 360
      CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCGCGAGGA GCCTGGCCCA 420
      GGATGCCCCA CCGCTTCCCG TGCCAGGGGT GCTTCTGAAG GAGTTCACITG TGTCCGGCAA 480
15     CATACTGACT ATCCGACTGA CTGCTGCAGA CCACGCCAA CTGCAGCTCT CCATCAGCTC 540
      CTGTCTCCAG CAGCTTTCCC TGTGTATGTG GATCACGCAG TGCTTTCTGC CCGTGTTTT 600
      GGCTCAGCTT CCCTCAGGGT AGAGGCGCTA AGCCAGCCCT GGCAGCCCTT CCTAGGTCAT 660
      GCCTCTCTCC CTAGGGAATG GTCCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
20     GTTTGTGCTT GGAGGAGGAC GGCTTACATG TTTGTTTCTG TAGAAAATAA AACTGAGCTA

```

Seq ID NO: 386 Protein sequence  
Protein Accession #: NP\_001318.1

```

25     1      11      21      31      41      51
      |      |      |      |      |      |
      MQAEGRGTTG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA 60
      PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAEALARRSLA QDAPPLPVP 120
      VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQLQLLLM WITQCFLPVF LAQPPSGQRR

```

Seq ID NO: 387 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 52..459

```

35     1      11      21      31      41      51
      |      |      |      |      |      |
      CCTCGTGGGC CTTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGAGC CATGCAGGCC 60
      GAAGGCCAGG GCACAGGGGG TTCGACGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT 120
      CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CCGGTGCCAC GGGCGGCAGA 180
40     GGTCCCGGGG GCGCAGGGG AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCGCGGGGGT 240
      CCGCATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CTGCGGGGC CAGGAGGCCG 300
      GACAGCCGCG TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
      ATCAGCTCCT GTCTCCAGCA GCTTCCCTG TTGATGTGGA TCACGCACTG CTTTCTGCCC 420
      GTGTTTTTGG CTACAGGCTC CTCAGGGCAG AGGCCTAAG CCCAGCCTGG CGCCCTTCC 480
45     TAGGTATATC CTCTCCCTT AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTTGTGGG 540
      GCCTGATTGT TTGTGCTGAG AGGAGGACGG CTTACATGTT TGTCTCTGTA GAAATAAAG 600
      CTGAGCTA

```

Seq ID NO: 388 Protein sequence  
Protein Accession #: Eos sequence

```

50     1      11      21      31      41      51
      |      |      |      |      |      |
      MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
55     PRGPHGGAAS AQDGRPCPGA RRPDSRLQLF RLTAADHRQL QLSISSCLQG LSLLMWITQC 120
      FLPVFLAQAP SQQRR

```

Seq ID NO: 389 DNA sequence  
Nucleic Acid Accession #: NM\_005562.1  
Coding sequence: 90..3671

```

60     1      11      21      31      41      51
      |      |      |      |      |      |
      ACAGCGGAGC GCAGAGTGAG AACCAACAAC CGAGGCGCCG GGCAGCGACC CCTGCAGCGG 60
      AGACAGAGAC TGAGCGGCCG GGCACCGCCA TGCTTGCCTT CTGGCTGGGC TGCTGCCTCT 120
65     GCTTCTCGCT CCTCTGCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
      ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGGAACTTCA CAGACAACT GGTAAATGGAT 240
      TCCGCTGCCT CAACTGCAAT GACAACACTG ATGGCATTCA CTGCGAGAAG TGCAAGAATG 300
      GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAAC TCCAAAGGTT 360
70     CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACCAGGT GTGACAGGAG 420
      CCAGATGCGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCAAG 480
      ACCAGAGACT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG 540
      ACCGCGGCCG CTGTGTCTGC AAGCCAGCTG TTACTGGAGA ACCTGTGAT AGGTGTCTGAT 600
      CAGGTTACTA TAATCTGGAT GGGGGGAACC CTGAGGGCTG TACCAGTGT TTCTGCTATG 660
75     GGCATTACAG CAGCTGCGCG AGCTCTGAG AATACAGTGT CCATAAGATC ACCTCTACCT 720
      TTCAATCAGA TGTGTATGGC TGAAGGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC 780
      AATGGTCACA GCGCCATCAA GATGTGTTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT 840
      TTGTGGCTCC TGCCAAATTT CTTGGGAATC AACAGGTGAG CTATGGGCAA AGCCTGTCTT 900
      TTGACTACCG TGTGGACAGA GGAGGCAGAC ACCCATCTGC CCATGATGTG ATTCTGGAAG 960
80     GTGCTGTGCT ACGGATCACA GCTCCCTTGA TGCCACTTGG CAAGACACTG CCTTGTGGGC 1020
      TCACCAAGAC TTACACATTC AGGTAAATG AGCATCCAAG CAATAATTGG AGCCCCAGC 1080
      TGAGTTACTT TGAGTATCTG GGAATCTCAC AGCCCTCCG ATCCGAGCTA 1140
      CATATGGAGA ATACAGTACT GGGTACATTG ACAATGTGAC CCTGATTTC GCGCCCTG 1200
      TCTCTGAGC CCCAGCACCC TGGGTGTAAC AGTGTATATG TCCTGTTGGG TACAAGGGGC 1260
      AATTCTGCCA GGATTGTGCT TCTGGCTACA AGAGAGATTC AGCGAGACTG GGGCCTTTG 1320

```

	GCACCTGTAT	TCCTTGTAAC	TGTCAAGGGG	GAGGGGCTTG	TGATCCAGAC	ACAGGAGATT	1380
	GTTATTACAG	GGATGAGAAT	CCTGACATTG	AGTGTGCTGA	CTGCCCAATT	GGTTTCTACA	1440
	ACGATCCGCA	CGACCCCCCG	AGCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTCAGCTGCT	1500
5	CAGTGATGCC	GGAGACGGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTACCCGGTG	1560
	CCCCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGGACCC	CTTTGGTGAA	CATGGCCAG	1620
	TGAGGCTTG	TCAGCCTGT	CAATGCAACA	ACAATGTGGA	CCCCAGTGCC	TCTGGGAATT	1680
	GTGACCGCT	GACAGGCAGG	TGTTTGAAGT	GTATCCACAA	CACAGCCGGC	ATCTACTGCG	1740
	ACCAGTGCAA	AGCAGGCTAC	TTCCGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAAGTGT	1800
10	GAGCTTGCAA	CTGTAACCCC	ATGGGCTCAG	AGCCTGTAGG	ATGTCGAAGT	GATGGCACCT	1860
	GTGTTTGCAA	GCCAGGATTT	GGTGGCCCCA	ACTGTGAGCA	TGGAGCATT	AGCTGTCCAG	1920
	CTGTCTATAA	TCAGTGAAG	ATTGAGATGG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAATGG	1980
	AGGCCCTGAT	TTCAAAGGCT	CAGGGTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040
	GCAGGATGCA	GCAGGCTGAG	CAGGCCCTTC	AGGACATTCT	GAGAGATGCC	CAGATTTTCT	2100
	AAGGTGCTAG	CAGATCCCTT	GGTCTCCAGT	TGGCCAGAGT	GAGGAGCCAA	GAGAACAGCT	2160
15	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAAG	AGTTCCGGCT	CTGGGAAGTC	2220
	AGTACCAGAA	CCGAGTTCGG	GATACTCACA	GGCTCATCAC	TCAGATGCAG	CTGAGCCTGG	2280
	CAGAAAGTGA	AGCTTCTCTG	GGAAACACTA	ACATTCCTGC	CTCAGACCAC	TACGTGGGGC	2340
	CAAAATGGCTT	TAAAGTCTTG	GCTCAGGAGG	CCACAAGATT	AGCAGAAAGC	CACGTTGAGT	2400
20	CAGCCAGTAA	CATGGAGCAA	CTGACAAGGG	AAACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
	CACTGGTGCG	CAAGGCCCTG	CATGAAGGAG	TCCGGAAGCG	AAGCGGTAGC	CCGGACGGTG	2520
	CTGTGGTGCA	AGGGCTTGTG	GAAAAATTGG	AGAAAACCAA	GTCCCTGGCC	CAGCAGTTGA	2580
	CAAGGGAGGC	CACCTCAAGCG	GAAATTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640
	TCCGTGATTG	AGTGTCTCGG	CTTCAGGGAG	TCAGTGATCA	GTCTTTTCAG	GTGGAAAGAG	2700
25	CAAAGAGGAT	CAAAACAAAA	GCGGATTCAC	TCTCAACGCT	GGTAACCAAG	CATATGGATG	2760
	AGTTCAAGCG	TACACAAAAA	AATCTGGGAA	ACTGGAAAGA	AGAAGCACAG	CAGCTCTTAC	2820
	AGAAATGGAAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCGTGCC	AATCTTGCTA	2880
	AAAGCAGAGC	ACAAGAAGCA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTTGAGAGCA	2940
	TCCTTAAAAA	CCTCAGAGAG	TTTGACCTCG	AGGTGGACAA	CAGAAAAGCA	GAAGCTGAAG	3000
30	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060
	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAATGGGG	3120
	CCGGGGAGGC	CTCGGAAATC	TCCAGTGAGA	TGAAACAGGA	GATTGGGAGT	CTGAACCTGG	3180
	AAGCCAATGT	GACAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAGA	3240
	GTGAGATGAG	GGAAAGTGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
35	TGGATGCAGT	ACAGATGGTG	ATTACAGAAG	CCCAGAAGGT	TGATACCAGA	GCCAAGAACG	3360
	CTGGGGTTAC	AATCCAAGAC	ACACTCAACA	CATTAGACGG	CCTCCTGCAT	CTGATGGACC	3420
	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAGCTT	TCCCGAGCCA	3480
	AGACCCAGAT	CAACAGCCAA	CTGCGGCCCA	TGATGTCAGA	GCTGGAAGAG	AGGGCACGTC	3540
	AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
40	AGAACTTGGA	GAAACATTAG	GACAACTTGC	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
	AGCAACAGTG	AAGCTGCCAT	AAATATTTCT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
	GGCTCGGGAG	CCATGTCATG	TGAGTGGGTG	GGATGGGGAC	ATTTGAACAT	GTTTAATGGG	3780
	TATGCTCAGG	TCAACTGACC	TGACCCCAT	CCTGATCCCA	TGGCCAGGTG	GTTGTCTTAT	3840
	TGCACCATAC	TCTTGTCTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
45	ATGATCAAGG	ATCTGGACCC	CAAAGAATAG	ACTGGATGGA	AAGACAAACT	GCACAGGCAG	3960
	ATGTTTGCCT	CATAATAGTC	GTAAGTGGAG	TCTTGGAAAT	TGGACAAGTG	CTGTTGGGAT	4020
	ATAGTCAACT	TATTTCTTGA	GTAATGTGAC	TAAAGGAAAA	AACCTTTGACT	TTGCCCAGGC	4080
	ATGAAATCTT	TCTAATGTCT	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAT	4140
	ACTATTGCCT	CATATTGTCC	TCTGCAAGCT	TCTTGCTGAT	CAGAGTTTCT	CCTACTTACA	4200
50	ACCCAGGGTG	TGAACATGTT	CTCCATTTTC	AAGCTGGAAG	AAGTGAGCAG	TGTTGGAGTG	4260
	AGGACCTGTA	AGGCAGGCC	ATTCAGAGCT	ATGGTGCTTG	CTGGTGCTTG	CCACCTTCAA	4320
	GTCTCTGACC	TGGGCATGAC	ATCCTTTCTT	TTAATGATGC	CATGGCAACT	TAGAGATTGC	4380
	ATTTTATTTA	AAGCATTTTC	TACCAGCAAA	GCAAAATGTT	GGAAAGTATT	TACTTTTTCG	4440
	GTTTCAAAGT	GATAGAAAAG	TGTGGCTTGG	GCATTGAAAG	AGGTAAATTT	CTCTAGATT	4500
55	ATTAGTCTTA	ATTCAATCTT	ACTTTTTCGA	CACCAAAAAT	GATGCCGATC	AATGTATTTT	4560
	ATCTTATTTT	CTCAATCTTC	TCTCTCTTTC	CTCCACCCAT	AATAAGAGAA	TGTTCTCTACT	4620
	CACACTTCAG	CTGGGTCACT	TCCATCCCTC	CATTATCCTT	TCCATCCATC	TTTCCATCCA	4680
	TTACCTCCAT	CCATCCTTCC	AACATATATT	TATTGAGTAC	CTACTGTGTG	CCAGGGGCTG	4740
	GTGGGACAGT	GGTGACATAG	TCTCTGCCCT	CATAGAGTTG	ATTGCTAGT	GAGGAAGACA	4800
60	AGCATTTTAA	AAAAATAAAT	TTAAACTTAC	AACTTTTGTT	TGTCACAAGT	GGTGTTTATT	4860
	GCAATAACCG	CTTGGTTTGC	AACTCTTTTG	CTCAACAGAA	CATATGTTGC	AAGACCTCTC	4920
	CATGGGGGCA	CTTGAGTTTT	GGCAAGGCTG	ACAGAGCTCT	GGGTTGTGCA	CATTTCTTTG	4980
	CATTCCAGCT	GTCACTCTGT	GCCTTTCTAC	AACTGATTGC	AACAGACTGT	TGAGTTATGA	5040
	TAACACCATG	GGGAATTGCT	GGAGGAACCA	GAGGCACTTC	CACCTTGGCT	GGGAAGACTA	5100
65	TGGTGCTGCC	TTGCTTCTGT	ATTTCCTTGG	ATTTCTCTGA	AAGTGTTTTT	AAATAAGAA	5160
	CAATTGTTAG	ATGCC					

Seq ID NO: 390 Protein sequence  
 Protein Accession #: NP\_005553.1

70	1	11	21	31	41	51	
	MPALWLGCC	CFSLLLPAAR	ATSRREVDCD	NGKSRQCIFD	RELHRQTGNG	FRCLNCNDNT	60
	DGIHCEKCKN	GFYRHRERDR	CLPCNCSKSG	SLSARCDNSG	RCSCKPGVTG	ARCDRLCPGF	120
75	HMLTDAGCTQ	DQRLDLSKCD	CDPAGIAGPC	DAGRCVCKPA	VTGERCDRCR	SGYNNLDGGN	180
	PEGCTQCFCY	GHSASCRSSA	EYSVHKITST	FHQDVGWKA	VQRNGSPAKL	QWSQRHQDVF	240
	SSAQRLDPIVY	FVAPAKFLGN	QQVSYGQSL	FDYRVDRGGR	HPSAHDVILE	GAGLRITAPL	300
	MPLGKTLPCG	LTKYTFYRLN	EHPNSNWSQ	LSYFEYRRL	RNLALRIRA	TYGEYSTGYI	360
	DNVTILISAR	VSGAPAPWVE	QCICPVGYKG	QFCQDCASGY	KRDSARLGP	GTICPCNCQG	420
80	GGACDPDTGD	CYSGDENPDI	ECADCPIGFY	NDPHDPRSK	PCPCHNGFSC	SVMPEEEVV	480
	CNNCPFGVTG	ARCELADGTY	FGDPFGEHGP	VRPCQPCQCN	NNVDPASAGN	CDRLTGRCLK	540
	CIHNTAGIYC	DQCKAGYFEG	PLAPNPADKC	RACNCPNMG	EPVGCRRSDG	CVCKPFGGPG	600
	NCEHGAFCSP	ACYNQVKIQM	DQFMQQLQRM	EALISKAQGG	DGVVPDTELE	GRMQQAQAL	660
	QDILRDAQIS	EGASRLGLQ	LAKVRSQENS	YQSRLLDLKM	TVERVRALGS	QYQNRVRDTH	720
	RLITQMQLSL	ABSEASLGNT	NIPASDHYVG	PNGFKSLAQE	ATRLAESHVE	SASNMEQLTR	780

ETEDYSKQAL SLVRKALHEG VSGSGSPDG AVVQGLVEKL ETKSLAQQL TREATQAEIE 840  
 ADRSYQHSRLR LLDVSRLQGV VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNLG 900  
 NWKEBAQQLL QNGKSGREKS DQLLSRANLA KSRQAEALSM GNATFYEVEE ILKNLREFDL 960  
 QVDNRKAEAE EAMKRLSYIS QKVSDASDKT QQAERALGSA AADAQRAKNG AGEALEISSE 1020  
 IEQEIGSLNL EANVTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE 1080  
 AQKVDTRAKN AGVTIQDTLN TLDGLHLHMD QPLSVDEEGL VLLQKLSRA KTQINSQRLP 1140  
 MMSELEERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ

Seq ID NO: 391 DNA sequence

Nucleic Acid Accession #: AF101051.1

Coding sequence: 221.856

1 11 21 31 41 51  
 | | | | |  
 15 GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCGGCC CCGGGCGCGG ACCCCAACCC 60  
 CGACCCAGAG CTTCTCCAGC GCGCGCGCAG CGAGCAGGGC TCCCGCCCTT AACTTCTCTC 120  
 CGCGGGGCCA GCCACCTTCG GGAGTCCGGG TTGCCACCTT GCAAACTCTC CGCCTTCTGC 180  
 ACCTGCCACC CCTGAGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAACG CGGGGCTGCA 240  
 GCTGTTGGGC TTCACTCTCG CCTTCTCTGG ATGGATCGGC GCCATCGTCA GCACTGCCCT 300  
 20 GCGCCAGTGG AGGATTACTT CCTATGCGCG CGACAACATC GTGACCGCCC AGGCCATGTA 360  
 CGAGGGGCTG TGGATGTCCT GCGTGTGCGA GAGCACCAGG CAGATCCAGT GCAAAGTCTT 420  
 TGACTCCTTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCCCTGA TGGTGGTTGG 480  
 CATCTCTCTG GGAGTGATAG CAATCTTTGT GCCCACCCTT GGCATGAAGT GTATGAAGTG 540  
 25 CTTGGAAGAC GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTCTT 600  
 TCTTGCAGGT CTGGCTATTT TAGTTGCCAC AGCATGGTAT GGCAATAGAA TCGTTCAAGA 660  
 ATTTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTTGGTCAGG CTCTCTTCAC 720  
 TGGCTGGGCT GCTGCTTCTC TCTGCTTCTT GGGAGGTGCC CTACTTTGCT GTTCTCTGCC 780  
 30 CCGAAAAACA ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCCAGCGG 840  
 GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAAAATCA TGTGAAACA AACCGAAAT 900  
 GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA 960  
 GTATGGTATT ACATAACAAA CAAACACCA AAAAAACCAT GTGTTAAAT ACCTAGTGT 1020  
 AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT 1080  
 TTGTATTACT GCTTCCCATT GAGTAATCAT ACTCAAATGG GGAAGGGGT GCTCCTTAAA 1140  
 35 TATATATAGA TATGTATATA TACATGTTTT TCTATTAAAA ATAGACAGTA AAATACTATT 1200  
 CTCATTATGT TGATACTAGC ATACTTAAAA TATCTCTAAA ATAGGTAAAT GTATTTAATT 1260  
 CCATATTGAT GAAGATGTTT ATTGGTATAT TTTCTTTTTC GTCCTTATAT ACATATGTAA 1320  
 CAGTCAAAATA TCATTACTC TTCTTCATTA GCTTTGGGTG CTTTGGCCAC AAGACCTAGC 1380  
 CTAATTTACC AAGGATGAAT TCCTTCAATT CTTCATGCGT GCCCTTTTCA TATACTTATT 1440  
 40 TTATTTTTTA CCATAATCTT ATAGCACTTG CATCGTTATT AAGCCCTTAT TTGTTTTGTG 1500  
 TTTCAATTGG CTCATCTTCC TGAATCTAAC ACATTTCTAT GCCTACATTT TAGTTTCTAA 1560  
 AGCCAAGGAG AATTTTATTAC AAATCAGAAC TTTGGAGGCA AATCTTTCTG CATGACCAA 1620  
 GTGATAAATT CCTGTTGACC TTCCACACA ATCCCTGTAC TCTGACCAT AGCACTCTTG 1680  
 TTTGCTTTGA AAATATTTGT CCAATTGAGT AGCTGCATGC TGTTCGCCCA GGTGTTGTAA 1740  
 45 CACAACCTTA TTGATTGAAT TTTTAAGCTA CTTATTCTAT GTTTTATATC CCCCTAAACT 1800  
 ACCTTTTTGT TCCCATTTCC TTAATTGTAT TGTTTTCCCA AGTGAATTA TCATGCGTTT 1860  
 TATATCTTCC TAATAAGGTG TGGTCTGTTT GTCTGAACAA AGTGCTAGAC TTTCTGGAGT 1920  
 GATAATCTGG TGACAAATAT TCTCTCTGTA GCTGTAAACA AGTCACTTAA TCTTCTTACC 1980  
 TCTTTTTTCT ATCTGCCAAA TTGAGATAAT GATACTTAAC CAGTTAGAAG AGGTAGTGTG 2040  
 50 AATATTAATT AGTTTATATT ACTCTCATTC TTTGAACATG AACTATGCCT ATGTAGTGTG 2100  
 TTTATTGCT CAGCTGGCTG AGACACTGAA GAAGTCACTG AACAAAACTT ACACACGTAC 2160  
 CTTCACTGTA TTCATGCTCT TCCTCTCTCT ACCAGTCTAT TTCCACTGAA CAAACCTTAC 2220  
 ACACATACCT TCATGTGGTT CAGTGCCTTC CTCTCTCTAC CAGTCTATT CCACCTGAACA 2280  
 AAACCTACGC ACATACCTTC ATGTGGCTCA GTGCCCTTCT CTCTCTACCA GTCTATTTCC 2340  
 55 ATTCTTTCAG CTGTGCTGTA CATGTTGTG CTCTGTTCCA TTTTAAACAA TGCTCTTACT 2400  
 TTTCCAGTCT GTACAGAAAG CTATTTCAT TGAGCAAGAT GATGTATGGA AAGGGTGTG 2460  
 GCACTGGTGT CTGGAGACCT GGATTGAGT CTGTTGCTA TCAATCACCG TCTGTGTTG 2520  
 AGCAAGGCTT TTGGCTGCTG TAAGCTTATT GCTTCATCTG TAAGCGGTGG TTTGTAATTC 2580  
 CTGATCTTCC CACCTCACAG TGATGTTGTG GGGATCCAGT GAGATAGAAT ACATGTAAGT 2640  
 60 GTGGTTTTGT AATTTGAAAA GTGCTATACT AAGGGAAAGA ATTGAGGAAT TAACTGCATA 2700  
 CGTTTTGTGT TTGCTTTTCA AATGTTTGAA AATAAAAAAA TGTTAAGAAA TGGGTTTCTT 2760  
 GCCTTAACCA GTCTCTCAAG TGATGAGACA GTGAAGTAAA ATTGAGTGCA CTAACGAAT 2820  
 AAGATTCTGA GGAAGTCTTA TCTTCTGCAG TGAGTATGGC CCAATGCTTT CTGTGGCTAA 2880  
 ACAGATGTAA TGGGAAGAAA TAAAAGCCTA CGTGTGGTA AATCCAACAG CAAGGGAGAT 2940  
 65 TTTTGAATCA TAATAACTCA TAAGGTGCTA TCTGTTCAAT GATGCCCTCA GAGCTCTTGC 3000  
 TGTTAGCTGG CAGCTGACGC TGCTAGGATA GTTAGTTTGG AAATGGTACT TCATAATAAA 3060  
 CTACACAAGG AAAGTCAGCC ACCGTGCTTT ATGAGGAATT GGACCTAATA AATTTTAGTG 3120  
 TGCCCTCCAA ACCTGAGAAT ATATGCTTTT GGAAGTAAA ATTTAAATGG CTTTGGCCAC 3180  
 ATACATAGAT CTTCAATGAT GTGTAGTGTA ATTCCATGTG GATATCAGTT ACCAAACATT 3240  
 70 ACAAATAAAT TTTATGGCCC AAAATGACCA ACGAAATGT TACAATAGAA TTTATCCAAT 3300  
 TTTGATCTTT TTATATTCTT CTACCACACC TGGAAACAGA CCAATAGACA TTTTGGGGTT 3360  
 TTATAATGGG AATTTGTATA AAGCATTAAT CTTTTCAAT AAATTGTTTT TTAATTTAAA 3420  
 AAAAGGAAAA AAAAAAAAAA AAA

Seq ID NO: 392 Protein sequence

Protein Accession #: AAD16433.1

1 11 21 31 41 51  
 | | | | |  
 80 MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGL WMSCVSQSTG 60  
 IQICKVFDLS LNLSSLTQAT RALMVVGILL GVIAIFVATV GMKCMKLED DEVQKMRMAV 120  
 IIGAILFLAG LAIILVATWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCLLGG 180  
 LLCCSCPRKT TSYPTPRPYP KPAPSSGKDY V

Seq ID NO: 393 DNA sequence  
Nucleic Acid Accession #: NM\_006180.1  
Coding sequence: 352..2820

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
CCCCCATTCG CATCTAACAA GGAATCTGCG CCCAGAGAG TCCCGGACGC CGCCGGTCGG 60
TGCCCGGCGC GCCGGGCCAT GCAGCGACGG CCGCCGCGGA GCTCCGAGCA GCGGTAGCGC 120
CCCCCTGTAA AGCGGTTGCG TATGCCGGGA CCACTGTGAA CCCTGCCGCC TGCCGGAAACA 180
CTCTTCGCTC CGGACCAAGCT CAGCCTCTGA TAAGCTGGAC TCGGCACGCC CGCAACAAGC 240
ACCGAGGAGT TAAGAGAGCC GCAAGCGCAG GGAAGGCCCTC CCGCACGGG TGGGGGAAAG 300
CGGCCGGTGC AGCGCGGGGA CAGGCACTCG GGCTGGCACT GGCTGCTAGG GATGTCGTCC 360
TGGATAAGGT GGCATGGACC CGCCATGGCG CGGCTCTGGG GCTTCTGCTG GCTGGTTGTG 420
GGCTTCTGGA GGGCCGCTTT CGCCTGTCCC ACGTCTGCA AATGCAGTGC CTCTCGGATC 480
TGGTGACGCG ACCCTTCTCC TGGCATCGTG GCATTTCCGA GATTGGAGCC TAACAGTGTA 540
GATCCTGAGA ACATCACCGA AATTTTCATC GCAAAACCAGA AAAGGTTAGA AATCATCAAC 600
GAAGATGATG TTGAAGCTTA TGTGGGACTG AGAAATCTGA CAATTGTGGA TTCTGGATTA 660
AAATTTGTGG TCATAAAGC ATTTCTGAAA AACAGCAACC TGCAGCACAT CAATTTTACC 720
CGAAACAAAC TGACGAGTTT GTCTAGGAAA CATTTCCGTC ACCTTGACTT GTCTGAACTG 780
ATCCTGGTGG GCAATCCATT TACATGCTCC TGTGACATTA TGTGGATCAA GACTCTCCAA 840
GAGGCTAAAT CCAGTCCAGA CACTCAGGAT TTGTACTGCC TGAATGAAAG CAGCAGAAT 900
TTTCCCTCGG CAAACCTGCA GATACCCAAT TGTGGTTTGC CATCTGCAAA TCTGGCCGCA 960
CCTAACCTCA CTGTGGAGGA AGGAAAGTCT ATCACATTAT CCGTAGTGT GGCAGGTGAT 1020
CCGGTTCCTA ATATGTATTG GGATGTTGGT AACCTGGTTT CCAACATAT GAATGAAACA 1080
AGCCACACAC AGGGCTCCTT AAGGATAACT AACATTTTCA CCGATGACAG TGGGAGCAG 1140
ATCTCTTGTG TGGCGGAAAA TCTTGTAGGA GAAGATCAAG ATTCTGTCAA CCTCACTGTG 1200
CATTTTGCAC CAACTATCAC ATTTCTCGAA TCTCCAACCT CAGACCACCA CTGGTGCATT 1260
CCATTCACTG TGAAGGCCAA CCCAAACCA CGCCTTCAGT GGTTCATATA CGGGGCAATA 1320
TTGAATGAGT CCAAAATACAT CTGTACTAAA ATACATGTTA CCAATCACAC GGAGTACCAC 1380
GGCTGCCTCC AGCTGGATAA TCCCACTCAC ATGAACAATG GGGACTACAC TCTAATAGCC 1440
AAGAATGAGT ATGGGAAGGA TGAGAAACAG ATTTCTGCTC ACTTCATGGG CTGGCCTGGA 1500
ATTGACGATG GTGCAAAACC AAATTATCCT GATGTAATTT ATGAAGATTA TGGAACTGCA 1560
GCGAATGACA TCGGGGACAC CACGAACAGA AGTAATGAAA TCCCTTCCAC AGACGTCAC 1620
GATAAACCAG CTCGGGAACA TCTCTCGTCC TATGCTGTGG TGGTGATTGC GTCTGTGGTG 1680
GGATTTTGCC TTTTGGTAAT GCTGTTTCTG CTTAAGTTGG CAAGACACTC CAAATTGGGC 1740
ATGAAAGGCC CAGCCTCCGT TATCAGCAAT GATGATGACT CTGCCAGCCC ACTCCATCAC 1800
ATCTCCAATG GGAGTAACAC TCCATCTTCT TCGGAAGGTG GCCCAGATGC TGTCAATTAT 1860
GGAATGACCA AGATCCCTGT CATTGAAAAT CCCCACTACT TTGGCATCAC CAACAGTCAG 1920
CTCAAGCCAG ACACATTGTG TCAGCACATC AAGCGACATA ACATTGTCTT GAAAGGGGAG 1980
CTAGGCGAAG GAGCCTTTGG AAAAGTGTTT CTAGCTGAAT GCTATAACCT CTGTCCTGAG 2040
CAGGACAAGA TCTTGGTGGC AGTGAAGACC CTGAAGGATG CCAGTGACAA TGCACGCAAG 2100
GACTTCCACC GTGAGGCCGA GCTCCTGACC AACCTCCAGC ATGAGCACAT CGTCAAGTTC 2160
TATGGCGTCT GCGTGGAGGG CGACCCCTCT ATCATGGTCT TTGAGTACAT GAAGCATGGG 2220
GACCTCAACA AGTTCTCTAG GGCACACGGC CCTGATGCCG TGCTGATGGC TGAGGGCAAC 2280
CCGCCCACGG AACTGACGCA GTGCGAGATG CTGCATATAG CCCAGCAGAT CGCCGCGGGC 2340
ATGGTCTACC TGGCGTCCCA GCACCTCTGT CACCGCGATT TGGCCACCAG GAACTGCCTG 2400
GTGCGGGAGA ACTTGTGTTG GAAAACGGG GACTTTGGGA TGTCCCGGGA CGTGTACAGC 2460
ACTGACTACT ACAGGGTCGG TGGCCACACA ATGCTGCCCA TTCGCTGGAT GCCTCCAGAG 2520
AGCATCATGT ACAGGAAATT CACGACGGAA AGCGACGTCT GGAGCCTGGG GGTCTGTGTT 2580
TGGGAGATTG TCACCTATGG CAACAGCCCC TGGTACCAGC TGTCAACAAA TGAGGTGATA 2640
GAGTGTATCA CTCAGGGCCG AGTCTCTCAG CGACCCCGCA CGTGCCCCCA GGAGGTGTAT 2700
GAGCTGATGC TGGGGTGTCT GCAGCGAGAG CCCCACATGA GGAAGACAT CAAGGGCATC 2760
CATACCCTCC TTCAGAACTT GGCCAAGGCA TCTCCGGTCT ACCTGGACAT TCTAGGCTAG 2820
GGCCCTTTTC CCCAGACCGA TCCTTCCCAA CGTACTCCTC AGACGGGCTG AGAGGATGAA 2880
CATCTTTTAA GTGCCGCTGG AGGCCACCAA GCTGCTCTCC TTCACTCTGA CAGTATTAAC 2940
ATCAAGAGCT CCGAGAAGCT CTCGAGGGAA GCAGTGTGTA CTCTTCTATC CATAGACACA 3000
GTATTGACTT CTTTGTGGA TTTATCTTTT CTCTCTTTC ATCTCCCTTG GTTGTCTCTT 3060
TTTCTTTTTT TAAATTTTCT TTTTCTTCTT TTTTCTGCTC TTCCCTGCTT CAGGATCTTT 3120
ACCTTTCTT TTTGATCAAT CTGGCTTCTG CATTACTATT AACTCTGCAT AGACAAAGGC 3180
CTTAACAAAC GTAATTTGTT ATATCAGCAG CACTCCAGT TTGCCACCA CAACTAACAA 3240
TGCCTTGTG TATTCTTGCC TTTGATGTGG ATGAAAAAAA GGGAAAAACA ATATTTCACT 3300
TAAACTTTGT CACTTCTGCT GTACAGATAT CGAGAGTTTC TATGGATTCA CTTCTATTTA 3360
TTTATTATTA TTACTGTTCT TATTGTTTTT GGATGGCTTA AGCCTGTGTA TAAAAAGAA 3420
AACTGTGTTT CAATCTGTGA AGCCTTTATC TATGGGAGAT TAAACCAGA GAGAAAGAA 3480
ATTTATTATG AACCGCAATA TGGGAGGAAC AAAGACAACC ACTGGGATCA GCTGGTGTCA 3540
GTCCTTACTT AGGAAATACT CAGCAACTGT TAGCTGGGAA GAATGTATTC GGCACCTTCC 3600
CCTGAGGACC TTTCTGAGGA GTAAAAAGAC TACTGGCCTC TGTGCCATGG ATGATTCTTT 3660
TCCCATCACC AGAAATGATA GCGTGCAGTA GAGAGCAAAG ATGGCTT

```

Seq ID NO: 394 Protein sequence  
Protein Accession #: NP\_006171.1

```

75      1      11      21      31      41      51
      |      |      |      |      |      |
MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCKCSA SRIWCSDFSP GIVAFPRLEP 60
NSVDPENITE IFIANQKRL E IINEDDVEAY VGLRNLTIVD SGLKFVAHKA FLKNSNLQHI 120
NFTRNKLTSL SRKFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
SKNIPLANLQ IPNCGLPASN LAAPNLIVVEE GKSITLSCSV AGDPVPMNYW DVGNLVSXHM 240
NETSHTQSSL RITNISDD S KQISCAVEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360
LIAKNEYGKD EKQISAHFYM WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGPASV ISNDDDSASP 480
LHHISNGSNT PSSSEGGPDA VIIGMTKIPV IENPQYFGIT NSQLKPDFTV QHIKRHNIVL 540
KRELGEAGFG KVFLAECCYNL CPEQDKLLVA VKTLKDASDN ARKDFHREAE LLTNLQHEHI 600

```

VKFGVVCVEG DPLIMVFEYM KHGDLNKFRL AHGPDVAVLMA EGNPPTELTQ SQMLHIAQQI 660  
 AAGMVYLASQ HFVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYRVG GHTMLPIRWM 720  
 PPESIMYRKF TTESDVVSLG VVLWEIFTYG KQWPYQLSNN EVIECITQGR VLQRPRTCPQ 780  
 EVYELMLGCW QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG

Seq ID NO: 395 DNA sequence  
 Nucleic Acid Accession #: AF410899  
 Coding sequence: 483..2999

1 11 21 31 41 51  
 GGGAGCAGGA GCCTCGCTGG CTGCTTCGCT CGCGCTCTAC GCGCTCAGTC CCCGGCGGTA 60  
 GCAGGAGCCT GGACCCAGGC GCCGGCGGCG GGCCTGAGGC GCCCGAGCCC GGCCTCGAGG 120  
 TGCATACCGG ACCCCCATTC GCATCTAACA AGGAATCTGC GCCCCAGAGA GTCCCGGACG 180  
 CCGCCGGTGC GTGCCCGGCG CGCCGGGCGCA TGCAGCGACG GCCCGCGCGG AGCTCCGAGC 240  
 AGCGGTAGCG CCCCCCTGTA AAGCGGTTTCG CTATGCCGGG ACCACTGTGA ACCCTGCCGC 300  
 CTGCCGGAAC ACTCTTCGCT CCGGACCAGC TCAGCCTCTG ATAAGCTGGA CTCGGCACGC 360  
 CCGCAACAAAG CACCGAGGAG TTAAGAGAGC CGCAAGCGCA GGGAAAGGCCT CCCCGCACGG 420  
 GTGGGGGAAA GCGGCGGCTG CAGCGCGGGG ACAGGCACTC GGGCTGGCAC TGGCTGCTAG 480  
 GGATGTCGTC CTGGATAAGG TGGCATGGAC CCGCCATGGC GCGGCTCTGG GGCTCTGCT 540  
 GGCTGGTTGT GGGCTTCTGG AGGGCCGCTT TCGCCTGTCC CACGTCTGCG AAATGCAGTG 600  
 CCTCTCGGAT CTGGTGCAGC GACCCCTCTC CTGGCATCGT GGCATTTCCG AGATTGGAGC 660  
 CTAACAGTGT AGATCTGAG AACATCACCG AAATTTTCAT CGCAAAACCAG AAAAGGTTAG 720  
 AAATCATCAA CGAAGATGAT GTTGAAGCTT ATGTGGGACT GAGAAATCTG ACAATTGTGG 780  
 ATTCGGAATT AAAATTTGFG GCTCATAAAG CATTCTGAA AAACAGCAAC CTGCAGCACA 840  
 TCAATTTTAC CCGAAACAAA CTGACGAGTT TGTCTAGGAA ACATTTCCGT CACCTTGACT 900  
 TGTCTGAAC TATCTCTGGT GGCAATCCAT TTACATGCTC CTGTGACATT ATGTGGATCA 960  
 AGACTCTCCA AGAGGCTAAA TCCAGTCCAG ACACTCAGGA TTTGTACTGC CTGAATGAAA 1020  
 GCAGCAAGAA TATTCCTCTG GCAACCTGCG AGATACCCAA TTGTGGTTTG CCATCTGCAA 1080  
 ATCTGGCCCG ACCTAACCTC ACTGTGGAGG AAGGAAAGTC TATCACATTA TCCTGTAGTG 1140  
 TGGCAGGTGA TCCGGTTCCT AATATGTATT GGGATGTTGG TAACCTGGTT TCCAAACATA 1200  
 TGAATGAAC AAGCCACACA CAGGGCTCCT TAAGGATAAC TAACATTTC A TCCGATGACA 1260  
 GTGGGAAGCA GATCTCTTGT GTGGCGGAAA ATCTTGTAAG AGAAGATCAA GATTCTGTCA 1320  
 ACCTCACTGT GCATTTTGA CCAACTATCA CATTCTCGA ATCTCCAACC TCAGACCACC 1380  
 ACTGGTGCA TCCATTCAT GTGAAAGGCA ACCCCAAACC AGCGCTTCAG TGGTTCTATA 1440  
 ACGGGGCAAT ATTGAATGAG TCCAAATACA TCTGTAATA AATACATGTT ACCAATCACA 1500  
 CGGAGTACCA CGGCTGCCCT CAGCTGGATA ATCCCACTCA CATGAACAAT GGGGACTACA 1560  
 CTCTAATAGC CAAGAATGAG TATGGGAAGG ATGAGAAACA GATTTCGTCT CACTTCATGG 1620  
 GCTGGCCTGG AATTGACGAT GGTGCAAAAC CAAATTATCC TGATGTAATT TATGAAGATT 1680  
 ATGGAAGTGC AGCGAATGAC ATCGGGGACA CCACGAACAG AAGTAATGAA ATCCCTTCCA 1740  
 CAGAGTCCAC TGATAAAACC GGTGCGGAAC ATCTCTCGGT CTATGCTGTG GTGGTGATTG 1800  
 CGTCTGTGGT GGGATTTTGC CTTTTGGTAA TGCTGTTTCT GCTTAAGTTG GCAAGACACT 1860  
 CCAAGTTTGG CATGAAAGAT TTCTCATGGT TTGGATTTGG GAAAGTAAAA TCAAGACAAG 1920  
 GTGTTGGGCC GTTCTCCGTT ATCAGCAATG ATGATGACTC TGCCAGCCCA CTCATCACA 1980  
 TCTCCAATGG GAGTAACACT CCATCTTCTT CGGAAGGTGG CCCAGATGCT GTCATTATTG 2040  
 GAATGACCAA GATCCCTGTC ATTGAAATC CCCAGTACTT TGGCATCACC AACAGTCAGC 2100  
 TCAAGCCAGA CACATTTGTT CAGCACATCA AGCGACATAA CATTGTTCTG AAAAGGGAGC 2160  
 TAGGCGAAGS AGCCTTTGGA AAGTGTTCCT TAGCTGAATG CTATAACCTC TGTCTCTGAGC 2220  
 AGGACAAGAT TTGTGTGGCA GTGAAGACCC TGAAGGATGC CAGTGACAA TGCACGCAAG 2280  
 ACTTCCACCG TGAGGCCGAG CTCCTGACCA ACCTCCAGCA TGAGCACATC GTCAAGTTCT 2340  
 ATGGCGTCTG CGTGGAGGGC GACCCCTCTA TCATGGTCTT TGAGTACATG AAGCATGGGG 2400  
 ACCTCAACAA GTTCTCTCAG GCACACGGCC CTGATGCCGT GCTGATGGCT GAGGGCAACC 2460  
 CGCCACAGGA ACTGACGAGC TCGCAGATGC TGCATATAGC CCAGCAGATC GCGCGGGGCA 2520  
 TGGTCTACCT GGCCTCCAG CACTTCGTGC ACCGCGATT TGGCCACCAG AACTGCCTGG 2580  
 TCGGGGAGAA CTTGCTGGTG AAAATCGGGG ACTTTGGGAT GTCCCGGGAC GTGTACAGCA 2640  
 CTGACTACTA CAGGGTCTGT GGCACACAAA TGCTGCCCAT TCGCTGGATG CCTCCAGAGA 2700  
 GCATCATGTA CAGGAATTC ACAGCGGAAA GCGACGCTCT GAGCCTGGGG GTCGTGTTGT 2760  
 GGGAGATTTT CACCTATGGC AAACAGCCCT GGTACCAAGT GTCAAACAAT GAGGTGATAG 2820  
 AGTGTATCAC TCAGGGCCGA GTCTGCAGC GACCCCGCAC GTGCCCCAG GAGGTGTATG 2880  
 AGCTGATGCT GGGGTGCTGG CAGCGAGAGC CCCACATGAG GAAGAATATC AAGGGCATCC 2940  
 ATACCTCTCT TCAGAACTTG GCCAAGGCAT CTCGGTCTA CTGGACAT TTAGGCTAGG 3000  
 GCCCTTTTCC CCAGACCGAT CCTTCCCAAC GTACTCTCTA GACGGGCTGA GAGGATGAAC 3060  
 ATCTTTTAAC TGCCGCTGGA GGCACCAAG CTGCTCTCTT TCACTCTGAC AGTATTAAAC 3120  
 TCAAGACTC CGAGAAGCTC TCGAGGGAAG CAGTGTGTAC TTCTTCATCC ATAGACACAG 3180  
 TATTGACTTC TTTTGGGCAT TATCTCTTTC TCTCTTTCCA TCTCCCTTGG TTGTTCTTTT 3240  
 TTCTTTTTTT AAATTTTCTT TTTCTTCTT TTTTCTGCT TCCCTGCTTC ACGATTCTTA 3300  
 CCCTTTCTTT TGAATCAAT TGGCTTCTGC ATTACTATTA ACTCTGCATA GACAAAGGCC 3360  
 TTAACAAACG TAATTTGTGA TATCAGCAGA CACTCCAGTT TGCCCAACC AACTAACAT 3420  
 GCCTTGTGT ATTCTGCTT TTGATGTGGA TGAACAAAAG GGAACAAACA TATTTCACTT 3480  
 AAACCTTGTG ACTCTGCTG TACAGATATC GAGAGTTTCT ATGGATTAC TTCTATTAT 3540  
 TTATTATTAT TACTGTCTT ATTGTTTTTG GATGGCTTAA GCCTGTGTAT AAAAAAGAAA 3600  
 ACTTGTGTTA AATCTGTGAA GCCTTTATCT ATGGGAGATT AAAACCAAG AGAAAGAAAG 3660  
 TTTATTATGA ACCGCAATAT GGGAGGAACA AAGACAACCA CTGGGATGAG CTGGTGTGAG 3720  
 TCCCTACTTA GGAATACTC AGCAACTGTT AGCTGGGAAG AATGTATTCG GCACCTTCCC 3780  
 CTGAGGACCT TCTGAGGAG TAAAAAGACT ACTGGCCTCT GTGCCATGGA TGATTCTTTT 3840  
 CCCATACCA GAAATGATAG CGTGCAGTAG AGAGCAAGA TGGCTTCCGT GAGACACAAG 3900  
 ATGGCGCATA GTGTGCTCGG ACACAGTTT GTCTCTGTA GTTGTGATGA TAGCACTGGT 3960  
 TTGTTTCTCA AGCGCTATCC ACAGAACCTT TGTCAACTTC AGTTGAAAAG AGGTGGATTG 4020  
 ATGTCCAGAG CTCATTTCCG GGTGAGGTGG GAAAGCC

Seq ID NO: 396 Protein sequence  
 Protein Accession #: AAL67965.1

1 11 21 31 41 51

	MSSWIRWHGP	AMARLWGFCE	LUVGFWRAAF	ACPTSCKCSA	SRIWCSDPSP	GIVAFPRLEP 60
	NSVDPENITE	IFIANQKRLE	IINEDDVEAY	VGLRNLITVD	SLKLFVAHKA	FLKNSNLQHI 120
5	NFTRNKLTSL	SRKHFRHLDL	SELILVGNPF	TCSCDIMWIK	TLQEAQSSPD	TQDLYCLNES 180
	SKNIPLANLQ	IPNCGLPAN	LAAPNLTVEE	GKSITLSCSV	AGDPVPNNYW	DVGNLVSKHM 240
	NETSHTQSSL	RITNISDDSD	GKQISCVAEN	LVGEDQDSVN	LTVHFAPIT	FLESPTSDDH 300
	WCIPFTVKGN	PKPALQWFYN	GAILNESKYI	CTKIHVTNHT	EYHGCLQLDN	PTHMNGDYT 360
	LIAKNEYGKD	EKQISAHFMG	WPGIDDGANP	NYPDVIYEDY	GTAANDIGDT	TNRSNEIPST 420
10	DVTDKTGREH	LSVYAVVVIA	SVVGFCLLMV	LFLKLARHS	KFGMKDFSWF	GFGKVKSRQG 480
	VGPASVISND	SDSASPLHHI	SNGSNTPSSS	EGGPDVAVIG	MTKIPVNIENP	QYFGITNSQL 540
	KPDTFVQHIK	RHNIVLKRLE	GEGAFGKVFL	AECYNLCPEQ	DKILVAVKTL	KDASDNARKD 600
	FHREAEELLN	LQHEHIVKFY	GVCVEGDPLI	MVFEYMKHGD	LNKFLRAHGP	DAVLMAEGNP 660
	PTELTQSQML	HIAQQIAAGM	VYLASQHFVH	RDLATRNCLV	GENLLVKIGD	FGMSRDVYST 720
15	DYYRVGGHTM	LPIRWMPPEP	IMYRKFTTES	DVWSLGVVLW	EIFTYQKQPW	YQLSNNEVIE 780
	CITQGRVLQR	PRTCPQEVYE	LMLGCCWQREP	HMRKNIKGIH	TLLQNLAKAS	PVYLDILG

Seq ID NO: 397 DNA sequence  
Nucleic Acid Accession #: AB052906  
Coding sequence: 74..814

	1	11	21	31	41	51	
	AAAACCTTGA	GGTGATTCAT	CTTCCAGGCT	CTCCTTCCAT	CAAGTCTCTC	CTCCCTAGCG	60
25	CTCTGGGTCC	TTAATGGCAG	CAGCCGCCGC	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	120
	GCTCCTGCTG	TCCGGCTGGT	CCCGGGCTGG	GCGAGCCGAC	CCTCACTCTC	TTTGCTATGA	180
	CATCACCGTC	ATCCCTAAGT	TCAGACCTGG	ACCACGGTGG	TGTGCGGTTC	AAGGCCAGGT	240
	GGATGAAAG	ACTTTTCTTC	ACTATGACTG	TGGCAACAAG	ACAGTCAAC	CTGTCAGTCC	300
	CTTGGGGAAG	AACTAAATG	TCACAACGGC	CTGGAAGCA	CAGAACCAG	TACTGAGAGA	360
30	GCTGGTGGAG	ATACTTACAG	AGCAACTGCG	TGACATTGAG	CTGGAGAATT	ACACACCCAA	420
	GGAAACCCCTC	ACCTTGACAG	CCAGGATGTC	TTGTGACAG	AAAGCTGAAG	GACACAGCAG	480
	TGATCTTGG	CAGTTTCAGT	TCGATGGGCA	GATCTTCTCT	CTCTTTGACT	CAGAGAAGAG	540
	AATGTGGACA	ACGGTTCATC	CTGAGGCCAG	AAAGATGAAA	GAAAAGTGGG	AGAATGACAA	600
	GGTGTGGCC	ATGTCTCTCC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
35	CTTCTTGATG	GGCATGGACA	GCACCCCTGA	GCCAAAGTGA	GGAGCACCAC	TCGCCATGTC	720
	CTCAGGCACA	ACCCAATCA	GGGCCACAGC	CACCACCTCT	ATCCTTTGCT	GCCTCTCAT	780
	CATCCTCCCC	TGCTTCATCC	TCCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTAA	840
	AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
	CCAGCTGCC	ACGACCTACG	GTGTATGTCC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	960
40	TGGACCAAT	AGCTCATCA	CTGCCCTGAT	TCCTTTTGCC	AACAATTTTA	CCAGCAGTTA	1020
	TACCTAACAT	ATTATGCAAT	TTTCTCTTGG	TGCTACCTGA	TGGAATTCCT	GCACTTAAAG	1080
	TTCTGGCTGA	CTAAACAAGA	TATATCATTT	TCTTTCTTCT	CTTTTGTGTT	GGAAAATCAA	1140
	GTACTTCTTT	GAATGTATGAT	CTCTTCTTGG	CAAAATGATAT	TGTCACTAAA	ATAATCACGT	1200
	TAGACTTCAG	ACCTCTGGGG	ATTCTTTCCG	TGTCCTGAAA	GAGAATTTT	AAATTTATTA	1260
45	ATAAGAAAAA	ATTATATATA	ATGATTGTTT	CCTTAGTAA	TTTATTGTTT	TGTACTGATA	1320
	TTTAAATAAA	GAGTTCTATT	TCCCAAAAAA	AAAAAATAAA	AA		

Seq ID NO: 398 Protein sequence  
Protein Accession #: BAB61048.1

	1	11	21	31	41	51	
	MAAAATKIL	LCLPLLLLLS	GWSRAGRADE	HSLCYDITVI	PKFRPGPRWC	AVQGVQDEKT	60
	FLHYDCGNKT	VTPVSPGLKK	LNVTTAWKAQ	NPVLREVVDI	LTEQLRDIQL	ENYTPKEPLT	120
55	LQARMSCEBQ	AEHSSSGSQ	FSFDGQIFLL	FDSEKRMWTT	VHPGARKMKE	KWENDKVVM	180
	SFHYFSMGDC	IGWLEDFLMG	MDSTLEPSAG	APLAMSSGTT	QLRATATTLLI	LCCLLIILPC	240
	FILPGI						

Seq ID NO: 399 DNA sequence  
Nucleic Acid Accession #: NM\_001898.1  
Coding sequence: 57..482

	1	11	21	31	41	51	
	GGCTCTCACC	CTCCTCTCCT	GCAGCTCCAG	CTTGTGCTC	TGCCCTTGAG	GAGACCATGG	60
65	CCCAGTATCT	GAGTACCCCTG	CTGCTCCTGC	TGGCCACCTT	AGCTGTGGCC	CTGGCCTGGA	120
	GCCCCAAGGA	GGAGGATAGG	ATAATCCCGG	GTGGCATCTA	TAAACGAGAC	CTCAATGATG	180
	AGTGGGTACA	CGGTGCCCTT	CACTTCGCCA	TCAGCGAGTA	TAAACAAGCC	ACCAAAGATG	240
	ACTACTACAG	ACGTCCGCTG	CGGGTACTAA	GAGCCAGGCA	ACAGACCGTT	GGGGGGGTGA	300
70	ATTACTTCTT	CGACGTAGAG	GTGGGCCGCA	CCATATGTAC	CAAGTCCCAG	CCCAACTTGG	360
	ACACCTGTGC	CTTCCATGAA	CAGCCAGAAC	TGCAGAAGAA	ACAGTTGTGC	TCTTTTCGAA	420
	TCTACGAAGT	TCCTCTGGAG	AACAGAAAGT	CCCTGGTGAA	ATCCAGGTGT	CAAGAATCCT	480
	AGGGATCTGT	GCCAGGCCAT	TCGCACCAGC	CACCACCCAC	TCCCACCCCT	TGTAGTGCTC	540
	CCACCCCTGG	ACTGGTGGCC	CCACCTCTGC	GGGAGGCCTC	CCCATTGTGC	TGCGCCAAAG	600
75	GACAGACAGA	GAAGGCTGCA	GGAGTCTCTT	GTGTCTCAGC	AGGGCGCTCT	GCCCTCCCTC	660
	CTTCTTCTT	GCTTCTAATA	GCCCTGGTAC	ATGGTACACA	CCCCCCCACC	TCCTGCAATT	720
	AAACAGTAGC	ATCGCC					

Seq ID NO: 400 Protein sequence  
Protein Accession #: NP\_001889.1

	1	11	21	31	41	51	
	MAQYLSTLLL	LLATLAVALA	WSPKEEDRII	PGGIYNADLN	DEWVQRALHF	AISEYNKATK	60
80	DDYYRRPLRV	LRARQQTVGG	VNYFFDVEVG	RTICTKSQPN	LDTCAPHEQP	ELQKKQLCSF	120

EIYEVWPWENR RSLVKSRQCE S

Seq ID NO: 401 DNA sequence

Nucleic Acid Accession #: NM\_003976.2

Coding sequence: 299..961

5

10

15

20

25

30

35

40

45

50

55

60

65

70

75

80

```

1      11      21      31      41      51
|      |      |      |      |      |
CTCTGAGCTT CTCTGAGCCT TGTTTGCTCA TCTGGAATAA GGGGATTAAA CCATTACCT 60
CATGGAGTTG TGAAGAATA GCTGCAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG 120
CTACTTCTGC TGGGTGTAGT CTAGCTGTGT AGGCCCTTGT TTCTCACCCT GGAGAACTG 180
GGGTGGCAGG CCGGTCCCCC ACAAAAGATA ACTCATCTCT TAATTGCAA GCTGCCTCAA 240
CAGGAGGGTG GGGGAACAGC TCAACAATGG CTGATGGGCG CTCTGGTGT TGATAGAGAT 300
GGAACCTGGA CTTGAGGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GCGGCAGCC 360
TGCCCTGTGG CCCACCTGG CCGCTCTGGC TCTGCTGAGC AGCGTCGAG AGGCCTCCCT 420
GGGCTCCGCG CCCCAGAGCC CTGCCCCCG CGAAGGCCCC CCGCTGTGCC TGGCGTCCCC 480
GCCTCGCCAC CTGCGGGGG GACGCACGGC CCGCTGGTGC AGTGAAGAG CCCGCGGCC 540
GCCGCGCAG CTTCTCGGC CCGCGCCCC GCGCCTGCA CCCCCTCTG CTCTCCCGC 600
CGGGGGCCGC GCGGCGCGG CTGGGGGCC GGGCAGCCGC GCTCGGCGC GGGGGCGCG 660
GGGTGCGCG CTGCGCTCGC AGCTGGTGCC GGTGCGCGC CTGCGCCTGG GCCACCGCTC 720
CGACGAGCTG GTGCGTTTCC GCTTCTGCAG CCGCTCCTGC CCGCGCGCGC GCTCTCCACA 780
CGACCTCAGC CTGGCCAGCC TACTGGGCGC CCGGGCCCTG CGACCGCCCC CGGGCTCCCG 840
GCCCCTCAGC CAGCCCTGCT GCCGACCAC GCGCTACGAA GCGGTCTCCT TCATGGACGT 900
CAACAGCACC TGGAGAACCG TGGACCGCCT CTCCGCCACC GCCTGCGGCT GCCTGGGCTG 960
AGGGCTCGCT CCAGGGCTTT GCAGACTGGA CCCTTACCGG TGGCTCTTCC TGCCTGGGAC 1020
CTTCCGCGAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGGCT CAAAGCTGAG 1080
AGGCCCTTAC CCGTGGGTGA TGGATATCAT CCCCAGACAG GTGAAGGGAC AACTGACTAG 1140
CAGCCCCAGA GCCCTCACC TGCGGATCCC AGCCTAAAAG ACACCAGAGA CCTCAGCTAT 1200
GGAGCCCTTC GGACCCACTT CTCACAGACT CTGGCACTGG CCAGGCCTCG AACCTGGGAC 1260
CCCTCTCTCG ATGAACACTA CAGTGGCTGA GGCATCAGCC CCCGCCAGG CCCTGTAGGG 1320
ACAGCATTTG AAGGACACAT ATTGCAGTTG CTGGTTGAA AGTGCTGTG CTGGAAGTGG 1380
CCTGTACTCA CTCATGGGAG CTGGCCCC

```

Seq ID NO: 402 Protein sequence

Protein Accession #: NP\_003967.1

1 11 21 31 41 51

| | | | | |

MELGLGLST LSHCPWRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60

PAGHLPGGRT ARWCSGRRAR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120

RGCRRLRQLV FVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180

RPVSQPCRP TRYEAVSFMD VNSTWRTVDR LSATACGLG

Seq ID NO: 403 DNA sequence

Nucleic Acid Accession #: NM\_057091.1

Coding sequence: 783..1445

50

55

60

65

70

75

80

85

90

95

100

105

110

115

120

125

130

135

140

145

150

155

160

165

170

175

180

185

190

195

200

205

210

215

220

225

230

235

240

245

250

255

260

265

270

275

280

285

290

295

300

305

310

315

320

325

330

335

340

345

350

355

360

365

370

375

380

385

390

395

400

405

410

415

420

425

430

435

440

445

450

455

460

465

470

475

480

485

490

495

500

505

510

515

520

525

530

535

540

545

550

555

560

565

570

575

580

585

590

595

600

605

610

615

620

625

630

635

640

645

650

655

660

665

670

675

680

685

690

695

700

705

710

715

720

725

730

735

740

745

750

755

760

765

770

775

780

785

790

795

800

805

810

815

820

825

830

835

840

845

850

855

860

865

870

875

880

885

890

895

900

905

910

915

920

925

930

935

940

945

950

955

960

965

970

975

980

985

990

995

1000

1005

1010

1015

1020

1025

1030

1035

1040

1045

1050

1055

1060

1065

1070

1075

1080

1085

1090

1095

1100

1105

1110

1115

1120

1125

1130

1135

1140

1145

1150

1155

1160

1165

1170

1175

1180

1185

1190

1195

1200

1205

1210

1215

1220

1225

1230

1235

1240

1245

1250

1255

1260

1265

1270

1275

1280

1285

1290

1295

1300

1305

1310

1315

1320

1325

1330

1335

1340

1345

1350

1355

1360

1365

1370

1375

1380

1385

1390

1395

1400

1405

1410

1415

1420

1425

1430

1435

1440

1445

1450

1455

1460

1465

1470

1475

1480

1485

1490

1495

1500

1505

1510

1515

1520

1525

1530

1535

1540

1545

1550

1555

1560

1565

1570

1575

1580

1585

1590

1595

1600

1605

1610

1615

1620

1625

1630

1635

1640

1645

1650

1655

1660

1665

1670

1675

1680

1685

1690

1695

1700

1705

1710

1715

1720

1725

1730

1735

1740

1745

1750

1755

1760

1765

1770

1775

1780

1785

1790

1795

1800

1805

1810

1815

1820

1825

1830

1835

1840

1845

1850

1855

1860

1865

1870

1875

1880

1885

1890

1895

1900

1905

1910

1915

1920

1925

1930

1935

1940

1945

1950

1955

1960

1965

1970

1975

1980

1985

1990

1995

2000

2005

2010

2015

2020

2025

2030

2035

2040

2045

2050

2055

2060

2065

2070

2075

2080

2085

2090

2095

2100

2105

2110

2115

2120

2125

2130

2135

2140

2145

2150

2155

2160

2165

2170

2175

2180

2185

2190

2195

2200

2205

2210

2215

2220

2225

2230

2235

2240

2245

2250

2255

2260

2265

2270

2275

2280

2285

2290

2295

2300

2305

2310

2315

2320

2325

2330

2335

2340

2345

2350

2355

2360

2365

2370

2375

2380

2385

2390

2395

2400

2405

2410

2415

2420

2425

2430

2435

2440

2445

2450

2455

2460

2465

2470

2475

2480

2485

2490

2495

2500

2505

2510

2515

2520

2525

2530

2535

2540

2545

2550

2555

2560

2565

2570

2575

2580

2585

2590

2595

2600

2605

2610

2615

2620

2625

2630

2635

2640

2645

2650

2655

2660

2665

2670

2675

2680

2685

2690

2695

2700

2705

2710

2715

2720

2725

2730

2735

2740

2745

2750

2755

2760

2765

2770

2775

2780

2785

2790

2795

2800

2805

2810

2815

2820

2825

2830

2835

2840

2845

2850

2855

2860

2865

2870

2875

2880

2885

2890

2895

2900

2905

2910

2915

2920

2925

2930

2935

2940

2945

2950

2955

2960

2965

2970

2975

2980

2985

2990

2995

3000

3005

3010

3015

3020

3025

3030

3035

3040

3045

3050

3055

3060

3065

3070

3075

3080

3085

3090

3095

3100

3105

3110

3115

3120

3125

3130

3135

3140

3145

3150

3155

3160

3165

3170

3175

3180

3185

3190

3195

3200

3205

3210

3215

3220

3225

3230

3235

3240

3245

3250

3255

3260

3265

3270

3275

3280

3285

3290

3295

3300

3305

3310

3315

3320

3325

3330

3335

3340

3345

3350

3355

3360

3365

3370

3375

3380

3385

3390

3395

3400

3405

3410

3415

3420

3425

3430

3435

3440

3445

3450

3455

3460

3465

3470

3475

3480

3485

3490

3495

3500

3505

3510

3515

3520

3525

3530

3535

3540

3545

3550

3555

3560

3565

3570

3575

3580

3585

3590

3595

3600

3605

3610

3615

3620

3625

3630

3635

3640

3645

3650

3655

3660

3665

3670

3675

3680

3685

3690

3695

3700

3705

3710

3715

3720

3725

3730

3735

3740

3745

3750

3755

3760

3765

3770

3775

3780

3785

3790

3795

3800

3805

3810

3815

3820

3825

3830

3835

3840

3845

3850

3855

3860

3865

3870

3875

3880

3885

3890

3895

3900

3905

3910

3915

3920

3925

3930

3935

3940

3945

3950

3955

3960

3965

3970

3975

3980

3985

3990

3995

4000

4005

4010

4015

4020

4025

4030

4035

4040

4045

4050

4055

4060

4065

4070

4075

4080

4085

4090

4095

4100

4105

4110

4115

4120

4125

4130

4135

4140

4145

4150

4155

4160

4165

4170

4175

4180

4185

4190

4195

4200

4205

4210

4215

4220

4225

4230

4235

4240

4245

4250

4255

4260

4265

4270

4275

4280

4285

4290

4295

4300

4305

4310

4315

4320

4325

4330

4335

4340

4345

4350

4355

4360

4365

4370

4375

4380

4385

4390

4395

4400

4405

4410

4415

4420

4425

4430

4435

4440

4445

4450

4455

4460

4465

4470

4475

4480

4485

4490

4495

4500

4505

4510

4515

4520

4525

4530

4535

4540

4545

4550

4555

4560

4565

4570

4575

4580

4585

4590

4595

4600

4605

4610

4615

4620

4625

4630

4635

4640

4645

4650

4655

4660

4665

4670

4675

4680

4685

4690

4695

4700

4705

4710

4715

4720

4725

4730

4735

4740

4745

4750

4755

4760

4765

4770

4775

4780

4785

4790

4795

4800

4805

4810

4815

4820

4825

4830

4835

4840

4845

4850

4855

4860

4865

4870

4875

4880

4885

4890

4895

4900

4905

4910

4915

4920

4925

4930

4935

4940

4945

4950

4955

4960

4965

4970

4975

4980

4985

4990

4995

5000

5005

5010

5015

5020

5025

5030

5035

5040

5045

5050

5055

5060

5065

5070

5075

5080

5085

5090

5095

5100

5105

5110

5115

5120

5125

5130

5135

5140

5145

5150

5155

5160

5165

5170

5175

5180

5185

5190

5195

5200

5205

5210

5215

5220

5225

5230

5235

5240

5245

5250

5255

5260

5265

5270

5275

5280

5285

5290

5295

5300

5305

5310

5315

5320

5325

5330

5335

5340

5345

5350

5355

5360

5365

5370

5375

5380

5385

5390

5395

5400

5405

5410

5415

5420

5425

5430

5435

5440

544



```

1      11      21      31      41      51
5  MELGLGGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPPVLAS 60
    PAGHLPGGRT ARWCSEGRARR PPPQPSRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
    RGCLRLSQLV PVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
    RPVSQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGCLG

```

Seq ID NO: 405 DNA sequence  
Nucleic Acid Accession #: NM\_057160.1  
Coding sequence: 1..714

```

1      11      21      31      41      51
15 ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCAAGGCC 60
    CACCTGGGTG CCCTCTTTCT CCCTGAGGCT CCACTTGGTC TCTCCGCGCA GCCTGCCCTG 120
    TGGCCACACC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCG CAGAGGCCTC CCTGGGCTCC 180
    GCGCCCCGCA GCCCTGCCCC CCGCGAAGGC CCCCAGCCTG TCCTGGCGTC CCCCAGCGGC 240
20 CACCTGCCCG GGGGACGCAC GCGCCGCTGG TGCAGTGGAA GAGCCCGCGC GCCGCGCGCG 300
    CAGCCTTCTC GGGCCGCGCC CCGCCGCGCT GCACCCCAT CTGCTCTTCC CCGCGGGGCG 360
    CCGCGGGCGC GGGCTGGGGG CCGGGGACAG CCGCTCGGG CAGCGGGGGC GCGGGGCTGC 420
    CGCTGCGCT CGCAGCTGGT GCGGTGCGC GCGCTCGGCC TGGGCCACCG CTCCGACGAG 480
    CTGGTGGCTT TCCGCTTCTG CAGCGGCTCC TGCCGCGCGC CGCGCTCTCC ACACGACCTC 540
25 AGCCTGGCCA GCCTACTGGG CGCCGGGGCC CTGCGACCGC CCCCAGGCTC CCGGCCCTGC 600
    AGCCAGCCCT GCTGCCGACC CACGCGCTAC GAAGCGGTCT CCTTCATGGA CGTCAACAGC 660
    ACCTGGAGAA CCGTGACCGC CCTCTCCGCC ACCGCTCGCG GCTGCCTGGG CTGAGGGCTC 720
    GCTCCAGGGC TTTCAGAGCT GGACCTTAC CGGTGGCTCT TCCTGCCTGG GACCCTCCCG 780
    CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAAGCT GAGAGCCCCC 840
    TACCGGTGGG TGATGGATAT CATCCCCGAA CAGGTGAAGG GACAACTGAC TAGCAGCCCC 900
30 AGAGCCCTCA CCTGCGGAT CCCAGCCTAA AAGACACCA AGACCTCAGC TATGGAGCCC 960
    TTGGAAGGAC CTCTCAGAG ACTCTGGCAC TGGCCAGGCC TCGAAGCTGG GACCCTCCT 1020
    CTGATGAACA CTACAGTGGC TGAGGCATCA GCCCCGCGCC AGGCCCTGTA GGGACAGCAT 1080
    TTGAAGGACA CATATTGCA TTGCTTGGT GAAAGTGCCT GTGCTGGAAC TGGCCTGTAC 1140
35 TCACTCATGG GAGCTGGCCC C

```

Seq ID NO: 406 Protein sequence  
Protein Accession #: NP\_476501.1

```

1      11      21      31      41      51
40 MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS 60
    APRSPAPREG PPPVLASPAH HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120
    RAARAGGPGS RARAAGARGC RLRSQLVFVR ALGLGHRSD LVRFRFCSGS CRRARSPHDL 180
45 SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

```

Seq ID NO: 407 DNA sequence  
Nucleic Acid Accession #: NM\_057090.1  
Coding sequence: 29..715

```

1      11      21      31      41      51
50 CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTGGA CTGGAGGCC TCTCCAGCT 60
    GTCCCACTGC CCCTGGCCTA GCGGCGAGGC TCCACTTGGT CTCGCCGCGC AGCCTGCCCT 120
55 GTGGCCCAAC CTGGCCGCTC TGGCTCTGCT GAGCAGCGTC GCAGAGGCTC CCCTGGGCTC 180
    CGCGCCCGCG AGCCCTTGCC CCGCGAAGG CCCCAGCCTG GTCTGGCGT CCCCAGCGGC 240
    CCACCTGCGG GGGGACGCA CCGCCGCTG GTGCACTGGA AGAGCCCGGC GCGCGCGGCC 300
    GCAGCCTTCT CCGCCCGCGC CCGCCCGGCC TGCACCCCA TCTGCTCTTC CCGCGGGGG 360
    CCGCGCGCGC CCGGCTGGGG GCGCGGCGAG CCGCGCTCGG GCAGCGGGGG CCGGGGGCTG 420
    CCGCTGCGC TCGCAGCTGG TCGCGGTGCG CCGCTCGGC CTGGGCCACC GCTCCGACGA 480
    GCTGTGCGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCGC GCGCGCTCTC CACACGACCT 540
    CAGCCTGGCC AGCCTACTGG GCGCCGGGGC CCTGCGACCG CCCCAGGCTC CCGGCCCGT 600
    CAGCCAGCCC TGCTGCCGAC CCACGCGCTA CGAAGCGGTC TCCTTCATGG ACGTCAACAG 660
    CACCTGGAGA ACCGTGGACC GCCTCTCCGC CACCGCCTGC GGCTGCCTGG GCTGAGGCT 720
    CGCTCCAGGG CTTTGCAGAC TGGACCTTA CCGGTGGCTC TTCTGCCTG GAGCCCTCC 780
    GCAGAGTCCC ACTAGCCAGC GGCCTCAGCC AGGGACGAAG GCCTCAAAGC TGAGAGGCC 840
    CTACCGGTGG GTGATGGATA TCATCCCCGA ACAGGTGAAG GGACAACTGA CTAGCAGCCC 900
    CAGAGCCCTC ACCCTGCGGA TCCCAGCCTA AAAGACACCA GAGACCTCAG CTATGGAGCC 960
    CTTCGAGCCC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTCGAACCTG GAGCCCTCC 1020
70 TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCGCGC CAGGCCCTGT AGGGACAGCA 1080
    TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAGTGCCT TGTGCTGGAA CTGGCCTGTA 1140
    CTCACCTCATG GGAGCTGGCC C

```

Seq ID NO: 408 Protein sequence  
Protein Accession #: NP\_476431.1

```

1      11      21      31      41      51
80 MELGLGGLST LSHCPWPRRQ APLGLSAQPA LWPTLAALAL LSSVAEASLG SAPRSPAPRE 60
    GPPPVLASPA GHLPGGRTAR WCSGRARRPP PQPSRPAPP PAPPSPALPRG GRAARAGGPG 120
    SRARAAGARG CLRLSQLVPV RALGLGHRSD ELVRFRFCSG SCRRARSPHD LSLASLLGAG 180
    ALRPPPGSRP VSQPCCRPTR YEAVSFMDVN STWRTVDRLS ATACGCLG

```

Seq ID NO: 409 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..1746

5	1	11	21	31	41	51	
	ATGCCACTGA	AGCATTATCT	CCTTTTGCTG	GTGGGCTGCC	AAGCCTGGGG	TGCAGGGTTG	60
	GCCTACCATG	GCTGCCCTAG	CGAGTGTACC	TGCTCCAGGG	CCTCCCAGGT	GGAGTGCACC	120
	GGGGCACGCA	TTGTGGCGGT	GCCCAACCCT	CTGCCCTGGA	ACGCCATGAG	CCTGCAGATC	180
10	CTCAACAGCG	ACATCACTGA	ACTCAATGAG	TCCCCGTTCC	TCAATATCTC	AGCCCTCATC	240
	GCCCTGAGGA	TTGAGAAGAA	TGAGCTGTGC	CGCATCACGC	CTGGGGCCTT	CCGAAACCTG	300
	GGCTCGTGC	GCTATCTCAG	CCTCGCCAAC	AACAAGCTGC	AGGTTCTGCC	CATCGGCCTC	360
	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAAGT	GTTGCAGATC	420
	CAGCCGGCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCAC	480
15	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCACGAA	GCTCAATCTG	540
	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACCTGGG	CAATCTCCAG	600
	GTCCCTCCGGC	TGTATGAGAA	CAGGCTCACG	GATATCCCCA	TGGGCACITT	TGATGGGCTT	660
	GTTAACTGCG	AGGAACTGCG	TCTACAGCAG	AACCAGATTG	GACTGCTCTC	CCCTGGTCTC	720
	TTCCACAACA	ACCACAACCT	CCAGAGACTC	TACCTGTCCA	ACAACCACAT	CTCCAGCTG	780
20	CCACCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTCC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTCGGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
	TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTTGATT	TGAGCCGCAA	TCAGATCAGC	TTCATCTCCC	CGGGTGCCCT	CAACGGGCTA	1020
	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
25	TTCCGCATGT	TGGCCAACTT	GCAGAACATC	TCCCTGCAGA	ACAATCGCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCGSCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCCAG	1200
	CTGGAGAACT	TGCCCCCTCG	CATCTTCGAT	CACCTGGGGA	AACCTGTGTA	GCTGCGGCTG	1260
	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCCG	TCCGCAACTG	GCTCTGTCTC	1320
	AACCAAGCCTA	GGTTAGGGAC	GGACACTGTA	CCTGTGTGTT	TCAGCCCAGC	CAATGTCCGA	1380
30	GGCCAGTCCC	TCATTATCAT	CAATGTCAAC	GTGTGCTTTC	CAAGCGTCCA	TGTCCCTGAG	1440
	TGTGCTAGTT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
	TCCGTCTCTT	CTACCACTGA	GCTAACCAAG	CCTGTGGAAG	ACTACACTGA	CTGACTACC	1560
	ATTGAGTCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCCAGAG	CGGGCTGGCC	1620
	ATTGCGGCCA	TTGTAAATGG	CATTGTGCCC	CTGGCCTGCT	CCCTGGCTGC	CTGCGTGGGC	1680
35	TGTTGCTGCT	GCAAGAAAGAG	GAGCCAAAGCT	GTCTGTATGC	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAAAGAG	GCAGGCTGGA	GCAGGGCTGG	GGAATGATGG	GACTGGAGGA	CCTGGGAATT	1800
	TCATCTTTCT	GCCTCCACCC	CTGGGTCCAT	GGAGCTTTCC	CGTGATTGCT	CTTCTGTGCC	1860
	CTAGATAAAG	GTGTGCTTAC	CTCTTCTCTA	CTTGCCCTGAT	TCTCCCGTAG	AGAAGCAGGT	1920
	CGTGCCGGAC	CTTCTTACAA	TCAGGAAGAT	AGATCCAAC	GGCCATGGCA	AAAGCCCTGG	1980
40	GGATTTCGCA	TTCATACCCC	TGGGCTTCCT	TCGAGAGGGC	TCTTCTCTCA	AATCCTCCCC	2040
	ACCTGTCTCT	CAAGAACAGC	CTTCCCTGCG	CCCAGGCCCC	CTCCGGGCTC	CTGTAGACTC	2100
	AGTTAGTCCA	CAGCTGCTCT	ACTTCGTGGG	AATAGTTCTC	CGCTGAGATA	GCCCCTCTCG	2160
	CCTAAGTATT	ATGTAAGTGT	ATTTCCCTTC	TTTTGTTTCT	CTTGTTTGTG	CTATGGCTTG	2220
	ACCCAGCATG	TCCCCTCAAA	TGAAAGTTCT	CCCCTTGATT	TTCTGCTCCT	GAAGGCAGGG	2280
45	TGAGTTCTCT	CCTCAAGAGAA	GACTTCAAAC	CATTTAAGTG	GTTCCTTAAG	AGCCGTCAAT	2340
	CAGCTGTGTT	TTGGGGATGC	TATGAAAGAG	AGAAGGAAAA	TCATGCCGCT	CAGTTCTTGG	2400
	AGACAGAAGA	GCCGTCTATC	GTGTCTCACT	TGTGATTTTT	ATCTGGAAAA	GGAGAGAAACA	2460
	CCCCAGCACA	GCAAGCTCAG	CCTTTTAGAG	AAGGATATTT	CCAAACTGCA	AACCTTGCTT	2520
	TGAAAAGTTT	AGCCCTTTAA	GGAAATGAAAT	CATGTAGAAAT	TTTGGACTTC	TAAAAACATT	2580
50	AAAAATCAGCT	TATTAATACG	GGATAGAGAA	AGAAATCTGG	TGCTGGGGGG	TCCCTGTGTT	2640
	CACCCCTAGA	GTTTGTTTTA	AAATTTTAA	TGAAGCATG	TGAAGTGATC	STGCAGAAAA	2700
	GTGGGAACAT	GATAGTGAT	GGCTTGGTGG	ATTTTCACAA	ACTGAACATA	CCTGTGTAAT	2760
	CAGCATCTAG	ACCCAGACCC	AGAGCATCAC	AAATATCCCC	CATCCTGGGC	TTTTCCCAAG	2820
	GGAGATGGGG	GCTTCTGTAAG	ATGGACTTAC	CTGGGACCTG	CCCCCATGCA	GCCAGGACGG	2880
55	TCCCCCACA	GTCAAGCTGT	GCAAGGCCCC	CGTGGCCAGG	GGTGGAGGAG	AATATGTGGG	2940
	TGTGGACAGG	ATGGGAGACT	GTGGCTGAA	CAGGAGATT	TATTATATCT	GGAGACCTTG	3000
	AGAGACCCCTG	AGACCTGGGG	CACCATGGCT	GGCCAGGTCA	GAAGCATCCT	GACTGCAGAG	3060
	GTCCGTGCAG	CCACACCCCT	TTCCCTGCCA	GCAAGTTGTC	TGCGGCTCAT	CGGAGGCCCC	3120
	TCCGCTGGA	GCCTTCTATG	GACGTGATAT	GCCTGTATCT	GTTTTAAATT	TTCATTCTTC	3180
60	ACTTAGGGGA	AGTGAATCG	CTCAGAGATG	AGATCCTTTA	ATTGAAAAAC	AAGTGTAAAC	3240
	GAATCTAGTG	TCTTTCTAAT	GTGGTAAAT	TCTCCATCAA	CATCAAGTGC	AGCTGGCAGC	3300
	TGAACCTCAG	AATCTCACTT	ACAGCAGGCG	ACACGGGGGT	ACACCGATGG	GTCACACTGG	3360
	GTCTGGGGGG	TCCCTGGAGC	TCTCTCTGCG	TGTGGTCTGG	TTAGGAGTTG	AGTTGTTTGC	3420
	TCCAGGGTTA	TTCTCTCTCT	CGAGTCACAG	TCACACGAAT	ACCTGCCTTC	TCTGGCTTTC	3480
65	CTGCTATACA	CATATTACAA	TGGCGTCAA	GAAGTTAGGC	TCATGGCAAC	GTGTGTCTTT	3540
	CTCTGGACAA	CTGGCCAGT	TTACAGTGAA	ATGGAGAATT	TCAGGTCTCC	ACGTCTGCCC	3600
	AGGAAAGAAC	TTCACTGAC	TCCACGGGGA	TCTGGAATC	CACGACCAAT	CCCGATCGGC	3660
	TCTTATAGC	TCCCCGCTCC	ACAAGACACC	TGTGCTTTGG	AAATCCACCA	CCAATCCCGA	3720
	TCCGCTCTTA	TTAGCTCCCC	GCTCCACAAG	ACACCTGTGA	TCTGGAATC	TACCACCAAT	3780
70	CCCGATCGGC	TCTTATTAGC	TCCCCGCTCC	ACAAGACACC	TGTGACATCC	TCCAGGGCCA	3840
	CAGGAGCAGC	TGCTGACCAAG	TTTTCCTTC	CAGTTCTCTG	ACAAAAAGTG	TCCAGAGGGC	3900
	TGTTTGCAAA	CAGTAGTGCA	CTTTGTAGCT	TTTCAACCTC	TGTCCAGGG	AATCTAGGAG	3960
	AGATGAGGCC	CGTCAGATG	AAGAGATGTC	ATCCCCCAG	GGTCTCCAAG	GCAATTCAC	4020
	ACTATTGGTG	GCACCTGGAG	GACATGCACC	AAGGCTTGCC	AGAGCCAACA	GGAAGTGAGC	4080
75	CCAGAGCATG	GCACATGAGC	ATCACCCGCT	GATGGTGGCC	TGCTGTGCCT	GGTGCCAACA	4140
	GGGGCATCCC	GGCCCGTACC	CCTCCAGACA	GGAAGCATGG	GTTCGCCAC	AGACCTGTGC	4200
	GGTGCTCCTG	TGAGTGGCCT	CCAGATGTCT	TTGTGCATAG	GCACAAGTGG	GCCAGGGCTG	4260
	GAGGGAGGTG	GGAAACCTCA	TCATCCGGTG	GGCCCTGCCA	ATCTTAACCC	AGAACCTTTA	4320
	GGTATTCTCTG	GCAATGAGCA	TGACATTGGA	GCACCTTCTT	CTCCAGCCAG	AGGCTGACCT	4380
	GAGGGCCACT	GTCTCTCAGT	GACACCAACC	AGGAGCAACC	TAGGTGAGGG	GTGAGGGCCC	4440
80	CCTTATGTGA	ACCTCTTGCC	TCTTCTTTTC	TCCCATCAGA	GTGGTTGGAT	GGAGCCATTG	4500
	GCCTCCTTTT	CTTCAGCGGG	CCCTTCAACC	TCTCTGCACC	ATGTTGTCTG	GCTGAGGAGC	4560
	TACTAGAAAA	GCTGAGTGGG	GTCTCCTTTC	CAACAGGATG	ATGCATTTGC	TCAATTTCTA	4620
	GGGCTGGAAT	GAGCCGGCTG	GTCCCCCAGA	AAGCTGGAGT	GGGGTACAGA	GTTTCAATTTT	4680

5 CCTCTCTGTT TACAGCTCCT TGACAGTCCC ACGCCCATCT GGAGTGGGAG CTGGGAGTTA 4740  
 GTGTTGGAGA AGAAACAACA AAAGCCAAT AGAACCAC TA TTTTAAAAA GTGCTTACTG 4800  
 TGCACAGATA CTCTTCAAGC ACTGGACGTG GATTCTCTCT CTAGCCCTCA GCACCCCTGC 4860  
 GGTAGGAGTG CCGCTCTTAC CCACCTTGTA TGGGGTACAG AGGCACTTGC TCTTCTGCAT 4920  
 GGTGTTCAAT AGGCTGGGAG TTTTATTAT CTCTTCAAACT TTTGTACAAG AGCTCATGGC 4980  
 TTGTCTTGGG CTTTCGTCAT TAAACCAAAG GAAATGGAAG CCATTCCCCT GTTGCTCTCC 5040  
 TTAGTCTTGG TCATCAGAAC CTCACTTGGT ACCATATAGA TCAAAAGCTT TGTAAACCACA 5100  
 GGAAAAAATA AACTCTTCCA TCCCTTAAAG AATAGAATAG TTTGTCCCTC TCATGGGAAT 5160  
 TGGGCTGTAT GTATATTGTT CTTCCTCCTT AGAATTAGA GATACAAGAG TTCTACTTAG 5220  
 10 AACTTTTCAT GGACACAATT TCCACAACCT TTCAGATGCT GATGTAGAGC TATTGGGAAA 5280  
 GAACTTCCAA ACTCAGGAAG TTTGCAGAGA GCAGACAGCT AGAGATAACT CGGGACCCAG 5340  
 AGTTGGTCGA CAGATGTTAG ATGTATCCTA GCTTTTAGCC ATAAACCACT CAAAGATTCA 5400  
 GCCCCAGAT CCCACAGTCA GAACTGAATC TGCCTTGTG GGAAGCCAGC AGTGGCCTTG 5460  
 GGAAGGAAGC CATGGCTGTG GTTCAGAGAG GGTGGGCTGG CAAGCCACTT CCGGGGAAAA 5520  
 15 CTCCTTCCGC CCCAGGTTT TCTTCTCTT AAGGAGAGAT TGTCTCTACC AACCCGCTGC 5580  
 CTTTCATGCT CTTTCAAAGC TAGATCATGT TTGCCTTGCT TAGAGAATTA CTGCAAATCA 5640  
 GCCCCAGTGC TTGGCGATGC ATTTACAGAT TTCTAGGCCC TCAGGGTTTT GTAGAGTGTG 5700  
 AGCCCTGGTG GGCAGGGTTG GGGGGTCTGT CTTCTGCTGG ATGTGCTTGT TAATCCATTT 5760  
 20 GGTGTACAGA ATCAACAATA AATAATATAC ATGTAT

Seq ID NO: 410 Protein sequence  
 Protein Accession #: BAB84587.1

25 1 11 21 31 41 51  
 | | | | |  
 MPLKHYLLLL VGCQAWAGL AYHGCPSSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60  
 LINTHITELNE SPFFINISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPGL 120  
 FGQLDSLESLL LSSNQQLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAED HLVGLTKLNL 180  
 30 GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQO NQIGLLSPGL 240  
 FHNHNLQRL YLSNNHISQL PPSIFMQLFQ LNRLTLFGNS LKELSLGIFG PMPNLRRLWL 300  
 YDNHSSLPD NVFSNLRQLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLGDNV 360  
 FRMLANLQNI SLQNNRLRQL PGNIFANVNG LMAIQLQNNQ LENLEPLGIFD HLGKLCBLRL 420  
 YDNPWRCDSY ILPLRNWLLL NQPRLGTDIV PVCFSFANVR GQSLIIINVN VAVPSVHVPE 480  
 VPSYETPWPY PDTSPYDPT SVSSTELTS PVEDYDILT IQVTDDRSMV GMTQAQSGLA 540  
 35 IAAIVIGIVA LACSLAACVG CCCCKKRSQA VLMQMKAPNE C

Seq ID NO: 411 DNA sequence  
 Nucleic Acid Accession #: XM\_098151  
 Coding sequence: 1..447

40 1 11 21 31 41 51  
 | | | | |  
 ATGATGCATT TGCTCAATTC TCAGGGCTGG AATGAGCCGG CTGGTCCCCC AGAAAGCTGG 60  
 AGTGGGGTAC AGAGTTCAGT TTCTCTCTCT GTTACAGCT CCTTGACAGT CCCACGCCCA 120  
 45 TCTGGAGTGG GAGCTGGGAG TCAGTGTGGG AGAAGAAACA ACAAAAGCCA ATTAGAACCA 180  
 CTATTTTAA AAAGTGCTTA CTGTGCACAG ATACTCTTCA AGCATTGGAC GTGGATTCTC 240  
 TCTCTAGCCC TCAGCACCCC TGCGGTAGGA GTGCCGCCCT TACCCACTTG TGATGGGGTA 300  
 CAGAGGCACT TGCTCTCTG CATGGTGTTC AATAGGCTGG GAGTTTATT TATCTCTTCA 360  
 50 AACTTTGTAC AAGAGCTCAT GGCTTGTCTT GGGCTTTCGT CATTAAACCA AAGGAAATGG 420  
 AAGCCATTCC CCTGTTGCTC TCCTTAG

Seq ID NO: 412 Protein sequence  
 Protein Accession #: XP\_098151

55 1 11 21 31 41 51  
 | | | | |  
 MMHLNSQGW NEPAGPPESW SGVQSSVFLS VYSSLTVPRP SGVAGSQCW RRNNKSQLEP 60  
 LFLKSAYCAQ ILFKHWIWL SLALSTPAVG VPPLPTCDGV QRHLLECMVF NRLGVLFISS 120  
 60 NFVQELMACL GLSSLNQRKW KPFPCCSP

Seq ID NO: 413 DNA sequence  
 Nucleic Acid Accession #: NM\_002658.1  
 Coding sequence: 77..1372

65 1 11 21 31 41 51  
 | | | | |  
 GTCCCCGCG CCGCGTCGCG CCCTCCTGCC GCAGGCCACC GAGGCCGCCG CCGTCTAGCG 60  
 CCCCGACCTC GCCACCATGA GAGCCCTGCT GGCGCGCCTG CTTCTCTGCG TCCTGGTCTG 120  
 70 GAGCGACTCC AAAGGCAGCA ATGAACCTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA 180  
 TGGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAAA 240  
 GAAATTCGGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300  
 TCACCTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCCTGGAA 360  
 CTCTGCCACT GTCCTTCAGC AAACGTACCA TGCCACAGA TCTGATGCTC TTCAGCTGGG 420  
 CCTGGGGAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCTT GGTGCTATGT 480  
 75 GCAGGTGGCG CTAAAGCCGC TTGTCCAAGA GTGCATGGTG CATGACTGCG CAGATGGAAA 540  
 AAAGCCCTCC TCTCTCCAG AAGAATTAAA ATTTCACTGT GGCACAAAAGA CTCTGAGGCC 600  
 CCGCTTTAAG ATTATTGGGG GAGAATTAC CACCATCGAG AACCAACCTT GGTTCGCGGC 660  
 CATCTACAGG AGGCACCGGG GGGGCTCTGT CACCTACGTG TGTGGAGGCA GCCTCATCAG 720  
 80 CCCTTGCTGG GTGATCAGCG CCACACACTG CTTCAATTGAT TACCCAAAAGA AGGAGGACTA 780  
 CATCGTCTAC CTGGTCTCGT CAAGGCTTAA CTCCAACACG CAAGGGGAGA TGAAGTTTGA 840  
 GGTGGAAAAC CTCATCTAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA 900  
 CATTGCCTTG CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCCGCACTAT 960  
 ACAGACCATC TGCCCTGCCCT CGATGTATAA CGATCCCCAG TTTGGCACAA GCTGTGAGAT 1020  
 CACTGGCTTT GGAAAAGAGA ATCTACCGA CTATCTCTAT CCGGAGCAGC TGAATATGAC 1080

5  
10  
15  
20

```

TGTGTGAAG CTGATTTCCT ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAGT 1140
CACCACCAAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCTT GCCAGGGAGA 1200
CTCAGGGGGA CCCCTCGTCT GTTCCCTCCA AGGCCGCGAT ACTTTGACTG GAAATGTGAG 1260
CTGGGGCCGT GGATGTGCCC TGAAGGACAA GCCAGGCGTC TACACGAGAG TCTCACACTT 1320
CTTACCCTGG ATCCGCAGTC ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC 1380
AGGGAGGAAA CGGGCACCAC CCGCTTCTCT GCTGGTTGTC ATTTTTCAG TAGAGTCATC 1440
TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCCTGTGG 1500
CACCACCAGG GTGAACGACA ATAGCTTTAC CCTCACGGAT AGGCCTGGGT GCTGGCTGCC 1560
CAGACCCTCT GGCCAGGATG GAGGGGTGGT CCTGACTCAA CATGTTACTG ACCAGCAACT 1620
TGTCTTTTTC TGGACTGAAG CCGTCAGGAG TTA AAAAGGG CAGGGCATCT CCTGTGCATG 1680
GGCTCGAAGG GAGAGCCAGC TCCCCCGACC GGTGGGCATT TGTGAGGCC ATGGTTGAGA 1740
AATGAATAAT TTCCCAATTA GGAAGTGTA GCAGCTGAGG TCTCTTGAGG GAGCTTAGCC 1800
AATGTGGGAG CAGCGGTTTG GGGAGCAGAG AACTAACGA CTTCAGGGCA GGGCTCTGAT 1860
ATCCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTTGCACACT TGTGTGTGG 1920
GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCCTT 1980
AAACTGTGTG GACTGTGTAT CCACACAGAG TGGTCTTTCT GGAGAGGTTA TAGGTCACCTC 2040
CTGGGGCCCT TGGGGTCCCC CACGTGACAG TGCCTGGGAA TGTACTTAT CTGCAGCATG 2100
ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT 2160
ATCCCTTCTT TTTAGCCTAG TTTATCCAA CTCTACTGGG TGGGTGAGG ACCACTCCTT 2220
ACACTGAATA TTTATATTTT ACTATTTTTA TTTATATTTT TGTAAATTTA AATAAAGTG 2280
ATCAATAAAA TGTGATTTT CTGA

```

Seq ID NO: 414 Protein sequence  
Protein Accession #: NP\_002649.1

25  
30  
35

```

1 11 21 31 41 51
| | | | |
MRALLARLLL CVLVVSDSKG SNEHQVPSN CDCLNGGTCV SNKYFSNIHW CNCPKKFGGQ 60
HCEIDKSKTK YEGNGHFYRG KASTDTMRP CLPWNSATVL QQTYHAHRSD ALQLGLGKHN 120
YCRNPDNRNR PWCVYQVGLR PLVQECMVHD CADGKPKSSP PEELKFQCGQ KTLRPRFKII 180
GGEFTTIENQ WFFAAIYRRH RGGSVTVYCG GSLISPCWVI SATHCFIDYP KKEDYIVYLG 240
RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHNDIALLK IRSKEGRCAQ PSRTIQTICL 300
PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLKMTVVKLI SHRECQPHY YGSEVTTKML 360
CAADPQWKTD SCQDSDGGPL VCSLQGRMTL TGVSWGRGC ALKDKPGVYT RVSHFLPWIR 420
SHTKEENGLA L

```

Seq ID NO: 415 DNA sequence  
Nucleic Acid Accession #: NM\_024422.1  
Coding sequence: 202..2907

40  
45  
50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
CGCCAAAGGA AAAGCCCTT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC 60
CTCTCCGCGC GCCCACCTC CTCCGCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC 120
GCTCCGCGCG CGGCCCTGCG CCGCGGAGC CCTCCTACCC CGGCCGACG CTCGGCCGCG 180
GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCT CCGGCTCCTG GAACGGAGCC 240
CTCTGCCGCG TGCTCTGCT GACCTCGCG ATCTTAATAT TTGCCAGTGA TGCCTGCAAA 300
AATGTGACAT TACATGTTCC CTCCAACTA GATGCCGAGA AACTTGTGG TAGAGTTAAC 360
CTGAAAGAGT GCTTTACAGC TGCAAACTA ATTCATTCAA GTGATCCTGA CTTCCAAATT 420
TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATCTAT TGTCTCTCGA GAAGAGAAGT 480
TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGG 540
GAGCATCAA CAAAGGTCCT AAAGAAAAGA CATACTAAAG AAAAAGTTCT AAGGCGCGCC 600
AAGAGAAGAT GGGCTCCAAT TCCTTGTTGG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660
CTTTTCTTCT AACAGGTTCA ATCTGACAG GCCCAAACT ATACCATATA CTATTCCATA 720
AGAGGTCCTG GTTCAGTCCA AGAACCTCGG AATTATTTT ATGTGGAGAG AGACACTGGA 780
AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
TTTGCAACAA CTCCAGATGG GTATACTCCA GAACCTCCAC TGCCCTTAAT AATCAAAATA 900
GAGGATGAAA ATGATAACTA CCAATTTTT ACAGAAGAAA CTTATACTTT TACAATTTTT 960
GAAAATTGCA GAGTGGGCA TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020
GACACGATGC ACACAGCCT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCCACC 1080
CTATTTTCTA TGCATCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
GAGTTAATTG ACAAGTACCA GTTGAAAATA AAAGTACAAG ACATGGATGG TCAGTATTTT 1200
GGTCTACAGA CAACTTCAAC TTGTATCATT AACATTGATG ATGTAATGA CCACTTGCCA 1260
ACATTTACTC GTACTTCTTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAATC 1320
TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATCTG CTAAGTGGAG AGCTAATTAT 1380
ACCATTTTAA AGGGCAATGA AAATGGCAAT TTTAAATTTG TAACAGATGC CAAAACCAAT 1440
GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500
CAAATTTGGT TAGTTAATGA AGCTCCATT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
AGCACAGCAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGCCCTGA GTGTAACCCT 1620
CCAATACAGA CTGTTGCGAT GAAAGAAAAT GCAGAAGTGG GAACAACAAG CAATGGATAT 1680
AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAAGTATG 1740
CCAACAGGGT GGGTCACCAT TGTAGAAAAT ACAGGATCAA TCAAAGTTT CAGAAGCCTG 1800
GATAGAGAGG CAGAGACCAT CAAAATGGC ATATATAATA TTACAGTCTT TGCATCAGAG 1860
CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC 1920
AGCCCATTC TACCTAAAA GACAGTGATC ATCTGCAAA CCACCATGTC ATCTGCGGAG 1980
ATTGTTGCGG TTGCTCTGTA TGAGCCTATC CATGGCCAC CCTTTGACTT TAGTCTGGAG 2040
AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA 2100
CGTCTTTCTT ATCAGAATGA TCCTCCATTT GGCTCATATG TAGTACCTAT AACAGTGAGA 2160
GATAGACTTG GCATGTCTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220
GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGA 2280
AAGTGGGCCA TCCTTGCAAT ATTGTTGGGC ATAGCATTGC TCTTTTGCAT CCGTTTACG 2340
CTGGTCTGTG GGGCTTCTGG GACGTCTAAA CAACCAAAAG TAATTCCTGA TGATTTAGCC 2400
CAGCAGAAC TAATTGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGGC 2460
AATGGCTTCA CAACCTGAAC TGTGGCGCT TCTGCTCAGG GAGTTTGTGG CACCGTGGGA 2520

```

TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAAGGAGG ACACCAGACC 2580  
 TCGGAATCCT GCCGGGGGGG TGGCCACCAT CACACCCTGG ACTCCTGCAG GGGAGGACAC 2640  
 ACGGAGGTGG ACAACTGCAG ATACACTTAC TCGGAGTGGC ACAGTTTTAC TCAGCCCCGT 2700  
 CTTGGTGAAG AAGTGTATCT GTGTAATCAA GATGAAAATC ACAAGCATGC CCAAGACTAT 2760  
 GTCCGTGACAT ATAACATATGA AGGAAGAGGA TCGGTGGCTG GGTCTGTAGG TTGTTGCAGT 2820  
 GAACGACAAG AAGAAGATGG GCTTGAATTT TTGGATAATT TGGAGCCCAA ATTTAGGACA 2880  
 CTAGCAGAAG CATGCATGAA GAGATGAGTG TGTCTAATA AGTCTCTGAA AGCCAGTGGC 2940  
 TTTATGACTT TTAACAAAAA TTACAAACCA AGAATTTTTT AAAGCAGAAG ATGCTATTG 3000  
 TGGGGGTTTT TCTCTCATT TTTGGATGGA ATCTCTTTGG TCAAAATGCAC ATTTACAGAG 3060  
 AGACACTATA AACAGTACA CAAATTTTTT AATTTTTTACA TATTTTTTAAA TTAATTATCT 3120  
 TCTATCCAAG GAGGTCTACA GAGAAATTAA AGTCTGCCTT ATTTGTTACA TTTGGGTATA 3180  
 ATGACAACAG CCAATTTATA GTGCAATAAA ATGTAATTAA TTCAAGTCTT TATTATAGAC 3240  
 TATTTGAAGC ACAACCTAAT GGAAATTTGT AGAGACCTTG CTTTAACTT ATCTCCAGTT 3300  
 AATTAAGTGT TCATGTGGTG CTTGGAAACT GTTGTTTTCC TGAACATCTA AAGTGTGTAG 3360  
 ACTGCATTCT TGCATTATT TTATTCTTGT AATGTGACCT TTTACTGTG CAAAGGGAGA 3420  
 TTTCTAGCCA GGCATTGACT ATTACAATTT CATT

Seq ID NO: 416 Protein sequence  
 Protein Accession #: NP\_07740.1

1 11 21 31 41 51  
 MEARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLHVP SKLDAEKLVG RVNLKECFTA 60  
 ANLIHSSDPD FQILEDGSVY TTNTILLSSE KRSFTILLSN TENQEKKKIF VFLEHQTKVL 120  
 KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PPFLLQVQV SDTAQNYTIY YSIRGPGVDQ 180  
 EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPELPLPLI IKIEDENDNY 240  
 PIFTEETYTF TIFENCVRGT TVQVVCATDK DEPDTHMTRL KYSIIQGVPP SPTLFSMHPT 300  
 TVGIVTTSSQ LDRELIDKYQ LKIKVQMDMG QYFGLQTTST CIINIDVDND HLPFTFRTSY 360  
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KTNIEGVLV 420  
 KPLNLYEEKQ MIQIGVVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480  
 KENAEVGTTS NGYKAYDEPT RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540  
 KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDPD 600  
 EPIHGPPPDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFGSYVVP I TVRDRMGSS 660  
 VTSLDVTLCD CITENDCTHR VDPRIIGGGV QLKGWAILAI LLGIALLFICI LFTLVCGASG 720  
 TSKQPKVIPD DLAQONLVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780  
 QETIEMVKGG HQTSESCRGA GHHTLDSR GRGVSAGSVG CCSEREQEDG LEFLDNLEPK FRTLAECMK 840  
 CNQDENHKHA QDYVLTYNYE

Seq ID NO: 417 DNA sequence  
 Nucleic Acid Accession #: NM\_004949.1  
 Coding sequence: 202..2745

1 11 21 31 41 51  
 CGCCAAAGGA AAAGCCCTTT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC 60  
 CTCTCCGCGC GCCCCACCTC CTCCGCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC 120  
 GCTCCGCGCG CGGCCCTCGC CCCGCGGAGC CCTCTACCC CGGCCCGACG CTCGGCCCGC 180  
 GACCTGCCCC GAGCCCTCTC CATGGAGGCA GCCCGCCCTT CCGGCTCCTG GAACGGAGCC 240  
 CTCTGCCGCG TGCTCCTGCT GACCCCTCGC ATCTTAATAT TTGCCAGTGA TGCTGCAAAA 300  
 AATGTGACAT TACATGTTCC CTCCAAACTA GATGCCGAGA AACTTGTGG TAGAGTTAAC 360  
 CTGAAAGAGT GCTTTACAGC TGCAATCTA ATTCAATCAA GTGATCCTGA CTTCCAAATT 420  
 TTGGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCTCTCGA GAAGAGAAAT 480  
 TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGG 540  
 GAGCATCAA CAAAGTCTCT AAAGAAAAGA CATACTAAAG AAAAAGTTCT AAGGCGCGCC 600  
 AAGAGAAGAT GGGCTCCAAT TCCTTGTTCG ATGCTAGAAA ACTCCTTGGG TCCTTTTCCA 660  
 CTTTTCCTTC AACAGTTCA ATCTGACACG GCCCAAACT ATACCATATA CTATTCCATA 720  
 AGAGGTCTCT GAGTTGACCA AGAACCTCGG AATTTATTTT ATGTGGAGAG AGACACTGGA 780  
 AACTTGTATT GTACTCGTCC TGTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840  
 TTTGCAACAA CTCCAGATGG GTATACTCCA GAACCTCCAC TGCCCTTAAT AATCAAAATA 900  
 GAGGATGAAA ATGATAACTA CCCAATTTTT ACAGAAGAAA CTTATACTTT TACAATTTTT 960  
 GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020  
 GACACGATAG ACACACGCGT GAAGTACTCC ATCATTGGGC AGGTGCCACC ATCACCACCC 1080  
 CTATTTTCTA TGCATCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140  
 GAGTTAATG ACAAGTACCA GTTGAAAATA AAAGTACAAG ACATGGATGG TCAGTATTTT 1200  
 GGTCTACAGA CAACTTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA 1260  
 ACATTTACTC GTACTTCTTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAAATC 1320  
 TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAACCTGGAG AGCTAATTAT 1380  
 ACCATTTTAA AGGGCAATGA AAATGGCAAT TTTAAATTTG TAACAGATGC CAAACCAAT 1440  
 GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500  
 CAAATTTGGT TAGTTAATGA AGCTCCATTT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560  
 AGCAGACGAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAACCCT 1620  
 CCAATACAGA CTGTTCCGAT GAAAGAAAAT GCAGAAGTGG GAACAACAAG CAATGGATAT 1680  
 AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAAGTATG 1740  
 CCAACAGGGT GGGTCACCAT TGATGAAAAT ACAGGATCAA TCAAGATTTT CAGAAGCCTG 1800  
 GATAGAGAGG CAGAGACCAT CAAAATGGC ATATATAATA TTACAGTCCCT TGCATCAGAC 1860  
 CAAGGAGGGA GAAATGTAC GGGGACACTG GGCATTATAC TTCAAGACGT GAATGATAAC 1920  
 AGCCCATTC TACCTAAAAA GACAGTGATC ATCTGCAAC CCACCATGTC ATCTGCGGAG 1980  
 ATTTGTGCGG TTGATCTTGA TGAGCCTATC CATGGCCAC CCTTTGACTT TAGTCTGGAG 2040  
 AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAATTAATGA TACAGCAGCA 2100  
 CGTCTTTTCT ATCAGAAATGA TCCTCCATTT GGCTCATATG TAGTACCTAT AACAGTGAGA 2160  
 GATAGACTTG GCATGTCTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220  
 GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG TTGGAGGAGT ACAACTTGA 2280  
 AAGTGGGCCA TCCTTGCAAT ATTGTGAGGC ATAGCATTGC TCTTTTGCAT CCTGTTTACG 2340

5 CTGGTCTGTG GGGCTTCTGG GACGCTCTAA CAACCAAAAG TAATTCCTGA TGATTAGGCC 2400  
 CAGCAGAACC TAATTGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGCG 2460  
 AATGGCTTCA CAACCCAAC TGTGGGCGCT TCTGCTCAGG GAGTTTGTGG CACCGTGGGA 2520  
 TCAGGAATCA AAAACGGAGG TCAGGAGACC ATCGAAATGG TGAAGGAGG ACACCAGACC 2580  
 TCGGAATCCT GCCGGGGGGC TGGCCACCAT CACACCCTGG ACTCCTGCAG GGGAGGACAC 2640  
 ACGGAGGTGG ACAACTGCAG ATACACTTAC TCGGAGTGGC ACAGTTTAC TCAGCCCCGT 2700  
 CTTGGTGAAG AATCCATTAG AGGACACACT CTGATTAAAA ATTAACAAT GAAAGAAAGT 2760  
 GTATCTGTGT AATCAAGATG AAAATCACAA GCATGCCCAA GACTATGTCC TGACATATAA 2820  
 10 CTATGAAGA AGAGGATCGG TGGCTGGGTC TGTAGTTGT TGCAGTGAAC GACAAGAAGA 2880  
 AGATGGGCTT GAATTTTGG ATAATTGGA GCCCAAATT AGGACACTAG CAGAAGCATG 2940  
 CATGAAGAGA TGAGTGTGTT CTAATAAGTC TCTGAAAGCC AGTGGCTTTA TGACTTTTAA 3000  
 AAAAAATTAC AAACCAAGAA TTTTAAAG CAGAAGATGC TATTTGTGGG GGTTTTCTC 3060  
 TCATTATTG GATGAATCT CTTTGGTCAA ATGCACATT ACAGAGAGAC ACTATAAACA 3120  
 15 AGTACACAAA TTTTCAAT TTTACATATT TTAAATTAC TTATCTTCTA TCCAAGGAGG 3180  
 TCTACAGAGA AATTAAAGTC TGCCTTATTT GTTACATTG GGTATAATGA CAACAGCCAA 3240  
 TTTATAGTGC AATAAATG AATTAATTCA AGTCCTTATT ATAGACTATT TGAAGCACAA 3300  
 CCTAATGGAA AATTGTAGAG ACCTTGCTTT AACATTATCT CCAGTTAATT AAGTGTTCAT 3360  
 GTGGTGGCTG GAAACTGTTG TTTTCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT 3420  
 20 ATTATTTTAT TCTTGTAAATG TGACCTTTTC ACTGTGCAAA GGGAGATTTC TAGCCAGGCA 3480  
 TTGACTATTA CAATTCATT

Seq ID NO: 418 Protein sequence  
 Protein Accession #: NP\_004940.1

25 1 11 21 31 41 51  
 MEAARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLHVP SKLDAEKLVG RVNLKECFTA 60  
 ANLIHSSDDP FQILEDGSVY TTNITLSSSE KRSFTILLSN TENQEKKKIF VFLEHQTKVL 120  
 30 KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPFLQVQV SDTAQNYTIY YSIRGPGVDQ 180  
 EPRNLFYVER DTGNLYCTRP VDREQYESFE IIAFATTPDG YTPLEPLPLI IKIEDENDNY 240  
 PIFTEETYTF TIFENCRVGT TVGQVCATDK DEPDTHMTRL KYSIIGQVPP SPTLFSMHPT 300  
 TGVITTTSSQ LDRELIDKYQ LKIKVQDMDG QYFGLQTTST CIINIDVDND HLPTFTRTSY 360  
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKNE NGNFKIVTDA KINEGVLCVV 420  
 35 KPLNYEEKQQ MILQIGVNE APFSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVRM 480  
 KENAEVGTTS NGYKAYDPET RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540  
 KNGIYNITVL ASDQGGRTCT GTLGIILODV NDNSPFIPKK TVIICKPTMS SAEIVAVDPD 600  
 EPIHGPPDF SLESTSEVQ RMWRLKAIND TAARLSYQND PPFSGYVVI TVRDLGMSS 660  
 40 VTSLDVTLCD CITENDCTHR VDPRIIGGGV QLGKWAIIAI LLGIALLFICI LFTLVCGASG 720  
 TSKQPKVIPD DLAQNLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVGSGIKNGG 780  
 QETIEMVKGK HQTSESCRGA GHHHTLDSR GGHTEVDNCR YTYSEWHSFT QPRLGEESIR 840  
 GHTLIKN

Seq ID NO: 419 DNA sequence  
 Nucleic Acid Accession #: NM\_002722.1  
 Coding sequence: 14..301

45 1 11 21 31 41 51  
 ACTCTGGACT CCGGATGGCT GCCGCACGCC TCTGCCTCTC CCTGCTGCTC CTGTCCACCT 60  
 GCGTGGCTCT GTTACTACAG CCACTGCTGG GTGCCAGGG AGCCCCACTG GAGCCAGTGT 120  
 50 ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCACGTA TGCAGCTGAT CTCCGTAGAT 180  
 ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAAGACA CAAAGAGGAC ACGCTGGCCT 240  
 TCTCGGAGTG GGGGTCCCCG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGGACTTAT 300  
 55 AATGCCACCT TCTGTCTCCT ACGACTCCAT GAGCAGCGCC AGGCCAGCTC TCCCCTCTGC 360  
 ACCCTTGGCT CTGGCCAAAG CTTGCTCCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420  
 AAGCC

Seq ID NO: 420 Protein sequence  
 Protein Accession #: NP\_002713.1

60 1 11 21 31 41 51  
 MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPEQMAQYA ADLRRYINML 60  
 65 TRPRYKGRHK EDTLAFSEWG SPHAAPFREL SPLDL

Seq ID NO: 421 DNA sequence  
 Nucleic Acid Accession #: NM\_032545.1  
 Coding sequence: 46..718

70 1 11 21 31 41 51  
 AAAGTATCT TCAATGCACT AAGAGAAGGA GACTCTCAAA CCAAAAATGA CTGGAGGGCA 60  
 CCAATGTCAGG CTTCTGTTTA CCGTCAGTTT GGCATTACAG ATCATCAATT TGGGAAACAG 120  
 75 CTATCAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTTG CCACTCAGAA 180  
 GCACCCAGAG TCACCGCTCA ACTGGACCTC CAGTCATTTC GGAGAGGTGA CTGGGAGCGC 240  
 CGAGGGCTGG GGGCCGGAGG AGCCGCTCCC TACTCCCGG GCTTTCGGAG AGGGTGCCTC 300  
 CGCGCGGCGG CGTGTCTGCA GGAACGCGCG TACCTGCGTG CTGGGCAGCT TCTGCGTGTG 360  
 CCGCGCCAC TTACACGGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC 420  
 80 CCTGGAGCAC GGAACCTGGA CCCTCCGCGC CTGCCACCTC TGCAAGTGCA TCTTCGGGGC 480  
 CCTGCACGTC CTCCCCCTCC AGACGCCTGA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC 540  
 CCACGCTCAC GGGCCGAGCG CCGGGGGCGC GCCCAGCCTG CTACTCTTGC TGCCCTGCGC 600  
 ACTCCTGCAC GCCTCTCTGC GCCCGGATGC GCCCGCGCAC CCTCGGTCCC TGGTCCCTTC 660  
 CGTCTCCAG CGGAGCGGCG GCCCCTGCGG AAGGCCGGA CTTGGGCATC GCCTTTAATT 720  
 TTCTATGTTG TAAATAATAG ATGTGTTTAG TTTACCGTAA GCTGAAGCAC TGGGTGAATA 780

TTTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840  
AAAAAA

Seq ID NO: 422 Protein sequence  
Protein Accession #: NP\_115934.1

1 11 21 31 41 51  
| | | | |  
MTWRHHVRL L FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSEHFG 60  
VTGSAEGWGP EEPLPYSAF GEGASARPRC CRNGGTCVLG SFCVCPAHT GRYCEHDQRR 120  
SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL 180  
LLPCALLHRL LRPDAPAPHR SLVPSVLQRE RRPCGRPLG HRL

Seq ID NO: 423 DNA sequence  
Nucleic Acid Accession #: NM\_006533.1  
Coding sequence: 72..467

1 11 21 31 41 51  
| | | | |  
AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT 60  
CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT 120  
TCTCCGGACC TGGTGTCAGG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180  
CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240  
CCGACTGCCG ATTCCTGACC ATTCACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300  
AGGGCCGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360  
CTGCTCGCCT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAGACC CTGAAACCTG 420  
GCAAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG 480  
CTGGCCCTGC CGTTTCCCTT CCTTGGGTTT ATGCAAATAC AATCAGCCCA GTGCAAAAC

Seq ID NO: 424 Protein sequence  
Protein Accession #: NP\_006524.1

1 11 21 31 41 51  
| | | | |  
MARSLVCLGV IILLSAFSGP GVRGGMPKPL ADRKLCADQE CSHPISTMAVA LQDYMADPCR 60  
FLTIRHQVYV YVFSKLLKRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD 120  
VKTDKWDYFC Q

Seq ID NO: 425 DNA sequence  
Nucleic Acid Accession #: NM\_080870.1  
Coding sequence: 3..710

1 11 21 31 41 51  
| | | | |  
AGATGACACA AGTCACAGAA AAGTCCACAG AACACCCAGA AAAGACCACG TCAACCACAG 60  
AGAAAAACAC AAGAACCCCA GAAAAGCCTA CGCTATACTC AGAGAAGACC ATATGCACCA 120  
AAGGGA AAAA CACACCAAGT CCAGAAAAGC CTACAGAAAA CCTGGGGAAC ACCACACTGA 180  
CCACTGAGAC CATAAAAGCC CCAGTAAAGT CCACAGAAAA CCCAGAAAAA ACAGCAGCAG 240  
TCACAAAGAC TATAAAACCT TCAGTCAAGG TCACAGGAGA CAAATCTCTC ACTACTACCT 300  
CTTCTCATCT AAATAAAACT GAAATTACTC ATCAGGTGCC CACTGGTCTT TTCACCTCA 360  
TTACATCTAG AACGAAGCTG AGTTCTATCA CATCAGAAAG CACAGGAAAC GAGAGCCATC 420  
CATACCTCAA TAAAGATGGC TCACAGAAAG GTATCCACGC TGGACAGATG GGAGAGAATG 480  
ATTCATTCCC TGCATGGGCC ATAGTTATTG TGGTCTTGGT GGTCTGTGATT CTCCTCTCTG 540  
TGTTCTCTGG CCTGATCTTC TTGGTCTCCT ATATGATGCG GACACGCCGC ACCTAATCCC 600  
AGAACACCCA GTACAATGAT GCAGAGGATG AGGGTGGCCC CAATTCTTAC CCGGTCTACC 660  
TGATGGAGCA GCAGAATCTT GGCATGGGCC AGATCCCTTC CCCACGGTGA TCTTGGAGTA 720  
GGCGCCACGC CCGGCTCTCT CCATGCTCTG CCCCTTTCTT GGATGAGGAA CCGGACTCAC 780  
AATTCTATT TCCGGGACTA CAGGAAGGGC AGAGAATACT GACGGTTACC AGTATTAACC 840  
CTTCATCTGT TCTTGAAACT GGTGGGGGAA TGAGGTGATA AGCAAGGAGG GTGTAAAGTT 900  
AGGGGACAAA GAAGAAGAA TGAATAATAC GAGCAGACAT TCTCTGTAGA AGGTAATGGT 960  
CTGAGAATGA AAAGGTGTTT GATGGACATG TTGTGGGGGC ACCAATGCAG AACACTGCAC 1020  
TGAGTCTCTA AGGAAGGACA GGAGCCTTAT AGGCAATGCC CCAGACTGAC TTGTGAGTGG 1080  
GGTTTATGGG GAAAGGGAGG GACTGAGGGC AGAGTCTCTG GGTTCAGGA CAGCATTATG 1140  
TTATTTCAT TCACTATTAC TTAAGAGTTT GTGTGTAAAC AGGCTCATCT CTGAGTTCTC 1200  
AGGACCCTTG CCCCCACCCC CATTTTTTTA ATGAAAAAAA AAAACAAAAA AACCGATCC 1260  
AAGAAGAAAA GAGAAATTTT TTCTTCTCC ACTCTCTCCA TGCCCTGGAG AAAAAAAGT 1320  
CCAGAAAGAA TCATAAATAT CTCTCATCTA CATGGTTGCT TCCTCTCTCT CCCAAATCCC 1380  
TTAGTTTTC TAAATGTCTA CAGTGGACGC CCTGTTGGTT TGGCTTGCTG GGTGTGGGGT 1440  
GGACACGCAA GGAGGGGATT TTTATTGGC CAGCAGTCTC ACCCACTGAT CTCCACCCCA 1500  
GACCTTCCCT GATTGGTGTC TCAGCATTTA TTTTCTGTG TCTTCCACCA AAAGCCAGCT 1560  
GTAGCTTTAT CTCGTAAAG TTACCATCT TCTCTACTGT CCCCATTCTC TCTCTCCCA 1620  
CCTTACCCCC AGATTCAGT TTTCTCTCT GTAGGCATT CATCTGTGTG TGTCTCTGG 1680  
ATTTCTCTC TCTCTCTTA TGGCCATTTC ACCTTATTAC TGATTGGGTA GAGGGGAAA 1740  
AGGAGAATGA TGATGATAGT TTCTTCTCT CTATTGACCT TTTTATAAT AAAGTATAAC 1800  
ATGTT

Seq ID NO: 426 Protein sequence  
Protein Accession #: NP\_543146.1

1 11 21 31 41 51  
| | | | |  
MTQVTEKSTE HPEKTTSTTE KTRTPEKPT LYSEKTICTK GKNTVPVEPK TENLGNITLI 60  
TETIKAPVKS TENEKTAAY TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI 120  
TSRTKLSSIT SEATGNESHP YLNKDGSKQG IHAGQMGENG SFPAAVIVIV VLVAVILLV 180

FLGLIFLVSY MMTRRTLQ NTQYNDAEDE GGPNSYPVYL MEQQNLGMGQ IPSPR

Seq ID NO: 427 DNA sequence  
Nucleic Acid Accession #: XM\_069480.1  
Coding sequence: 1..4383

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

1 11 21 31 41 51  
ATGGACACTG TGCTGGTGCT GCTCCTGGGC CTGCAGGCCT TGGCCGGACC CAGTCCGAAG 60  
CCCCAGAAAG ACTCTGTCTC AGACTGGGCC ATTGTGTGA TCACTCTCAC TTTGGTGCCA 120  
GCAATTGTCA GCCTAATGTA CGGTATCAAG AAGGCCCTGCC AGTTCGGAG GGAGATGAGT 180  
CTGGGGTGTG GCTGTGGCTC TGTGACCCCT TACAGCAGCC ACCATGAGGG GGAGGCTGCC 240  
AGCCAGCGCT ACTCTTGTC AATGAAAGCT TCTTGGGGGG CAGGTGCTAC TACATTCCAA 300  
GAATATCAGA AAATCGGGGA ACTCTCAACA TCCGATCACA TATTCCCTCT CACTCCAGGC 360  
CTTGTTTATA GTATCCCTTT TGATCACAAT GTTCTGCATT CAGGACAAAG ACCTCCAGAG 420  
CTCCCTAAAT CTACAGAAAT CCATGAGCAA AAACGCCACT GCAACACCAC ACGCCATTCT 480  
AAGCCAACCTG ACAAGCCTAC AGGCAACTCC AAAACTATAG ACCACAAAAG CTCTACAGAT 540  
AATCATGAGG CTCTCCACAC TTCTGAAGAA AACTCCAGCA ACCAAGGGAA AGACCCAATG 600  
ATCCGGAACC AGCGCTCTGT TGATCCTGCT GACTCCACTA CCACACATAA AGAATCCGCT 660  
GGAAAAAACA ATATAACGCC AGCACCACAG AGCAAAATAA ACTGTGCTAA GTCCACAACA 720  
GGCAATCAAT CGGTAAACAAG AAAATCAGAT AAAACTGGAA GACCTTTGGA AAAGTCCATG 780  
AGTACTTTGG ATAAGACAAG TACCAGCTCA CATAAGACTA CAACTTCTCT CCACAACCTA 840  
GGCAATTACAG AGACCAAGCA AAAAAGCACA TCTTTTCCAG AAAAACTCAC AGCAGCCTCA 900  
AAAAACAACAT ACAAGACCAC AGGAACCCCA GAAGAGTCAG AAAAACTGA AGATTCCAGA 960  
ACAACAGTTG CTTACAGACA GCTCCTGACA AAAACTACAA AAAACATACA AGAGACCATA 1020  
TCAGCCAATG AGCTCACACA ATCTCTAGCA GAGCCTACAG AACATGGAGG AAGGACAGCC 1080  
AATGAGAAAC ACACACCATC CCCAGCAGAG CCTACAGAAA ATAGAGAAAG GACAGCCAAT 1140  
GAGAACACCA CACTATCCCC AGCAGAGCCT ACAGAAAATA GAGAAAGGAC AGCCAATGAG 1200  
AACACCGCAC CATTTCCAGC AGGGCCTACA GAAAATAGAG AAATGACAGC CAATGAGAAT 1260  
ACCACACTAT TCCCAGCAGA GCCTACAGAA CATGGAGAAA GGACAGCCAA TGAGAACACC 1320  
ACACCATCCC CAGCAGAGCC TACAGAACAT GGAGAAAGGA CAGCCAATGA GAACACTACA 1380  
CCATCCCCAG CAGAGCCTAC AGAACATGGA GAAAGGACCC CATTTGCCAA TGACAAAACC 1440  
ACATCATCCT CAGCAGAGTC TACAGAACAT GGAGAAAGGA CCCCCTGGC CAACGAGAAC 1500  
ACCACACCAT CCCCAGCAGA GCCTACAGAA AATAGAGAAA GGACAGCCAA TGAGAACACC 1560  
ACACCATCCC CAGCAGGGCC TACAGAAAAC AGAGAAACGA CAGCCAACGA GAAGACCACA 1620  
CTATCCCCAG TAGAGCCTAC AGAAAAATAGA GAAACAACAG CCAATGAGAA GACCACACCA 1680  
TCCCCAGCAG AGCCTACAGA AAATGGACAA AGGACCCCAT TTGCCAATGA GAAAACCACA 1740  
TCATCCTCAG CAGAGCCTAC AGAACACGGA GAAAGGACCC CACTGGCCAA TGAGAACACC 1800  
ACACCATCCC CAGCAGAGCC TACAGAAAAT AGAGAAAGGA CAGCCAATGA GAAGACCACA 1860  
CCATCCCCAG CAGAGCCTAC AGAAAAATAGA GAAACAACAG CCAATGAGAA GACCACACCA 1920  
ACGCCATCTC TAGCAGAGCC TACAGAAAAT GGACAAAGGA CCCCATTGTC CAATGAGAAG 1980  
ACCACATCAT CTTACAGAGA GCCTACAGAA CACGAAAGAA GGACTCCACT GGCCAATGAG 2040  
AACACCACAC CATCCCCGGC AGAGCCTACA GAAATAGAG AAAGGACAGC CAATGAGAAC 2100  
ACCACACCAT CCCCAGCAGG GCCTACAGAA AATAGAGAAA TGACAGCCAA CGAGAAGACC 2160  
ACACTATTC CAGCAGAGCC TACAGAAAAT AGAGAAAGGA CAGCCAATGA GAAGACCACA 2220  
TCATCCCCAG CAGAGCCTAC AGAAAAATAGA CAAAGGACCC CATTTGCCAA TGAGAAAACC 2280  
ACATCATCCC CAGCAGAGCC TACAGAACAC GGAGAAAGGA CCCCCTGGC CAATGAGAAC 2340  
ACCACACTAT CCCCAGCAGA GCCTACAGAA AATAGAGAAA GGACAGCCAA TGAGAGACC 2400  
ACACCATPCC CAGCAGAGCC TACAGAAAAT AGAGAAAGGA CAGCCAATGA GAACACCACA 2460  
CCATCCCCAG CACAGCCTAC AGAAAAATAGA GAAACAACAG CCAATGAGAA GACCACACCA 2520  
ACACCATCTC TAGCAGAGCC TACAGAAAAT GGAAAAAGGA CCCCATTGTC CAATGAGAAG 2580  
ACCACATCAT CTTACAGAGA GCCTACAGAA CACGCAGAAA GGACTCCACT GGCCAATGAG 2640  
AACACCAAT CATCCCCAGC AGAGCCTACA GAAATAGAG AAAGGACAGC CAATGAGAAG 2700  
ACCACACAAT TCCCAGCAGA GCCTACAGAA AATAGAGAAA GCACAGCCAA TGAGAAGACC 2760  
ACACCATTCC CAGCAGAGCC TACAGAAAAT AGAGAAAGGA CAGCCAATGA GAACACCACA 2820  
CTATCCCCAG CAGAGCCTAC AGAACATGAA GAAATGACCC CATTGGCCAA TGAGAAGACC 2880  
ACACTATCCC CAGCAGAGCC TACAGAAAAT GGAGAAAGGA CCCCATTGTC CAATGAGAAG 2940  
ACCACACCAT CTTACAGAGA GCCTACAGAA CATGGAGAAA GGACCCCTCT GGCCAATGAG 3000  
ATCACCACAC CATCCCGAGC AGAGCCTACA GAACATGGAG AAAGGATAGC CAATGAGAAG 3060  
GCCACACCAT CCCCAGCAAA GCCTACAGAA CATGGAGAAA GGACAGCCAA TGAGAAGACC 3120  
ACACCATCCT CAGCAGAGCC TACAGAAAAT GGAGAAAGGA CCCCCTGGC CAATGAGAAC 3180  
ACCACAACAT CCCCACAGAA GTCTACAGAA CATGGAGAAA GGACAGCCAA TGAGAAGACC 3240  
ACACCATCCC CAGCAGAGCC TACAGAACAT GGAGAAAGGA CACCATCAGC CAATGAGAAG 3300  
ACCATACCAT CTCCAGCAAA GCCTACAGAA CACGAAAGAA TGACCCCTATC GGCCAATGAG 3360  
AACACCACAC CATCCCCAGT AAAGCCTACA GAACATGGAG AAAAGACTAC ATTGGCCAAT 3420  
GAGAAGATCA CACTATCCCC AGAAGGGCCT ACAGAACATG GAGCAAAAAC TACGTCGGCC 3480  
AATGAGAAGA TCACACCATC CTAGCAAGG CCTACAGAAC ATGGAGAAAG GACCACATCA 3540  
CCCAATGACA AGATCACCTC ATCTGCAGCA GAGTCTACAG AACATAGAGA TAGGGCTACA 3600  
TCAGCCAATG TGATCACACC AGCCCCAGCA GAGCCTATAA AACATGCAAA AAGGACCACA 3660  
TTGGCCCATG AGAAGATGAC ACAAGTCACA GAAAAGTCCA CAGAACACCC AGAAAAGACC 3720  
ACGTCAACCA CAGAGAAAAC CACAAGAACC CCAGAAAAGC CTACGCTATA CTCAGAGAAG 3780  
ACCATATGCA CCAAGGGGAA AAACACACCA GTCCCAGAAA AGCCTACAGA AAACCTGGGG 3840  
AAACACCACAG TGACCACTGA GACCATAAAA GCCCCAGTAA AGTCCACAGA AAACCCAGAA 3900  
AAAAACGACG CAGTCACAAA GACTATAAAA CCTTCAGTCA AGGTCACAGG AGACAAATCT 3960  
CTCACTACTA CTTCTTCTCA TCTAAATAAA ACTGAAGTTA CTCATCAGGT GCCCACTGGT 4020  
TCTTTACCCC TCATTACACT TAGAACGAAG CTGAGTTCTA TCACATCAGA AGCCACAGGA 4080  
AACGAGAGCC ATCCATACCT CAATAAAGAT GGCTCACAGA AAGGTATCCA CGCTGGACAG 4140  
ATGGGAGAGA ATGATTCAAT CCCTGCATGG GCCATAGTTA TTGTGGTCTT GGTGGCTGTG 4200  
ATTCTCTCTT TGGTGTTCCT TGGCCTGATC TTTCTGGTCT CCTATATGAT GCGGACACGC 4260  
CGCACACTAA CCCAGAACAC CCAGTACAAT GATGCAGAGG ATGAGGGTGG CCCCAATTCC 4320  
TACCCGGTCT ACCTGATGGA GCAGCAGAA CTGCGCATGG GCCAGATCCC TTCCCCACGG 4380  
TGA



Seq ID NO: 428 Protein sequence  
Protein Accession #: XP\_069480.1

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
MDTVLVLLLG LQALAGSPSP POKDSVSDWA IVLITLTLVA AIVSLMYGIK KACQFRREMS 60
LGCGCGSVTP YSSHHEGEAA SQRYSCQMKA SWGAGATTFO EYQKTGELST SDHIFPLTPG 120
LVYSIPFDHI VLHSGQRPPE LPKSTEIHEQ KRHCNTRHS KPTDKPTGNS KTIDHKSSTD 180
NHEAPPTSEE NSSNQGDPM IRNQRSVDPA DSTTHKESA GKKHITPAK SKINCRKSTT 240
10    GKSTVTRKSD KTRGRPLEKSM STLDKTSTSS HKTTSFHNHNS GNSQTKQKST SFPEKITAAS 300
      KTTYKTTGTP EEEKTEDSR TTVASDKLLT KTTKNIQETI SANELTQSLA EPTHEGGRTA 360
      NENNTSPSPAE PTENRRTAN ENTTLSPAEP TENRERTANE NTAPFPAGPT ENREMTANEN 420
      TTLFPAEPT EHGERTANENT TPSPAEPTEH GERTANENTT PSPAEPTEHG ERTPFANDKT 480
15    TSSSAESTEH GERTPLANEN TTPSPAEPTE NRERTANENT TSPAPAGPTEN RETTANEKTT 540
      LSPVEPTENR ETTANEKTTT SPAEPTENGQ RTPFANEKTT SSSAEPTHEG ERTPLANENT 600
      TPSPAEPTEH RERTANEKTT PSPAEPTEH GERTANENTT TSPSPAEPTEH GRTPTFANEK 660
      TTSSSAEPT EHEERTPLANE NTTPSPAEPTE ENRERTANEN TTPSPAEPTE NREMTANEK 720
      TLFPAEPTEN RERTANEKTT SSPAEPTENG QRTPFANEKTT TSSPAEPTEH GERTPLANEN 780
20    TTLSPAEPTE NRERTANEKTT TFFPAEPTEN RERTANENTT PSPAQPTENG DRTPLANEK 840
      TPLSPAEPTEH GKRTPFANEK TTSSSAEPT HAERTPLANE NTSSSPAEPTE ENRERTANEK 900
      TTQFPAEPT NRESTANEKTT TFFPAEPTEN REWTANENTT LSPAEPTEHE EMTPLANEK 960
      TPLSPAEPTEH GERTPTFNEK TTPSSAEPT EHGERTPLANE ITTPSRAEPT EHGERIANEK 1020
      ATPSPAEPTEH HGETTVNEDT TPSSAEPTEN GERTPLANEN TTSPTESTE HGERTANEK 1080
25    TPSPAEPTEH GERTPSANEK TTPSPAEPTE HEEMTPSANE NTTPSPVKPT EHGEKTTLAN 1140
      EKITLSPGEP TEHGAKTTSA NEKITPSLAK PTEHGERTS PNDKITSSAA ESTEHRDRAT 1200
      SANVITPAPA EPIKHAKTIT LAHEKMTQVT EKSTHEPEKT TSTTEKTRT PEKPTLYSEK 1260
      TICTKGKNTV VPEKPTENLG NTTLTETETIK APVKSTENPE KTAAVTKTIK PSVKVTGDKS 1320
      LTTTSSHLNK TEVTHQVPTG SFTLITSRTK LSSITSEATG NESHPYLNKD GSQKGIHAGQ 1380
30    MGENDSFPAP AIVIVLVAV ILLLVFLGLI FLVSYMMRTR RTLTQNTQYN DADEGGPNS 1440
      YPVYLMQEQN LGMGQIPSPR

```

Seq ID NO: 429 DNA sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..10674

```

35    1      11      21      31      41      51
      |      |      |      |      |      |
ATGTGGCCTC GCCTGGCCTT TTGTTGCTGG GGTCTGGCGC TCGTTTCGGG CTGGGCGACC 60
40    TTTACAGAGA TGTCCTCCGTC GCGCAATTTC AGCTTCCGCC TCTTCCCGGA GACCGCGCCC 120
      GGGGCCCCCG GGAGTATCCC CGCGCCGCCC GCTCCTGGCG ACGAAGCGGC GGGGAGCAGA 180
      GTGGAGCGGC TGGGCCAGGC GTTCCGCGCA CGCGTGCGGC TGCTGCGGGA GCTCAGCGAG 240
      CGCTCGGAGC TTGTCTCTCT GGTGGATGAT TCGTCCAGCG TGGGCGAAGT CAACCTCCGC 300
      AGCGAGCTCA TGTTCGTCGG CAAGCTGCTG TCCGACTTCC CCGTGGTGCC CACGGCCACG 360
45    CGCGTGCCCA TCGTGACCTT CTGTCACCAAG AACTACGTGG TGCCGCGCGT CGATTACATC 420
      TCCACCCGCC GCGCGCGCCA GCACAAGTGC GCGCTGCTCC TCCAAGAGAT CCCTGCCATC 480
      TCCTACCGAG GTGGCGGCAC CTACACCAAG GCGCCTTCC AGCAAGCCGC GCAAAATCTT 540
      CTTTCATGCTA GAGAAACATC AACAAAGTT GTATTCTCA TCACTGATGG ATATTCCAAT 600
      GGGGGAGACC CTAGACCAAT TGCAGCGTCA CTGCGAGATT CAGGAGTGA GATCTTCACT 660
      TTTGGCATAT GGCAGGGGAA CATTCGAGAG CTGAATGACA TGGCTTCCAC CCCAAAGGAG 720
50    GAGCACTGTT ACCTGCTACA CAGTTTGAAG GAATTTGAGG CTTTAGCTCG CCGGGCATTG 780
      CATGAAGATC TACCTCTGAG GAGTTTATT CAAGATGATA TGGTCCACTG CTCATATCTT 840
      TGTGATGAAG GCAAGGACTG CTGTGACCGA ATGGGAAGCT GCAAATGTGG GACACACACA 900
      GGCCATTTTG AGTGCATCTG TGAAAAGGGG TATTACGGGA AAGGTCTGCA GTATGAATGC 960
      ACAGCTTGCC CATCGGGGAC ATACAAACCT GAAGGCTCAC CAGGAGGAAT CAGCAGTTGC 1020
55    ATTCCATGTC CTGATGAAA TACACCTCT CCACCTGGA GCACATCCCC TGAAGACTGT 1080
      GTCTGCAGAG AGGGATACAG GGCATCTGGC CAGACCTGTG AACTGTGCTA CTGCCCTGCC 1140
      CTGAAGCCTC CCGAAATATG TTACTTTATC CAAAACACTT GCAACAACCA CTTCAATGCA 1200
      GCCTGTGGGG TCCGATGTCA CCTGTGATTT GATCTTGTGG GAAGCAGCAT CTCTTATGT 1260
60    CTACCAATG GTTTGTGGTC CGGTTTCAGAG AGCTACTGCA GAGTAAGAAC ATGCCTCAT 1320
      CTCCGCCAGC CGAACATGAG CCACATCAGC TGTCTACAA GGGAAATGTT ATATAAGACA 1380
      ACATGTTTGG TTGCTGTGTA TGAAGGGTAC AGACTAGAAG GCAGTGATAA GCTTACTTGT 1440
      CAAGGAAACA GCCAGTGGGA TGGGCCAGAA CCCCCTGTG TGGAGCGCCA CTGTTCCACC 1500
      TTTAGATGTC CCAAAGATGT CATCATATCC CCCCACAACT GTGGCAAGCA GCCAGCCAAA 1560
65    TTTGGGACGA TCTGCTATGT AAGTTGCCGC CAAGGGTTCA TTTTATCTGG AGTCAAAGAA 1620
      ATGCTGAGAT GTACCACTTC TGGAAATATG AATGTCTGG TTCAGGCAGC TGTGTGTAAA 1680
      GACGTGGAGG CTCTCAAAAT CAACGTCTCT AAGGACATAG AGGCTAAGAC TCTGGAACAG 1740
      CAAGATCTCT CCAATGTTAC CTGGCAGATT CCAACAGCTA AAGACAACTC TGGTGAAGAA 1800
      GTGTCACTCC ACGTTTATCC AGCTTTCACC CCACCTTACC TTTTCCCAAT TGGAGATGTT 1860
70    GCTATCGTAT ACACGGCAAC TGACCTATCC GGCAACCAG CCAGCTGCAT TTTCCATATC 1920
      AAGGTTATTG ATGCAGAAC ACCTGTCTAT GACTGTGTGA GATCTCCACC TCCCGTCCAG 1980
      GTCTCGGAGA CGGTACATGC CGCAAGCTGG GATGAGCCTC AGTTCTCAGA CAACTCAGGG 2040
      GCTGAATTGG TCATTACCAG AAGTCATACA CAAGGAGACC TTTTCCCTCA AGGGGAGACT 2100
      ATAGTACAGT ATACAGCCAC TGACCCCTCA GGCAATAACA GGACATGTGA TATCCATAT 2160
75    GTCATAAAAG GTTCTCCCTG TGAAATTTCCA TTCACACCTG TAAATGGGGA TTTTATATGC 2220
      ACTCCAGATA ATACTGGAGT CCACTGTACA TTAACCTGCT TGGAGGGCTA TGATTTCACA 2280
      GAAGGGTCTA CTGACAAAGT TTATTGTGCT TATGAAGATG GCGTCTGGAA ACCAACATAT 2340
      ACCACTGAAT GGCCAGACTG TGCCAAAAAA CGTTTTCGCA ACCACGGGTT CAAGTCTTT 2400
      GAGATGTTCT ACAAGAGCAG TCGTTGTGAT GACACAGATC TGATGAAGAA GTTTTCTGAA 2460
80    GCATTTGAGA CGACCTTGGG AAAAATGGTC CCATCATTTT GTAGTGATGC AGAGGACATT 2520
      GACTGCAGAC TGAGAGGAGAA CCTGACCAAA AAATATTGCC TAGAATATAA TTATGACTAT 2580
      GAAAATGGCT TTGCAATTGG ACCAGGTGGC TGGGGTGCAG CTAATAGGCT GGATTACTCT 2640
      TACGATGACT TCCTGGACAC TGTGCAAGAA ACAGCCACAA GCATCGGCAA TGCCAAGTCC 2700
      TCACGGATTA AAAGAAATGC CCCATTATCT GACTATAAAA TTAAGTTAAT TTTTAACATC 2760
      ACAGCTAGTG TGCCATTACC CGATGAAAGA AATGATACCC TTGAATGGGA AAATCAGCAA 2820

```

	CGACTCCTTC	AGACATTGGA	AACTATCACA	AATAAACTGA	AAAGGACTCT	CAACAAAGAC	2880
	CCCATGTATT	CCTTTCAGCT	TGCATCAGAA	ATACCTATAG	CCGACAGCAA	TTTATTAGAA	2940
	ACAAAAAAGG	CTTCCCCCTT	CTGCAGACCA	GGCTCAGTGC	TGAGAGGGCG	TATGTGTGTC	3000
5	AATTGGCCCTT	TGGGAACCTA	TTATAATCTG	GAACATTTCA	CCTGTGAAAG	CTGCCGGATC	3060
	GGATCCCTATC	AAGATGAAGA	AGGGCAACTT	GAGTGCAAGC	TTTGCCCTTC	TGGGATGTAC	3120
	ACGGAATATA	TCCATTCAAG	AAACATCTCT	GATTGTAAAG	CTCAGTGTAA	ACAAGGCACC	3180
	TACTCATACA	GTGGACTTGA	GACTTGTGAA	TCGTGTCCAC	TGGGCACTTA	TCAGCCAAAA	3240
	TTTGGTTCCC	GGAGCTGCCT	CTCGTGTCCA	GAAAAACACT	CAACTGTGAA	AAGAGGAGCC	3300
10	GTGAACATTT	CTGCATGTGG	AGTTCCTTGT	CCAGAAGGAA	AATTCTCGCG	TTCTGGGTTA	3360
	ATGCCCTGTC	ACCCATGTCC	TCGTGACTAT	TACCAACCTA	ATGCAGGGAA	GGCCTTCTGC	3420
	CTGGCCTGTC	CCTTTATATG	AACTACCCCA	TTCTGCTGGT	CCAGATCCAT	CACAGAATGT	3480
	TCAACTTCAG	TTCTGAATAT	TACTATTTTC	GGTGGATTTG	GGCATCTGGA	GTGTGTTAAAT	3540
	TGTCCTTCTG	AGGTTTTCCTA	TGAATGCTTC	TTTAACCCCTT	GCCACAATAG	TGGAACCTGC	3600
15	CAGCAACTTG	GGCGTGGTTA	TGTTTGTCTC	TGTCACCTTG	GATATACAGG	CTTAAAGTGT	3660
	GAAACAGACA	TCGATGAGTG	CAGCCCACTG	CCTTGCCTCA	ACAATGGAGT	TTGTAAGAC	3720
	CTAGTTGGGG	AAATCAATTG	TGAGTGCCCA	TCAGGTACCA	CAGGTGAGCG	GTGTGAAGAA	3780
	AATATAAATG	AGTGTAGCTC	CAGTCTCTGT	TTAAATAAAG	GAATCTGTGT	TGATGGTGTG	3840
	GCTGGCTATC	GTTCACATG	TGTGAAAGGA	TTTGTAGGCC	TGCATTGTGA	AACAGAAATC	3900
20	AATGAATGCC	AGTCAAACCC	ATGCTTAAAT	AATGCAGTCT	GTGAAGACCA	GGTTGGGGGA	3960
	TTCTTGTGCA	AATGCCACCC	TGGATTTTTG	GGTACCCGAT	GTGGAAAGAA	CGTCGATGAG	4020
	TGCTTCAGTC	AGCCATGCAA	AAATGGAGCT	ACCTGTAAAG	ACGGTGCCAA	TAGCTTCAGA	4080
	TGCCCTGTGT	CAGCTGGCTT	CACAGGATCA	CAGTGTGAAT	TGAACATCAA	TGAATGTGAG	4140
	TCTAATCCAT	GTAGAAATCA	GGCCACCTGT	GTGGATGAAT	TAAATTCTA	CAGTTGTAAA	4200
25	TGTCAGCCAG	GATTTTCAGG	CAAAAGGTGT	GAAACAGAAC	AGTCTACAGG	CTTTAACCTG	4260
	GATTTTGAAG	TTTCTGGCAT	CTATGGATAT	GTCTAGCTAG	ATGGCATGCT	CCCATCTCTC	4320
	CATGCTCTAA	CCTGTACCTT	CTGGATGAAA	TCTCTGACG	ACATGAACCTA	TGGAACACCA	4380
	ATCTCCTATG	CAGTTGATAA	CGGCAGCGAC	AATACCTTGC	TCTCTGACTGA	TTATAACGGC	4440
	TGGGTTCTTT	ATGTGAATGG	CAGGGAAAAG	ATAACAAACT	GTCCCTCGGT	GAATGATGGC	4500
30	AGATGGCATC	ATATTGCCAT	CACITGGACA	AGTGCCAAATG	GCATCTGGAA	AGTCTATATC	4560
	GATGGGAAAT	TATCTGACGG	TGGTGTCTGG	CTCTCTGTGT	GTGTTGCCAT	ACCTGGTGGT	4620
	GGTGGCTTAG	TTCTGGGGCA	AGAGCAAGAC	AAAAAAGGAG	AGGGATTGAG	CCCAGCTGAG	4680
	TCTTTTGTGG	GCTCCATAAG	CCAGCTCAAC	CTCTGGGACT	ATGTCTCTGT	TCCACAGCAG	4740
	GTGAAGTCAAC	TGGCTACCTC	CTGCCCAGAG	GAACCTCAGTA	AAGGAAACGT	GTTAGCATGG	4800
35	CCTGATTTCT	TGTCAGGAAT	TGTGGGGAAA	GTGAAGATCG	ATTCTAAGAG	CATATTTTGT	4860
	TCTGATTGCC	CACGCTTAGG	AGGGTCAGTG	CCTCATCTGA	GAACCTGCATC	TGAAGATTTA	4920
	AAGCCAGGTT	CCAAAGTCAA	TCTGTTCTGT	GATCCAGGCT	TCCAGCTGGT	CGGGAACCCCT	4980
	GTGCACTACT	GTCTGAATCA	AGGACAGTGG	ACACAACCCAC	TTCCCTCACTG	TGAACGCATT	5040
	AGCTGTGGGG	TGCCACCTCC	TTTGGAGAAT	GGCTTCCATT	CAGCCGATGA	CTTCTATGCT	5100
40	GGCAGCACAG	TAACTTACCA	GTGCAACAAT	GGCTACTATC	TATTGGGTGA	CTCAAGGATG	5160
	TTCTGTACAG	ATAATGGGAG	CTGGAACGGC	GTTCACCAT	CCTGCCTTGA	TGTCGATGAG	5220
	TGTGCACTTG	GATCAGATTG	TAGTGAGCAT	GCTTCTTGCC	TGAACGTAGA	TGGATCCTAC	5280
	ATATGTTTCT	GTGTCCCAAC	GTACACAGGA	GATGGGAAAA	ACTGTGCAGA	ACCTATAAAA	5340
	TGTAAGGCTC	CAGGAATCC	GGAAAATGGC	CACCTCCTCAG	GTGAGATTTA	TACAGTAGGT	5400
45	GCCGGAGTCA	CATTTTCTGT	TCAGGAAGGA	TACCAGTTGA	TGGGAGTAAC	CAAAATCACA	5460
	TGTTTGGAGT	CTGGAGAATG	GAATCATCTA	ATACCATATT	GTAAGCTGTG	TTTATGTGGT	5520
	AAACCCGCTA	TTCCAGAAAA	TGGTTGCATT	GAGGAGTTAG	CATTTACTTT	TGGCAGCAAA	5580
	GTGACATATA	GGTGTAAATA	AGGATATACT	CTGGCCGGTG	ATAAAGAATC	ATCCTGTCTT	5640
	GCTAACAGTT	CTTGGAGTCA	TTCCCTCTCT	GTGTGTGAAC	CAGTGAAGTG	TTCTAGTCCG	5700
50	GAAATATATA	ATAATGGAAA	ATATATTTTG	AGTGGGCTTA	CCTACCTTTC	TACTGCATCA	5760
	TATTCATGCG	GTGTCCCAAC	CAGCTTACAG	GGCCCTTCCA	TTATTGAATG	CACGGCTTCT	5820
	GGCATCTGGG	ACAGAGCGCC	ACCTGCCTGT	CACCTCGTCT	TCTGTGGAGA	ACCACCTGCC	5880
	ATCAAAGATG	CTGTCAATAC	GGGGAATAAC	TTCACTTTCA	GGAACACCGT	CACCTTCACT	5940
	TGCAAAAGAG	GCTATACTCT	TGCTGGTCTT	GACACCATTG	AATGCCTGGC	CGACGGCAAG	6000
55	TGGAGTAGAA	GTGACCAAGA	GTGCTGGCT	GTCTCCTGTG	ATGAGCCACC	CATTGTGGAC	6060
	CACGCCCTCT	CAGAGACTGC	CCATCGGCTC	TTTGAGACA	TTGCATTCTA	CTACTGCTCT	6120
	GATGGTTACA	GCCTAGCAGA	CAATTCCAG	CTTCTCTGCA	ATGCCAGGG	CAAGTGGGTA	6180
	CCCCCAGAA	GTCAAGACAT	GGCCCGTTGT	ATAGCTCATT	TCTGTGAAAA	ACCTCCATCG	6240
	GTTTTCTATA	GCATCTTGGG	ATCTGTGAGC	AAAGCAAAAT	TTGCAGCTGG	CTCAGTTGTG	6300
60	AGCTTTAAAT	GCATGGGAAG	CTTTGTACTG	AACACCTCAG	CAAAGATTGA	ATGTATGAGA	6360
	GGTGGGCAGT	GGAACCCCTT	CCCCATGTCC	ATCCAGTGCA	TCCCTGTGCG	GTGTGGAGAG	6420
	CCACCAAGCA	TCATGAATGG	CTATGCAAGT	GGATCAAAT	ACAGTTTGTG	AGCCATGGTG	6480
	GCTTACAGCT	GCAACAAGGG	GTCTACATC	AAAGGGGAAA	AGAAGAGCAC	CTGCGAAGCC	6540
	ACAGGGCAGT	GGAGTAGTCC	TATACCGACG	TGCCACCCGG	TATCTTGTGG	TGAACCACTT	6600
65	AAGGTTGAGA	ATGGCTTTCT	GGAGCATACA	ACTGGCAGGA	TCTTTGAGAG	TGAAGTGAGG	6660
	TATCAGTGTA	ACCCGGGGCTA	TAAGTCAGTC	GGAAGTCCCTG	TATTTGTCTG	CCAAGCCAAT	6720
	CGCCACTGGC	ACAGTGAATC	CCCTCTGATG	TGTGTTCCTC	TCGACTGTGG	AAAACTCTCC	6780
	CCGATCCAGA	ATGGCTTCAT	GAAAGGAGAA	AACCTTGAAG	TAGGGTCCAA	GGTTCAAGTT	6840
	TTCTGTAATG	AGGGTTATGA	GCTTGTGGT	GACAGTTCTT	GGACATGTCA	GAAATCTGGC	6900
70	AAATGGAATA	AGAAGTCAAA	TCCAAAGTGC	ATGCCTGCCA	AGTGCCCAAG	GCCGCCCTCT	6960
	TTGGAAAACC	AGCTAGTATT	AAAGGAGTTG	ACCACCGAGG	TAGGAGTTGT	GACATTTTCC	7020
	TGTAAGAAG	GGCATGTCTT	GCAAGGCCCT	TCTGTCTTGA	AATGCTTGCC	ATCCAGCAAA	7080
	TGGAATGACT	CTTCCCTGT	TTGTAAGATT	GTCTTTTGTG	CCCCACCTCC	CCTAATTTCC	7140
	TTTGGTGTCC	CCATTCTCTC	TTCTGCTCTT	CATTTTGGAA	GTACTGTCAA	GTATTTCTGT	7200
75	GTAGGTGGGT	TTTTCTTAAG	AGGAAATTCT	ACCACCTCT	GCCAACCTGA	TGGCACCTGG	7260
	AGCTCTCCAC	TGCCAGAATG	GTTCAGATG	GAATGTCCCC	AACCTGAGGA	AATCCCCAAT	7320
	GGAATCATTT	ATGTGCAAGG	CCTTGCCTAT	CTCAGCACAG	CTCTCTATAC	CTGCAAGCCA	7380
	GGCTTTGAAT	TGGTGGGAAA	TACTACCACC	CTTTGTGGAG	AAAATGGTCA	CTGGCTTGGG	7440
	GGAAAACCCA	CATGTAAGC	CATTGAGTGC	CTGAAACCCA	AGGAGATTTT	GAATGGCAAA	7500
80	TTCTCTTACA	CGGACCTACA	CTATGGACAG	ACCGTTACCT	ACTCTTGCAA	CCGAGGCTTT	7560
	CGGCTCGAAG	GTCCCACTGC	CTTGACCTGT	TTAGAGACAG	GTGATTGGGA	TGTAGATGCC	7620
	CCATCTTGCA	ATGCCATCCA	CTGTGATTCC	CCACAACCCA	TTGAAAATGG	TTTTGTAGAA	7680
	GGTGCAGATT	ACAGCTATGG	TGCCATAATC	ATCTACAGTT	GCTTCCCTGG	GTTCAGGGTG	7740
	GCTGGTCAAT	CCATGCAGAC	CTGTGAAGAG	TCAGGATGGT	CAAGTTCCAT	CCCAACATGT	7800
	ATGCCAATAG	ACTGTGGCCT	CCCTCCTCAT	ATAGATTTTG	GAGACTGTAC	TAAACTCAAA	7860

5 GATGACCAGG GATATTTTGA GCAAGAAGAC GACATGATGG AAGTTCCATA TGTGACTCCT 7920  
 CACCTCTCCT ATCAATTTGGG AGCAGTGGCT AAAACCTGGG AAAATACAAA GGAGTCTCCT 7980  
 GCTACACATT CATCAAACCT TCTGTATGGT ACCATGGTTT CATAACCTG TAATCCAGGA 8040  
 TATGAACCTT TGGGGAACCC TGTGCTGATC TGCCAGGAAG ATGGAACCTG GAATGGCAGT 8100  
 GCACCATCCT GCATTTCAAT TGAATGTGAC TTGCCTACTG CTCCTGAAAA TGGCTTTTTG 8160  
 CGTTTTACAG AGACTAGCAT GGGAAAGTGT GTGCAGTATA GCTGTAAACC TGGACACATT 8220  
 CTAGCAGGCT CTGACTTAAG GCTTTGTCTA GAGAATAGAA AGTGGAGTGG TGCCTCCCCA 8280  
 CGCTGTGAAG CCATTTCAATG CAAAAAGCCA AATCCAGTCA TGAATGGATC CATCAAAGGA 8340  
 10 AGCAACTACA CATACTGAG CACGTTGTAC TATGAGTGTG ACCCCGGATA TGTGCTGAAT 8400  
 GGCACGTAGA GAGAAACATG CCAGGATGAC AAAAACTGGG ATGAGGATGA GCCCATTTGC 8460  
 ATTCTGTGG ACTGCAGTTC ACCCCAGTC TCAGCCATG GCCAGGTGAG AGGAGACGAG 8520  
 TACACATTCC AAAAAGAGAT TGAATACACT TGCAATGAAG GGTTCCTGCT TGAGGGAGCC 8580  
 AGGAGTCGGG TTGTCTTGGC CAATGGAAGT TGGAGTGGAG CCACCTCCGA CTGTGTGCCT 8640  
 15 GTCAGATGTG CCACCCCGCC ACAACTGGCC AATGGGGTGA CGGAAGGCCT GGACTATGGC 8700  
 TTTCAAGAG AAGTAACATT CCACTGTAC GAGGGCTACA TCTTGACGG TGCTCCAAA 8760  
 CTCACCTGTC ATCAGATGG CAACTGGGAT GCAGAGATTC CTCTCTGTAA ACCAGTCAAC 8820  
 TGTGGACCTC CTGAAGATCT TGCCCATGGT TTCCCTAATG GTTTTTCTCT TATTCTATGG 8880  
 GGCATATATC AGTATCAGTG CTTTCTGGT TATAAGCTCC ATGGAATTC ATCAAGAAGG 8940  
 20 TGCTCTCCA ATGGCTCCTG GAGTGGCAGC TCACCTTCCT GCCTGCCTTG CAGATGTTCC 9000  
 ACACCAAGTA TTGAATATGG AACTGTCAAT GGGACAGATT TTGACTGTGG AAAGGCAGCC 9060  
 CGGATTCACT GCTTCAAAGG CTTCAAGCTC CTAGGACTTT CTGAAATCAC CTGTGAAGCC 9120  
 GATGGCCAGT GGAAGCTCTG GTTCCCCAC TGTGAACACA CTCTCTGTGG TTCTCTTCCA 9180  
 ATGATACCAA ATGCGTTCAT CAGTGAGACC AGCTCTTGA AGGAAAATGT GATAACTTAC 9240  
 25 AGCTGCAGGT CTGGATATGT CATAAAGGC AGTTCAGATC TGATTGTGAC AGAGAAAGG 9300  
 GTATGGAGCC AGCCTTATCC AGTCTGTGAG CCCTTGTCTT GTGGGTCCCC ACCGTCTGTC 9360  
 GCCAATGCAG TGGCAACTGG AGAGGCACAC ACCTATGAAA GTGAAGTGAA ACTCAGATGT 9420  
 CTGGAAGGTT ATACGATGGA TACAGATACA GATACATTCA CCTGTGAGAA AGATGGTCGC 9480  
 TGGTCCCTG AGAGAATCTC CTGCAGTCTT AAAAAATGTC CTCTCCCGGA AAACATAACA 9540  
 30 CATATACTTG TACATGGGGA CGATTTTCA GTGAATAGGC AAGTTTCTGT GTCATGTGCA 9600  
 GAAGGGTATA CCTTTGAGG AGTTAAACA TCAGTATGTC AGCTTGATGG AACCTGGGAG 9660  
 CCACCATTTT CCATGAACT TTGCAGTCCA GTTCTTGTG GGAACCTGA AAGTCCAGAA 9720  
 CATGGATTG TGGTTGGCAG TAAATACACC TTTGAAAGCA CAATTATTTA TCAGTGTGAG 9780  
 CCTGGCTATG AACTAGAGGG GAACAGGGAA CGTGTCTGCC AGGAGAACAG ACAGTGGAGT 9840  
 35 GGAAGGGTGG CAATATGCAA AGAGACCAGG TGTGAACTC CACTTGAATT TCTCAATGGG 9900  
 AAAGCTGACA TTGAAACAG GACGACTGGA CCCAACGTGG TATATTCTG CAACAGAGGC 9960  
 TACAGTCTTG AAGGCCATC TGAGGCACAC TGCACAGAA ATGGAACCTG GAGCCACCA 10020  
 GTCCCTCTCT GCAAACCAAA TCCATGCCCT GTTCTTTTG TGATCCCGA GAATGCTCTG 10080  
 CTGTCTGAAA AGGAGTTTAT TGTGTATCAG AATGTGTCCA TCAATGTAG GGAAGGTTTT 10140  
 40 CTGTCTGAGG CCCACGGCAT CATTACCTGC AACCCGACG AGACGTGGAC ACAGACAAGC 10200  
 GCCAATGTG AAAAATCTC ATGTGGTCCA CCAGCTCAG TAGAAAATGC AATTGCTCGA 10260  
 GGCGTACATT ATCAATATGG AGACATGATC ACCTACTCAT GTTACAGTGG ATACATGTTG 10320  
 GAGGGTTTTT TGAGGAGTGT TTGTTAGAA AATGGAACAT GGACATCAC TCTTATTGTC 10380  
 AGAGCTGTCT GTCGATTTCC ATGTGAGAA GGGGGCATCT GCCAACGCCC AAATGCTTGT 10440  
 45 TCCTGTCCAG AGGGCTGGAT GGGGCGCTC TGTGAAGAAC CAATCTGCAT TCTTCCCTGT 10500  
 CTGAACGGAG TCGCTGTGT GGGCCCTTAC CAGTGTGACT GCCCGCTGG CTGGACGGGG 10560  
 TCTGCTGTC ATACAGCTGT TTGCCAGTCT CCCTGCTTAA ATGGTGGAAA ATGTGTAAGA 10620  
 CCAAACCGAT GTCAGTGTCT TTCTTCTTGG ACGGGACATA ACTGTCCAG GTAA

Seq ID NO: 430 Protein sequence  
 Protein Accession #: FGENSEH predicted

50  
 1 11 21 31 41 51  
 MWPRLAFCW GLALVSGWAT FQOMSPSRNF SFRLFPETAP GAPGSIPAPP APGDEAAGSR 60  
 55 VERLQAFRR RVRLLRELSE RLELVFLVDD SSSVGEVNF SELMFVRKLL SDFPVVPTAT 120  
 RVAIVTFSSK NVVVRVDYI STRRARQHKC ALLLQEIPI SYRGGGTYT GAFQQAQIL 180  
 LHARENSTKV VFLITDGYSN GGDPRPIAAS LRDSQVEIFT FGIWQGNIRE LNDMASTPKE 240  
 60 EHCYLLHSFE EPEALARRAL HEDLPSSGFI QDDMVHCSYL CDEGDKCCDR MGSCCKGTHT 300  
 GHFEICCEKG YYGKGLQYEC TACPSGTYPK EGSPPGSISS IPCPDENHTS PPGSTSPEDC 360  
 VCREGVRASG QTCELVHCPA LKPPENGYFI QNTCNNHFNA ACGVRCHPGF DLVGSIIILC 420  
 LPNGLWSGSE SYCRVRTCPH LRQPKHGHIS CSTREMLYKT TCLVACDEGY RLEGSDKLTC 480  
 QGNSQWDGPE PRCVERHCST FQMPKDVII PHNCGKQPAK FGITCYVSCR QGFILSGVKE 540  
 65 MLRCTTSGKW NVGVQAQVCK DVEAPQINCP KDIEAKTLEQ QDSANVTWQI PTAKDNSGEK 600  
 VSVHVPFAFT PPYLFPPIGDV AIVYTATDLS GNQASCFIHI KVIDAEPPVI DWCRSPPPVQ 660  
 VSEKVHAASW DEPOFSDNSG AELVITRSH T QGDLFPQGET IVQYTATDPS GNNRTCDIHI 720  
 VIKGSPCEIP FTFVNGDFIC TPDNTGVNCT LTCLEGYDFT EGSTDKYICA YEDGVWKPTY 780  
 TTEWPDCAKK RFANHGFKSF EMFYKAARCD DTDLMKKFSE AFETTLGKMV PSFCSDAEDI 840  
 70 DCLREENLTK KYCLEVNYDY ENGFAIGPGG WGAANRLDYS YDDFLDTVQE TATSIGNAKS 900  
 SRIKRSAPLS DYKIKLIFNI TASVPLPDER NDTLEWENQQ RLLQTLTIT NKLRKTLNKD 960  
 PMYSFQAL ILIADNSNLE TTKASPFRCR GSVLGRMCV NCPLGTYYNL EHFTCESCRI 1020  
 GSYQDEBQGL ECKLCPGSMY TEYIHSRNI DCKAQCKQGT YSYSGLETCE SCPLGTYQPK 1080  
 FGSRSLSCSP ENTSTVKRGA VNISACGVPC PEGKFSRSLG MPCHPCPRDY YQPNAGKAFK 1140  
 75 LACPFYGTTP FAGRSITEC STSVINITIF GGFHLELLN CPSEVFHECF FNPCHNSGTC 1200  
 QQLGRGYVCL CPLGYTGLKC ETDIDECSPL PCLNNGVCKD LVGEFICECP SGYTGORCEE 1260  
 NINECSSSPC LNKIGICVDGV AGYRCTCVKG FVGLHCETE NEQSNPCLN NAVCEDQVGG 1320  
 FLCKCPGFL GTRCGKNVDE CLSQPCNKA TCKDGANSFR CLCAAGFTGS HCELNINECQ 1380  
 SNPCRQATC VDELSNYSCK CQPGFSKRC ETEQSTGFNL DFEVSGIYGY VMLDGMPLPSL 1440  
 80 HALTCTFWMK SSDDMNYGTP ISYAVDNGSD NTLLLTDYNG WVLYVNGREK ITNCPVNDG 1500  
 RWHIAITWT SANGIKVYI DGKLSDDGAG LSVGLPIPGG GALVLQEQD KKGEGFSPA 1560  
 SFVGSISQLN LWDVLSFPQQ VKSLATSCPE ELKSGNVLAW PDFLSGIVGK VKIDSISIFC 1620  
 SDCPRLGGSV PHLRTASEDL KPGSKVNLFC DPGFQLVGNP VQVCLNQGW TQPLPHCERI 1680  
 SCGVPPPLEN GFHSADDFYA GSTVTYQCNN GYLLGDSRM FCTDNGSWNG VSPSCLDVDE 1740  
 CAVGSDCSEH ASCLVNVDGSY ICSCVPPYTG DGKNCAPFIK CKAPGNPENG HSSGEIYTVG 1800  
 AGVTFSQCEG YQLMGVTKIT CLBSGEWNHL IPYCKAVSCG KPAPENGCI EELAFTEGSK 1860

VTIRCCKNGYT LAGDKESSCL ANSSWSHSP VCEPVKCSSP ENINNGKYIL SGLTYLSTAS 1920  
 YSCDTGYSLQ GPSIIETAS GIWDRAPPAC HLVFCGEPPA IKDAVITGNN FTFRNTVTYT 1980  
 CKEGYTLAAGL DTIECLADGK WSRSDQQLA VSCDEPPIVD HASPETAHRL FGDIAPFYCS 2040  
 DGYSLADNSQ LLCNAQKQKV PPEGQDMPC IAHFCEKPPS VSYSILESVS KAKFAAGSVV 2100  
 5 SFKCMGEFVL NTSAKIECMR GGQWNPSPMS IQCIPVRCGE PPSIMNGYAS GSNYSFGAMV 2160  
 AYSCNKGFIY KGEKKSTCEA TGQWSSPIPT CHPVSCGEP KVENGFLEHT TGRIFESEVR 2220  
 YQCNPGYKSV GSPVFCQAN RHWSESPML CVPLDCGKPP PIQNGFMKGE NFEVGSKVQF 2280  
 FCNEGYELVG DSSWTCQKSG KWNKSNPKC MPAKCEPPL LENQLVLKEL TTEVGVVTF 2340  
 10 CKEGHVLQGP SVLKCLPSQ WNDSPFPCKI VLCTPPPLIS FGVPIPPSAL HFGSTVKYSC 2400  
 VGGFFLRGNS TTLCPQDGTW SSPLPECVFV ECPQPEIIPN GIIDVQGLAY LSTALYTCCK 2460  
 GFELVGNNTT LCGENGHWLG GKPTCKAIEC LKPKELNKG FSYTDLHYGQ TVTYSCNRGF 2520  
 RLEGPSALTC LETGDWDVDA PSCNAIHCD S PQIENGFEVE GADYSYGAI IYSCFPGFQV 2580  
 AGHAMQTCEE SGWSSSIPTC MPIDCGLPPH IDFGDCTKLK DDQGYFEQED DMMEVPYVTP 2640  
 15 HPPYHLGAVA KTWENTKESP ATHSSNPLYG TMVSYTCNPG YELLGPNVLI CQEDGTWNGS 2700  
 APSICISIECD LPTAPENGFL RFTETSMGSA VQYSCPKPHI LAGSDDLRLCL ENRWKSGASP 2760  
 RCEAISCKKP NPVMNGSEIKG SNYTYLSTLY YECDPGYVLN GTERRTCQDD KNWDEDEPIC 2820  
 IPVDCSSPPV SANGQVRGDE YTFQKEIEYT CNEGFLLGGA RSRVCLANGS WSGATPDCVP 2880  
 VRCATPPQLA NGVTEGLDYG FMKEVTFHCH EGYILHGAPK LTCQSDGNWD AEIPLCKPVN 2940  
 CGPPEDLAHG FPNNGFSFIHG GHIQYQCFPG YKLHGNSSRR CLSNGSWSGS SPSCLPCCRS 3000  
 20 TPVIEYGTVN GTDHDGCKAA RIQCFKGFKL LGLSEITCEA DGQWSSGFPH CEHTSCGSLP 3060  
 MIPNAFISSET SSWKENVITY SCRSGYVIQ SSDLICTEKG VWSQPYPVCE PLSCGSPSPV 3120  
 ANAVATGEAH TYESEVKLRC LEGYTMDTDT DTFTCQKDG R WFERISCSP KKCPLEPENIT 3180  
 HILVHGGDFS VNRQVSVSCA EGYTFEGVNI SVCQLDGTWE PPFSDSCSP VSCGKPESPE 3240  
 HGFVVGSKYT FESTIYQCE PGYELEGNRE RVCQENRQWS GGVAIKETR CETPLEFLNG 3300  
 25 KADIENTRTG PNVVYSCNRG YSLEGPSEAH CTENGWWSHP VPLCKPNPCP VPVFIPEAL 3360  
 LSEKEFYVDQ NVSICKREGE LLQGHGIITC NPDETWTQTS AKCEKISCP PAHVENAIAR 3420  
 GVHYQYGDMI TYSCYSGYML EGFLRSVCL E NGTWTSPPIC RAVCRFPQN GGICQRPNAC 3480  
 SCPEGWMGRL CREPICILPC LNGGRCAVAPY QCDCFPGWG SRCHTAVCQS PCLNGGKCVR 3540  
 30 PNRCHLSSW TGHNCRR

Seq ID NO: 431 DNA sequence

Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..390

1 11 21 31 41 51  
 ATGAGGTTCA GTGTCTCAGG CATGAGGACC GACTACCCCA GGAGTGTGCT GGCTCCTGCT 60  
 TATGTGTCTAG TCTGTCTCCT CCTCTTGTGT CCAAGGGAAG TCATCGCTCC CGCTGGCTCA 120  
 40 GAACCATGGC TGTGCCAGCC GGCACCCAGG TGTGGAGACA AGATCTACAA CCCCTGGAG 180  
 CAGTGTCTGT ACAATGACGC CATCGTGTCC CTGAGCGAGA CCCGCCAATG TGGTCCCCC 240  
 TGCACCTTCT GGCCTGCTT TGAGCTCTGC TGTCTTGATT CCTTTGGCCT CACAAACGAT 300  
 TTTGTTGTGA AGCTGAAGGT TCAGGGTGTG AATTCACAGT GCCACTCATC TCCCATCTCC 360  
 AGTAAATGTG AAAGAGGCCG GATATGTTAG

Seq ID NO: 432 Protein sequence

Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
 MRFSVSGMRT DYPRSVLAPA YVSVCLLLLC PREVIAPAGS EPWLCQPAPR CGDKIYNPLE 60  
 QCCYNDAIVS LSETRQCGPP CTFWPCFELC CLDSFGLTND FVVKLVQGV NSQCHSSPIS 120  
 SKCERGRIC

Seq ID NO: 433 DNA sequence

Nucleic Acid Accession #: NM\_007231.1  
Coding sequence: 89..2017

1 11 21 31 41 51  
 60 TAGGAACAGG GGAGAGTGCA CCTGCTACCA GTCAAGCTCA GCCAGACTGC AAGAGGAGGC 60  
 GAGCGGAGC CAGCCGAGGG AGTGAACCAT GGACAAGTGG AAATGCCCGA GTTCTCTCAA 120  
 GTGACGGGAG AAGGAGAAAG TGTGCGCTTC ATCAGAGAAT TTCCATGTTG GTGAAAATGA 180  
 TGAGAAATCAG GACCGTGGTA ACTGGTCCAA AAAATCGGAT TATCTTCTAT CTATGATTGG 240  
 65 ATACGCAGTG GGATTAGGAA ATGTGTGGAG ATTTCCATAT CTGACCTACA GCAATGGTGG 300  
 AGGCGCCTTC TTGATACCTT ATGCAATTAT GTTAGCATTG GCTGGTTTAC CTTTGTCTCT 360  
 TCTGGAGTGT TCACTGGGAC AATTGCTAG CTTAGGTCCA GTTTCAGTTT GGAGGATTCT 420  
 TCCATGTGTT CAAGGTGTGG GAATTACAAT GGTCTGTATC TCCATTTTIG TGACAATCTA 480  
 TTACAATGTC ATAATTGCCT ATAGTCTTTA CTACATGTTT GCTTCTTTTC AAAGTGAAC 540  
 70 ACCATGGAAA AATTGTCTCT CGTGGTCAGA TAAAACTGT AGCAGATCAC CAATAGTAAC 600  
 TCACTGTAAT GTGAGTACAG TGAATAAAGG AATACAAGAG ATCATCCAAA TGAATAAAG 660  
 CTGGGTAGAC ATCAACAATT TTACCTGCAT CAACGGCAGT GAAATTTATC AGCCAGGGCA 720  
 GCTTCCCACT GAACAATATT GGAATAAAGT GGCCTCCAA CGGTCAAGTG GAATGAATGA 780  
 GACTGGAGTA ATTGTTTGGT ATTTAGCACT TTGTCTTCTT CTGGCTTGGC TCATAGTTGG 840  
 75 AGCAGCACTA TTTAAGGAA TCAAAATCGT TGGCAAGGTG GTATATTTTA CAGCTCTTTT 900  
 CCCCTATGTG GTCCCTACTCA TCCTGTGTAGT ACGAGGTGCA ACTCTGGAGG GTGCTTCAA 960  
 AGGCATTTC TACTATATTG GAGCCAGTC AAATTTTACA AAACCTAAGG AAGCTGAGGT 1020  
 ATGGAAAGAT GCTGCCACTC AGATATTTTA CTCCCTTTCA GTGGCTTGGG GTGGCTTAGT 1080  
 TGCTCTATCA TCTTACAATA AGTTCAAAA CAACTGCTTC TCTGATGCCA TTGTGGTTTG 1140  
 80 TTTGACAAAC TGTCTCACTA CGGTGTTTGC TGGATTGCT ATTTTCTCTA TATTGGGACA 1200  
 CATGGCCCAT ATATCTGGAA AGGAAGTTTC TCAAGTTGTA AAATCAGGTT TTGATTGGC 1260  
 ATTCAATGCC TATCCAGAGG CTCTAGCCCA ACTCCAGGT GGTCCATTTT GGTCCATATT 1320  
 ATTTTCTTCA ATGCTTTTAA CTTTGGGTCT CGATTCTCAG TTTGCTTCA TTTGAAACGAT 1380  
 CACAACAACA ATTCAAGATT TATTCCCAA AGTGATGAAG AAAATGAGG TTCCCATAC 1440  
 TTTGGGTGTC TGCTTGGTTT TGTTCTCCT TGCTCTGCTC TGTGTGACTC AGGCTGAAT 1500

TTACTGGGTT CATCTGATTG ACCACTTCTG TGCTGGATGG GGCATTTTAA TTGCAGCTAT 1560  
 ACTGGAGCTA GTTGGAAATCA TCTGGATTTA TGGAGGGAAC AGATTCATTG AGGATACAGA 1620  
 AATGATGATT GGAGCAAAGA GGTGGATATT CTGGCTATGG TGGAGAGCTT GCTGGTTTGT 1680  
 AATTACGCCT ATCCCTTTGA TTGCAATATT TATCTGGTCA TTGGTGCAAT TTCATAGACC 1740  
 TAATTATGGC GCAATCCCAT ACCCTGACTG GGGAGTTGCT TTAGGCTGGT GTATGATTGT 1800  
 TTTCTGCATT ATTTGGATAC CAATTATGGC TATCATAAAA ATAATTCAGG CTAAAGGAAA 1860  
 CATCTTTCAA CGCCCTATAA GTTGTGTCAG ACCAGCTTCT AACTGGGGTC CATACCTGGA 1920  
 ACAACATCGT GGGGAAAGAT ATAAAGACAT GGTAGATCCT AAAAAAGAGG CTGACCATGA 1980  
 AATACCTACT GTTAGTGGCA GCAGAAACC GGAATGAGAT CTCATTGAAA AAAATATATG 2040  
 ATTGTATAAT GTGATTTTTT TTAGAATAGG GGGAACTTGA TTTATTGTG TGTAACTGA 2100  
 ATAGGAAAAA GTACATACTA TGTTCATGAT AGTGTGATTT TTTTCACATT TAAGCAGGAA 2160  
 TGCAATATAA AAATGTGAAT CTCTTAATTC TCAGCCATGT GCTTATTATA TTTCTTTTAA 2220  
 GATTGTCTAT CTGTATAACA CACACACACA CACCTAAGAG TCCTATTTC ACAATTATAT 2280  
 TTTTGTAAAT AGTATATGCA TTTTAAATAC ATTGGAGGCT TTATTTTGAA CTAATTCTCT 2340  
 AGAGAATAGT TATATTTTCT ATTACACAAG TTAAAAATA TTATTAACCT GTATTTTCTT 2400  
 AATATACAAT CTATCTTTTC CACAAATATG AGTGGGAAAT AAATCAGCAC ATTTGAAAGA 2460  
 AAGTGTTAAA ACTGAAGGCC TCACCTTAAT AGAAACGTGA TAAATATATG GACAAATGGA 2520  
 CTATACATAC TATAAGAGGA CTGTAGTTTA ATACTTTTGA CCCAAATATG TTTAAAAACA 2580  
 TCGTGCATTT GTTACAGCTC ATGTTTTCTA TATGAACCTA GTCATTAAATG TTCITTATAA 2640  
 AAAGTGAAAT AAGATGGAAG AATTAGGATC CTACAGCCAG TACGTGATAA ATCTAGAAAA 2700  
 TTGAGTTTTG AGTACCTCTT TTCCCATATA CAATCTTCTC TCCTTAGGTA ATTTGGAAGA 2760  
 AAACATGAC CCATTTAATT TCTATTGTGT TTCACCAAAAT TCAGTGTGTG TCATTATACC 2820  
 TCTCTGAAAT ATAGGTTTAA TTTCAAAATG AATATGGACT TAAATGTTAA TGAGAAACTG 2880  
 GCTTTAATCA ATCTTAGCAT TTTTATTCTG TAATACAGGG CTGATAGAGT GATTTTGTCT 2940  
 TATATGAGTC AGTTACTACT TACAGGTGAT AACTTGCTA CTATTGGAAG ATAAAGTTGT 3000  
 CAAACTGTGC AAGAATGAGA AAAGCCAAAT TAGAAATCC TATGTCCTAG TTTCTTACC 3060  
 AAGGATAATT AAATATATCA CTAAGAGCTT TATATATTGA TTATATATTG TTGCAACTG 3120  
 GTTTAAGCAT CATAGCCTAT GATGATAAAC ACTGCCTATA TATGTAAATA GCTTTTCATC 3180  
 AATTCTTAAA TTTCTTAACC TAGGCTTCAG GGAGCATATG AAACCAAAAT TATATGGAAC 3240  
 ATTTTCTGTG TGTACATGTA CATGCAATTT TCTAGGGAGA GAGTCCGTAG GTTTATCAGA 3300  
 ATATCAAGGA AAACGTGTAC CCAAGAAGT TTAAGAATCA CATACAGTGC TGCTGGCTTT 3360  
 TTGTGCTTGG CAAATGAGTG ACAATAGAAG AAATAAATTT TCTTACACAT TTTAAAACGT 3420  
 TTTCTCTTCC TTGTGATTGA AGATGAAAGG AGTAAGAAAT TAAGGCATTT GTTTAATTAA 3480  
 TACTGGTAAC TTATTAGGG GGGAGGGGAC ATGAAGGTAG GTAATAGGT AGGCCTCTAA 3540  
 TTGAACCACT TCTCTAAGTT ATGTACGTAT ATATAAGCTG AAATGTGTGT TGACATTCTG 3600  
 AGGGTTTTCT TTTTCTTTTT CCTTTTTTTT TTTTGTGGT GGGGGGCTGG GGGTCAGAGT 3660  
 CTGTCTCTGT TGCCCTGGGT GGAGTGCAGT GGCATGATCT CAGCTCACTG CAACCTCTGC 3720  
 CTTCGGAATT CAAATGATTC TCTGCTCA GCCTCTGAG TAGCTGGGAC TACAGGTGCC 3780  
 CGCCACCACA CCAGCTAATT TTTGTATTTT TAGTAGAGGC GAAGTTTCCC CATGTTGGCC 3840  
 AGGCTGGTCT TGAACCTCCG ACCTCAAGTG ATCTGTCTAC CTCGGCCTCC TAAAGTGCTG 3900  
 AGAATACAGG TGTAGCCAC CGTGCCCGGC CCATCTAAG GGTTTTCTTT GAAGACAGGT 3960  
 CAAATGCTGT TAGTAAGTTT CAGGAGATTG TTAATTCCTC AGTTATACCA GATTTTATAA 4020  
 AATATTGAG AATAGATGGC TAACAAGAGG TTAGAAATAC TTTTCCTTAA TTTTAAATCCA 4080  
 CAGTATGTTA CATGCATTCT ACCACTACAT TTGGTGCTA TTTAAGGTGT GCAATTTTCT 4140  
 ATAGGTGACT TTTGCAATT AGGGAAGATT TGGGCATATT AAATGAAAGA ATATCTAATT 4200  
 GGGGGAGGTG TGAAGGAAA GAAATCTTT TCAAAAGCTG ACCACAAAGA GTAGTTAAAA 4260  
 GTTTTTGTCA CTATCTTAC AAGTGTGTA AGCACAGATT TCAACAGAGT GCTTGGCATA 4320  
 TTGTAGGGTG CTCAATGGTG GTTTTATTA TTATTACTCA GATTCCACAG TGGCAAGAAA 4380  
 CATCATCTA CATAATGGAA AACATTTACA TCAATCCCA CTACTTTAA TGCGAACTTG 4440  
 GAGATAATT ATGGTATTGT ATTGTAAACC ATTAATGAAA ACTTTTTCAC AGTTGAGTGA 4500  
 AATTAATC ACTATATCTC

Seq ID NO: 434 Protein sequence  
 Protein Accession #: NP\_009162.1

1 11 21 31 41 51  
 MDKCLKPSFF KCREKEKVSA SSENPHVGEN DENQDRGNWS KKS DYLLSMI GYAVGLGNVW 60  
 RFPYLTYNSG GGAFLIPYAI MLALAGLPLF FLECSLGQFA SLGPVSVWRI LPLFQGVGIT 120  
 MVLISIFVTI YYNVIAIYSL YYMFASFQSE LPWKNCSSWS DKNCRSPIV THCNVSTVVK 180  
 GIQEIIMNK SWVDINNFTC INGSEIYQPG QLPSEQYWNK VALQRSSGMN ETGVIVWYLA 240  
 LCLLLAWLIV GAALFKGIKS SGKVVFYFAL FPYVLLILL VRGATLEGAS KGISYYIGAQ 300  
 SNFTKLKEAE VVKDAATQIF YSLSVWAGGL VALSSYNKFK NNCFSDAIVV CLTNCLTSVF 360  
 AGFAIFSILG HMAHISGKEV SQVVKSGFDL AFIAYPEALA QLPGGPFWSI LFFFMLLTLG 420  
 LDSQFASIE ITTTIQDLFP KVMKKMRVPI TLGCLLVLF LGLVCVTQAG IYVHVLIDHF 480  
 CAGWGILIAE ILELVGIWI YGGRNFIEDT EMMIGAKRWI FWLWWRACWF VITPILLIAI 540  
 FIWSLVQFHR PNYGAIPYD WGVALGWCM VFCIIWIPIM AIIKIIQAKG NIFQRLISCC 600  
 RPASNWGPYL EQHRGERYKD MVDPKKEADH EIPTVSGSRK PE

Seq ID NO: 435 DNA sequence  
 Nucleic Acid Accession #: M18728.1  
 Coding sequence: 51..1085

1 11 21 31 41 51  
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60  
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120  
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180  
 ATGTCGCAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAA CCTGCCCCAG AATCGTATTG 240  
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300  
 TAGGAACCTA ACAAGCTCAC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360  
 ATGCATCCCT GCTGATCCAG AACGTACACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420  
 TCATAAGATC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGAGAC 480  
 TGCCCAAGCC CTCCATCTCC AGCAACAAC CCAACCCCGT GGAGGACAAG GATGCTGTGG 540

CCTTCACCTG TGAACCTGAG GTTCAGAAACA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600  
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCCTC ACTCTACTCA 660  
 GCCTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720  
 ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCTC 780  
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840  
 ACCCACTGCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900  
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960  
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020  
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080  
 TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140  
 GAATTCCTCT AGCTCCCTCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200  
 CTCGTCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA 1260  
 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAAC TAGAGA CAGTCAAAC 1320  
 GCAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380  
 AACAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440  
 TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500  
 GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAAAAG 1560  
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620  
 AAATGTACAG TGGTCTTTT CAGAGTTGGA CTCTAGACT CACCTGTCTC CACTCCCTGT 1680  
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740  
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAACAT GGCTAAATAC AATGGGTATC 1800  
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATAGG CTACACTCAT 1860  
 CTGACTCAT TTTTATTCTA TTTTGTGTTG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920  
 CTCTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980  
 CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040  
 GGCTGGAATT ACAAAACCTA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100  
 ATAAAGGCC CAAATGGTGG TAACGTGATA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160  
 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220  
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAATTTAAAA AAAAAAAGA 2280  
 ACACAGGAGA TTCCAGTCTA CTGTAGTTAG CATAATACAG AAGTCCCCTC TACTTTAACT 2340  
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400  
 TGTTCCTTTC TTCCAATTG ACAAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460  
 CTATCACTGT ACTTGTAGAG TGGTGTCTGT TTAATTCATA AATCACAAAT AAAAGCCAAT 2520  
 TAGCTCTATA ACT

Seq ID NO: 436 Protein sequence  
 Protein Accession #: AAA59907.1

1 11 21 31 41 51  
 MGPPSAPPCR LHPVPWKEVLL TASLLTFWNP PTTAKLTIES TPFNVAEGKE VLLLAHNLPO 60  
 NRIGYSWYKG ERVDGNLIV GYVIGTQQAT PGPAYSGRET IYPNASLLIQ NVTQNDTGFY 120  
 TLQVIKSDLV NEBATQQFHV YPELPKPSIS SNNSNPVEDK DAVAFTEPE VQNTTYLWVW 180  
 NGQSLPVSPP LQLSNGNMTL TLLSVKRNDG GSYECEIQNP ASANRSDPVT LNVLYGPDVP 240  
 TISPSKANYR PGENLNLSCH AASNPPAQYS WFINGTFQQS TQELFIPNIT VNNSGSYMCO 300  
 AHNATGLNR TTVMTITVSG SAPVLSAVAT VGITIGVLAR VALI

Seq ID NO: 437 DNA sequence  
 Nucleic Acid Accession #: M18728.1  
 Coding sequence: 1355..1657

1 11 21 31 41 51  
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60  
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCCCTGCTC ACAGCCTCAC 120  
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180  
 ATGTGCGAGA GGGGAAGGAG GTTCTTCTAC TCGCCCAACA CCTGCCCCAG AATCGTATTG 240  
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300  
 TAGGAACCTA ACTAGTACTC CCAGGGCCCC CATACAGTGG TCGAGAGACA ATATACCCCA 360  
 ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACAAG 420  
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCCGACA GTTCCATGTA TACCCGGAGC 480  
 TGCCCAAGCC CTCCTATCTC AGCAACAACCT CCAACCCCGT GGAGGACAAG GATGCTGTGG 540  
 CCTTCACCTG TGAACCTGAG GTTCAGAAACA CAACCTACCT GTGTGGGTA AATGGTCAGA 600  
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCCTC ACTCTACTCA 660  
 GCGTCAAAAG AACCATGACA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720  
 ACCGCAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCTC 780  
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCCTGCCAC GCAGCCTCTA 840  
 ACCCACTGCG ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900  
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960  
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020  
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080  
 TATAGCAGCC CTGGTGTATT TTCGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140  
 GAATTCCTCT AGCTCCCTCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200  
 CTCGTCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAATT TAAAGGGAAA 1260  
 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAAC TAGAGA CAGTCAAAC 1320  
 GCAAACCATG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380  
 AACAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTGTCTCT TGCTTATGCC 1440  
 TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500  
 GGGTAACCTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTTAC ATAAAAAAG 1560  
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTC 1620  
 AAATGTACAG TGGTCTTTT CAGAGTTGGA CTCTAGACT CACCTGTCTC CACTCCCTGT 1680  
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740  
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAACAT GGCTAAATAC AATGGGTATC 1800  
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATAGG CTACACTCAT 1860

CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920  
 CTCTTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980  
 CTCTAAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040  
 GGCTGGAATT ACAAAAGTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100  
 ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160  
 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220  
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAATTTAAAA AAAAAAAGA 2280  
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTCT TACTTTAACT 2340  
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400  
 TGTTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460  
 CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAAT AAAAGCCAAT 2520  
 TAGCTCTATA ACT

Seq ID NO: 438 Protein sequence  
 Protein Accession #: AAA59908.1

1 11 21 31 41 51  
 | | | | | |  
 MDSFSQDVKT RLLIMIRLLP PFNLSLLMPA SFAWQDDAVI SISQEVASEG NLTECQIYLV 60  
 NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELDF

Seq ID NO: 439 DNA sequence  
 Nucleic Acid Accession #: M18728.1  
 Coding sequence: 2370..2501

1 11 21 31 41 51  
 | | | | | |  
 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60  
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120  
 TTCTAACCTT CTGGAACCCA CCCACCACTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180  
 ATGTCGCAGA GGGGAAGGAG GTTCTTCTAC TCGCCACAAA CCTGCCCCAG AATCGTATTG 240  
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300  
 TAGGAAGTCA ACAGAGCTACC CCAGGGCCCG CATACAGTGG TCGAGAGACA ATATACCCCA 360  
 ATGCATCCCT GCTGATCCAG AACGTCACCC AGAATGACAC AGGATTCTAT ACCCTACAAG 420  
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCCGACA GTTCCATGTA TACCCGGAGC 480  
 TGCCCAAGCC CTCCTACTCC AGCAACCACT CCAACCCCGT GGAGGACAAG GATGCTGTGG 540  
 CCTTCACCTG TGAACCTGAG GTTCAGAACCA CAACCTACCT GTGGTGGGTA AATGGTCAGA 600  
 GCCTCCCGGT CAGTCCCAGG CTGCAGCTGT CCAATGGCAA CATGACCCTC ACTCTACTCA 660  
 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAAT ACAGAACCCA GCGAGTGCCA 720  
 ACCGCAAGTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTCCCC 780  
 CCTCAAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCAC GCAGCCTCTA 840  
 ACCCACCTGC ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900  
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCATAACT 960  
 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCCTG 1020  
 TCCTCTCAGC TGTGGCCACC GTCGGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080  
 TATAGCAGCC CTGGTGATT TTCGATATT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140  
 GAATCTTCT AGCTCCTCCA ATCCCATT TATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200  
 CTCGTCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAATC AATGAAAT TAAAGGGAAA 1260  
 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAAT 1320  
 GCAACCATG CTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380  
 AACAGACTC CTCATCATGA TAAGGCTCTT ACCCCCTTTT AATTTGTCCT TGCTTATGCC 1440  
 TGCCTCTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAGAAG TAGCTTCAGA 1500  
 GGGTAACCTTA ACAGAGTGTG AGATCTATCT TGTCAATCCC AACGTTTAC ATAAAAAAG 1560  
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CCGTGTGTTT 1620  
 AAATGTACAG TGGTCCCTTT CAGAGTTGGA CTCTAGACT CACCTGTTCT CACTCCCTGT 1680  
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740  
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAAACAT GGCTAAATAC AATGGGTATC 1800  
 GCTGAGACTA AGTGTAGTAA ATTAACAAAT GTGCTGCTTG GTTAAATGG CTACACTCAT 1860  
 CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920  
 CTCTTGGTAT TACCCTCCTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980  
 CTCFAAAGC TTTAAATGTC TGCATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040  
 GGCTGGAATT ACAAAAGTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100  
 ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160  
 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACTGAAAT 2220  
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAAA CAATTTAAAA AAAAAAAGA 2280  
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTCT TACTTTAACT 2340  
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCAA TGTATTATT TCTGTGGTTC 2400  
 TGTTTCCTTG TTCCAATTG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460  
 CTATCACTGT ACTGTAGAG TGGTGCTGCT TTAATTCATA AATCACAAAT AAAAGCCAAT 2520  
 TAGCTCTATA ACT

Seq ID NO: 440 Protein sequence  
 Protein Accession #: AAA59909.1

1 11 21 31 41 51  
 | | | | | |  
 MLTNVFISVV LFPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

Seq ID NO: 441 DNA sequence  
 Nucleic Acid Accession #: NM\_002381.2  
 Coding sequence: 64..1524

1 11 21 31 41 51

	1	11	21	31	41	51	
	AAATCCGAGC	CTCGCGTGGG	CTCCTGGCCC	CCGACGGACA	CCACCAGGCC	CACGGAGCCC	60
	ACCATGCCGC	GCCCGGCCCC	CGCGCGCCGC	CTCCCGGGAC	TCCTCCTGCT	GCTCTGGCCG	120
5	CTGCTGCTGC	TGCCCTCCGC	CGCCCCCGAC	CCCGTGGCCC	GCCCGGGCTT	CCGGAGGCTG	180
	GAGACCCGAG	GTCCCGGGGG	CAGCCCTGGA	CGCCGCCCTT	CTCCTGCGGC	TCCCGACGGC	240
	GCGCCCGCTT	CCGGGACCAG	CGAGCCTGGC	CGCGCCCGCG	GTGCAGGTGT	TTGCAAGAGC	300
	AGACCCCTGG	ACCTGGTGT	TATCATTGAT	AGTTCTCGTA	GCGTACGGCC	CCTGGAATTC	360
	ACCAAAGTGA	AAACTTTTGT	CTCCCGGATA	ATCGACACTC	TGGACATTGG	GCCAGCCGAC	420
10	ACGCGGGTGG	CAGTGGTGAA	CTATGCTAGC	ACTGTGAAGA	TCGAGTTCCA	ACTCCAGGCC	480
	TACACAGATA	AGCAGTCCCT	GAAGCAGGCT	GTGGGTGAA	TCACACCTTT	GTCAACAGGC	540
	ACCATGTGAG	GCCTTAGCAT	CCAGACAGCA	ATGGACGAAG	CCTTCACAGT	GGAGGCAGGG	600
	GCTCGAGAGC	CCTCTTCTAA	CATCCCTAAG	GTGGCCATCA	TTGTTACAGA	TGGGAGGCC	660
	CAGGACCAGG	TGAATGAAGT	GGCGGCTCGG	GCCCAAGCAT	CTGGTATTGA	GCTCTATGCT	720
15	GTGGGCGTGG	ACCGGGCAGA	CATGGCGTCC	CTCAAGATGA	TGGCCAGTGA	GCCCTTAGAG	780
	GAGCATGTTT	TCTACGTGGA	GACCTATGGG	GTCAATTGAGA	AACTTTCCTC	TAGATTCCAG	840
	GAAACCTTCT	GTGCGCTGGG	CCCCTGTGTG	CTTGAACAC	ACCAAGTCCA	GCACGTCTGC	900
	ATCAGTGATG	GGGAAGGCAA	GCACCACTGT	GAGTGTAGCC	AAGGATACAC	CTTGAATGCC	960
	GACAAGAAAA	CGTGTTCAGC	TCTTGATAGG	TGTGCTCTTA	ACACCCACGG	ATGTGAGCAC	1020
20	ATCTGTGTGA	ATGACAGAGA	TGGCTCTTAT	CATTGTGAGT	GCTATGAAGG	TTATACCTTG	1080
	AATGAAGACA	GGAAACTTGG	TTCAGCTCAA	GATAAATGTG	CTTTGGGTAC	CCATGGGTGT	1140
	CAGCACATTT	GTGTGAATGA	CAGAACAGGG	TCCCATCATT	GTGAATGCTA	TGAGGGCTAC	1200
	ACTCTGAATG	CAGATAAAAA	AACATGTTCA	GTCCGTGACA	AGTGTGCCCT	AGGCTCTCAT	1260
	GGTTGCCAGC	ACATTTTGTG	GAGTGATGGG	GCCGCATCCT	ACCACTGTGA	TTGCTATCCT	1320
25	GGCTACACCT	TAAATGAGGA	CAAGAAAAACA	TGTTTCAAGG	CTGAGGAAGC	ACGAAGACTT	1380
	GTTTCCACTG	AAGATGCTTG	TGGATGTGAA	GCTACACTGG	CATTCCAGGA	CAAGGTGAGC	1440
	TCGTATCTTC	AAAGACTGAA	CACTAAACTT	GATGACATTT	TGGAGAAGTT	GAAAATAAAT	1500
	GAATATGAGC	AAATACATCG	TTAAATTGCT	CCAATTTCTC	ACCTGAAAAA	GTGACAGAGT	1560
	TGGTGTACTT	AATACCTATG	CATTCTTTTG	CACACCTGTT	ATTGCCAATG	TTCTGTCTAA	1620
30	TAATTTGCCA	TTATCTGTAT	TAATGCTTGA	ATATTACTGG	ATAAATTTGA	TGAAGATCTT	1680
	CTGCAGAAAT	AGCATGATT	TTCCAAGGAA	ATACATATGC	AGATACTTAT	TAAGAGCAAA	1740
	CTTTAGTGTC	TCTAAGTTAT	GACTGTGAAA	TGATTGGTAG	GAAATAGAAT	GAAAAGTTTA	1800
	GTGTTTCTTT	ATCTACTAAT	TGAGCCATTT	AATTTTAAAA	TGTTTATATT	AGATAACCAT	1860
	ATTCACAATG	GAAACTTTAG	GCTAGTTTTC	TTTTGATAGT	ATTTATAATA	TAAATCAATC	1920
35	TTATTACTGA	GAGTGCAAA	TGTACAAGGT	ATTTACACAT	ACAACCTCAT	ATAACTGAGA	1980
	TGAATGTAAT	TTGAACTGT	TTAACACTTT	TTGTTTTTTG	CTTATTTTGT	TGGAGTATTA	2040
	TTGAAGATGT	GATCAATAGA	TTGTAATACA	CATATCTAAA	AATAGTTAAC	ACAGATCAAG	2100
	TGAACATTAC	ATTGCCATTT	TTAATTCATT	CTGGTCTTTG	AAAGAAATGT	ACTACTAAAG	2160
	AGCACTAGTT	GTGAATTTAG	GGTGTAAAC	TTTTTACCAA	GTACAAAAAT	CCCAAAATTC	2220
40	CTTTATTATT	TTGCTTCAGG	ATCCAAGTGA	CAAAGTTATA	TATTTATATA	ATTGCTATAA	2280
	ATCGACAAAA	TCTAATGTTG	TCTTTTTTAA	GTTAGTGATC	CACCTGCCCT	AGCCTCCCAA	2340
	AGTGCTGGGA	TTACAGGCTT	GAAAGTCTAA	CTTTTTTTTA	CTTATATATT	TGATACATAT	2400
	AATTCTTTTG	GCTTTGAAAC	TTGCAACTTT	GAGAACAAAA	CAGTCCCTTA	AATTTTGCAC	2460
	TGCTCAATTC	TGTTTTTCGT	TTGCATTGTC	TTTAATATAA	TAAAGTTTAT	TACCTTTACA	2520
45	TATTATCATG	TCTATTTTGG	ATGACTCATC	AATTTTGCT	ATTAAAGATA	TTTCTTTAAA	2580
	TTAAAAAAA	AAAAAAA					

Seq ID NO: 442 Protein sequence  
Protein Accession #: NP\_002372.1

	1	11	21	31	41	51	
	MPRPAPARRL	PGLLLLLLWPL	LLLPSAAPDP	VARPGFRRLE	TRGPGGSPGR	RPSAPAPDGA	60
	PASGTSEPR	ARGAGVCKSR	PLDLVFIIDS	SRSVRPLEFT	KVKTFVSRIL	DTLDIGPADT	120
55	RVAVVNYAST	TKIEFLQAY	TDKQLKQAV	GRITPLSTGT	MSGLAIQTAM	DEAFTEVAGA	180
	REPSSNIPKV	AIIVTDGRPQ	DQVNEVAARA	QASGIELYAV	GVDRADMASL	KMMASEPLEE	240
	HVFYVETYG	IEKLSSRFQ	TFCALDPCVL	GTHQCQHVCI	SDGEGKIHCE	CSQYTYLNAD	300
	KKTCALDR	ALNTHGCEHI	CVNDRSGSYH	CECYEGYTLN	EDRKTCSAQD	KCALGTHGCG	360
	HICVNDRG	HHCECYEGT	LNADKKTCSV	RDKCALGSHG	CQHICVSDGA	ASYHCDCYFG	420
60	YTLNEDKKT	SATEEARRLV	STEDACGCEA	TLAFQDKVSS	YLQRLNKTLD	DILEKLKINE	480
	YQIHR						

Seq ID NO: 443 DNA sequence  
Nucleic Acid Accession #: NM\_016639.1  
Coding sequence: 40..429

	1	11	21	31	41	51	
	GCGGCGGGCG	CAGACAGCGG	CGGGCGCAGG	ACGTGCACTA	TGGCTCGGGG	CTCGCTGCGC	60
	CGGTGCTGCG	GGCTCCTCGT	GCTGGGGCTC	TGGCTGGCGT	TGCTGCGCTC	CGTGGCCGGG	120
70	GAGCAAGCGC	CAGGCACCGC	CCCCTGCTCC	CGCGGCAGCT	CCTGGAGCGC	GGACCTGGAC	180
	AAGTGCAATG	ACTGCGCGTC	TTGCAAGGCG	CGACCGCACA	GCGACTTCTG	CCTGGGCTGC	240
	GCTGCAGCAG	CTCTGCGCCC	CTTCCGGCTG	CTTTGGGCCA	TCCTTGGGGG	CGCTCTGAGC	300
	CTGACCTTCG	TGCTGGGGCT	GCTTCTGCG	TTTTTGGTCT	GGAGACGATG	CCGACGAGAG	360
	GAGAAAGTTA	CCACCCCATC	AGAGGAGACC	GGCGGAGAGG	GCTGCCACGC	TGTGGCGCTG	420
75	ATCCAGTGAC	AATGTGCCCC	CTGCCAGCCG	GGGCTCGCCC	ACTCATCATT	CATTATCCAA	480
	TTCTAGAGCC	AGTCTCTGCC	TCCACAGCGC	GGCGGGAGCC	AAGCTCCTCC	AACCACAAGG	540
	GGGGTGGGGG	GCGGTGAATC	ACCTCTGAGG	CCTGGGCCCA	GGGTTCAGGG	GAACCTTCCA	600
	AGGTGTCTGG	TTGCCCTGCC	TCTGGCTCCA	GAACAGAAAG	GGAGCCTCAC	GCTGGCTCAC	660
80	ACAAACACAG	TGACACTGAC	TAAGGAACTG	CAGCATTTGC	ACAGGGGAGG	GGGGTGCCTT	720
	CCTTCTCTAG	GACCTGGGGG	CCAGGCTGAC	TTGGGGGGCA	GACTTGACAC	TAGGCCCCAC	780
	TCACCTAGAT	GTCTCTGAAAT	TCCACACGGG	GGGTCAACCT	GGGGGGTTAG	GGACCTATTT	840
	TTAACACTAG	GGGCTGGCCC	ACTAGGAGGG	CTGGCCCTAA	GATACAGACC	CCCCAACTC	900
	CCCAAGCGG	GGAGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAATTTATT	960



AATAAAAGAA TCTTTAACTT TAAAAA AAAA

Seq ID NO: 444 Protein sequence  
Protein Accession #: NP\_057723.1

1	11	21	31	41	51	
MARGSLRRLL	RLVLGLWL	LLRSVAGEQA	PGTAPCSRGS	SWSADLDKCM	DCASCRARPH	60
SDFCLGCAAA	PPAPFRLLWP	ILGALSILTF	VLGLLSGFLV	WRRCRREKFP	TTPIETTGGE	120
GCPAVALIQ						

Seq ID NO: 445 DNA sequence  
Nucleic Acid Accession #: AF322916.1  
Coding sequence: 50..4300

1	11	21	31	41	51	
GCACCTCCGCA	GCCTTTAAGG	TTCGCGCGGG	GGCCAGGCAA	GAGTTAGCCA	TGAAGAGCCT	60
CAAGTCCCGC	CTGAGGAGGC	AGGACGTGCC	CGGCCCGCG	TCGTCTGGCG	CCGCCCGCGC	120
CAGCGCGCAT	GCAGCAGATT	GGAATAAATA	TGATGACCGA	TTGATGAAAG	CAGCAGAAAG	180
GGGGGATGTA	GAAAAAGTGA	CCTCAATCCT	TGCTAAAAAG	GGGGTCAATC	CAGGCAAACT	240
AGATGTGGAA	GGCAGATCTG	TCTTCCATGT	TGTGACCTCA	AAGGGGAATC	TTGAGTGTTT	300
GAATGCCATC	CTTATACATG	GAGTTGATAT	TACAACCACT	GACACTGCAG	GGAGAAATGC	360
TCTTCACCTG	GCTGCTAAGT	ATGGACATGC	ATTGTGCCTA	CAAAAACCTC	TACAGTACAA	420
TTGTCCCACT	GAGCATGCAG	ACCTGACGGG	AAGAACTGCA	CTTCAAAAAA	AAGCAATGGC	480
AGATTGTCTT	TCTAGCATAC	AGCTGCTTTG	TGACCATGGG	GCCTCTGTGA	ATGCCAAAGA	540
TGTAAGGAGG	CGGACACCA	TTGTTCTGGC	TACTCAGATG	AGTAGGCCAA	CAATATGTCA	600
ACTGCTGATA	GATAGAGGAG	CGGATGTTAA	TTCCAGAGAC	AAACAAACA	GAAGTGCCTT	660
CATGCTAGGT	TGCGAATATG	GTTGCAGAGA	TGCAGTAGAA	GTCTTAATTA	AAAAATGGTG	720
TGATATAAGC	TTGCTGGATG	CGCTTGGCCA	TGATAGTTCT	TACTATGCAA	GAATTTGGTG	780
CAATCTGGAC	ATTCTAACCT	TGTTGAAGAC	TGCATCGGAA	AATACCAACA	AAGGGAGAGA	840
ACTTTGGAAG	AAAGGACCAT	CTTTGCAACA	CGGAAATTTG	ACACACATGC	AAGATGAAGT	900
AAATGTGAAG	TCACATCAGA	GGGAGCATCA	AAATATTCAG	GATTTGGAGA	TTGAAAATGA	960
AGATTGAAA	GAGAGGTTGA	GAAAAATTCA	GCAAGAACAA	AGAATACTTT	TGGATAAAGT	1020
CAATGGTTTA	CAGTTACAGC	TGAATGAGGA	AGTTATGGTT	GCTGATGATC	TGGAAGCGA	1080
GAGAGAAAAG	CTGAAGTCCC	TTTTGGCAGC	TAAAGAAAAG	CAACATGAAG	AAAGCTTAAG	1140
GACTATTGAG	GCTCTGAAAA	ATAGATTTAA	ATATTTTGAG	AGTGATCATT	TAGGATCAGG	1200
AGTCATTTC	AGTAACCGAA	AAGAAGATAT	GCTTCTTAAA	CAAGGTCAGA	TGTATATGGC	1260
AGACTCACAG	TCTACTTCCC	CAGGTATACC	AGCCCATATG	CAAGCAGATG	CTATGTTAAG	1320
ACCTCTGGAA	CTATCTTTAC	CCAGTCAAA	GTCATACTCT	GAAAATGAAA	TTTTAAAGAA	1380
AGAGTTAGAA	GCAATGCGAA	CTTTCTGTGA	GTCAGCAAAA	CAAGACCGAC	TGAAGCTCCA	1440
AAATGAACAT	GCACACAAAG	TGGCAGAAAT	CAAGCTTTTA	GCATTAGAA	GTGAAAGGGT	1500
CAAGGAGGAT	TCAGATGAAC	AGATAAAGCA	ATTAGAAGAT	GCATTAAAA	ATGTGCAGAA	1560
GAGGATGTAT	GAGTCAAGAG	GTAAGTTTAA	ACAAATGCGA	ACCCATTTTC	TTGCCCTTAA	1620
AGAACACTTA	ACAAGTGAAG	CAGCCTCAGG	GAATCACAGA	CTAACCGAGG	AACTGAAGGA	1680
TCAGTTGAAA	GACTTGAAAG	TAAAATATGA	AGGTGCTTCA	GCAGAGTGG	GGAAATTAAG	1740
AAACCAATC	AAACAAATG	AGATGATAGT	AGAAGAGTTT	AAGAGGGATG	AAGGCAAGCT	1800
GATAGAAGAA	AATAAGCGAT	TACAGAAGGA	ACTTAGTATG	TGTGAATGG	AGCGAGAGAA	1860
GAAAGGAAGA	AAGGTCACAG	AGATGGAAGG	CCAGGCCAAA	GAATTTGTCAG	CGAAGTTGGC	1920
CCTTTCCATT	CCAGCTGAAA	AATTTGAAAA	CATGAAGAGC	TCATTATCAA	ATGAAGTGAA	1980
TGAGAAAGCA	AAAAAATTAG	TAGAAATGGA	AAGAGAACAT	GAAAAATCAC	TTAGTGAAAT	2040
TAGACAGTTA	AGAGAGAAAC	TTGAGAAATG	TAAAGCCAA	CTTGCTCAGC	ACGTCAAAAC	2100
AGAGGAACAT	GAACAGGTTA	AGAGCAGATT	AGAACAGAAA	TCAGGAGAAC	TTGGGAAGAA	2160
GATCACTGAG	TTAACAATTG	AAAATCAGAC	ACTACAAAAG	GAAATTGAAA	AAAGTTTATT	2220
GGATAATAAG	CTCCTCAAGG	AGCAAGCACA	TAACTTAACA	ATTGAAATGA	AAAATCATT	2280
TGTTCCCTTA	AAAGTAAAGT	AAGACATGAA	AAAGTCACAT	GATGCAATTA	TTGATGATCT	2340
TAATAGAAAG	CTTTTAGATG	TAACACAAA	ATATACAGAA	AAGAAGTTGG	AAATGGAGAA	2400
ATTGCTACTG	GAAATAGACA	GCTTAAGTAA	GGATGTAAGC	CGCCTAGAAA	CTGTGTTTGT	2460
ACCTCCTGAG	AAACATGAAA	AAGAGATAAT	AGCTCTGAAA	TCCAATATTG	TTGAACCTTA	2520
GAAACAGCTG	TCTGAACTTA	AGAAAAATG	TGGTGAAGAC	CAGGAGAAAA	TACACGCTCT	2580
CACATCTGAA	AACACTAACT	TGAAGAAGAT	GATGAGTAAT	CAGTATGTGC	CAGTTAAAC	2640
CCATGAAGAG	GTTAAAAATG	CACTGAATGA	CACGTTAGCC	AAAACTAACA	GAGAATTATT	2700
AGATGTGAAG	AAAAAATTG	AAGATATAAA	TCAGGAATTT	GTAATAATAA	AAGATAAGAA	2760
TGAAATATTA	AAAAGAAAC	TGGAAAACAC	TCAGAACCAA	ATAAAGCTG	AGTACATCAG	2820
CCTGGCAGAG	CACGAGGCAA	AGATGAGCTC	GCTAAGTCAG	AGCATGAGAA	AGGTGCAGGA	2880
TAGTAATGCT	GAAATCTTGG	CCAACTACAG	AAAAGGCCAA	GAAGAGATTG	TGACACTGCA	2940
TGCCGAAATT	AAAGCCGAGA	AGAAGGAGCT	CGACACAATA	CAAGAAATGCA	TTAAGGTAAA	3000
ATATGCCCCA	ATTGTCTAGT	TTGAGGAGTG	CGAGAGAAAA	TTTAAAGCAA	CAGAGAAAGA	3060
ACTAAAGAC	CAGTTATCAG	AGCAGACACA	AAAGTATAGT	GTCAGTGAAG	AAGAAGTCAA	3120
GAAAAACAAG	CAAGAGAAAT	ACAAGTTAAA	GAAGGAGATT	TTTACCCTTC	AGAAAGATTT	3180
GAGAGATAAG	ACAGTTCTCA	TTGAGAAATG	TCATGAAATG	GAAAGAGCAT	TAAGCAGAAA	3240
AACAGACGAG	CTAACAAAC	AGTTAAAGAA	CTTGTCACAG	AAATACACGG	AAGTAAAGAA	3300
TGTGAAGAG	AAGCTAGTAG	AAGAAATGTC	CAACACAGCT	TCTGAGATAC	TTGCAGTGCA	3360
AAATCTTTTG	CAAAAACAAC	ATGTTCCATT	GGAACAGGTT	GAGGCTCTGA	AAAAATCTCT	3420
TAATGGCACA	ATTGAAATC	TAAAGGAAGA	ACTGAAGAGT	ATGCAAGAGT	GTTACGAGAA	3480
AGAGCAGCAG	ACAGTGACCA	AACTGCATCA	ATTGTTGGAG	AATCAAAAGA	ACTCTTCTGT	3540
ACCCTGCGCA	GAGCATTTGC	AGATTAAAGA	AGCATTGAG	AAAGAAGTTG	GAATCATAAA	3600
AGCCAGCTTG	AGAGAAAAGG	AAGAAGAAAG	CCAAAACAAA	ATGGAAGAAG	TCTCCAAACT	3660
TCAGTCGAG	GTTTCAGAA	CTAAACAAAG	ATTAACAAA	TTAGAGACTA	GAGAGGTAGT	3720
TGACTTGCTT	AAATATAAAG	CAACAAAAG	TGATTGGAG	ACACAGATTT	CTAGCTTAAA	3780
TGAAAAATGT	GCCAACTCTG	ATAGAAAGTA	TGAGGAAGTA	TGTGAGGAAG	TTTTGCATGC	3840
CAAAAAGAAG	GAAATATCTG	CAAAAGATGA	GAAGGAATTA	CTGCATTTCA	GCATTGAGCA	3900
AGAAATTAAG	GATCAGAAGG	AACGATGTGA	TAAGTCCTTA	ACAACAATCA	CAGAGTTACA	3960
AAGAAGAATA	CAAGAATCTG	CTAAACAAAT	AGAAGCAAAA	GATAATAAGA	TAACCTGAAT	4020

GCTTAATGAT GTGGAAAGAT TAAACAGGC ACTCAATGGC CTTTCCCAAC TCACCTACAC 4080  
 AAGTGGGAAC CCCACCAAGA GGCAGAGCCA GCTGATTGAC ACTCTGCAGC ACCAAGTGAA 4140  
 ATCTCTGGAG CAACAGCTGG CCGATGCTGA CAGACAGCAC CAAGAAGTAA TTGCAATTTA 4200  
 TCGGACACAC CTTCTTAGTG CTGCACAGGG TCACATGGAT GAAGATGTTT AGGAGGCTCT 4260  
 GCTCCAGATC ATACAAATGC GGCAGGGGCT TGTGTGCTAG CCGTTAGCAC TGACTGCCAG 4320  
 TATCTGTTTT ATCTTGCTGG TGCTGAACAT TCTTTGTGCA ACTCCATGGT CTTTCTGGGC 4380  
 CTTACTGTGC TGGTATAATT AAAATAAAAT ATATTTTGTG CTGGGTGT

Seq ID NO: 446 Protein sequence

Protein Accession #: AAG49577.1

1 11 21 31 41 51  
 | | | | |  
 MKSLKSRLRR QDVPGPASSG AAAASAHAA WNKYDDRLMK AAERGDVEKV TSILAKKGVN 60  
 PGKLDVBRGS VFHVVTSGKN LECLNAILIH GVDITTSDDTA GRNALHLAAK YGHALCLQKL 120  
 LQYNCPTEHA DLQGRRTALQK KAMADCPSSI QLLCDHGASV NAKDVKGRTP LVLATQMSRP 180  
 TICQLLIDRG ADVNSRDQKN RTALMLGCEY GCRDAVEVLI KNGADISLLD ALGHDSSYYA 240  
 RIGDNLIDLT LLKTASENTN KGRRLWKKGP SLQQRNLTHM QDEVNVKSHQ REHQNIQDLE 300  
 IENEDLKERL RKIQQEQIRIL LDKVNGLQLO LNEEVMVADD LESEREKLKS LLAKEKQHE 360  
 ESLRTIEALK NRFKYFESDH LSGSGSHFSNR KEDMLLKQGG MYMADSQCTS PGIPAHMQSR 420  
 SMRLPLELSL PSQTSYSENE ILKKELEAMR TFCESAKQDR LKLQNLHLAK VAECKALALE 480  
 CERVKEDSDE QIKQLEDALK DVQKRMYESE GKVKQMOTHF LALKEHLTSE AASGNHRLTE 540  
 ELKDQLKDLK VKYEGASAEV GKLRNQIKQN EMIVEEFKRD EGKLIENKR LQKELSMCEM 600  
 EREKKGKRVK EMEGQAKELS AKLALSIPAE KFNEMKSSLS NEVNEKAKKL VEMEREHEKS 660  
 LSIRQLKRE LENVKAQLAQ HVKPEEHEQV KSRLEQKSSE LGKKITELTL KNQTLQKEIE 720  
 KVLVDNKLK EQAHNLTIEM KNHYVPLKVS EDMKKSHDAI IDDLNRKLLD VTQKYTEKKL 780  
 EMEKLLLEND SLKSDVSRLE TVFVPPKEKE KEIIALKSNI VELKKQLSEL KKKCGEDQEK 840  
 IHALTSENTN LKMMNSQYV FVKTHEEVKM TLNDTLAKTN RELLDVKKKF EDINQEPVKI 900  
 KDKNEILKRN LENTQNQIKA EYISLAHEHA KMSSLSQSMR KVQDSNAEIL ANYRKQGEIE 960  
 VTLLHAETKAQ KKELDITQEC IKVKYAPIVS FEBCERKFKA TEKELKDQLS EQTKYSVSE 1020  
 BEVKNKQEN DKLKKEIFTL QKDLRDKTVL IEKSHEMERA LSRKTDELNK QLKDLSQKYT 1080  
 EVKNVKEKLV EENAKQTSEI LAVQNLLQKQ HVPLEQVEAL KKSLLNGTIEN LKEELKSMQR 1140  
 CYEKEQQTVT KLHQLLENQK NSSVPLAEHL QIKAEFEKEV GIIKASLREK EESQNKME 1200  
 VSKLQSEVQN TKQALKKLET REVVDLSKYK ATKSDLETQI SSLNEKLANL NRKYEEVCEE 1260  
 VLHAKKEIS AKDEKELLHF SIEQEIKDQK ERCDKSLTTI TELQRRIQES AKQIEAKDNK 1320  
 ITELNDVER LKQALNGLSQ LTYTSGNPTK RQSQLIDTLQ HQVKSLEQQL ADADRQHQEV 1380  
 IAIYRTHLLS AAQGHMDEDV QEALLQIIQM RQGLVC

Seq ID NO: 447 DNA sequence

Nucleic Acid Accession #: NM\_003020.1

Coding sequence: 29..664

1 11 21 31 41 51  
 | | | | |  
 CGCTCCTCGG GCTGCCCTC GGTGACAAT GGTCTCCAGG ATGGTCTCTA CCATGCTATC 60  
 TGGCCTACTG TTTTGGCTGG CATCTGGATG GACTCCAGCA TTTGCTTACA GCCCCGGAC 120  
 CCCTGACCGG GTCCTCAGAAG CAGATATCCA GAGGCTGCTT CATGGTGTTA TGGAGCAATT 180  
 GGGCATTGCC AGGCCCCGAG TGGAAATATCC AGCTCACCAG GCCATGAATC TTGTGGGCCC 240  
 CCAGAGCATT GAAGGTGGAG CTCATGAAGG ACTTCAGCAT TTGGGTCCTT TTGGCAACAT 300  
 CCCCAACATC GTGGCAGAGT TGACTGGAGA CAACATTCCCT AAGGACTTTA GTGAGGATCA 360  
 GGGGTACCCA GACCTCCAA ATCCTGTGCC TGTGGGAAAA ACAGATGATG GATGCTTAGA 420  
 AAACACCCCT GACACTGCAG AGTTCACTCG AGAGTTCCAG TTGCACCAGC ATCTCTTTGA 480  
 TCCGGAACAT GACTATCCAG GCTTGGGCAA GTGGAACAAG AAACCTCCTT ACGAGAAGAT 540  
 GAAGGGAGGA GAGAGACGAA AGCGGAGGAG TGTCAATCCA TATCTACAAG GACAGAGACT 600  
 GGATAATGTT GTTGCAAAGA AGTCTGTCCC CCATTTTTC AATGAGGATA AGGATCCAGA 660  
 GTAAAGAGAA GATGCTAGAC GAAACCCAC ATTACCTGTT AGGCCTCAGC ATGCTTTATG 720  
 TGCACGTGTA AATGGAGTCC CTGTGAATGA CAGCATGTTT CTTACATAGA TAATTATGGA 780  
 TACAAGACAG CTGTATGTAG ATAGTGTATT GTCTTCACAC CGATGATTC GCTTTTGTGT 840  
 AAATAGATAA AAGAGCTTTT TTGTTCTTGG GGTTTTAAAT ATGTGAATCT GCAATGATCA 900  
 TAAAAATTAA AATGTGAATG TCAACAATAA AAAGCAAGAC TATGAAAGGC TCAGATTTCT 960  
 TGCAGTTTAA AATGGTGTCT GAGGTGTGAC TATTTTGGCC AAGTCTGTAG AAAGCTGTCA 1020  
 TTTGATTTTG ATTATGTAGT TCATCCAGCC CTGGGCATT GTTATACACC AGTAAAGAAG 1080  
 GCTGTACTCA AGAGGAGGAG CTGACACATT TCACTTGGCT GCGTCTTAAT AAACATGAAT 1140  
 GCAAGCATTG GC

Seq ID NO: 448 Protein sequence

Protein Accession #: NP\_003011.1

1 11 21 31 41 51  
 | | | | |  
 MYSRMVSTML SGLLFWLASS WTPAFAYSPP TPDRVSEADI QRLHGVMEQ LGIARPRVEY 60  
 PAHQAMNLVG PQSIEGGAHE GLQHLGPFNG IPNIVAELET DNIPKDFSED QGYPDPPNFC 120  
 PVGKTDDGCL ENTPTDABFS REFQLHQHLE DPEHDYPGLG KWNKKLLYEK MKGGERRKRR 180  
 SVNPLYQGQR LDNVVAKKSV PHFSDEDKDF E

Seq ID NO: 449 DNA sequence

Nucleic Acid Accession #: NM\_003816.1

Coding sequence: 79..2538

1 11 21 31 41 51  
 | | | | |  
 CGGCAGGGTT GGAATATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60  
 CCTGCGGAAT CGGCCGAGAT GGGGTCTGGC GCGCGCTTTC CCTCGGGGAC CCTTCGTGTC 120  
 CGGTGGTTGC TGTGTCTTGG CTTGTTGGGC CCAGTCCTCG GTGCGCGCGC GCCAGGCTTC 180

	CAACAGACCT	CACATCTTTC	TTCTTATGAA	ATTATAACTC	CTTGGAGATT	AACTAGAGAA	240
	AGAAGAGAAG	CCCCTAGGCC	CTATTCAAAA	CAAGTATCTT	ATGTTATTCA	GGCTGAAGGA	300
	AAAGAGCATA	TTATTCACTT	GGAAAGGAAC	AAAGACCTTT	TGCCTGAAGA	TTTTGTGGTT	360
5	TATACTTACA	ACAAGGAAGG	GACTTTAATC	ACTGACCATC	CCAATATACA	GAATCATTTG	420
	CATTATCGGG	GCTATGTGGA	GGGAGTTTAT	AATTCATCCA	TTGCTCTTAG	CGACTGTTTT	480
	GGACTCAGAG	GATTGCTGCA	TTTAGAGAAT	GCGAGTTATG	GGATTGAACC	CCTGCAGAAC	540
	AGCTCTCATT	TTGAGCACAT	CATTTATCGA	ATGGATGATG	TCTACAAAGA	GCCTCTGAAA	600
	TGTGGAGTTT	CCAACAAGGA	TATAGAGAAA	GAAACTGCAA	AGGATGAAGA	GGAAGAGCCT	660
10	CCCAGCATGA	CTCAGCTACT	TCGAAGAAGA	AGAGCTGTCT	TGCCACAGAC	CCGGTATGTG	720
	GAGCTGTTCA	TTGTCTGAGA	CAAGGAAAGG	TATGACATGA	TGGGAAGAAA	TCAGACTGCT	780
	GTGAGAGAAG	AGATGATTCT	CCTGGCAAAC	TACTTGGATA	GTATGTATAT	TATGTTAAAT	840
	ATTCGAATTG	TGCTAGTTGG	ACTGGAGATT	TGGACCAATG	GAAACCTGAT	CAACATAGTT	900
	GGGGGTGCTG	GTGATGTGCT	GGGGAACCTC	GTGCAGTGGC	GGGAAAAGTT	TCTTATCACA	960
15	CGTCGGAGAC	ATGACAGTGC	ACAGCTAGTT	CTAAGAAAAG	GTTTTGGTGG	AACTGCAGGA	1020
	ATGGCATTGG	TGGGAACAGT	GTGTTCAAGG	AGCCACGCAG	GCGGGATTAA	TGTGTTTGGA	1080
	CAATTCACCTG	TGGAGACATT	TGCTTCCATT	GTGCTCATG	AATTGGGTCA	TAATCTTGGA	1140
	ATGAATCACG	ATGATGGGAG	AGATTGTTCC	TGTGGAGCAA	AGAGCTGCAT	CATGAATTCA	1200
	GGAGCATCGG	GTTCCAGAAA	CTTTAGCAGT	TGCAGTGCAG	AGGACTTTGA	GAAGTTAACT	1260
20	TTAAATAAAG	GAGGAACTG	CCTTCTTAAT	ATTCCAAAGC	CTGATGAAGC	CTATAGTGCT	1320
	CCCTCCTGTG	GTAATAAGTT	GGTGGACGCT	GGGGAAGAGT	GTGACTGTGG	TACTCCAAAG	1380
	GAATGTGAAT	TGGACCTTTG	CTGCGAAGGA	AGTACCTGTA	AGCTTAAATC	ATTTGCTGAG	1440
	TGTGCATATG	GTGACTGTTG	TAAAGACTGT	CGGTTCCCTC	CAGGAGGTAC	TTTATGCCGA	1500
	GGAAAAACCA	GTGAGTGTGA	TGTTCCAGAG	TACTGCAATG	GTTCTTCTCA	GTTCTGTGAG	1560
25	CCAGATGTTT	TTATTTCAGAA	TGGATATCCT	TGCCAGAATA	ACAAAGCCTA	TTGCTACAAAC	1620
	GGCATGTGCC	AGTATTTATG	TGCTCAATGT	CAAGTCATCT	TTGGCTCAAA	AGCCCAAGGCT	1680
	GGCCCAAAAG	ATTGTTTCAT	TGAAGTGAAT	TCTAAAGGTG	ACAGATTTTG	CAATTGTGGT	1740
	TTCTCTGGCA	ATGAATACAA	GAAAGTGTGCC	ACTGGGAATG	CTTTGTGTGG	AAAGCTTCAG	1800
	TGTGAGAAATG	TACAAGAGAT	ACCTGTATTT	GGAATTTGTG	CTGCTATTAT	TCAAACGCCT	1860
30	AGTCGAGGCA	CCAAATGTTG	GGGTGTGGAT	TTCCAGCTAG	GATCAGATGT	TCCAGATCCT	1920
	GGGATGGTTA	ACGAAGGCAC	AAAATGTGGT	GCTGGAAAAG	TCTGTAGAAA	CTTCCAGTGT	1980
	GTAGATGCTT	CTGTTCTGAA	TTATGACTGT	GATGTTTCAG	AAAAGTGTCA	TGGACATGGG	2040
	GTATGTAATA	GCAATAAGAA	TTGTCACTGT	GAAAATGGCT	GGGCTCCCCC	AAATTGTGAG	2100
	ACTAAAGGAT	ACGGAGGAAG	TGTGGACAGT	GGACCTACAT	ACAATGAAAT	GAATACTGCA	2160
35	TTGAGGGACG	GACTTCTGGT	CTTCTTCTTC	CTAATTGTTT	CCCTTATTGT	CTGTGCTATT	2220
	TTTATCTTCA	TCAAGAGGGA	TCAACTGTGG	AGAAGCTACT	TCAGAAAGAA	GAGATCACAA	2280
	ACATATGAGT	CAGATGGCAA	AAATCAAGCA	AACCTTCTTA	GACAGCCGGG	GAGTGTTCCT	2340
	CGACATGTTT	CTCCAGTGTG	ACCTCCACGA	GAAGTTCCTA	TATATGCAAA	CAGATTTGCA	2400
	GTACCAACCT	ATGCAGCCAA	GCAACCTCAG	CAGTTCCCAT	CAAGGCCACC	TCCACCACAA	2460
40	CCGAAAGTAT	CACTCAGGGG	AACTTAATT	CCTGCCCGTC	CTGCTCCTGC	ACCTCCTTTA	2520
	TATAGTTCCC	TCACTTGATT	TTTTTAACCT	TCTTTTGTGA	AATGTCCTCA	GGGAAGTGAG	2580
	CTAATACTTT	TTTTTTTCT	TGATGTTTTT	TTGAAAAGCC	TTTCTGTTGC	AACTATGAAT	2640
	GAAAACAAAT	CACCACAAAA	CAGACTTCAC	TAACACAGAA	AAACAGAAAC	TGAGTGTGAG	2700
	AGTTGTGAAA	TACAAGGAAA	TGCAGTAAAG	CCAGGGAATT	TACAATAACA	TTTCCGTTTC	2760
45	CATCATTGAA	TAAGTCTTAT	TCAGTCATCG	GTGAGGTTAA	TGCACATAAT	ATGGATTTTT	2820
	TGAACATGTT	ATTGCAATGA	TTCTCAAATT	AACGTGATTG	GTGTAAGATT	TTTGTCTATT	2880
	AGTGTGTAAG	TGTTATTTCT	AATTTTCTAC	CTTAGTTATC	ATTAATGTAG	TTCTCTATTG	2940
	AACATGTGAT	AACTAATAC	CTGTGAAAAC	TGACTAATCA	GCTGCCAATA	ATATCTAATA	3000
	TTTTTCATCA	TGCACGAATT	AATAATCATC	ATACTCTAGA	ATCTTGTCTG	TCACCTACTA	3060
50	CATGAATAAG	CAAAATATTG	CTTCAAAAGA	ATGCACAAGA	ACCACAATTA	AGATGTCATA	3120
	TTATTTTGAA	AGTACAAAAT	ATACTAAAAG	AGTGTGTGTG	TATTCACGCA	GTACTCGCT	3180
	TCCATTTTCA	TGACCTTTCA	ACTATAGGTA	ATAACTCTTA	GAGAAATTAA	TTTAATATTA	3240
	GAATTTCTAT	TATGAATCAT	GTGAAAGCAT	GACATTCGTT	CACAATAGCA	CTATTTTAAA	3300
	TAAATTATAA	GCTTTAAGGT	ACGAAGTATT	TAATAGATCT	AATCAAAAT	GTGATTCAT	3360
55	GGCTATAATA	AAGCAGGAGC	AATATAAAAA	TCTTCAATCA	ATTGAACTTT	TACAAAACCA	3420
	CTTGAGAAAT	TCATGAGCAC	TTTAAATCT	GAACTTTCAA	AGCTTGTCTAT	TAAATCATT	3480
	AGAATGTTTT	CATTATCTAA	GGTGTGCTGG	GTGATGTAAA	ATATTAGACA	CTAATATTTT	3540
	CATAGAAAT	AGGCTGGAGA	AAGAAGGAAG	AAATGGTTTT	CTTAAATACC	TACAAAAAAG	3600
	TTACTGTGGT	ATCTATGAGT	TATCATCTTA	GCTGTGTTAA	AAATGAATTT	TTACTATGGC	3660
60	AGATATGGTA	TGGATCGTAA	AATTTTAAGC	ACTAAAAATT	TTTTCATAAC	CTTTCATAAT	3720
	AAAGTTTAAT	AATAGGTTTA	TTAACTGAAT	TTCAATTAGT	TTTTAAAAAG	GTTTTGTGGT	3780
	TGTGTATATA	TACATATACA	AATACAACAT	TTACAATAAA	TAAATACTCT	GAAATTCCTA	3840
	AAAAAATAAA	AAAAAATAAA	AAAAA				

Seq ID NO: 450 Protein sequence  
Protein Accession #: NP\_003807.1

	1	11	21	31	41	51	
70	MGSGARFSPG	TLRVRWLLLL	GLVGPVLGAA	RPGFQQTSHL	SSYEIITPWR	LTRERREAPR	60
	PYSKQVSYVI	QAEQKEHIH	LERNKDLLPE	DFVVYTYNKE	GTLLTDHPNI	QNHCHYRGYV	120
	EGVHNSIAL	SDCFGLRLGL	HLENASYGIE	PLQNSHFEH	IIRMDDVYK	EPLKCGVSNK	180
	DIEKETAKDE	EEEPSPMTQL	LRRRAVLFPQ	TRYVELFIVV	DKERYDMMGR	NQTAVREEMI	240
	LLANYLDSMY	IMLNIRIVLV	GLEIWTNGNL	INIVGGAGDV	LGNFVQWREK	FLITRRRHDS	300
75	AQLVLKKGFG	QCTAGMAFVGT	VCSRSHAGGI	NVFGQITVET	FASIVAHELG	HNLGMNHDDG	360
	RDCSCGAKSC	IMNSGASGR	NFSSCSAEDF	EKLTLNKGGN	CLLNIPKPE	AYSAPSCGNK	420
	LVDAGEECD	GTPKECELD	CCEGSTCKLK	SFAECAYGDC	CKDCRFLPGG	TLCRGKTSEC	480
	DVPEYCNSS	QFCQPDVFIQ	NGYPQNNKA	YCYNGMCQYY	DAQQVIFGS	KAKAAPKDCF	540
	IEVNSKGRDF	GNCGFSNGEY	KKCATGNALC	GKLQCEVQVE	IPVFGIVPAI	IQTSPRGTKC	600
80	WGVDFQLGSD	VDPDGMVNEG	TKCGAGKICR	NFQCVDAVSL	NYDCDVQKKK	HGHGVCNSNK	660
	NCHCENGWAP	PNCETKGYGG	SVDSGPTYNE	MNTALRDGLV	VFFFLIVPLI	VCAIFIFIKR	720
	DQLWRSYFRK	KRSQTYESDG	KNQANPSRQP	GSVPRHVSPL	TPPREVPIYA	NRFVAVPTYAA	780
	KQPPQFPSPR	PPQPKVSSQ	GNLIPARPAP	APPLYSSLT			

Seq ID NO: 451 DNA sequence  
Nucleic Acid Accession #: NM\_016650.1  
Coding sequence: 196..789

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      GGTTC AATA TATGC AGATG TCTCG ATATA GGAAT GAAAT TACGT CTTTG GAACA ACTTA 60
AATAAGTCAA ATATACTTGG AGCTTTAAAA ATTAAGGA GAGAGATTTC AGCACCTTTT 120
10    CTGCTGCCAT GACAACCATG CAAGGAATGG AACAGGCCAT GCCAGGGTTG GCCTGGTGTG 180
      CCCCAGCTGG GAAACATGGC TGTACATACAT TCACATCTGT GGAAAGGATT GCAAGAGAAG 240
      TTCTTGAAGG GAGAACCCAA AGTCCTTGGG GTTGTGCAGA TTCTGACTGC CCTGATGAGC 300
      CTTAGCATGG GAATAACAAT GATGTGTATG GCATCTAATA CTTATGGAAG TAACCCATT 360
      TCCGTGCATA TCGGGTACAC AATTTGGGGG TCAGTAATGT TTATTATTTC AGGATCCTTG 420
      TCAATTGCAG CAGGAATTAG AACTACAAAA GGCCTGGTCC GAGGTAGTCT AGGAATGAAT 480
15    ATACCAGCT CTGTACTGGC TGCATCAGGG ATCTTAATCA ACACATTAG CTGGCGTTT 540
      TATTCATTCC ATACCCTTA CTGTAAC TAC TATGGCACT CAAATAATTG TCATGGGACT 600
      ATGTCCATCT TAATGGGTCT GGAATGGCATG GTGCTCCTCT TAAGTGTGCT GGAATTTCTGC 660
      ATTGCTGTGT CCTCTCTGTC CTTTGGATGT AAAGTGTCTCT GTTGTACCCC TGGTGGGGTT 720
20    GTGTTAATTC TGGCATCACA TTCTCACATG GCAGAAACAG CATCTCCAC ACCACTTAAT 780
      GAGGTTGAG GCCAACAAAA GATCAACAGA CAAATGCTCC AGAAATCTAT GCTGACTGTG 840
      ACACAAGAGC CTCACATGAG AAATTACCAG TATCCAACTT CGATACTGAT AGACGTGTTG 900
      ATATTATTAT TATATGTAAT CCAATTATGA ACTGTGTGTG TATAGAGAGA TAATAAATTC 960
      AAAATTATGT TCTCATTTT TTCCCTGGAA CTCAATAACT CACTTCACTG GCTCTTTATC 1020
25    GAGAGTACTA GGAGTTAAAT TAATAAATAA TGCATTTAAT GAGGCCACAG GAAAAA

```

Seq ID NO: 452 Protein sequence  
Protein Accession #: NP\_057734.1

```

30    1      11      21      31      41      51
      |      |      |      |      |      |
      MAVIHS LHWK GLQEK FLKGE PKVLGV VQIL TALMS LSMGI TMMCM ASNTY GSNPI SVHIG 60
      YTIWGS VMFI ISGSL SIAAG IRTTK GLVVR SLGMN ITSSV LAASG ILINT FSLAF YSFHH 120
      PYCNYY GNSN NCHGT MSILM GLDGM VLLLS VLEFC IAVSL SAFGCK VLLCC TPGGV VLILP 180
35    SHSHMAETAS PTPLENEV

```

Seq ID NO: 453 DNA sequence  
Nucleic Acid Accession #: NM\_002091.1  
Coding sequence: 56..503

```

40    1      11      21      31      41      51
      |      |      |      |      |      |
      AGTCTCTGCT CTTCCAGGCC TCTCCGGCGC GCTCCAAGGG CTTCCCGTCG GGACCATGCG 60
      CGGCAGTGAG CTCCCGCTGG TCCTGCTGGC GCTGGTCCTC TGCCTAGCGC CCGGGGGGCG 120
45    AGCGGTCCCG CTGCTCTGCG GCGGAGGGAC CGTGTGACC AAGATGTACC CGCGCGGCAA 180
      CCACTGGGCG GTGGGGCACT TAATGGGGAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
      TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACATC AGGTGGGAAG AAGCTGCAAG 300
      GAATTTGCTG GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCAACCCAA 360
      GGCCTTGGGC AATCAGCAGC CTTCTGTGGA TTCAGAGGAT AGCAGCAACT TCAAGATGT 420
50    AGGTTCAAAA GCGAAAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
      CCCCAGCTG AACCAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAACCCC 540
      TAAGAGACTG AGTCTGCAA GCATCAGTTC TACGGATCAT CAACAAGATT TCCTTGTGCA 600
      AAATATTTGA CTATTCTGTA TCTTTCATCC TTGACTAAAT TCGTGATTTT CAAGCAGCAT 660
      CTTCTGTTT AAACCTGTTC GCTGTGAACA ATTGTGAAA AGAGTCTTCC AATTAATGCT 720
55    TTTTATATC TAGGCTACCT GTTGGTTAGA TTCAAGGCCC CGAGCTGTTA CCATTACAA 780
      TAAAGCTTA AACACAT

```

Seq ID NO: 454 Protein sequence  
Protein Accession #: NP\_002082.1

```

60    1      11      21      31      41      51
      |      |      |      |      |      |
      MRGSELPLVL LALVLCLAPR GRAVPLPAGG GTVLTMYPR GNHWAVGHLM GKKSTGESS 60
      VSERGSLKQQ LREYIRWEEA ARNLLGLIEA KENRNHQPPQ PKALGNQPS WDSEDSSNFK 120
65    DVGSKGKVGR LSAPGSQREG RNPQLNQ

```

Seq ID NO: 455 DNA sequence  
Nucleic Acid Accession #: NM\_016522.1  
Coding sequence: 265..1299

```

70    1      11      21      31      41      51
      |      |      |      |      |      |
      GCGGAAGCAG CGAGGAGGGA GCCCCCTTGG GCCGTCCTCC GTGGAACCGG TTTCCGAGG 60
      CTGGCAAAAG CCGAGGCTGG ATTTGGGGGA GGAATATTAG ACTCGAGGA GTCTGCGCGC 120
75    TTTTCTCTC CCCGCGCTC CCGGTCGCGG CGGGTTCAAC GCTCAGTCCC CGCGCTCGCT 180
      CCGCACCCCA CCCACTTCTT GTGCTCGCCC GGGGGGCGTG TGCCGTGCGG CTGCGGAGT 240
      TCGGGGAAGT TGTGGCTGTC GAGAATGGGG GTCTGTGGGT ACCTGTTCTT GCCCTGGAAG 300
      TGCCTCGTGG TCGTCTCTCT CAGGCTGCTG TTCCTGTAC CCACAGGAGT GCCCGTGC GC 360
      AGCGGAGATG CACCTTCCC CAAAGCTATG GACAACGTGA CGGTCCGCA GGGGAGAGC 420
80    GCCACCTCA GGTGCACTAT TGACAACCGG GTCACCCGGG TGGCCTGGCT AAACCGCAGC 480
      ACCATCTCT ATGCTGGGAA TGACAAGTGG TGCCTGGATC CTCGCTGGT CCTTCTGAGC 540
      AACACCCAAA CGCAGTACAG CATCGAGATC CAGAACGTGG ATGTGTATGA CGAGGGCCCT 600
      TACACCTGCT CGGTGCAGAC AGACAACCAC CCAAGACCT CTAGGGTCCA CCTCATTTGT 660
      CAAGTATCTC CAAAATTGT AGAGATTCTT TCAGATATCT CCATTATGA AGGGAACAAT 720
      ATTAGCTCA CCTGCATAGC AACTGGTAGA CCAGAGCCTA CGGTACTTGG GAGACATC 780

```

TCTCCCAAAG CGGTTGGCTT TGTGAGTGAA GACGAATACT TGGAAATTCA GGGCATCACC 840  
 CGGGAACAGT CAGGGGAGTA CGAGTGCAGT GCCTCCAATG ACGTGGCCGC GCCCGTGGTA 900  
 CGGAGAGTAA AGGTCAACCGT GAACTATCCA CCATACATTT CAGAAGCCAA GGGTACAGGT 960  
 GTCCCGCTGG GACAAAGGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCAGCAGAA 1020  
 TTCCAGTGGT ACAAGAGATGA CAAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080  
 AACAGACCTT TCCTCTCAAA ACTCATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140  
 TACACTTGGC TGGCCTCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTGGT 1200  
 CCAGGCGCCG TCAGCGAGGT GAGCAACGGC ACGTCGAGGA GGGCAGGCTG CGTCTGGCTG 1260  
 CTGCCTCTTC TGGTCTTGCA CCTGCTTCTC AAATTTTGAT GTGAGTGCCA CTCCCCCACC 1320  
 CGGGAAGAGC TGCCGCCACC ACCACCACA ACACAACAGC AATGGCAACA CCGACAGCAA 1380  
 CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACACAGC CTCATGGGAC AGAAATTGA 1440  
 GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTT AAAAAGAAA TTGAAAATTG 1500  
 CCTTGAGAT ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560  
 CCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGGCAG TGTGGGCAAG 1620  
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CACGTGGAAC ATTCTGGAGC TGGCCATCCC 1680  
 AAATTCATC AGTCCATAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740  
 CCGGCCCAAG CGTGGCGCTG CCGGCACCTT GGTAGACTGT GCCACCACGG CGTGTGTTGT 1800  
 GAAACGTGAA ATAAAAAGAG CAAAAA AAAA

Seq ID NO: 456 Protein sequence  
 Protein Accession #: NP\_057606.1

1 11 21 31 41 51  
 | | | | |  
 MGVCGLFLP WKCLVVVSLR LLFLVPTGVP VRSGDATFPK AMDNVTVRQG ESATLRCTID 60  
 NRVTRVAWLN RSTILYAGND KWCLDPRVVL LSNQTQYSI EIQNVVDVDE GPYTCVQTD 120  
 NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTCTAT GRPEPTVWR HISEPKAVGFV 180  
 SEDEYLEIQG ITRQSGDYE CSASNDVAAP VVRVKVTVN YPPYISEAKG TGVPGVKQGT 240  
 LQCBASAVPS AEFQWYKDDK RLIEGKGVK VENRPFLLSKL IFFNVSEHDY GNYTCVASNK 300  
 LGHTNASIML FGPAVSEVS NGTSRRAGCV WLLPLLVLHL LLKF

Seq ID NO: 457 DNA sequence  
 Nucleic Acid Accession #: NM\_012261.1  
 Coding sequence: 203..1045

1 11 21 31 41 51  
 | | | | |  
 GATTGCTCT GCCAGCAGT GTCGGTGCCG CGCTCGACAC CGAGTCCTAG CTAGGCGCTC 60  
 ACAGAATACG CGCTCCCTTC CTCGCCCTTC TCTGTCCCCC GCCTCTCGCT CACCCCGGCC 120  
 CACTCCAGCG GCGACTTTGA GGGATTCCCT CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180  
 CCTCATTCGG GGCAGTCCGA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240  
 ACTTCGAGTT CTCCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAGAAGT 300  
 GGAAATCTCT TCAGGCCTTT CCACTAACCC TGAAAAAGAT ATATTGTGG TGCGGGAAAA 360  
 TGGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATTT ATTGTACCTT ATGATGTGTG 420  
 GGCCAGCAAC GCGTCAATAT TGTACACAGA ACAGGCCGAT ATCGCATTGA CCGGGGGAGC 480  
 TGAGGTGAAG GGCCGCTGTG GCCACAGCCA GTCGGAGCTG CAAGTGTCTT GGGTGGATCG 540  
 CGCATATGCA CTCAAAATGC TCTTTGTAAA GGAAAGCCAC AACATGTCCA AGGGACCTGA 600  
 GGCGACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTACGAC TCCTCGGAGA AAACCCACTT 660  
 CAAAGACGCA GTCAGTCTGT GGAAGCACAC AGCCAACTCG CACCACCTCT CTGCCCTGGT 720  
 CACCCCGGCT GGGAAAGTCT ATGAGTGTCA AGCTCAACAA ACCATTTCAC TGGCCTCTAG 780  
 TGATCCGCGA AAGACGGTCA CCATGATCCT GTCTGCGGTC CACATCCAAC CTTTGTGACAT 840  
 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900  
 GGAAGAAAAC TTGCCCTTGA TTTTGGGGCT CATCTTGGGC CTCGTCATCA TGGTAACACT 960  
 CGCGATTTAC CACGTCCACC ACAAAATGAC TGCCCAACCAG GTGCAGATCC CTCGGGACAG 1020  
 ATCCAGTAT AAGCATATGG GCTAGAGGCC GTTAGGCAGG CACCCCTTAT TCCTGCTCCC 1080  
 CCAACTGGAT CAGGTAGAAC AACAAAGCA CTTTCCATC TTGTACACGA GATACACCAA 1140  
 CATAGCTACA ATCAACAGG CCTGGGTATC TGAGGCTTGC TTGGCTTGTG TCCATGCTTA 1200  
 AACCACGGA AGGGGGAGAC TCTTTCGGAT TTGTAGGGTG AAATGGCAAT TATTCTCTCC 1260  
 ATGCTGGGGA GGAGGGGAGG AGGGTCTCAG ACAGCTTTCG TGCTCATGGT GGCTTGGCTT 1320  
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGCCCCCAA AGTTTAGGGA 1380  
 TTGAAACAT GCTTCTTTGA GGAGGAAACC CCTTTAGGTT CAGAAGAATA TGGGGTGCTT 1440  
 TGCTCCCTTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAAAC 1500  
 TCATGCTCCC TGCAGCAAGA CCGCTGAAAG TGATTATGCT TTCTGGCTGG CATTCTGCAT 1560  
 GTTTAGTGAT TGTCTTGGGA ATGTTTCACT GCTACCCGCA TCCAGCGACT GCAGCACCAG 1620  
 AAAACGACTA ATGTAACATAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC 1680  
 GGGGGACCTG AAGAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAAATA AAACACACTA 1740  
 TTCTCTGGC

Seq ID NO: 458 Protein sequence  
 Protein Accession #: NP\_036393.1

1 11 21 31 41 51  
 | | | | |  
 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60  
 EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEBVKRCG HSQSELQVFW VDRAYALKML 120  
 FVKESHMMSK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHHLS ALVTPAGKSY 180  
 ECQAQQTISL ASSDPQKTVT MILSAVHIQF FDIISDFVFS EEHKCPVDER EQLEETLPLI 240  
 LGLILGLVIM VTLAIYVHH KMTANQVQIP RDRSQYKHM

Seq ID NO: 459 DNA sequence  
 Nucleic Acid Accession #: NM\_001169.1  
 Coding sequence: 85..870

1 11 21 31 41 51

5  
10  
15  
20  
25

	TAGGAGATAA		GAGTATCTTG		CACAGCAGGT		GCAGGTTTCC		CAGCAGCTCA		GGCAAGAGTC	60
	CGATGTTTGT		GCCATCTGAT		CCTGATGTCT		GGAGAGATAG		CCATGTGTGA		GCCTGAATTT	120
	GGCAATGACA		AGGCCAGGGG		GCCGAGCGTG		GGTGGCAGGT		GGCGAGTGTC		CTGGTACGAA	180
	CGGTTTGTGC		AGCCATGTCT		GGTCGAACTG		CTGGGCTCTG		CTCTCTTCAT		CTTCATCGGG	240
	TGCCTGTCCG		TCATTGAGAA		TGGGACGGAC		ACTGGGCTGC		TGCAGCCGGC		CCTGGCCAC	300
	GGGCTGGCTT		TGGGGCTCGT		GATTGCCACG		CTGGGGAAATA		TCAGTGGTGG		ACACTTCAAC	360
	CCTGCGGTGT		CCCTGGCAGC		CATGCTGATC		GGAGGCCTCA		ACCTGGTGAT		GCTCCTCCCG	420
	TACTGGGTCT		CACAGCTGCT		CGGGGGGATG		CTCGGGGCTG		CCTTGGCCAA		GGTGGTGAGT	480
	CCTGAGGAGA		GGTTCGGAA		TGCATCTGGG		GCGGCCTTTG		TGACAGTCCA		GGAGCAGGGG	540
	CAGGTGGCAG		GGGCGTTGGT		GGCAGAGATC		ATCCTGACGA		CGCTGCTGGC		CCTGGCTGTA	600
	TGCATGGGTG		CCATCAATGA		GAAGACAAAG		GGCCCTCTGG		CCCCGTCTCT		CATCGGCTTT	660
	GCCGTACCCG		TGGATATCCT		GGCTGGGGGC		CCTGTGTCTG		GAGGCTGCAT		GAATCCCGCC	720
	CGTGCTTTTG		GACCTGCGGT		GGTGGCCAA		CACCTGGAAT		TCCACTGGAT		CTACTGGCTG	780
	GGCCCACTCC		TGGCTGGCCT		GCTTGTGTGA		CTGCTCATT		GGTGCTTCAT		TGGAGATGGG	840
	AAGACCCGCG		TCATCTGAA		GGCTCGGTGA		GCAGAGCTCG		TGGGATTCCT		GCTGCTCCAG	900
	GTGTCTCTAG		CTACCTGTG		CCAGACTGAG		GACAGGGGAG		TTCTTGCATT		TCCTGCCAGG	960
	GCAGAGGCC		AGAGGAGCG		CCCCCTGCTT		CCACTGCTTG		GGCCTGCTTT		CTCAGATAGA	1020
	CTGACTGCTG		AGGAGGCTCT		AGGTTCTTGG		AATTCCTTTG		TGCTCATCAG		AGACCCAGC	1080
	CTGGGGAACA		CGCTGCCCGC		ACTGCCCAGA		GAGCAGTGCA		AACACCACAA		CACGAGCGTG	1140
	TTTCTTGAGA		GGAAATGCCC		CGAGTTGGAC		AAGGAGGCTG		TTTCTGCACA		TCAGTCTATT	1200
	TCCCGCACCC		CATTCTTTCG		TTGATTGCTT		TGTTGGGGGC		CTGGCCACTT		CCTTGCTTCT	1260
	CAAGCTGACA		ATTCTCACTT		TGCAATAAAT		AGTCCAGTGT		TTCTTTCAT			

Seq ID NO: 460 Protein sequence  
Protein Accession #: NP\_001160.1

30  
35

	1		11		21		31		41		51	
	MSGEIAMCEP		EPGNDKAREP		SVGGRWRVSW		YERFVQPCLV		ELLSALFIF		IGCLSVIENG	60
	TDTGLLQPAL		AHGLALGLVI		ATLGNISGGH		FNPVSLAAM		LIGGLNLVML		LPYVWSQLLG	120
	GMLGAALAKV		VSPERFWNA		SGAAFVTQVE		QGQVAGALVA		EIIITTLAL		AVCMGAINKE	180
	TKGPLAPFSI		GFAVTVDILA		GGPVSGGCMN		PARAFGPAVV		ANHWNFWIY		WLGPLLAGLL	240
	VGLLIRCFIG		DGKTRLILKA		R							

Seq ID NO: 461 DNA sequence  
Nucleic Acid Accession #: NM\_003226.1  
Coding sequence: 2..226

45  
50

	1		11		21		31		41		51	
	GATGCTGGGG		CTGGTCTTGG		CCTTGCTGTC		CTCCAGCTCT		GCTGAGGAGT		ACGTGGGCCT	60
	GTCTGCAAA		CAGTGTGCCG		TGCCGGCCAA		GGACAGGGTG		GACTGCGGCT		ACCCCATGT	120
	CACCCCAAG		GAGTGCAACA		ACCGGGGCTG		CTGCTTTGAC		TCCAGGATCC		CTGGAGTGCC	180
	TTGGTGTTC		AAGCCCTGA		CTAGGAAGAC		AGAATGCACC		TTCTGAGGCA		CCTCCAGCTG	240
	CCCCTGGGAT		GCAGGCTGAG		CACCCCTGCC		CGGCTGTGAT		TGCTGCCAGG		CACCTGTTCT	300
	CTCAGTTTTT		CTGTCCCTTT		GCTCCCGGCA		AGCTTTCTGC		TGAAAGTTCA		TATCTGGAGC	360
	CTGATGTCTT		AACGAATAAA		GGTCCCATGC		TCCACCCG					

Seq ID NO: 462 Protein sequence  
Protein Accession #: NP\_003217.1

55  
60

	1		11		21		31		41		51	
	MLGLVLALLS		SSSAEEYVGL		SANQCAVPAK		DRVDCGYPHV		TPKECNRRGC		CFDSRIPGVP	60
	WCFKPLTRKT		ECTF									

Seq ID NO: 463 DNA sequence  
Nucleic Acid Accession #: NM\_002993.1  
Coding sequence: 64..408

65  
70  
75  
80

	1		11		21		31		41		51	
	GGCACGAGCC		AGTCTCCGCG		CCTCCACCCA		GCTCAGGAAC		CCGCGAACC		TCTCTTGACC	60
	ACTATGAGCC		TCCCGTCCAG		CCGCGCGGCC		CGTGTCCCGG		GTCCCTTCGGG		CTCCTTGTGC	120
	GCGCTGCTCG		CGCTGCTGCT		CCTGCTGACG		CCGCCGGGGC		CCCTCGCCAG		CGCTGGTCCCT	180
	GTCTCTGCTG		TGCTGACAGA		GCTGCGTTGC		ACTTGTTTAC		GCGTTACGCT		GAGAGTAAAC	240
	CCCAAAACAG		TTGGTAAACT		GCAGGTGTTT		CCCGCAGGCC		CGCAGTGCTC		CAAGGTGGAA	300
	GTGGTAGCCT		CCCTGAAGAA		CGGGAAGCAA		GTTTGTCTGG		ACCCGGAAGC		CCCTTTTCTA	360
	AAGAAAGTCA		TCCAGAAAAT		TTTGGACAGT		GGAACAAGA		AAAACGTAGT		AACAAAAAAG	420
	ACCATGCATC		ATAAAAATTG		CCAGTCTTCA		GCGGAGCAGT		TTTCTGGAGA		TCCCTGGACC	480
	CAGTAAGAA		AAGAAGGAAG		GTTTGGTTTT		TTTCCATTTT		CTACATGGAT		TCCCTACTTT	540
	GAAAGAGTGT		GGGGAAGGCC		TACGCTTCTC		CCTGAAGTTT		ACAGCTCAGC		TAATGAAGTA	600
	CTAATATAGT		ATTTCACATA		TTTACTGTTA		TTTACCTGA		TAAGTTATTG		AACCCCTTGG	660
	CAATTGACCA		TATTTGTAGC		AAAGAATCAC		TGGTTATTAG		TCTTTCAATG		AATATTGAAT	720
	TGAAGATAAC		TATTTGTATT		CTATCATACA		TTCTTTAAAG		TCTTACCGAA		AAGGCTGTGG	780
	ATTTCTGATG		GAAATAATGT		TTTATTAGTG		TGCTGTTGAG		GGAGGTATCC		TGTTGTTCTT	840
	ACTCACTCTT		CTCATAAAT		AGGAAATATT		TTAGTTCTGT		TTTCTTGGGG		AATATGTTAC	900
	TCTTTACCCCT		AGGATGCTAT		TTAAGTTGTA		CTGTATTAGA		ACACTGGGTG		TGTCATACCG	960
	TTATCTGTGC		AGAATATATT		TCCTTATTCA		GAATTTCTAA		AAATTTAAGT		TCGTAAAGGG	1020
	CTAATATATT		CTCTTCCTAT		GGTTTATGAT		GTTTGTATGTC		TTCTTAGTAT		GGCATAATGT	1080
	CATGATTTAC		TCATTAACCT		TTGATTTTGT		ATGCTATTTT		TTCACTATAG		GATGACTATA	1140

ATTCTGGTCA CTAAATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC 1200  
 TGATTGTCTAA TTTACATAGA AATGTATTCT CITGGTTTTT TAAATAAAG CAAAATTAAC 1260  
 AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTTGAA CAATTGGAAT ATAAATTCAT 1320  
 CATTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380  
 TTTAAAGGTT TIGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440  
 AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCAAT 1500  
 TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAAAAAA AAAAAA

Seq ID NO: 464 Protein sequence  
 Protein Accession #: NP\_002984.1

1 11 21 31 41 51  
 MSLPSSRAAR VPGPSGLCA LLALLLLTTP PGPLASAGPV SAVLTELRCT CLRVTLRVNP 60  
 KTIQKLVFP AGPQCSKVEV VASLKNKQV CLDPEAPFLK KVIQKILDSG NKKN

Seq ID NO: 465 DNA sequence  
 Nucleic Acid Accession #: NM\_002038.2  
 Coding sequence: 108..500

1 11 21 31 41 51  
 GAACCGTTTA CTCGCTGCTG TGCCCATCTA TCAGCAGGCT CCGGGCTGAA GATTGCTTCT 60  
 CTTCTCTCCT CCAAGGTCTA GTGACGGAGC CCGCGCGCGG CGCCACCATG CGGCAGAAGG 120  
 CGGTATCGCT TTTCTTGTGC TACCTGCTGC TCTTCACTTG CAGTGGGGTG GAGGCAGGTA 180  
 AGAAAAAGTG CTCGGAGAGC TCGGACAGCG GCTCCGGGTT CTGGAAGGCC CTGACCTTCA 240  
 TGGCCGTCCG AGGAGGACTC GCAGTCGCCG GGCTGCCCGC GCTGGGCTTC ACCGGCGCCG 300  
 GCATCGCGCG CAACCTCGGTG GCTGCCCTCG TGATGAGCTG GTCTGCGATC CTGAATGGGG 360  
 CGCGCGTGCC CGCCGGGGGG CTAGTGGCCA CGCTGCAGAG CCTCGGGGCT GGTGGCAGCA 420  
 GCCTCGTCAT AGGTAATATT GGTGCCCTGA TGGGCTACGC CACCCACAAG TATCTCGATA 480  
 GTGAGGAGGA TGAGGAGTAG CCAGCAGCTC CCAGAACCCT TTCTTCCTTC TTGGCCTAAC 540  
 TCTTCCAGTT AGGATCTAGA ACTTTGCCCT TTTTTTTTTT TTTTTTTTTT TTTGAGATGG 600  
 GTTCTCACTA TATTGTCCAG GCTAGAGTGC AGTGGCTATT CACAGATGCG AACATAGTAC 660  
 ACTGCAGCCT CCAACTCCTA GCCTCAAGTG ATCCTCCTGT CTCAACCTCC CAAGTAGGAT 720  
 TACAAGCATG CGCCGACGAT GCCCAGAATC CAGAACCTTG TCTATCACTC TCCCCAACAA 780  
 CCTAGATGTG AAACAGAAAT AAACCTTACC CAGAAAA

Seq ID NO: 466 Protein sequence  
 Protein Accession #: NP\_002029.3

1 11 21 31 41 51  
 MRQKAIVSLFL CYLLLFCTSG VEAGKKKCE SSDSGSGFWK ALTFMAVGGG LAVAGLPALG 60  
 FTGAGIAANS VAASLMSWSA ILNGGGVPAG GLVATLQSLG AGGSSVVIGN IGALMGYATH 120  
 KYLDSEEDDE

Seq ID NO: 467 DNA sequence  
 Nucleic Acid Accession #: NM\_003469.2  
 Coding sequence: 92..1945

1 11 21 31 41 51  
 GAAACGGCCC GAGAAGCTCG CCCGGAGAAC GGGGAGGAAT ATGCTGTGGA GTCCTCTGTC 60  
 CATATAAACA AAAAGAGGAA ATCTTTCAAA CATGGCTGAA GCAAAGACCC ACTGGCTTGG 120  
 AGCAGCCCTG TCTCTTATCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180  
 TCAGAGAAAC CAGCTGCTTC AGAAAGAACC AGACCTCAGG TTGGAAATG TCCAAAAGTT 240  
 TCCCAGTCTT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACAAAGCTCA 300  
 TAAGGAAGAA AGCAGCCCAAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA 360  
 AAAAGAAAAT GGCATGAAA GCCACTTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG 420  
 GATGAGAATA ATACTCGAAG CTTTGAGACA GGCTGAAAT GAGCCTCAGT CTGCACCAAA 480  
 AGAAAATAAG CCCTATGCCT TGAATTCAGA AAAGAACTTT CCAATGGACA TGAGTGATGA 540  
 TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCCTATGTA 600  
 TGAAGAGAA TCCAGGGATA ACCCTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660  
 TACTCCTCAA AGCCTTGCTA CATTGGAATC TGTCTTCCAA GAGCTGGGGA AACTGACAGG 720  
 ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACTTTATA CGGATGATGA 780  
 AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTCGGGG GAGAAGACTG 840  
 GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAAGA 900  
 GAATATAGGA AAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT 960  
 CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT 1020  
 AATTGCTTAT TTGAAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080  
 AATGGGGGAA AGGGCCACCA GGCTTTTGA GAAACCTCTT GATTCTCAGT CTATTATCA 1140  
 GCTGATTGAA ATCTCAAGGA ATTTACAGAT ACCCCAGAA GACTTAATTG AGATGCTCAA 1200  
 AACTGGGGAG AAGCCGAATG GATCAGTGGA ACCGGAGCGG GAGCTTGACC TTCTGTTGA 1260  
 CCTAGATGAC ATCTCAGAGG CTGACTTAGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT 1320  
 CTCCAAGAGT GGTACCTTA AAACACCTGG TCGTGTGGG ACTGAGGCC TACCAGACGG 1380  
 GCTCAGTGTG GAGGATATTT TAAATCTTTT AGGGATGGAG AGTGCAGCAA ATCAGAAAAA 1440  
 GTCGTATTTT CCAATCCAT ATAACAGGA GAAAGTTCTG CCAAGGCTCC CTTATGGTGC 1500  
 TGGAGATCT AGATCGAACC AGCTTCCCAA AGCTGCCTGG ATTCCACATG TTGAAAACAG 1560  
 ACAGATGGCA TATGAAAACC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG 1620  
 GATGCTAGTT AAATACCTTG AGATCATTA TTAACACCAA GTGAAGCGAG TTCTGGTCA 1680  
 AGGCTCATCT GAGAGTGACC TGCAGGAAGA GGAACAAATT GAGCAGGCCA TCAAGAGCA 1740  
 TTTGAATCAA GGACGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGGTTCCC 1800  
 TGTGGGGCCC CCGAAGAAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860  
 AATGAAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGGAAGGG AGCATATTGC 1920

TAAGAGAGCA ATGGAAAATA TGTAAGCTGC TTTCATTAAT TACCCTACTT TCATTCTCTC 1980  
 CACCCCAAGC AATTCCTTTC ATTTCTCTTC AGTGTGTGA CTTCTATCCT GTTAACACTG 2040  
 TAATATCTTT AATGATGTA CAGGCAGATG AAACCAGGTC ACTGGGGAGT CTGCTTCATT 2100  
 TCCTCTGAGC TGTATCTTG TGTATGGATA TGTGTAAATG TTATGACTCC TTGATAAAAA 2160  
 ATTTATTATG TCCATTATTC AAGAAAGATA TCTATGACTG TGTTAATAG TATATCTAAT 2220  
 GGCTGTGGCA TTGTGATGC TCACATATGA TAAAAAGTG TCCTATAATT CTATTGAAAG 2280  
 TTTTAAATAT TTATTGAATT ATTTTGTTC TGTCTGTAGC GTTTTGTGGA GTACTGGACC 2340  
 AAAAAAATAA AGCATTATAA ATATA

Seq ID NO: 468 Protein sequence  
 Protein Accession #: NP\_003460.1

1 11 21 31 41 51  
 MAEAKTHWLG AALSLIPLIF LISGAEASF QRNQLQKEP DLRLNVQKF PSEPMIRALE 60  
 YIENLRQQAQ KEESPDPNP YQGVSVPLQQ KENGDESHLP ERDSLSEEDW MRIILEALRQ 120  
 AENEPQSAFK ENKPYALNSE KNFPMDMSDD YETQQWPERK LKHMQFPMPY EENSRLNPFK 180  
 RTNEIVEEQY TPQSIALTLES VFQELGKLTG PNNQKRERMD EQKLYTDDE DDIYKANNIA 240  
 YEDVVGGEEDW NPVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSQQLGI QEEDLRKESK 300  
 DQLSDDVSKV IAYLRLRVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRLNLI 360  
 PPEDLIEMLK TGEKPNGSVE PERELDLFVD LDDISEADLD HPDLFQNRML SKSGYPKTPG 420  
 RAGTEALPDG LSVEDILNLL GMESAANQKT SYFPNPYNQE KVLPRLPYGA GRSRSNQLPK 480  
 AAWIPHVENR QMAYENLNDK DQELGEYLAR MLVKYPEIIN SNQVKRVPGQ GSSEDDLQEE 540  
 EQIEQAIEKH LNQSSSQETD KLAPVSKRFP VGPPKNDITP NRQYWEDELL MKVLEYLNQE 600  
 KAEKGREHIA KRAMENM

Seq ID NO: 469 DNA sequence  
 Nucleic Acid Accession #: NM\_006398.1  
 Coding sequence: 19..516

1 11 21 31 41 51  
 GGCCCTTGT CTGCAGAGAT GGCTCCCAAT GCTTCTCTGCC TCTGTGTGCA TGTCCGTTCC 60  
 GAGGAATGGG ATTTAATGAC CTTTGATGCC AACCCATATG ACAGCGTGAA AAAAATCAAA 120  
 GAACATGTCC GGTCTAAGAC CAAGGTTCTCT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180  
 AAGATCTTAA AGCCACGGAG AAGCCTCTCA TCTTATGGCA TTGACAAAGA GAAGACCATC 240  
 CACCTTACCC TGAAGTGGT GAAGCCAGT GATGAGGAGC TGCCCTTGT TCTTGTGGAG 300  
 TCAGGTGATG AGGCAAGAG GCACCTCTCT CAGGTGCGAA GGTCACGCTC AGTGGCACAA 360  
 GTGAAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC 420  
 AATGGAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGGCATCAG AAAGGGCAAC 480  
 TTACTCTTCC TGCCATCTTA TTGTATTGGA GGGTGACCAC CCTGGGGATG GGGTGTGGC 540  
 AGGGGTCAA AAGCTTATTT CTTTAACTCT CTACTCAAC GAACACATCT TCTGATGATT 600  
 TCCCAAATAT AATGAGAATG AGATGAGTAG AGTAAGATTT GGGTGGGATG GGTAGGATGA 660  
 AGTATATTGC CCAACTCTAT GTTCTTTTGA TTCTAACACA ATTAATTAAG TGACATGATT 720  
 TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCAAAATAG AGCATTC

Seq ID NO: 470 Protein sequence  
 Protein Accession #: NP\_006389.1

1 11 21 31 41 51  
 MAPNASCLCV HVRSEEDWLM TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR 60  
 RSLSSYGIDK ERTIHLTLKV VKPSDEELPL FLVESGDEAK RHLLQVRRSS SVAQVKAMIE 120  
 TKTGIIPETQ IVTCNGKRLE DGRMMADYGI RKGNNLFLAS YCIGG

Seq ID NO: 471 DNA sequence  
 Nucleic Acid Accession #: XM\_094741.1  
 Coding sequence: 1..948

1 11 21 31 41 51  
 ATGAAGGCCA ACTACAGCGC AGAGGAGCGC TTTCTCTGTC TGGGTTTCTC CGACTGGCCT 60  
 TCCCTGCAGC CGGTCTCTTT CGCCCTTGTC CTCTGTGCT ACCTCCTGAC CTTGACGGGC 120  
 AACTCGGCGC TGGTGCTGCT GGCCTGCGC GACCCGCGCC TGCACACGCC CATGTACTAC 180  
 TTCTCTGCTC ACCTGGCCTT GGTAGACGCG GGCCTTCTCA CTAGCGTGGT GCCCGCGCTG 240  
 CTGGCAACCT TGCGCGGACC AGCGCTCTGG CTGCGCGGCA GCCACTGCAC GGCCAGCTG 300  
 TGCGCATCGC TGGCTCTGGG TTCGCGCGAA TGCGTCTCTC TGGCGGTGAT GGCTCTGGAC 360  
 CGCGCGCGCG CAGTGTGCGC CCCGCTGCGC TATGCGGGGC TCGTCTCCCC GCGCCTATGT 420  
 CGCACGCTGG CCAGCGCCTC CTGGCTAAGC GGCCTCACCA ACTCGGTGTC GCAACCCGCG 480  
 CTCCTGGCTG AGCGGCGGCT GTGCGCGCCC CGCCTGCTGG ACCACTTCAT CTGTGAGCTG 540  
 CCGCGTTGCT TCAAGCTGGC CTGCGGAGGC GACGGAGACA CTACCGAGAA CCAGATGTTT 600  
 GCCGCGCGCG TGGTCATCTT GCTGCTGCGG TTTGCGGTC TCTGCGCTC CTACGGTGCC 660  
 GTGGCCCGAG CTGTCTGTTG CATGCGGTTT AGCGGAGGCC GGAGGAGGCC GGTGGGACG 720  
 TGTGGGTCCC ACCTGACAGC CGTCTGCTG TTTACGGCT CGGCCATCTA CACCTACCTG 780  
 CAGCCCGCTG AGCGCTACAA CCAGGCACGG GGCAAGTTCT TATCGCTCTT CTACACCGTG 840  
 GTCACACCTG CTCTCAACCC GCTCATCTAC ACCCTCAGGA ATAAGAAAGT GAAGGGGGCA 900  
 GCGAGGAGGC TGCTGCGGAG TCTGGGGAGA GGCCAGGCTG GGCAGTGA

Seq ID NO: 472 Protein sequence  
 Protein Accession #: XP\_094741.1

1 11 21 31 41 51  
 MKANYSABER FLLLGFSWDP SLQPVLFALV LLCYLLTLTG NSALVLLAVR DPLRLTPMY 60



FLCHLALVDA GFTTSVVPPL LANLRGPALW LPRSHCTAQL CASLALGSAE CVLLAVMALD 120  
 RAAAVCRPLR YAGLVSPRLC RTLASASWLS GLTNSVAQTA LLAERPLCAP RLDDHFICEL 180  
 PALLKLACGG DGTITTENQMF AARVVILLLP FAVILASYGA VARAVCCMRF SGGRRRAVGT 240  
 CGSHLTAVCL FYGSAIYTYL QPAQRYNQAR GKFSVLFYTV VTPALNPLIY TLRNKKVKGA 300  
 ARRLRLSLGR GQAGQ

Seq ID NO: 473 DNA sequence  
 Nucleic Acid Accession #: NM\_001062.1  
 Coding sequence: 76..1380

1 11 21 31 41 51  
 | | | | |  
 GCTCTCATT CTTCTGCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG 60  
 TACACTGTTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTACTGTTT 120  
 TCTTTTATTC CAAGCCAAC ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180  
 CTAAACCTC TGTGAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC 240  
 AATGTTGTGT TGTCCCTCAA ACTTGTGGA ATCCAGATCC AAACCTGAT GCAAAAGATG 300  
 ATCCAACAAA TCAAAATACAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360  
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACGCTG AGGAAAACCTT AATATATGAT 420  
 TACCACCTGA CTGACAAGCT AGAAAATAAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480  
 CACAATGGCA CTCCCCTGAC TAACACTACT CAGCTCAGCC TGGACGTTT GGCCTTGTGT 540  
 CTGTGTAATG GGAAGTACT AACCAGCGAA GTTGTCAACC ACTTCATCTC TGAAAAATAA 600  
 AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CCTGGCTCTG 660  
 ACCTGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAG CAGATGAAGG CAGTTTAAAG 720  
 AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATTC TGTCTGAGAA AAAAGAAAA 780  
 GGTCTCATTT GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840  
 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAAACTC TGAATACAGT GCTCAGCGAA 900  
 ATTTCTCAAG GAGCAATCAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960  
 GGAAAGACCT TCTTGGATAT TAACAAAGAC TCTTCTTGGC TCTCTGCTTC AGGTAACCTC 1020  
 AACATCTCCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC 1080  
 GTCATTTACT CTGTGAGAA CAATGAAACA TATTTCACCA ATGTCAGTGT GCTAAATGGT 1140  
 TCTGTCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACAT ATTTGGTTTC 1200  
 ACAAATGGAG AGCGCTCATG GGGGCCCTAT ATCACTGTGA TTCAGGGCCT ATGTGCCAAC 1260  
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCACTGAG CCAAGGAGCT 1320  
 GGTAGTTACG TTGTCGCGAA TGGAGAAAAC TTGGAGGTTT GCTGGAGCAA ATACTAATAA 1380  
 GCCCAAACTT TCCTCAGCTG CATAAAATCC ATTTGCAGTG GAGTTCATG TTTATTGTCC 1440  
 TTATGCCTTC TTCTTCATTT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCTTCTC 1500  
 TCTCTACATG TTAATAAAA GTTGTGAAA GATTAAC

Seq ID NO: 474 Protein sequence  
 Protein Accession #: NP\_001053.1

1 11 21 31 41 51  
 | | | | |  
 MRQSHQLPLV GLLLSFPIPS QLCEICEVSE ENYIRLKPILL NTMIQSNYNR GTSAVNVVLS 60  
 LKLVGIQIQI LMQMKIQIYK YNVKSRSLSDV SSGELALIL ALGVCRNAEE NLIYDYHLTD 120  
 KLENKFQAEI EMQEAHNGTP LTNYYQLSLD VLALCLFNNG YSTAEEVNHF TPENKNYYFG 180  
 SQFSVDTGAM AVLALTCVKK SLINGQIKAD EGSLLNISIY TKSLEVKILS EKKENGLIGN 240  
 TFSTGEAMQA LPVSSDYINE NDWNCQQTILN TVLTEISQGA FSNPNAAQV LPALMGKTFE 300  
 DINKDSSCVS ASGNFCACAD EPITVTPPDS QSYISVNYSV RINETYFTNV TVLNGSVFLS 360  
 VMEKAQKMDN TTFGFTMEER SWGPYITCQ GLCANNDRT YWELLSGGEF LSQAGASYVV 420  
 RNGENLEVRW SKY

Seq ID NO: 475 DNA sequence  
 Nucleic Acid Accession #: NM\_004852.1  
 Coding sequence: 89..1546

1 11 21 31 41 51  
 | | | | |  
 GCCCCGCCCC GCCCGGGGCC CTGATGGACT GAATGAAGGC TGCCCTACACC GCCTATCGAT 60  
 GCCTCACCAA AGACCTAGAA CGTGCGCCAT GAACCCGAG CTGACAATGG AAAGTCTGGG 120  
 CACTTTGCAC GCGCGCGCGC GCGCGCGCAG TGGCGGGGGC GCGCGCGGGG GCGCGGGGGG 180  
 CGGCGCGGGG GCGCGGGGCC ATGAGCAGGA GCTGCTGGCC AGCCCGAGCC CCCACCAAGC 240  
 GCGCGCGGGC CCGCGTGGCT CGCTGCGGGG CCCTCCGCGC CCTCCAACCG CGCACCAGGA 300  
 GCTGGGCAGC GCGCGAGCGG CGGCAGCGGC GCGCTCGCGC TCGGCCATGG TCACCAGCAT 360  
 GGCCTCGATC CTGGACGGCG GCGACTACCG GCCCGAGCTC TCCATCCCGC TGCACCACGC 420  
 CATGAGCATG TCCTGCGACT CGTCTCCGCC TGGCATGGGC ATGAGCAACA CCTACACCAC 480  
 GCTGACACCG CTCACGCCG TGCCACCCAT CTCACCCGTG TCTGACAAAT TCCACCACCC 540  
 TCACCCGCAC CACCATCCGC ACCACCACCA CCACCACCAC CACCAGCGCC TGTCCGGCAA 600  
 CGTCAGCGGC AGCTTCACCC TCATGCGCGA CGAGCGCGGG CTCCCGGCCA TGAACAACCT 660  
 CTACAGTCCC TACAAGGAGA TGCCCGGCAT GAGCCAGAGC CTGTCCCGCC TGGCCGCCAC 720  
 GCGCTGGGGC AAGCGGCTAG GCGGCCCTCA CAACGCGCAG CAGAGTCTGC CCAACTACGG 780  
 TCCGCGGGC CAGCAACAAA TGCTCAGCCC CAACTTCGAC GCGCACCACA CTGCCATGCT 840  
 GACCCGCGGT GAGCAACACC TGTCCCGCGG CCTGGGCACC CCACCTGCGG CCATGATGTC 900  
 GCACCTGAAC GGCTTGACAC ACCCGGGCCA CACTCAGTCT CAGCGGCGCG TGTGGCACC 960  
 CAGTCGCGAG CGGCGCACTT CGTCTCATC GGGCTCGCAG GTGGCCACGT CGGCGCAGCT 1020  
 GGAAGAAATC AACACCAAAG AGGTGGCCCA GCGCATCACA GCGGAGCTGA AGCGCTACAG 1080  
 TATCCCCCAG GCGATCTTTG CGCAGAGGGT GCTGTGCCGG TCTCAGGGGA CTCTCTCCA 1140  
 CCTGCTCCGG AATCAAAAAC CGTGGAGTAA ACTCAAATCT GGCAGGGAGA CCTTCCGCGAG 1200  
 GATGTGGAAG TGGCTTCAGG AGCCCGAGTT CCAGCGCATG TCCGCTTAC GCCTGGCAGC 1260  
 GTGCAAAACG AAGAGCAAG AACCAACAAA AGACAGGAAC AATTCCAGA AGAAGTCCC 1320  
 CCTGGTGTTC ACTGACCTCC AACCGCGAAC ACTCTTGGCC ATCTTCAAGG AGAACAACG 1380  
 CCCGTCAAAG GAGATGCAGA TCACCATTTT CCAGCAGCTG GGCCTGGAGC TCACAACCGT 1440  
 CAGCAACTTC TCAATGAACG CCGCGCGCGG CAGCTGGAG AAGTGGCAAG ACATCTGAG 1500

CACAGGGGGC TCCTCGTCCA CCTCCAGCAC GTGTACCAAA GCATGATGGA AGGACTCTCA 1560  
 CTTGGGCACA AGTCACCTCC AATGAGGAC AACAGATACC AAAAGAAAAC AAAGGAAAAA 1620  
 GACACCGGAT TCCTAGCTGG GCCCTTCAC TGGTG

Seq ID NO: 476 Protein sequence  
 Protein Accession #: NP\_004843.1

1 11 21 31 41 51  
 MNPELTMESL GTLHGARGGG SGGGGGGGGG GGGGGPGHEQ ELLASPSPHH ARRGPGRSLR 60  
 GPPPPPTAHQ ELGTAATAAA AASRSAMVTS MASILDGGDY RPELSIPLHH AMSMSCDSSP 120  
 PGMGMSNTYT TLTPQLPLPP ISTVSDKFHH PHPHHHPHHH HHHHHQRLSG NVSGSFITLMR 180  
 DERGLPAMNN LYSYKEMPG MSQSLSPALAA TPLGNLGLGL HNAQQSLPNY GPPGHDKMLS 240  
 PNFDAAHTAM LTRGEQHLRS GLGTTPAAMM SHLNLGLHHPG HTQSHGVPVA PSRERPPSSS 300  
 SSSQVATSGQ LEEINTKEVA QRITAEKRY SIPQAIFAQR VLCSRSQGLS DLLRNPKPWS 360  
 KLKSGRETFR RMWKWLQEPF FORMSALRLA ACKRKEQEPN KDRNNSQKKS RLVTDLQRR 420  
 TLFAIFKENK RPSKEMQITI SQQLGLELTT VSNFFMNARR RSLEKWQDDL STGGSSSTSS 480  
 TCTKA

Seq ID NO: 477 DNA sequence  
 Nucleic Acid Accession #: NM\_013271.1  
 Coding sequence: 27..809

1 11 21 31 41 51  
 TCCGGAGCCA GGCCTCGCTGG GGCAGCATGG CGGGGTCGCC GCTGCTCTGG GGGCCGCGGG 60  
 CCGGGGGCGT CGGCCTTTTG GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCGCGC 120  
 TCTGCGCGCG GCCGTAAAG GAACCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG 180  
 AGACTGGCGC TCCTCGCCGC TTCCGGCGGT CAGTGCCCCG AGGTGAGGCG GCGGGGCGCG 240  
 TGCAGGAGCT GCGCGGGGCG CTGGCGCATC TGCTGGAGGC CGAACGTCAG GAGCGGGCGC 300  
 GGGCCGAGGC GCAGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG 360  
 TCTGGGGCGC CCCCCGCAAC TCTGATCCGG CTCTGGGCCT GGCACGACGAC CCGACGCGC 420  
 CTGCAGCGCA GCTCGCTCGC GCTCTGCTCC GCGCCCGCCT TGACCTGCC GCCCTAGCAG 480  
 CCCAGCTTGT CCCCCGCGCC GTCCCCGCGG CGGCGCTCCG ACCCCGCGCC CCGGTCTACG 540  
 ACGACGCGCC CCGCGGCCCG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600  
 CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660  
 TGGCAGCCCC GCGCCGCTC CGCCGTGCCG CCGACCACGA TGTGGGCTCT GAGCTGCCCC 720  
 CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAACGCGCT AGAGACCCCG GCGCCCCAGG 780  
 TGCTGCGAG CGCCTCTTTG CCACCTTGAG CACTGCCCCG ATCCCGTGCA CCCTGGGACC 840  
 CAGAAGTGCC CCGCCCATCC CGCCACCAGG ACTTCTCCCC GCCAGCACGT CCAGAGCAAC 900  
 TTACCCCGCG CAGCCAGCCC TCTCACCCGA GGATCCCTAC CCCCTGGCCC ACAATAACAT 960  
 GATCTGAGC

Seq ID NO: 478 Protein sequence  
 Protein Accession #: NP\_037403.1

1 11 21 31 41 51  
 MAGSPLLWGP RAGGVGLLV LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR 60  
 RSVPRGEAAG AVQELARALA HLLAERQER ARAEAQEAED QQARVLAQLL RVWGAPRNSD 120  
 PALGLDDDPD APAAQALARAL LRLRLDPAAL AAQLVPAPVP AALRPRPPV YDDGAPGPA 180  
 EEAGDETPDV DPELLRYLLG RILAGSADSE GVAAPRRLRR AADHDVGSSEL PPEGVLGALL 240  
 RVRKLETPAP QVPARLLLP

Seq ID NO: 479 DNA sequence  
 Nucleic Acid Accession #: NM\_002214  
 Coding sequence: 681..2990

1 11 21 31 41 51  
 CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGACG 60  
 CTGCCGACTT GTCTTTGCCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120  
 GTTGGCCTCC CTGCCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT 180  
 TCCCTCGAC CTGCGCGCGG TACCCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240  
 TAGGGTGGTT TCCCCCCAG CTTGGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300  
 CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT 360  
 TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT 420  
 TGGCCGTGCA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCCGTGCC GAGCCGGGAG 480  
 GGCCTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT 540  
 CCGAGCCGCG GGGTCCGCTT GCTAGGCTCG CGGAAAACGT CCTAGCGACA CTGCCCCGCG 600  
 GGGCCCGAGG TCGCCCGGGA GGCAGAGCCC GCGTCCGGA GGCAGCCAGG CGGCGGGCGC 660  
 GGGGCGGGCT GTTTTGCTAT ATGTGCGGCT CGGCCCTGGC TTTTITTAAC GCTGCAATTTG 720  
 TCTGCTGCA AAACGACCGG CGAGGTCCCG CCTGTTCTT CTGGGCAGCG TGGGTGTTT 780  
 CACTTGTCTT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840  
 CCTGTGCCAG GTGCCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA 900  
 TTTCAAGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTT CAATTTAATA AGCAAAGGCT 960  
 GCTCAGTTGA TTTCAATAGAA TACCATCTG TGCATGTTAT AATACCACT GAAATGAAA 1020  
 TTAATACCA GTGACACCA GGAGAAGTGT CTATCCAGCT CGGTCCAGGA GCCGAAGCTA 1080  
 ATTTTATGCT GAAAGTTTCA CCTCTGAAGA AATATCTGT GGTCTTTTAT TATCTTGTG 1140  
 ATGTCTCAGC ATCAATGAC AATAATATAG AAAAATTAAT TCCGTTGGA AACGATTAT 1200  
 CTAGAAAAAT AGCATTTTTC TCCGCTGACT TTCGCTTGG ATTTGGCTCA TACGTTGATA 1260  
 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT 1320  
 ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACA 1380  
 TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440

AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500  
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560  
 GCAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACTGCT 1620  
 5 ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680  
 ACAACAACAT TAATGTCTAT TTTGCAGTTC AAGGAAAACA ATTTCATTGG TATAAGGATC 1740  
 TTCTACCCCT CTTGCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800  
 ATAATTTGGT AGTGGAAAGC TATCAGAAGC TCATTTTCAGA AGTGAAAGTT CAGGTGGA 1860  
 ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920  
 10 CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCCTTTC AATGTAACAG 1980  
 TTCAATGAAA AAAATGTGAT GTCACAGGAG GAAAAAATA TGCAATAATC AAACCTATTG 2040  
 GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTGAG TGTGAGGACA 2100  
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAAG TGTTCCTAGT 2160  
 GTGATGAGAA TAAATGTCTAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220  
 15 ACAAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280  
 ACAAATTAAG GCTTGGAAAA GTGTATGGA AATACTGTGA AAAGGATGAC TTTTCTGTCT 2340  
 CATATCACC AAGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400  
 GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460  
 TCAATTCAA GGGCCAAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520  
 20 GCACCGATCC CAGGAGCATC GGCCTGCTCT GTGAACACTG CCCACCTGT TATACAGCCT 2580  
 GCAAGGAAAA CTGGAATTTG ATGCAATGCC TTCACCTCA CAATTTGTCT CAGGCTATAC 2640  
 TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAAACAAC GCATTATGTC GACCAAACTT 2700  
 CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAAATATTTT CATCATTTTC ATAGTTACAT 2760  
 TCTTGATTGG GTTGCTTAAA GTCCTGATCA TTAGACAGGT GATACTACAA TGAATAGTA 2820  
 25 ATAAATTAAG GTCCTCATCA GATTACAGAG TGTGAGCTCT AAAAAAGGAT AAGTTGATT 2880  
 TGCAAGTGT TTGCACAAGA GCAGTCACT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940  
 TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATT 3000  
 TTAACACATT AATGGGAAAC TGGAAATGTT AATAATTGCT CCTAAGATT ATAATTTTAA 3060  
 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT AACTCGAAC 3120  
 30 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180  
 AAAATGTGTC TTACTACTGT TTGAGACTAG TGTGCTGTTA GCACCTTACT GTAATATATA 3240  
 ACTTATTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300  
 TACCTGTTAT CCCTACGCTT CCCAGAGAGA ACAAATGCTGT GAGAGAGTTT AGCATTGTGT 3360  
 CACTACAAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420  
 35 TATATTCTAA GGTTCGCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480  
 ATGAATAAAT GATTGCTGTT TCACTCTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540  
 AAAGATTATT GCTTTTTTAA GTGTGTAGTT TTATGCATGT GTGTTTATGG TTTGCTTATT 3600  
 TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCCTCTT GCCTTTATGT TTTGTTTTCT 3660  
 TTTTACAGG ATAAAGTTTAT GTATGTCA CA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720  
 40 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT 3780  
 GAATGTTAA

Seq ID NO: 480 Protein sequence  
 Protein Accession #: NP\_002205

1 11 21 31 41 51  
 MCGSALAFFT AAFVCLQND RGPASFLWAA WVFSVLVLGL QGEDNRCASS NAASCARCLA 60  
 LGPECGWCQV EDFISGGSRS ERCDIVSNLI SKGCSVDSIE YPSVHVLIPT ENEINTQVTP 120  
 50 GEVSIQLRPG AEANFMKVH PLKKYPVDLY YLVDVSASMH NNIEKLNSVG NDLSRKMFAFF 180  
 SRDFRLGFGS YVDKTVSPYI SIHPERIHNQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA 240  
 VHRQKISGNI DTEGEGFDAM LQAAVCESHI GWRKEAKRL LVMTDQTSHL ALDSKLAGIV 300  
 VPNDGNCHLK NNVVVKSTTM EHPSLQVLSL KLIDNNINVI FAVQKGQFHW YKDLLPLPLP 360  
 TIAGEIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420  
 55 NVTSNDEVLV NVTVTMKKCD VTGKKNYAI KPIGFNETAK IHIHRNCSCQ CEDNRGPKGK 480  
 CVDETFLDSK CFQCDENKCH FDEDDQFSSES CKSHKDQFVC SGRGVCVCGK CSCCHKIKLKG 540  
 VYKGYCKKDD FSCPYHHGNL CAGHGECEAG RCQCFSGWEG DRQCQPSAAA QHCNVNSKGQV 600  
 CSGRGTCVCG RCECTDPRSI GRFCEHCPTC YTACKENWNC MQCLHPHNL QAILDQCKTS 660  
 CALMEQQHYV DQTSCECFSSP SYLRIFPIIF IVTFLIGLLK VLIIRQVILQ WNSNKKIKSSS 720  
 60 DYRVASASKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCNF

Seq ID NO: 481 DNA sequence  
 Nucleic Acid Accession #: NM\_003318.1  
 Coding sequence: 1..2574

1 11 21 31 41 51  
 ATGGAATCCG AGGATTTAAG TGGCAGAGAA TTGACAATTG ATTCCATAAT GAACAAAGTG 60  
 AGAGACATTA AAAATAAGTT TAAAAATGAA GACCTTACTG ATGAACTAAG CTTGAATAAA 120  
 70 ATTTCTGCTG ATACTACAGA TAACTCGGGA ACTGTTAACC AAATTATGAT GATGGCAAAC 180  
 AACCCAGAGG ACTGGTTGAG TTTGTTGCTC AAAGTAGAGA AAAACAGTGT TCCGCTAAGT 240  
 GATGCTCTTT TAAATAAATT GATTGGTCGT TACAGTCAAG CAATTGAAGC GCTTCCCCCA 300  
 GATAAATATG GCCAAATGA GAGTTTGTCT AGAATTCAAG TGAGATTGTC TGAATTAATA 360  
 GCTATTCAAG AGCCAGATGA TGCACGTGAC TACTTTCAAA TGGCCAGAGC AAATGCAAG 420  
 75 AAAATTGCTT TTGTTTCATAT ATCTTTTGCA CAATTTGAAC TGTCACAAGG TAATGTCAAA 480  
 AAAAGTAAAC AACTTCTTCA AAAAGCTGTA GAACGTGGAG CAGTACCACT AGAAATGCTG 540  
 GAAATTGCCC TGCGGAATT TAAACCTCAA AAAAAGCAGC TGCTTTTACA GGAGGAAAAA 600  
 AAGAATTAT CAGCATCTAC GGTATTAAC TCCCAAGAAT CATTTTCCGG TTCACTTGGG 660  
 CATTTACAGA ATAGGAACAA CAGTTGTGAT TCCAGAGGAC AGACTACTAA AGCCAGGTTT 720  
 80 TTATATGAG AGAATACATGCC ACCCAAGAT GCAGAAATAG GTTACCGGAA TTCATTGAGA 780  
 CAAACTAACA AAATTAACA GTCATGCCCA TTTGGAAGAG TCCAGATTAA CCTTCTAAAT 840  
 AGCCAGATT GTGATGTGAA GACAGATGAT TCAGTTGTAC CTTGTTTAT GAAAAGACAA 900  
 ACCTCTAGAT CAGAAATGCC AGATTGTGTT GTGCCTGGAT CTAACCAAG TGGAAATGAT 960  
 TCCTGTGAAT TAAGAAATTT AAAGTCTGTT CAAATAGTTC ATTTCAAGGA ACCTCTGGTG 1020  
 TCAGATGAAA AGAGTTCTGA ACTTATTAT ACTGATTCAA TAACCTGAA GAATAAAAGC 1080

5 GAATCAAGTC TTCTAGCTAA ATTAGAAGAA ACTAAAGAGT ATCAAGAACC AGAGGTTCCA 1140  
 GAGAGTAACC AGAAACAGTG GCAATCTAAG AGAAAGTCAG AGTGTATTAA CCAGAAATCCT 1200  
 GCTGCATCTT CAAATCACTG GCAGATTCCG GAGTTAGCCC GAAAAGTTAA TACAGAGCAG 1260  
 AAACATACCA CTTTTGAGCA ACCTGTCTTT TCAGTTTCAA AACAGTCACC ACCAATATCA 1320  
 ACATCTAAAT GGTTTGAGCCC AAAATCTATT TGTAAGACAC CAAGCAGCAA TACCTTGGAT 1380  
 GATTACATGA GCTGTTTTAG AACTCCAGTT GTAAAGAATG ACTTTCACC TGCTTGTGAG 1440  
 TTGTCAACAC CTTATGGCCA ACCTGCCTGT TTCAGCAGC AACAGCATCA AATACTTGCC 1500  
 ATTCCACTTC AAAATTTACA GGTTTTAGCA TCTTCTTCA CAAATGAATG CATTTCCGTT 1560  
 10 AAAGGAAGAA TTTATTCAT TTTAAAGCAG ATAGGAAGTG GAGGTTCAAG CAAGGTATTT 1620  
 CAGGTGTTAA ATGAAAGAA ACAGATATAT GCTATAAAAT ATGTGAACCT AGAAGAAGCA 1680  
 GATAACCAA CTCTTGATAG TTACCGGAAC GAAATAGCTT ATTTGAATAA ACTACAACAA 1740  
 CACAGTGATA AGATCATCCG ACTTTATGAT TATGAAATCA CGGACCAGTA CATCTACATG 1800  
 GTAATGGAGT GTGGAAATAT TGATCTTAAT AGTTGGCTTA AAAAGAAAAA ATCCATTGAT 1860  
 CCATGGGAAC GCAAGAGTTA CTGGAAAAAT ATGTTAGAGG CAGTTCACAC AATCCATCAA 1920  
 15 CATGGCATTG TTCACAGTGA TCTTAAACCA GCTAACTTTC TGATAGTTGA TGGAAATGCTA 1980  
 AAGCTAATTG ATTTTGGGAT TGCAAAACCA ATGCAACACG ATACAACAAG TGTTGTTAAA 2040  
 GATTCTCAGG TTGGCAGCAGT TAATATATAT CCACAGAAAG CAATCAAAGA TATGCTCTCC 2100  
 TCCAGAGAGA ATGGGAAATC TAAGTCAAAG ATAAGCCCCA AAAGTGATGT TTGGTCTTCA 2160  
 GGATGTATTT TGTACTATAT GACTTACGGG AAAACACCAT TTCAGCAGAT AATTAATCAG 2220  
 20 ATTTCTAAAT TACATGCCAT AATTGATCCT AATCATGAAA TTGAATTTCC CGATATTCCA 2280  
 GAGAAAGATC TTCAAGATGT GTTAAAGTGT TGTTTAAAAA GGGACCCAAA ACAGAGGATA 2340  
 TCCATTCCTG AGCTCCTGGC TCATCCCTAT GTTCAAATTC AAACCTATCC AGTTAAACCA 2400  
 ATGGCCAAGG GAACACTGAA AGAAATGAAA TATGTTCTGG GCCAACTTGT TGGTCTGAAT 2460  
 25 TCTCCTAACT CCATTTTGAA AGCTGCTAAA ACTTTATATG AACACTATAG TGGTGGTGAA 2520  
 AGTCATAATT CTTCTCTCTC CAAGACTTTT GAAAAAATAA GGGGAAAAAA ATGA

Seq ID NO: 482 Protein sequence  
 Protein Accession #: NP\_003309.1

30 1 11 21 31 41 51  
 MESEDLSGRE LTIDSIMNKV RDIKNKFKNE DLTDELSLNK ISADTTDMSG TVNQIMMMAN 60  
 NPEDWLSLLL KLEKNSVPLS DALLNKLIGR YSQAIEALPP DKYQGNESFA RIQVRFABLK 120  
 35 ATQEPDARD YFQMARANCK KFAFVHISFA QFELSQGNVK KSKQLLQKAV ERGAVPLEML 180  
 ETALRNLNLQ KQQLSEEEK KNLSASTVLT AQESFSGSLG HLQNRNNSCD SRGQTTKARF 240  
 LYGENMPPQD AEIGYRNSLR QTNKTKQSCP FGRVPVNLIN SPDCDVKTDD SVVPCFMKRO 300  
 TSSRCDRLV VPSKPSGND SCELRLKSV QNSHFKEPLV SDEKSSELI TDSITLKNKT 360  
 ESSLLAKLEE TKBYQPEPEV ESNQKQWQSK RKSECIQNPN AASSNHQWIP ELARKVNTAQ 420  
 40 KHTTFBQPVF SVSKQSPFIS TSKWFDPKSI CKTPSSNTLD DYMSCFRTPV VKNDFPPACQ 480  
 LSTPYGQAPC FQQQQHQILA TPLQNLQVLA SSSANECISV KGRIYSILKQ IGSGGSSKVF 540  
 QVLNEKKQIY AIKYVNLLEEA DNQTLDSYRN ETAYLNKLQQ HSDKIIRLYD YEITDQYIYM 600  
 VMBCGNIDLN SWLKKKKSID PWERKSYWKN MLEAVHTIHQ HGIVHSDLPK ANFLIVDGLM 660  
 KLIDFGLIANQ MQPDTTSSVVK DSQVGTVNYM PPEAIKDMSS SRENGKSKSK ISPKSDVWSL 720  
 45 GCILYMYTYG KTFPQQIINQ ISKLHAIIDP NHEIEFPDIP EKDLQDVLKC CLKRDPKQRI 780  
 SIPELLAHPY VQIQTHPVNQ MAKGTTEEMK YVLGQLVGLN SPNSILKAAK TLYEHYSGGE 840  
 SHNSSSSKTF EKKRGKK

Seq ID NO: 483 DNA sequence  
 Nucleic Acid Accession #: NM\_003667.1  
 Coding sequence: 1..2651

50 1 11 21 31 41 51  
 ATGGACACCT CCCGGCTCGG TGTGCTCCTG TCCTTGCTCG TGCTGCTGCA GCTGGCGACC 60  
 55 GGGGGCAGCT CTCCCAGGTC TGGTGTGTTG CTGAGGGGCT GCCCCACACA CTGTCAATTGC 120  
 GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG ACCTGGGGCT CTGGGAGCTG 180  
 CCTTCCAACC TCAGCGCTTT CACCTCTTAC CTAGACCTCA GTATGAACAA CATCAGTCAG 240  
 CTGCTCCCGA ATCCCCTGCC CAGTCTCCGC TTCTGGAGG AGTTACGTCT TCGCGGAAAC 300  
 60 GCTCTGACAT ACATTCCCAA GGGAGCATTC ACTGGCCTTT ACAGTCTTAA AGTTCTTATG 360  
 CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC TGCAGAATT TCGAAGCCTT 420  
 CAATCCCTGC GTCTGGATGC TAACCACATC AGCTATGTGC CCCCAGCTG TTTCACTGGC 480  
 CTGCAATCCC TGAGGCACCT GTGGCTGGAT GACAATGCGT TAACAGAAAT CCCCGTCCAG 540  
 GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG CCCTGAACAA AATACACCAC 600  
 65 ATACCAGACT ATGCCTTTGG AAACCTCTCC AGCTTGGTAG TTCTACATCT CCATAACAAT 660  
 AGAATCCACT CCCTGGGAAA GAAATGCTTT GATGGGCTCC ACAGCCTAGA GACTTTAGAT 720  
 TTAAATTACA ATAACTTGA TGAATTCCTC ACTGCAATTA GGACACTCTC CAACCTTAAA 780  
 GAACTACATT TCTATGACAA TCCCATCCAA TTTGTTGGGA GATCTGCTTT TCAACATTTA 840  
 70 CCTGAACATA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACTGAATT TCCTGATTTA 900  
 ACTGGAACAG CAAACCTGGA GAGTCTGACT TTAAGTGGAG CACAGATCTC ATCTCTTCTT 960  
 CAAACCGTCT GCAATCAGTT ACCTAATCTC CAAGTGCTAG ATCTGTCTTA CAACCTATTA 1020  
 GAAGATTAC CCAAGTTTTC AGTCTGCCAA AAGCTTCAGA AAATGACCT AAGACATAAT 1080  
 GAAATCTACG AAATTAAGT TGACACTTTC CAGCAGTTGC TTAGCCTCCG ATCGCTGAAT 1140  
 TTGGCTTGA ACAAAATGTC TATTATTCAC CCCAATGCAT TTTCCACTTT GCCATCCCTA 1200  
 75 ATAAAGCTGG ACCATCTCGT CAACCTCCTG TCGTCTTTTC CTATAACTGG GTTACATGGT 1260  
 TTAACCTACT TAAATTAAC AGGAAATCAT GCCTTACAGA GCTTGATATC ATCTGAAAAC 1320  
 TTTCCAGAAC TCAAGGTTAT AGAAATGCCT TATGCTTACC AGTGTCTGTC ATTTGGAGTG 1380  
 TGTGAGAATG CCTATAAGAT TTCTAATCAA TGGAATAAAG GTGACAACAG CAGTATGGAC 1440  
 GACCTTCATA AGAAAGATGC TGGAAATGTT CAGGCTCAAG ATGAACGTGA CCTTGAAGAT 1500  
 80 TTCCTGCTGT ACTTTGAGGA AGACCTGAAA GCCCTTCATT CAGTGCAGTG TTCACCTTCC 1560  
 CCAGGCCCTC TCAAACCTCG TGAACACCTG CTGTATGGCT GGCTGATCAG AATTGGAGTG 1620  
 TGGACCATAG CAGTTCTGCG ACTTACTTGT AATGCTTTGG TGACCTCAAC AGTTTTCAGA 1680  
 TCCCCTCTGT ACATTTCCCC CATTAAACTG TTAATTGGGG TCATGCGCAG AGTGAACATG 1740  
 CTCACGGGAG TCTCAGTGC CGTGCTGGCT GGTGTGGATG CGTTCACCTT TGGCAGCTTT 1800  
 GCACGACATG GTGCCTGGTG GAGACTTGGG GTTGGTTGCC ATGTCATTGG TTTTGTGTC 1860

ATTTTGTGCTT CAGAATCATC TGTTCCTCTG CTTACTCTGG CAGCCCTGGA GCGTGGGTTC 1920  
 TCTGTGAAAT ATTCTGCAAA ATTTGAAACG AAAGCTCCAT TTTCTAGCCT GAAAGTAATC 1980  
 ATTTTGTCTCT GTGCCCTGCT GGCCTTGACC ATGGCCGCGAG TTCCCTGCTT GGGTGGCAGC 2040  
 AAGTATGGCG CCTCCCTCTCT CTGCCTGCCT TTGCCTTTTG GGGAGCCCGAC CACCATGGGC 2100  
 TACATGGTCCG CTTCTCATCTT GCTCAATTCC CTTTGCTTCC TCATGATGAC CATTGCCCTAC 2160  
 ACCAAGCTCT ACTGCAATTT GGACAAGGGA GACCTGGAGA ATATTTGGGA CTGCTCTATG 2220  
 GTAAACACA TTGCCCTGTT GCTCTTCACC AACTGCATCC TAAACTGCC TGTGGCTTTC 2280  
 TTGTCTTCTT CCTCTTTAAT AAACCTTACA TTTATCAGTC CTGAAGTAAT TAAGTTTATC 2340  
 TCTTCTGGTGG TAGTCCCACT TCCTGCATGT CTCAATCCCC TTCTCTACAT CTTGTTCAAT 2400  
 CCTCACTTTA AGGAGGCTCT GGTGAGCCTG AGAAAGCAAA CCTACGCTG GACAAGATCA 2460  
 AAACACCCAA GCTTGATGTC AATTAACCTCT GATGATGTCG AAAACAGTC CTGTGACTCA 2520  
 ACTCAAGCCT TGGTAACCTT TACCAGCTCC AGCATCACTT ATGACCTGCC TCCCAGTTCC 2580  
 GTGCCATCAC GCCTTATCC AGTGACTGAG AGCTGCCATC TTTCTCTGT GGCATTTGTC 2640  
 CCATGTCTTA A

Seq ID NO: 484 Protein sequence  
 Protein Accession #: NP\_003658.1

1 11 21 31 41 51  
 | | | | |  
 MDT SRLGVLL SLPVLLQLAT GSSSFRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVL 120  
 LQNNQLRHVP TEALQNLRSQ QSLRLDANHI SYVPPSCFSG LHSRLHLWLD DNALTEIPVQ 180  
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETL 240  
 LNYNNLDEFP TAIRTLNLK ELHFYDNPIQ FVGRSAFQHL PELRLTLNG ASQITEFPDL 300  
 TGTANLESLT LTGAQISSLP QTVCNQLPNL QVLDLSYNLL EDLPSFSVCQ KLQKIDLRHN 360  
 BIYEIKVDTF QQLSLRLSLN LAWNKIAIHH PNAFSTLPSL IKLDDLSSNLL SSFPITGLHG 420  
 LTHLKLGTGN ALQSLISSEN FPELKVIEPM YAYQCCAFGV CENAYKISNQ WNKGDNSMMD 480  
 DLHKKDAGMF QAQDERDLED FLDDFEEDLK ALHSVQCSFS PGPFPKCEHL LDGWLIRIGV 540  
 WTI AVLALTC NALVTSTVFR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDATFTGFSF 600  
 ARHGAWWENG VGCHVIGFLS IFASESSVFL LTLAALERGF SVKYSKAFET KAPFSSLKVI 660  
 ILLCALLALT MAAPVLLGGS KYGASPLCLP LPFGEPSTMG YMVALILLNS LCFLMMTIAY 720  
 TKLYCNLDKG DLENLWDCSM VKHIALLLFT NCILNCPVAF LSFSSSLINLT FISPEVIKFI 780  
 LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS 840  
 TQALVTFTSS SITYDLPPSS VPSPAYPVTB SCHLSSVAFV PCL

Seq ID NO: 485 DNA sequence  
 Nucleic Acid Accession #: NM\_005756.1  
 Coding sequence: 73..3117

1 11 21 31 41 51  
 | | | | |  
 AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60  
 CTCGCGGTCA GGATGGTTTT CTCTGTCAGG CAGTGTGGCC ATGTGTGGCAG AACTGAAGAA 120  
 GTTTTACTGA CGTTCAGAT ATTCCTTGTC ATCATTGTCT TCCATGTCTG TCTGGTAACA 180  
 TCCCTGGAAG AAGATATCTA TAATTCCAGT TTGTCAACCAC CACCTGCTAA ATTATCTGTT 240  
 GTACGTTTTG CCCCCCTCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300  
 AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAAATCA CTATAGTAAA AACCTTCAAT 360  
 GCTTCAGGGC TCAAAACCCA GAGAAATATC TGCAATTTGT CATCTATTGT CAATGACTCA 420  
 GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAA 480  
 CAACATATAA CGAATGGCAC CTTAACTGGA GTCTGTCTCT TAAGTGAAT AAAACGCTCA 540  
 GAGCTCAACA AAACCTTGCA AACCTTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600  
 GAGGCCCAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA 660  
 TGTGCTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTGCGAC CAATGGAAACA CTGCTGCTGT 720  
 TCTGTGAGGA TACCTCTGCC TTCTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780  
 CAGGATCCCA TTGCTGTCTCT TGCTGACCAT CCACGTGGCC CACCATTTC TTCCAGCCAA 840  
 TCCATCCCG TGGTGCTCTG GGCACATGTG CTTTCCAGG TCCCAAAAGC TACCTCTTTT 900  
 GCTGAGCCTC CAGATTATTC ACCTGTGACC CACAATGTTT CCTCTCCAAT AGGGGAGATT 960  
 CAACCCCTTT CACCCAGGCC TTCAGTCCCT ATAGCTTCCA GCCCTGCCAT TGACATGCCC 1020  
 CCACGCTCTG AAACGATCTC TTCCCTATG CCCCACACCC ATGTCTCCGG CACCCACCT 1080  
 CCTGTGAAAG CCTCATTTTC CTCTCCACC GTGTCTGCCC CTGCGAATGT CAACACTACC 1140  
 AGCGCACCTC CTGTCCAGAC AGACATCGTC AACACCAGCA GTATTCTGTA TCTTGAGAAC 1200  
 CRAAGTGTG AGATGGAGAA GGCTCTGTCC TTGGGCAGCC TGGAGCCTAA CCTCGCAGGA 1260  
 GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCCTCCG CTGACATGCT GGCCCCCTCTG 1320  
 GCTCAAAGAT TGCTGAAAGT AGTGGATGAC ATTTGGCTTAC AGCTGAACCT TTCAAACACG 1380  
 ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440  
 TTCAACACAA CTACCTTTGT GGCCCAAGAC CCTGCAAAATC TTCAGGTTTC TCTGGAAACC 1500  
 CAAGCTCCTG AGAACAGTAT TGGCACAATT ACTCTTCCTT CATCGCTGAT GAATAATTTA 1560  
 CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTTTTGA AACACCTGCT 1620  
 TTGTTTCAAG ATCTCTCCCT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT 1680  
 GTTGCAAAAC TGACCCGTGAG GAACCTTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740  
 AACCAGAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGGT 1800  
 GGCAGAGGAG GCTGGTCAGA CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAAACC 1860  
 ATCTGTACCT GTAGCCATCT AACAAAGCTT GGCCTTCTGC TGGACCTATC TAGGACATCT 1920  
 GTGCTGCTCT CTCAAAATGAT GGCTCTGACG TTCATTACAT ATATTGTTG TGGGCTTTCA 1980  
 TCAATTTTTT TGTGAGTGAC TCTTGTAACC TACATAGCTT TTGAAAGAT CCGGAGGGAT 2040  
 TACCCTTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CCTGGTCTTC 2100  
 CTCTCTGACT CGTGGATTGC TCTGTATAAG ATGCAAGGCC TCTGCATCTC AGTGGCTGTA 2160  
 TTTTCTCAT ATTCTCTCTT GGTCTCATTC ACATGGATGG CCCTAGAAGC ATTCCATATG 2220  
 TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATCTGTC 2280  
 ATTGTGCTT GGGGGGTACC AGCTGTGGTT GTGACCATCA TCCTGACTAT ATCCCCAGAT 2340  
 AACTATGGGC TTGGATCCTA TGGGAAATTC CCCAATGGTT CACCGGATGA CTTCTGCTGG 2400  
 ATCAACAACA ATGCAATTAT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTTC 2460  
 CTGACGTCGA GCATGTTTAT TGTGCTCCTG GTTCAGTCTT GTCGAATTA AAAGAAGAAG 2520

5  
10  
15  
20  
25  
30  
35

```

CAACTGGGAG CCCAGCGAAA AACCAGTATT CAAGACCTCA GGAGTATCGC TGGCCTTACA 2580
TTTTTACTGG GAATAACTTG GGGCTTTGCC TTCTTTGCCCT GGGGACCAGT TAACGTGACC 2640
TTCATGTATC TGTTTGCCAT CTTTAATACC TTACAAGGAT TTTTCATATT CATCTTTTAC 2700
TGTTGGGCCA AAGAAAATGT CAGGAAGCAA TGGAGGCGGT ATCTTTGTTG TGGAAAGTTA 2760
CGGCTGGCTG AAAATTCTGA CTGGAGTAAA ACTGCTACTA ATGGTTTAAA GAAGCAGACT 2820
GTAAACCAAG GAGTGTCCAG CTCTTCAAAAT TCCTTACAGT CAAGCAGTAA CTCCACTAAC 2880
TCCACCACAC TGCTAGTGAA TAATGATTGC TCAGTACACG CAAGCGGAAA TGGAAATGCT 2940
TCTACAGAGA GGAATGGGGT CTCTTTTAGT GTTCAGAATG GAGATGTGTG CCTTCACGAT 3000
TTCACTGGAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCCGT 3060
ATGGCTCTCA GAAGGACTTC AAAGCGGGGA AGCTTACACT TTATTGAGCA AATGTGATTC 3120
CTTTCTTCTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA 3180
CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT 3240
AAGCTAATTA AGGCGGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300
TTTAGACATT TCTGATTGGG TTTCTTATCT TTCATTTTAT AAGAAGGTTG GTTTTAAACA 3360
ATACACTAAG AATGACTCCT ATAAAGAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420
TTTAAAGAGG CTAAGTTATC TTTGATAACA TCATATAAAG CAACTGTGTA CTTCAGCCTG 3480
TTGGTGAGTT TAGTTGTGCA TGCCCTTTGT GTATATAAGC TAAATTCTAG TGACCCATGT 3540
GTCAAAAATC TTACTTCTAC ATTTTCTTGT ATTTATTTTC TACTGTGTAA ATGTATTCTT 3600
TTGTAGAATC ATGGTTGTTT TGTCTCACGT GATAATTCAG AAAATCCTTG CTCGTTCCGC 3660
AAATCCTAAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA 3720
TCAAGAAATA ATGATCCAG CAGACTGAG AAAATGTAA GAGACAGTGC CACAGTTAGC 3780
TCATACAGTG CTTTGTAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840
TGGGTCAATG CTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900
GTGCACGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCATCCTC CTGACCGCAT 3960
CCCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020
AGAGGGATGA ACTGTCTACC AGACCATGTG TCAGGAAAAT TGTGAACGTA GATGAGGTAC 4080
ATACACTGCC GCTTCTCAA TCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC 4140
CTTCTCTTAA AAAGGTACAT ATATATGGAA AAAAATCATA TTGCCGTCTT TAAAAGGCA 4200
ACTGCATGGT ACATTGTGTA TTGTATGAC TGGTACACTC TGGCCCAGCC AGAGCTATAA 4260
TTGTTTTTTA ATATGTGCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320
GGGAACCTGC CTACACTGCT ATTGTGCTA CATGTATCGA GCCTTGATTG CTCCTAGTTA 4380
TATACAGGGT CTATCTTGCT TCCTACCTAC ATCTGCTTGA CCACTGCTTC AAGTACATCC 4440
TTATTAGGAA CATTTCAAAC CCCTTTTAGT TAAGTCTTTC ACTAAGGTTT TCTTGATAT 4500
ATTTCAAGTG AATGTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560
CTGACTTGTC TTTGCAATAT TTCTTTCTG ATTTATTTAA TTTTCTTGA TTTATATGTT 4620
AAAAATCAAA ATGTTAAAAA CAATGAAATA AATTGTCAGT TAAGA

```

Seq ID NO: 486 Protein sequence  
Protein Accession #: NP\_005747.1

40  
45  
50  
55  
60

```

1 11 21 31 41 51
| | | | |
MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSP PAKLSVVSFA 60
PSSNEVETTS LNDVTLSELL SNETGVKQPR NICNLSSICN DSAFFRGEIM PQYDKESTVP 120
QNQHITNGTL TGVLSLSELK RSELNKLQT LSETYFIMCA TAEAQSTLNC TFTIKLNNTM 180
NACAVIAALE RVKIRPMEHC CCSVRIPCPS SPEELEKLQC DLQDPVCL A DHPGRPPFSS 240
SQSIPVVPRA TVLSQVPKAT SFAEPPDYSP VTHNVSPIG EIQPLSPQPS APIASSPAID 300
MPPQSETISS PMPQTHVSGT PPPVKASFSS PTVSAPANVN TTSAPPVQTD IVNTSSISDL 360
ENQVLQMEKA LSLGLEPNL AGEMINQVSR LLHSPDMLA PLAQRLLKV DDIGLQLNFS 420
NTTISLTPS LALAVIRVNA SSENTTFVA QDPANLQVSL ETQAPENSIG TITLPSLMLN 480
NLPAHDMELA SRVQNFNFFET PALFQDPSLE NLSLISYVIS SSVANLTVRN LTRNVTVTLK 540
HINPSQDELT VRCVFWDLGR NGGRGWSDN GCSVKDRRLN ETICTCSHLT SFGVLLDLR 600
TSVLPAQMA LTFITYIGCG LSSIFLSVTL VTYIAFEKIR RDYPSKILIQ LCAALLLNL 660
VFLDSWIAL YMQGLCISV AVFLHYFLV SFTWMGLEAF HMYLALVKVF NTYIRKYILK 720
FCIVGWGVA VVMTIILTIS PDNYGLGSYG KFPNGSPDDF CWINNNNAVFI ITVVGYFCVI 780
FLLNVSMFIV VLVQLCRIKK KQLGAQRKT SIQDLRSIAG LTFLLGITWG FAFFAWGPVN 840
VTFMYLFAIF NTLQGFIFIFI FYCVAKENVR KQWRRYLCCG KLRLAENS DW SKTATNGLKK 900
QTVNQGVSSS SNSLQSSNS TNSTLLVNN DCSVHASNG NASTERNGVS FSVQNGDVCL 960
HDFTGKQHMF NEKEDSCNGK GRMALRRTSK RGLSHFIEQM

```

Seq ID NO: 487 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2904

65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
ATGGTTTCT CTGTCAGGCA GTGTGGCCAT GTTGGCAGAA CTGAAGAAGT TTTACTGACG 60
TTCAAGATAT TCCTTGTCAT CATTGTCTT CATGTCGTTT TGGTAACATC CCTGGAAGAA 120
GATACTGATA ATTCAGTTT GTCACCACCA CCTGATGTTA CTTAAGCTT ACTCCCTTCA 180
AACGAAACAG AAAAACTAA AATCATTATA GTAAAAACCT TCAATGCTTC AGGCGTCAA 240
CCCCAGAGAA ATATCTGCAA TTTGTCTATC ATTTGCAATG ACTCAGCATT TTTTAGAGGT 300
GAGATCATGT TCAATATGA TAAAGAAAGC ACTGTTCCCC AGAATCAACA TATAACGAAT 360
GGCACCTTAA CTGGAGTCTT GTCTCTAAGT GAATTAACA CATTAAATTG TACATTCACA 420
ATAAACTGA ATAATACAAT GAATGCATGT GCTGTAATAG CTGCTTTGGA AAGAGTAAAG 480
ATTGCAACAA TGAACACTG CTGCTGTCTT GTCAGGATAC CCTGCCCTTC CTCCCAGAA 540
GAGTTGGAAA AGCTTCAGTG TGACCTGCAG GATCCCATTG TCTGTCTTGC TGACCATCCA 600
CGTGGCCAC CATTTCTTC CAGCCAATCC ATCCCACTGG TGCCTCGGGC CACTGTGCTT 660
TCCAGGTTCC CCAAGCTAG CTCTTTTGCT GAGCCTCCAG ATTATTCACT TGTGACCCAC 720
AATGTTCCCT CTCCTCAATAG GGAGATTCAA CCCCTTTCAC CCCAGCCTTC AGCTCCATA 780
GCTTCCAGCC CTGCCATTGA CATGCCCCCA CAGTCTGAAA CGATCTCTTC CCTTATGCCC 840
CAAAACCATG TCTCCGGCAC CCCACTCCT GTGAAAGCCT CATTTCTCTC TCCCACCGTG 900
TCTGCCCTG CGAATGTCAA CACTACCAGC GCACCTCCTG TCCAGACAGA CATCGTCAAC 960
ACCAGCAGTA TTTCTGATCT TGAGAACCAA GTGTTGCAGA TGGAGAAGGC TCTGTCTTGT 1020
GGCAGCCTGG AGCCTAACCT CGCAGGAGAA ATGATCAACC AAGTCAGCAG ACTCCTTCAT 1080

```

5	TCCCCGCGCTG	ACATGCTGGC	CCCTCTGGCT	CAAAGATTGC	TGAAAGTAGT	GGATGACATT	1140
	GGCCTACAGC	TGAACCTTTT	AAACACGACT	ATAAGTCTAA	CCTCCCCTTC	TTTGGCTCTG	1200
	GCTGTGATCA	GAGTGAATGC	CAGTAGTTTC	AACACAACCTA	CCTTTGTGGC	CCAAGACCTT	1260
	GCAAATCTTC	AGGTTTCTCT	GGAAACCCAA	GCTCCTGAGA	ACAGTATTGG	CACAATTACT	1320
	CTTCCTTCAT	CGCTGATGAA	TAATTTACCA	GCTCATGACA	TGGAGCTAGC	TTCCAGGGTT	1380
	CAGTTCAATT	TTTTTGAAAC	ACCTGCTTTG	TTTCAGGATC	CTTCCCTGGA	GAACCTCTCT	1440
	CTGATCAGCT	ACGTCATATC	ATCGAGTGT	GCAAACCTGA	CCGTCAGGAA	CTTGACAAGA	1500
	AACGTGACAG	TCACATTTAA	GCACATCAAC	CCGAGCCAGG	ATGAGTTAAC	AGTGAGATGT	1560
10	GTATTTTGGG	ACTTGGGCAG	AAATGGTGGC	AGAGGAGGCT	GGTCAGACAA	TGGCTGCTCT	1620
	GTCRAAGACA	GGAGATTGAA	TGAAACCATC	TGTACCTGTA	GCCATCTAAC	AAGCTTCGGC	1680
	GTTCTGCTGG	ACCTATCTAG	GACATCTGTG	CTGCTGCTC	AAATGATGGC	TCTGACGTTT	1740
	ATTACATATA	TTGGTTGTGG	GCTTTTCATCA	ATTTTCTGT	CAGTGACTCT	TGTAACCTAC	1800
	ATAGCTTTTG	AAAAGATCCG	GAGGGATTAC	CCTTCCAAAA	TCCTCATCCA	GCTGTGTGCT	1860
	GCTCTGCTTC	TGCTGAACCT	GGTCTTCCTC	CTGACTCGT	GGATTGCTCT	GTATAAGATG	1920
15	CAAGGCTCT	GCATCTCAGT	GGCTGTATTT	CTTCATTATT	TTCTCTGGT	CTCATTCACA	1980
	TGGATGGGCC	TAGAAGCAIT	CCATATGTAC	CTGGCCCTTG	TCAAAGTATT	TAATACTTAC	2040
	ATCCGAAAAAT	ACATCCTTAA	ATTCTGCATT	GTCGGTTGGG	GGGTACCAGC	TGTGGTTGTG	2100
	ACCATCATCC	TGACATATAT	CCAGATAAAC	TATGGGCTTG	GATCCTATGG	GAAATTCCTC	2160
	AATGGTTTAC	CGGATGACTT	CTGCTGGATC	AACAACAATG	CAGTATTCTA	CATTACGGTG	2220
20	GTGGGATATT	TCTGTGTGAT	ATTTTGTGCT	AACGTCAGCA	TGTTTCATTGT	GGTCTCTGGT	2280
	CAGCTCTGTC	GAATTAATAA	GAAGAAGCAA	CTGGGAGCCC	AGCGAAAAAC	CAGTATTCAC	2340
	GACCTCAGGA	GTATCGCTGG	CCTTACATT	TACTGGGAA	TAAGTGGGG	CTTTCCTTTC	2400
	TTTGCTGGG	GACCACTTAA	CGTGACCTTC	ATGTATCTGT	TGCCATCTT	TAATACCTTA	2460
	CAAGGATTTT	TCATATTCAT	CTTTTACTGT	GTGGCCAAAG	AAAAATGTCAG	GAAGCAATGG	2520
25	AGGCGGTATC	TTTGTGTGTT	AAAGTTACGG	CTGGCTGAAA	ATTCTGACTG	GAGTAAAACT	2580
	GCTACTAATG	TTTAAAGTAA	GCAGACTGTA	AACCAAGGAG	TGTCAGCTC	TTCAAATTC	2640
	TTACAGTCAA	GCAGTAACTC	CACTAACTCC	ACCACACTGC	TAGTGAATAA	TGATTGCTCA	2700
	GTACACGCAA	GCGGGAATGG	AAATGCTTCT	ACAGAGAGGA	ATGGGGTCTC	TTTTAGTGT	2760
30	CAGAATGGAG	ATGTGTGCTT	TCACGATTTT	ACTGGAAAAC	AGCAGATGTT	TAACGAGAAG	2820
	GAAGATTCTT	GCAATGGGAA	AGGCCGTATG	GCTCTCAGAA	GGACTTCAAA	GCGGGGAAGC	2880
	TTACACTTTA	TTGAGCAAAT	GTGA				

Seq ID NO: 488 Protein sequence  
Protein Accession #: Eos sequence

35	1	11	21	31	41	51	
	MVFSVRQCGH	VGRTEEVLLT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSP	PDVTLSLLPS	60
	NETEKTKITI	VKTFNAGSVK	PQRNICNLSS	ICNDSAFFRG	EIMFQYDKES	TVFPQNHITN	120
40	GLTLGVLSLS	ELMNLNCTFT	IKLNNMTNAC	AVIAALERVK	IRPMEHCCCS	VRIPCPSPE	180
	ELEKLQCDLQ	DPVIVCLADHP	RGPPFSSSSQS	IPVVPRAITVL	SQVPKATSPA	EPDYSPTV	240
	NVSPPIGEIQ	PLSPQPSAPI	ASSPAIDMPP	QSETISSPMP	QTHVSGTPPP	VKASFSSPTV	300
	SAPANVNTTS	APPVQTDIVN	TSSISDLENQ	VLQMEKALSL	GSLEPNLAGE	MINQVSRLLH	360
	SPPDMLAPLA	QRLKVVDDI	GLQLNFSNTT	ISLTSPLSAL	AVIRVNASSF	NTTTFVAQDP	420
45	ANLQVSLLET	APENSIGTIT	LPSSLMNNLP	AHDMELASRV	QFNFFETPAL	FQDPSLENLS	480
	LISYVSISSV	ANLTVRNLRT	NVTVTLLKHIN	PSQDELTVRC	VFWDLGRNGG	RGWSDNGCS	540
	VKDRRLNETI	CTCSHLTSFG	VLLDLRSITSV	LPAQMMALTF	ITYIGCGLSS	IFLSVTLVTY	600
	IAFEKIRRDY	PSKILILQCA	ALLLLNLVFL	LDSWIALYKM	QGLCISVAVF	LHYFLLVSFT	660
	WMGLEAFHMY	LALVVKVNTY	IRKYILKFCI	VGWGVPAVVV	TIILTISPDPN	YGLGSYGFKP	720
50	NGSPDDFCWI	TENNAVFYITV	VGYPVIFLL	NVSMFIVVLV	QLCRIKKKKQ	LGAQRKTSIQ	780
	DLRSIAGLTF	LLGTTWGFAT	FAWGPVNVTF	MYLFAIFNTL	QGFFIFIFYC	VAKENVRKQW	840
	RRYLCCGKLR	LAENSWSKLT	ATNLGKKQTV	NQGVSSSSNS	LQSSSNSTNS	TTLLVNNDCS	900
	VHASGNNGAS	TERNGVSFSV	QNGDVCLHDF	TGKQHFNEK	EDSCNGKGRM	ALRRTSKRGS	960
55	LHFIEQM						

Seq ID NO: 489 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2811

60	1	11	21	31	41	51	
	ATGGTTTTCT	CTGTCAGGCA	GTGTGGCCAT	GTTGGCAGAA	CTGAAGAAGT	TTTACTGACG	60
	TTCAAGATAT	TCCTTGTCAT	CATTGTCTTT	CATGTCGTTT	TGGTAACATC	CCTGGAAGAA	120
	GATACTGATA	ATTCCAGTTT	GTCACCACCA	CCTGAGGTTG	AAACAACAAG	CCTCAATGAT	180
65	GTTACTTTAA	GCTTACTCCC	TTCAAACGAA	ACAGGCGTCA	AACCCACAG	AAATATCTGC	240
	AATTGTGTCAT	CTATTGTCAA	TGACTCAGCA	TTTTTTAGAG	GTGAGATCAT	GTTTCAATAT	300
	GATAAAGAAA	GCACGTGTTT	CCAGAATCAA	CATATAACGA	ATGGCACCTT	AACTGGAGTC	360
	CTGTCTCTAA	GTGAATTAAT	ACGCTCAGAG	CTCAACAAAA	CCCTGCAAAC	CCTAAGTGAG	420
70	ACTTACTTTA	TAATGTGTGC	TACAGCAGAG	GCCCAAAGCA	CATTAAATTG	TACATTACAC	480
	ATAAACTGTA	ATAATACAAT	GAATGCATGT	GCTGTAATAG	CTGCTTTGGA	AAGAGTAAAG	540
	ATTGACCAAA	TGGAACACTG	CTGCTGTTCT	GTCAGGATAC	CCTGCCCTTC	CTCCCCAGAA	600
	GAGTTGGAAA	AGCTTCAGTG	TGACCTGCAG	GATCCCATTT	TCTGTCTTGC	TGACCATCCA	660
	CGTGGCCCAT	CATTTTCTTC	CAGCCAATCC	ATCCAGTGG	TGCGCTCGGC	CACGTGCTTT	720
75	TCCCAGGTCC	CCAAAGCTAC	CTCTTTTGCT	GAGCCTCCAG	ATTATTACCC	TGTGACCCAC	780
	AATGTTCCCT	CTCCAATAGG	GGAGATTCAA	CCCCTTTTAC	CCCAGCCTTC	AGCTCCCAT	840
	GCTTCCAGCC	CTGCCATTGA	CATGCCCCCA	CAGTCTGAAA	CGATCTCTTC	CCCTATGCC	900
	CAAACCCATG	TCTCCGGCAC	CCCACCTCTT	GTGAAAGCCT	CATTTTCTCT	TCCCACCGTG	960
	TCTGCCCCCT	CGAATGTCAA	CACTACCAGC	GCACCTCCTG	TCCAGACAGA	CATCGTCAAC	1020
80	ACCAGCAGTA	TTCTGTGATC	TGAGAACCAA	GTGTTGCAGA	TGGAGAAAGC	TCTGTCTTCT	1080
	GGCAGCCTGG	AGCCTTAACCT	CGCAGGAGAA	ATGATCAACC	AAGTCAGCAG	ACTCCTTCAT	1140
	TCCCCGCGCT	ACATGCTGGC	CCCTCTGGCT	CAAAGATTGC	TGAAAGTAGT	GGATGACATT	1200
	GGCCTACAGC	TGAACCTTTT	AAACACGACT	ATAAGTCTAA	CCTCCCCTTC	TTTGGCTCTG	1260
	GCTGTGATCA	GAGTGAATGC	CAGTAGTTTC	AACACAACCTA	CCTTTGTGGC	CCAAGACCTT	1320
	GCAAATCTTC	AGGTTTCTCT	GGAAACCCAA	GCTCCTGAGA	ACAGTATTGG	CACAATTACT	1380

	CTTCCTTCAT	CGCTGATGAA	TAATTTACCA	GCTCATGACA	TGGAGCTAGC	TTCCAGGGTT	1440
	CAGTTCAATT	TTTTTGAAAC	ACCTGCTTTG	TTTCAGGATC	CTTCCTCGGA	GAACCTCTCT	1500
	CTGATCAGCT	ACGTATATC	ATCGAGTGT	GCAAACCTGA	CCGTGAGGAA	CTTGACAAGA	1560
5	AACGTGACAG	TCACATTAAC	GCACATCAAC	CCGAGCCAGG	ATGAGTTAAC	AGTGAGATGT	1620
	GTATTTTGGG	ACTTGGGCG	AAATGGTGGC	AGAGGAGGCT	GGTCAGACAA	TGGCTGCTCT	1680
	GTCAAAGACA	GGAGATTGAA	TGAAACCATC	TGTACCTGTA	GCCATCTAAC	AAGCTTCGGC	1740
	GTTCTGCTGG	ACCTATCTAG	GACATCTGTG	CTGCTGCTC	AAATGATGGC	TCTGACGTTT	1800
	ATTACATATA	TTGGTTGTGG	GCTTTCATCA	ATTTTCTGT	CAGTGACTCT	TGTAACCTAC	1860
	ATAGCTTTTG	AAAAGATCCG	GAGGGATTAC	CCTTCCAAAA	TCCTCATCCA	GCTGTGTGCT	1920
10	GCTCTGCTTC	TGCTGAACCT	GGCTTTCCTC	CTGGACTCGT	GGATTGCTCT	GTATAAGATG	1980
	CAAGGCCTCT	GCATCTCAGT	GGCTGTATTT	CTTCATTAT	TTCTCTTGGT	CTCATTCACA	2040
	TGGATGGGCC	TAGAAGCATT	CCATATGTAC	CTGGCCCTTG	TCAAAGTATT	TAATACTTAC	2100
	ATCCGAAAA	ACATCCTTAA	ATTCTGCATT	GTCCGTTGGG	GGGTACCAGC	TGTGGTTGTG	2160
	ACCATCATCC	TGACTATAT	CCCAGATAAC	TATGGGCTTG	GATCCTATGG	GAAATTCCTC	2220
15	AAATGGTTAC	CGGTGACCTT	CTGCTGGATC	AACAACAATG	CAGTATTCTA	CATTACGGTG	2280
	GTGGGATATT	TCTGTGTGAT	ATTTTGTCTG	AACGTGAGCA	TGTTTCTTGT	GGTCTTGGTT	2340
	CAGCTCTGTC	GAATTAACAA	GAAGAAGCAA	CTGGGAGCCC	AGCGAAAAAC	CAGTATTCAA	2400
	GACCTCAGGA	GTATPCGCTG	CCTTACATTT	TTACTGGGAA	TAACTTGGGG	CTTTCCTTCT	2460
20	TTTGCTGGG	GACCAAGTAA	CGTGACCTTC	ATGTATCTGT	TTGCCATCTT	TAATACCTTA	2520
	CAAGGATTTT	TCATATTCAT	CTTTTACTGT	GTGGCCAAAG	AAAATGTCAG	GAAGCAATGG	2580
	AGGCGGTATC	TTTGTGTGTT	AAAGTTACGG	CTGGCTGAAA	ATTCTGGAAA	TGCTTCTACA	2640
	GAGAGGAATG	GGGTCTCTTT	TAGTGTTCAG	AATGGAGATG	TGTGCCTTCA	CGATTTCACT	2700
	GGAAACAGC	ACATGTTTAA	CGAGAAGGAA	GATTCCTGCA	ATGGGAAAGG	CCGTATGGCT	2760
25	CTCAGAAGGA	CTTCAAAGCG	GGGAAGCTTA	CACTTTATTG	AGCAATGTG	A	

Seq ID NO: 490 Protein sequence  
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
30	MVFSVRQCGH	VGRTEEVLLT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSP	PEVETTSIND	60
	VTLSLLPSNE	TGKVPQRNIC	NLSSICNDAS	FFRGEIMFOY	DKESTVPQNG	HITNGTLTGV	120
	LSLSELKRSE	LNKILQTLSE	TYFIMCATAE	AQSTLNCFTT	IKLMNTMNAC	AVIAALERVK	180
	IRPMEHCCE	VRIPCPSSPE	ELEKLQCDLQ	DPIVCLADHP	RGPPFSSSQS	IPVVPRTVL	240
35	SQVFKATSE	EPDPYSPVTH	NVPSPIGEIQ	PLSPQPSAPI	ASSPAIDMPP	QSETISSPMP	300
	QTHVSGTPFP	VKAGFSSPTV	SAPANVNTTS	APPVQTDIVN	TSSISDLNEN	VLQMEKALSL	360
	GSLEPNLAGE	MINQVSRLLH	SPPDMLAPLA	QRLKVVDDI	GLQLNFSNTT	ISLTSPSLAL	420
	AVIRVNASSF	NTTTFVAGDP	ANLQVSLQET	APENSIGTIT	LPSSLMNNLP	AHDMELASRV	480
	QNFVFETPAL	FQDPSLENLS	LISYVISSSV	ANLTVRNLTR	NVTVLKHIN	PSQDELTVRC	540
40	VFWDLGRNGG	RGWSDNGCS	VKDRRLNETI	CTCSHLTSEF	VLLDLSTSV	LPAQMMALTF	600
	ITYIGCGLSS	IFLSVTLVTV	IAFEKIRRDY	PSKILQLCA	ALLLLNLVFL	LDSWIALYKM	660
	QGLCISVAVF	LHYFLLVSTF	WMGLEAFHMY	LALVKVFNTY	IRKYLKFCI	VGWGVPAVVV	720
	TIILTISPDN	YGLGSYKXFP	NGSPDDFCWI	NNNAVFIYIT	VGYFCVIFLL	NVSMFIVVLV	780
45	QLCRKIKKKQ	LGAQRKTSIQ	DLRSIAGLTF	LLGITWGFAP	FAWGPVNVTF	MYLFAIFNTL	840
	QGFIFIFIFC	VAKENVRKQW	RRYLCCGKLR	LAENSGNAST	ERNGVSVSVQ	NGDVCLHDF	900
	GKQHMFNKE	DSCNGKGRMA	LRRTSKRGSL	HFIEQM			

Seq ID NO: 491 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..3045

	1	11	21	31	41	51	
55	ATGGTTTTCT	CTGTGAGGCA	GTGTGGCCAT	GTGGGAGGAA	CTGAAGAAGT	TTTACTGACG	60
	TTCAAGATAT	TCCTTGTCTT	CATTTGTCTT	CATGTCGTTT	TGGTAACATC	CCTGGAAGAA	120
	GATACTGATA	ATTCAGTTT	GTCACCAACA	CCTGCTAAAT	TATCTGTTGT	CAGTTTGGCC	180
	CCCTCCTCCA	ATGAGGTTGA	AACAACAAGC	CTCAATGATG	TTACTTTAAG	CTTACTCCCT	240
	TCAAACGAAA	CAGAAAAAAC	TAAAACTACT	ATAGTAAAAA	CCTTCAATGC	TTCAGGCGTC	300
60	AAACCCGAGA	GAAATATCTG	CAATTTGTCA	TCTATTGTC	ATGACTCAGC	ATTTTCTAGA	360
	GGTGAGATCA	TGTTTCAATA	TGATAAGGAA	AGCACTGTTT	CCCAGAATCA	ACATATAACG	420
	AATGGCACCT	TAACTGGAGT	CCTGTCTCTA	AGTGAATTAA	AACGCTCAGA	GCTCAACAAA	480
	ACCTGCAAAA	CCCTAAGTGA	GACTTACTTT	ATAATGTGTG	CTACAGCAGA	GGCCCCAAGC	540
	ACATTAAAT	GTACATTCAC	AATAAACTG	AATAATACAA	TGAATGCATG	TGCTGCAATA	600
	GCCGCTTTGG	AAAGAGTAAA	GATTCGACCA	ATGGAACACT	GCTGCTGTTT	TGTGAGGATA	660
65	CCCTGCCCTT	CTCCCCCAGA	AGAGTTGGGA	AAGCTTCAGT	GTGACCTGCA	GGATCCCAT	720
	GTCTGTCTTG	CTGACCATCC	ACGTGGCCCA	CCATTTTCTT	CCAGCCAATC	CATCCCACTG	780
	GTGCCTCGGG	CCACTGTGCT	TTCCCAAGTC	CCCAAGGCTA	CCTCTTTTGC	TGAGCCTCCA	840
	GATTATTAC	CTGTGACCCA	CAATGTTCCC	TCTCCAATAG	GGGAGATTCA	ACCCCTTTCA	900
70	CCCCAGCCTT	CAGCTCCCAT	AGCTTCCAGC	CCTGCCATTG	ACATGCCCCC	ACAGTCTGAA	960
	ACGATCTCTT	CCCTATGCCC	CCAAACCCAT	GTCTCCGGCA	CCCCACCTCC	TGTGAAAGCC	1020
	TCATTTTCTT	CTCCCAACCT	GTCTGCCCTT	GCGAATGTCA	ACACTACCAG	CGCACCTCCT	1080
	GTCCAGACAG	ACATCGTCAA	CACCAGCAGT	ATTCTGTATC	TTGAGAACCA	AGTGTGTCAG	1140
	ATGGAGAAGG	CTCTGTCTTT	GGGAGCCCTG	GAGCCTAAC	TCCGAGGAGA	AATGATCAAC	1200
75	CAAGTCAGCA	GACTCCTTCA	TTCCCGCCTT	GACATGCTGG	CCCCTCTGGC	TCAAAGATTG	1260
	CTGAAAGTAG	TGGATGATAT	TGGCCTACAG	CTGAACCTTT	CAAACACGAC	TATAAGTCTA	1320
	ACCTCCCTCT	CTTTGGCTCT	GGCTGTGATC	AGAGTGAATG	CCAGTAGTTT	CAACACAAC	1380
	ACCTTTGTGG	CCCAAGACCC	TGCAAACTTT	CAGGTTTCTC	TGGAAACCCA	AGCTCCTGAG	1440
	AACAGTATTG	GCACAATTAC	TCTTCTTCTA	TCGCTGATGA	ATAATTTACC	AGCTCATGAC	1500
80	ATGGAGCTAG	CTTCCAGGGT	TCAGTTCAAT	TTTTTTGAAA	CACCTGCTTT	GTTCAGGAT	1560
	CCTTCCCTGG	AGAACCTCTC	TCTGATCAGC	TACGTATAT	CATCGAGTGT	TGCAAACTG	1620
	ACCGTCAGGA	ACTTGACAA	AAAGCTGACA	GTCACATTAA	AGCACATCAA	CCCGAGCCAG	1680
	GATGAGTTAA	CAGTGAGATG	TGTATTTTGG	GACTTGGGCA	GAAATGTTGG	CAGAGGAGGC	1740
	TGGTCAGACA	ATGGCTGCTC	TGTCAAAGAC	AGGAGATTGA	ATGAAACCAT	CTGTACCTGT	1800
	AGCCATCTAA	CAAGCTTCGG	CGTTCTGCTG	GACCTATCTA	GGACATCTGT	GCTGCCTGCT	1860



5	CAAAATGATGG	CTCTGACGTT	CATTACATAT	ATTGGTTGTG	GGCTTTCATC	AATTTTCTG	1920
	TCAGTGACTC	TTGTAACCTA	CATAGCTTTT	GAAAAGATCC	GGAGGGATTA	CCCTTCCAAA	1980
	ATCCTCATCC	AGCTGTGTGC	TGCTCTGCTT	CTGCTGAACC	TGGTCTTCCT	CCTGGACTCG	2040
	TGGATTGCTC	TGTATAAGAT	GCAAGGCCTC	TGCATCTCAG	TGGCTGTATT	TCTTCATTAT	2100
	TTTCTCTTGG	TCTCATTAC	ATGGATGGGC	CTAGAAGCAT	TCCATATGTA	CCTGGCCCTT	2160
	GTCAAAGTAT	TTAATACTTA	CATCCGAAAA	TACATCCTTA	AATTCCTGCAT	TGTGGGTGG	2220
	GGGGTACCAG	CTGTGGTGTG	GACCATCATC	CTGACTATAT	CCCCAGATAA	CTATGGGCTT	2280
	GGATCCATATG	GGAAATCCCC	CAATGGTTCA	CCGGATGACT	TCTGCTGGAT	CAACAACAAT	2340
	GCAGTATTCT	ACATTACGGT	GGTGGGATAT	TTCTGTGTGA	TATTTTGTCT	GAACGTCAGC	2400
10	ATGTTCAATTG	TGGTCCTGGT	TCAGCTCTGT	CGAATTAAAA	AGAAGAAGCA	ACTGGGAGCC	2460
	CAGCGAAAAA	CCAGTATTTA	AGACCTCAGG	AGTATCGCTG	GCCTTACATT	TTTACTGGGA	2520
	ATAACTTGGG	GCTTTGCCTT	CTTTGCCTGG	GGACCAGTTA	ACGTGACCTT	CATGTATCTG	2580
	TTTGGCATCT	TTAATACCTT	ACAAGGATTT	TTTATATTCA	TCITTTTACTG	TGTGGCCAAA	2640
	GAAAATGTCA	GGAAGCAATG	GAGGCGGTAT	CTTTGTTGTG	GAAAGTTACG	GCTGGCTGAA	2700
15	AATTCCTGACT	GGAGTAAAAA	TGCTACTAAT	GGTTTAAAGA	AGCAGACTGT	AAACCAAGGA	2760
	GTGTCCAGCT	CTTCAAATTC	CTTACAGTCA	AGCAGTAACT	CCACTAACTC	CACCACACTG	2820
	CTAGTGAATA	ATGATTGCTC	AGTACACGCA	AGCGGGAATG	GAAATGCCTC	TACAGAGAGG	2880
	AATGGGGTCT	CTTTTAGTGT	TCAGAATGGA	GATGTGTGCC	TTTACGATTT	CCTGGGAAAA	2940
20	CAGCACATGT	TTAACGAGAA	GGAAGATTCC	TGCAATGGGA	AAGGCCGTAT	GGCTCTCAGA	3000
	AGGACTTCAA	AGCGGGGAAG	CTTACACTTT	ATTGAGCAAA	TGTGA		

Seq ID NO: 492 Protein sequence

Protein Accession #: Eos sequence

25	1	11	21	31	41	51	
	MVFSVRQCGH	VGRTEBEVLT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSPP	PAKLSVVSFA	60
	PSSNEVETTS	LNDVTLSLLP	SNETEKTKIT	IVKTFNAGSV	KPQRNICNLS	SICNDSAFFR	120
30	GEIMFQYDKE	STVPQNHIT	NGTLTGVLSL	SELKRSELNK	TLQTLSETYF	IMCATAEAS	180
	TLNCTFTIKL	NNTMNACAAI	AALERVKIRP	MEHCCCSVRI	PCPSSPEELG	KLQCDLQDPI	240
	VCLADHPRGP	PFSSSQSPV	VPRATVLSQV	PKATSFABPP	DYSPVTHNPV	SPIGEIQPLS	300
	PQPSAPIASS	PAIDMPPQSE	TISSPMPQTH	VSGTPPPVK	SFSSTVTSAP	ANVNNTSAPP	360
	VQTDIVNTSS	ISDLENQVLQ	MEKALSLGSL	EPNLAGEMIN	QVSRLLHSPP	DMLAPLAQRL	420
35	LKVVDIDIGLQ	LNFNTTISL	TSPSLALAVI	RVNASSFNNT	TFVAQDPANL	QVSLETQAPE	480
	NSIGTITLPS	SLMNNLPAHD	MELASRVQFN	FFETPALFQD	PSLENLSLIS	YVSSSVANL	540
	TVRNLTRNVT	VTLKHINPSQ	DELTVRCVFW	DLGRNGGRGG	WSDNGCSVKD	RRLNETICTC	600
	SHLTSFGVLL	DLRSFVLP	QMMALTFTTY	IGCGLSSIFL	SVTLTVYIAF	EKIRRDYPSK	660
	ILIQLCALL	LLNLVFLDS	WIALYKMQGL	CISVAVFLHY	FLVSFTWMG	LEAFHMYLAL	720
40	VKVFNTRYRK	YILKFCIVGW	GVPVAVVTII	LTISPNDYGL	GSYGFKNPNS	PDDFCWINNN	780
	AVFYITVVG	FCVIFLLNVS	MFIVVLVQLC	RIKKKKQLGA	QRKTSIQDLR	SIAGLTFFLG	840
	ITWGFAPFAW	GPVNVTFMVL	FAIFNTLQGF	FIFIFYCVAK	ENVRKQWRRY	LCCGKLRLAE	900
	NSDWSKTATN	GLKKQTVNQ	VSSSSNSLQS	SSNSTNSTTL	LVNNDSCVHA	SGNGMASTER	960
	NGVSFSVQNG	DVCLHDFTEG	QMFNEKEDS	CNGKGRMALR	RTSKRGSLEH	IEQM	

Seq ID NO: 493 DNA sequence

Nucleic Acid Accession #: NM\_015507

Coding sequence: 241..1902

50	1	11	21	31	41	51	
	CCGCAGAGGA	GCCTCGGCCA	GGCTAGCCAG	GGCGCCCCCA	GCCCTCCTCC	AGGCCGCGAG	60
	CGCCCTCGCC	CGGGTGCCCTG	GCCTCCCTC	CCAGACTGCA	GGGACAGCAC	CCGGTAACTG	120
	CGAGTGGAGC	GGAGGACCCG	AGCGGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
55	GGGTCCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
	ATGCCCTCTG	CCTGGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
	GGGAACGCGG	CCAGTCAAG	GCATCACGGG	TTGTTAGCAT	CGGCACGTCA	GCCTGGGGTC	360
	TGTCATATG	GACTAAACT	GGCTGCTGC	TACGGCTGGA	GAAGAACACG	CAAGGGAGTC	420
	TGTGAAGCTA	CATGCGAACC	TGGATGTAAG	TTTGGTGAGT	GCGTGGGACC	AAACAAATGC	480
60	AGATGCTTTC	CAGGATACAC	CGGGAAAACC	TGCAGTCAAG	ATGTGAATGA	GTGTGGAATG	540
	AAACCCCGGC	CATGCCAAC	CAGATGTGTG	AATACACACG	GAAGCTACAA	GTGCTTTTGC	600
	CTCAGTGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
	ATAAATGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTCCCT	GTGTCCATCC	720
	TCAGGACTCC	GCCTGGCCCC	AAATGGAAGA	GACTGTCTAG	ATATTGATGA	ATGTGCCTCT	780
65	GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTTGGAAG	CTACTACTGC	840
	AAATGTCACA	TGTGTTTCGA	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
	AATGAATGTA	CTATGGATAG	CCATACGTGC	AGCCACCATG	CCAATTGCTT	CAATACCCAA	960
	GGGTCTTCCA	AGTGTAATAG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCG	GTGTTCTGCT	1020
	ATCCCTGAAA	ATTCTGTGAA	GGAAGTCCTC	AGAGCACCTG	GTACCATCAA	AGACAGAATC	1080
70	AAGAAGTTGC	TTGCTCACAA	AAACAGCATG	AAAAAGAAGG	CAAAAATTAA	AAATGTTACC	1140
	CCAGAACCCA	CCAGGACTCC	TACCCCTAAG	GTGAACTTGC	AGCCCTTCAA	CTATGAAGAG	1200
	ATAGTTTCCA	GAGCGGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GAAAATGAAA	1260
	GAGGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAAGCCCTGA	AGAATGACAT	AGAGGAGCGA	1320
	AGCCTGCGAG	GAGATGTGTT	TTTCCCTAAG	GTGAATGAAG	CAGGTGAATT	CGGCCTGATT	1380
75	CTGTTCCAAA	GGAAGCGCCT	AACTTCCAAA	CTGGAACATA	AAGATTTAAA	TATCTCGGTT	1440
	GACTGCAGCT	TCAATCATGG	GATCTGTGAC	TGGAACACAG	ATAGAGAAGA	TGATTTTGAC	1500
	TGGAATCCTG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGGCA	1560
	GGTCACAAGA	AAGACATTGG	CCGATTGAAA	CTTCTCCTAC	CTGACCTGCA	ACCCCAAAGC	1620
	AACTTCTGTT	TGCTTCTTTG	TTACCGGCTG	GCCGGAGACA	AAGTCGGGAA	ACTTCGAGTG	1680
80	TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAAGA	CCACGAGTGA	GGATGAAAAG	1740
	TGGAAGACAG	GGAAAATTCA	GTTGTATCAA	GGAACCTGAT	CTACCAAAG	CATCATTTT	1800
	GAAGCAGAAC	GTGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGT	1860
	TCAGGCTTAT	GTCCAGATAG	CCTTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
	TTGACTTTGT	ATGTCAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCATT	1980
	TTAGAATTAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCTT	2040

TCTTGATATA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100  
 TTCTGAAATC TTTCACATTT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCCCTCCT 2160  
 CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220  
 TAGAAAAAAA AGCACAGAGA AATGTTTAACT TGTGTTGACTC TTATGATACT TCTTGGAAAC 2280  
 5 TAGACATCA AAGATAGACT TTGCTTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340  
 TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA

Seq ID NO: 494 Protein sequence  
 Protein Accession #: NP\_056322

1 11 21 31 41 51  
 | | | | |  
 15 MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRNSKGV 60  
 CEATCEPGCK FGECVGPENK RCFFPGYTGKT CSQDVNECGM KPRPCQHRV NTHGSYKCF 120  
 LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEPQCLCPSS SGLRLAPNGR DCLDIDECAS 180  
 GKVICPYNRR CVNTFGSYYC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNQ 240  
 GSFKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KLLAHKNSM KKKAKIKNVT 300  
 20 PEPTRTPTPK VNLQPFNYE IVSRGGNSHG GKKGNEEKMK EGLEDEKREE KALKNDIEER 360  
 SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHIGCD WKQDREDDFD 420  
 WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFYDRL AGDKVKGKLRV 480  
 FVKNNSNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGGKKTG EIAVDGVLLV 540  
 SGLCPDSLLS VDD

Seq ID NO: 495 DNA sequence  
 Nucleic Acid Accession #: NM\_003506.1  
 Coding sequence: 259..2379

1 11 21 31 41 51  
 | | | | |  
 30 GCAGCTCCAG TCCCGGACGC AACCCCGGAG CCGTCTCAGG TCCCTGGGGG GAACGGTGGG 60  
 TTAGACGGGG ACGGGAAGGG ACAGCGGCCT TCGACCGCCC CCCGAGTAAT TGACCCAGGA 120  
 CTCATTTTCA GGAAGCCTG AAAATAGATA AAATAGTGAA ATGAGGAATT TGAACATTTT 180  
 35 ATCTTTGGAT GGGGATCTTC TGAGGATGCA AAGAGTGATT CATCCAAGCC ATGTGGTAAA 240  
 ATCAGGAATT TGAAGAAAAA GGAGATGTTT ACATTTTGTG TGACGTGTAT TTTTCTACCC 300  
 CTCCTAAGAG GGCACAGTCT CTTACCTGT GAACCAATTA CTGTTCACAG ATGTATGAAA 360  
 ATGGCCTACA ACATGACGTT TTTCCCTAAT CTGATGGGTC ATTTAGACCA GAGTATTGCC 420  
 GCGGTGGAAA TGGAGCATTT TCTTCTCTC GCAATCTGG AATGTTCCAC AAACATTGAA 480  
 40 ACTTTCCTCT GCAAGCATTT TGTACCAACC TGCATAGAAC AAATTCATGT GGTTCACCTT 540  
 TGTCTGTAAC TTTGTGAGAA AGTATATTCT GATTGCAAAA AATTAATTGA CACTTTTGGG 600  
 ATCCGATGGC CTGAGGAGCT TGAATGTGAC AGATTACAAT ACTGTGATGA GACTGTTCTT 660  
 GTAACCTTTG ATCCACACAC AGAATTTCTT GGTCTCTAGA AGAAACAGA ACAAGTCCAA 720  
 AGAGACATTT GATTTTGTGT TCCAAGGCAT CTTAAGACTT CTGGGGGACA AGGATATAAG 780  
 45 TTTCTGGGAA TTAGCCAGTG TCGCGCTCCA TCGCCCAACA TGTATTTTAA AAGTGATGAG 840  
 CTAGAGTTTG CAAAAAGTTT TATTGGAACA GTTCAATAT TTTGTCTTTG TGCAACTCTG 900  
 TTCACATTTT TTACTTTTTT AATTGATGTT AGAAGATTCA GATACCCAGA GAGACCAATT 960  
 ATATATTACT CTGCTCTGTT CAGCATTGTA TCTCTTATGT ACTTCATTGG ATTTTGTGCTG 1020  
 GGCGATAGCA CAGCCTGCAA TAAGGCAGAT GAGAAGCTAG AACTTGGTGA CACTGTTGTC 1080  
 50 CTAGGCTCTC AAAATAAGGC TTGCACCGTT TTGTTTCATG TTTTGTATTT TTTCACAATG 1140  
 GCTGGCCTG TGTGGTGGGT GATTCTTACC ATTACTTGGT TCTTAGCTGC AGGAAGAAAA 1200  
 TGGAGTTGTG AAGCCATCGA GCAAAAAGCA GTGTGGTTTC ATGCTGTTGC ATGGGGAACA 1260  
 CAGAGTTTCC TGACTGTTAT GCTTCTTGCT CTGAACAAAG TTGAAGGAGA CAACATTAGT 1320  
 GGAGTTTGCT TGTGTGGCCT TTATGACCTG GATGCTTCTC GCTACTTTGT ACTCTTGCCA 1380  
 55 CTGTGCCTTT GTGTGTTTGT TGGGCTCTCT CTCTTTTATG CTGGCATTAT TTCCTTAAAT 1440  
 CATGTTTCGAC AAGTCATACA ACATGATGGC CGGAACCAAG AAAAATAAAA GAAATTTATG 1500  
 ATTTCGAATTG GAGTCTTCAG CGGCTTGAT CTGTGCCAT TAGTGACACT TCTCGGATGT 1560  
 TACGTCATG AGCAAGTGAA CAGGATTACC TGGGAGATAA CTGGGCTCTC TGATCATTGT 1620  
 CGTCAGTACC ATATCCCATG TCCTTATCAG GCAAAAGCAA AAGCTCGACC AGAATTGGCT 1680  
 60 TTAATTTATG TAAATACCT GATGACATTA ATTGTTGGCA TCTCTGCTGT CTTCTGGGTT 1740  
 GGAAGCAAAA AGACATGCAC AGAATGGGCT GGGTTTTTAA AACGAAATCG CAAGAGAGAT 1800  
 CCAATCAGTG AAGTCGAAG AGTACTACAG GAATCATGTG AGTTTTCTT AAAGCACAAT 1860  
 TCTAAAGTTA AACACAAAAA GAAGCACTAT AAACCAAGTT CACACAAGCT GAAGGTCATT 1920  
 TCCAAATCCA TGGGAACCAAG CACAGGAGCT ACAGCAAATC ATGGCACTTC TGCAGTAGCA 1980  
 65 ATTACTAGCC ATGATTACCT AGGACAAGAA ACTTTGACAG AAATCCAAAC CTCACCAGAA 2040  
 ACATCAATGA GAGAGGTGAA AGCGGACGGA GCTAGCACCC CCAGGTTAAG AGAACAGGAC 2100  
 TGTGGTGAAC CTGCCCTGCC AGCAGCATCC ATCTCCAGAC TCTCTGGGGA ACAGGTCGAC 2160  
 GGGGAAGGGCC AGGCAAGGCG TGTATCTGAA AGTGCGCGGA GTGAAGGAAG GATTAGTCCA 2220  
 AAGAGTGATA TTACTGACAC TGGCCTGGCA CAGAGCAACA ATTGCAAGGT CCCAGTTTCT 2280  
 70 TCAGAACCAA GCAGCCTCAA AGGTTCCACA TCTCTGCTTG TTCAACCCAGT TTCAGGAGTG 2340  
 AGAAAAAGAG AGGGAGGTGG TTGTCAATCA GATACITGAA GAACATTTT TCTCGTTACT 2400  
 CAGAAGCAAA TTTGTGTTAC ACTGGAAGTG ACCTATGCAC TGTTTTGTAA GAATCACTGT 2460  
 TACGTTCTCT TTTTGCACAT AAAGTTGCAAT TGCCTACTGT TATACTGGAA AAAATAGAGT 2520  
 75 TCAAGAATAA TATGACTCAT TTACACAAAA GGTAAATGAC AACAATATAC CTGAAAACAG 2580  
 AAATGTGCAG GTTAATAATA TTTTTTTAAT AGTGTGGGAG GACAGAGTTA GAGGAATCTT 2640  
 CCTTTTCTAT TTATGAAGAT TCTACTCTTG GTAAGAGTAT TTTAAGATGT ACTATGCTAT 2700  
 TTTACCTTTT TGATATAAAA TCAAGATATT TCTTTGCTGA AGTATTTAAA TCTTATCCTT 2760  
 GTATCTTTTT ATACATATTT GAAAATAAGC TTATATGTAT TTGAACCTTT TTGAAATCCT 2820  
 80 ATTCAGATAT TTTTATCATG CTATTGTGAT ATTTAGCAC TTTGGTAGCT TTTACACTGA 2880  
 ATTTCTAAGA AAATTGTAAG ATAGTCTTCT TTTTACTGTG AAAAAAGAT ATACCAAAAA 2940  
 GTCTTATAAT AGGAATTTAA CTTTAAAAAC CCACCTTATG ATACCTTACC ATCTAAAAATG 3000  
 TGTGATTTTT ATAGTCTCGT TTAGGAATT TCACAGATCT AAATTAATGA CTGAAAATAA 3060  
 GGTGCTTACT CAAAGAGTGT CCACTATTGA TTGTATTATG CTGCTCACTG ATCCTTCTGC 3120  
 ATATTTAAAA TAAATGTCT TAAAGGGTTA GTAGACAAAA TGTTAGTCTT TTGTATATTA 3180  
 GGCCAAGTGC AATTGACTTC CTTTTTTTAA TGTTCATGA CCACCCATTG ATTTGATTAT 3240

AACCACTTAC AGTTGCTTAT ATTTTGTGTT TTAACCTTTG TTTCTTAACA TTAGAATAT 3300  
TACATTTTGT ATTATACAGT ACCTTTCTCA GACATTTTGT AG

Seq ID NO: 496 Protein sequence  
Protein Accession #: NP\_003497.1

5  
10  
15  
20

1	11	21	31	41	51	
MEMFTFLITC	IFLPLLRGHS	LFTCEPITVP	RCMKMAYNMT	FFPNLMGHYD	QSIAAVEMEH	60
FLPLANLECS	PNITFLCKA	FVPTCIEQIH	VVPPCRKLCE	KVYSDCKCLI	DTFGIRWPPE	120
LECDRLQYCD	ETVPTVTFDPH	TEFLGPQKKT	EQVQRDIGFW	CPRHLKTSYG	QGYKFLGIDQ	180
CAPPCPNMYF	KSDELEFAKS	FIGTVSIFCL	CATLFTFLTTF	LIDVRRFRYP	ERPIIYYSVC	240
YSIVSLMYFI	GFLLDGSDTAC	NKADEKLELG	DTVVLGSSQNK	ACTVLFMLLY	FFTMAGTVVWW	300
VILTITWFLA	AGRKWSCEAI	EQKAVWFHAV	AWGTPGFLTIV	MLLALNKVEG	DNISGVCFVG	360
LYDLASRYF	VLLFLCLCVF	VGLSLLAGI	ISLNHVRQVI	QHDGRNQEKL	KKFMIRIGVF	420
SGLYLVPLVT	LLGCVYVQV	NRITWEITW	SDHCRQYHIP	CPYQAKAKAR	PELALFMIKY	480
LMTLIVGISA	VFWVGSKKTC	TEWAGFFKRN	RKRDPISER	RVLQESCEFF	LKHNSKVKKH	540
KKHYKPSSHK	LKVISKSMGT	STGATANHGT	SAVAITSHDY	LQGETLLEIQ	TSPETSMREV	600
KADGASTPRL	REQDCGEFAS	PAASISRLSG	EQVDGKGQAG	SVSESARSEG	RISPKSDITD	660
TGLAQSNLQL	VPSSEPPSSL	KGSTSLLVHP	VSGVRKEQGG	GCHSDT		

Seq ID NO: 497 DNA sequence  
Nucleic Acid Accession #: NM\_005046  
Coding sequence: 16..777

25  
30  
35  
40  
45

1	11	21	31	41	51	
GGATTTCGGG	GCTCCATGGC	AAGATCCCTT	CTCCTGCCCC	TGCAGATCCT	ACTGCTATCC	60
TTAGCCTTGG	AAATGTCAGG	AGAAGAAGCC	CAGGGTGACA	AGATTATTGA	TGGCGCCCCA	120
TGTGCAAGAG	GCTCCACCCC	ATGGCAGGTG	GCCCTGTCTA	GTGGCAATCA	GCTCCACTGC	180
GGAGGCGTCC	TGGTCAATGA	GCGCTGGGTG	CTCACTGCCG	CCCACTGCAA	GATGAATGAG	240
TACACCGTGC	ACCTGGGCAG	TGATACGCTG	GGCGACAGGA	GAGCTCAGAG	GATCAAGGCC	300
TCGAAGTCAT	TCCGCCACCC	CGGCTACTCC	ACACAGACCC	ATGTTAATGA	CCTCATGCTC	360
GTGAAGCTCA	ATAGCCAGGC	CAGGCTGTCA	TCCATGGTGA	AGAAAGTCAG	GCTGCCCTCC	420
CGCTGCGAAC	CCCCCTGGAAC	CACCTGTACT	GTCTCCGGCT	GGGGCACAC	CACGAGCCCA	480
GATGTGACCT	TTCCTCTGTA	CCTCATGTGC	GTGGATGTCA	AGCTCATCTC	CCCCCAGGAC	540
TGCACGAAGG	TTTACAAGGA	CTTACTGGAA	AATTCCATGC	TGTGCGCTGG	CATCCCCGAC	600
TCCAAGAAAA	ACGCTCTCAA	TGGTGACTCA	GGGGGACCGT	TGGTGTGCAG	AGGTACCCTG	660
CAAGGTCTGG	TGTCTCTGGG	AACCTTCCCT	TGCGGCCAAC	CCAATGACCC	AGGAGTCTAC	720
ACTCAAGTGT	GCAAGTTTAC	CAAGTGGATA	AATGACACCA	TGAAAAAGCA	TCGCTAACGC	780
CACACTGAGT	TAATTAACCTG	TGTGCTTCCA	ACAGAAAAATG	CACAGGAGTG	AGGACGCCGA	840
TGACCTATGA	AGTCAAATTT	GACTTTACCT	TTCCTCAAAG	ATATATTTAA	ACCTCATGCC	900
CTGTTGATAA	ACCAATCAAA	TTGGTAAAGA	CCTAAACCA	AAACAAATAA	AGAAACACAA	960
AACCTCAA						

Seq ID NO: 498 Protein sequence  
Protein Accession #: NP\_005037

50  
55

1	11	21	31	41	51	
MARSLLLPLQ	ILLLSLALET	AGEEAQGDKI	IDGAPCARGS	HPWQVALLSG	NQLHCGGVLV	60
NERWVLTAAH	CKMNEYTVHL	GSDTLGDRRA	QRIKASKSFR	HPGYSTQTHV	NDLMLVKLNS	120
QARLSSMVKK	VRLPSRCEPP	GTCTVSGWG	TTTSPDVTFP	SDLMCVDVKL	ISPQDCTKVY	180
KDLLENSMLC	AGIPDSKINA	CNGDSGGPLV	CRGTLQGLVS	WGTFPCGPQN	DPGVYTQVCK	240
FTKWINDTMK	KHR					

Seq ID NO: 499 DNA sequence  
Nucleic Acid Accession #: NM\_007196  
Coding sequence: 182..962

60  
65  
70  
75  
80

1	11	21	31	41	51	
GTTCCACAGAA	GCTCCCCAGG	CTCTAGTGCA	GGAGGAGAAG	GAGGAGGAGC	AGGAGGTGGA	60
GATTCCCACTG	TAAAGAGCTC	CAGAATCGTG	TACCAGGCAG	AGAACTGAAG	TACTGGGGGCC	120
TCCTCCACTG	GGTCCGAATC	AGTAGGTGAC	CCCGCCCTTG	GATTCTGGAA	GACCTCACCA	180
TGGGACGCCC	CCGACCTCGT	GCGGCCAAGA	CGTGGATGTT	CCTGCTCTTG	CTGGGGGGAG	240
CCTGGGCAGG	ACACTCCAGG	GCACAGGAGG	ACAAGGTGCT	GGGGGGTCAT	GAGTGCCAAAC	300
CCCATTCGCA	GCCTTGGCAG	GCGGCCCTTG	TCCAGGGCCA	GCAACTACTC	TGTGGCGGTG	360
TCCTTGTAGT	TGGCAACTGG	GTCTTACAG	CTGCCCACTG	TAAAAAACCG	AAATACACAG	420
TACGCCTGGG	AGACCAACAG	CTACAGAATA	AAGATGGCCC	AGAGCAAGAA	ATACCTGTGG	480
TTCACTCCAT	CCCAACCCCC	TGCTACAACA	GCAGCGATGT	GGAGGACCAC	AACCATGATC	540
TGATGCTTCT	TCAACTGCGT	GACCAAGCAT	CCCTGGGGTC	CAAAGTGAAG	CCCATCAGCC	600
TGGCAGATCA	TTGCACCCAG	CCTGGCCAGA	AGTGCACCGT	CTCAGGCTGG	GGCACTGTCA	660
CCAGTCCCGG	AGAGAAATTT	CCTGACACTC	TCAACTGTGC	AGAAGTAAAA	ATCTTTCCCC	720
AGAAGAAGTG	TGAGGATGCT	TACCCGGGGC	AGATCACAGA	TGGCATGGTC	TGTGCAGGCA	780
GCAGCAAGAG	GGCTGACACG	TGCCAGGGCG	ATTCTGGAGG	CCCTCTGGTG	TGTGATGGTG	840
CACCTCCAGG	CATCACATCC	TGGGGCTCAG	ACCCTGTGG	GAGGTCCGAC	AAACCTGGCG	900
TCTATACCAA	CATCTGCCGC	TACCTGGACT	GGATCAAGAA	GATCATAGGC	AGCAAGGGCT	960
GATTCTAGGA	TAAGCACTAG	ATCTCCCTTA	ATAAACTCAC	AACCTCTC		

Seq ID NO: 500 Protein sequence  
Protein Accession #: NP\_009127

1	11	21	31	41	51
---	----	----	----	----	----

5 MGRPRPRAAK | TWMFLLLLLG | AWAGHSRAQE | DKVLGGHECQ | PHSQPWQAAAL | FQGQQLLCGG 60  
 VLVGGNWLVT | AAHCKKPKYT | VRLGDHSLQN | KDGPEQEIPV | VQSIHPHCYN | SSDVEDHNHD 120  
 LMLQLLRDQA | SLGSKVKPIS | LADHCTQPGQ | KCTVSGWGTV | TSPRENFPDT | LNCAEVKIFP 180  
 QKKCEDAYPG | QITDGMVCAG | SSKGADTCQG | DSGGPLVCDG | ALQGITSWGS | DPCGRSDKPG 240  
 VYTNICRYLD | WIKKIIGSKG

Seq ID NO: 501 DNA sequence  
 Nucleic Acid Accession #: NM\_006103  
 Coding sequence: 29..406

15 1 | 11 | 21 | 31 | 41 | 51  
 CACCTGCACC | CCGCCCGGGC | ATAGCACCAT | GCCTGCTTGT | CGCCTAGGCC | CGCTAGCCGC 60  
 CGCCCTCCTC | CTCAGCCTGC | TGCTGTTCGG | CTTCAACCCTA | GTCTCAGGCA | CAGGAGCAGA 120  
 GAAGACTGGC | GTGTGCCCGC | AGCTCCAGGC | TGACCAGAAC | TGACAGCAAG | AGTGCCTCTC 180  
 GGACAGCGAA | TGCGCCGACA | ACCTCAAGTG | CTGCAGCGCG | GGCTGTGCCA | CCTTCTGCCT 240  
 TCTCTGCCCA | AATGATAAGG | AGGGTTCCCTG | CCCCCAGGTG | AACATTAACT | TTCCCCAGCT 300  
 CGGCCTCTGT | CGGGACCAGT | GCCAGGTGGA | CAGCCAGTGT | CCTGGCCAGA | TGAATGCTG 360  
 20 CGCAATGGC | TGTGGGAAGG | TGTCTGTGT | CACTCCCAAT | TTCTGAGGTC | CAGCCACCAC 420  
 CAGGCTGAGC | AGTGAGGAGA | GAAAGTTTCT | GCCTGGCCCT | GCATCTGTTT | CCAGCCACC 480  
 TGCCCTCCCC | TTTTTCGGGA | CTCTGTATTC | CCTCTGGGCG | TGACCACAGC | TTCTCCCTTT 540  
 CCAACCAAT | AAGTAACCA | CTTTCAGCAA | AAAAAAAAAA | AAAAA

25 Seq ID NO: 502 Protein sequence  
 Protein Accession #: NP\_006094

30 1 | 11 | 21 | 31 | 41 | 51  
 MPACRLGPLA | AALLLSLLLF | GFTLVSGTGA | EKTGVCPQLQ | ADQNTQECV | SDSECADNLK 60  
 CCSAGCATFC | LLCPNDRKES | CPQVNINFPQ | LGLCRDQCQV | DSQCPGQMKC | CRNGCGKVSC 120  
 VTPNF

35 Seq ID NO: 503 DNA sequence  
 Nucleic Acid Accession #: NM\_002407  
 Coding sequence: 65..352

40 1 | 11 | 21 | 31 | 41 | 51  
 CCTCCACAGC | AACTTCCTTG | ATCCCTGCCA | CGCAGGACTG | AACACAGACA | GCAGCCGCCT 60  
 CGCCATGAAG | CTGCTGATGG | TCCTCATGCT | GGCGGCCCTC | CTCCTGCACT | GCTATGCAGA 120  
 TTCTGGCTGC | AAATCCTGGG | AGGACATGGT | TGAAAAGACC | ATCAATTCCG | ACATATCTAT 180  
 ACCTGAATAC | AAAGAGCTTC | TTCAAGAGTT | CATAGACAGT | GATGCCGCTG | CAGAGGCTAT 240  
 45 GGGGAAATTC | AAGCAGTGT | TCCTCAACCA | GTCACATAGA | ACTCTGAAAA | ACTTTGGACT 300  
 GATGATGATC | ACAGTGTACG | ACAGCATTGT | GTGTAAATAT | AAGAGTAATT | AACTTTACCC 360  
 AAGGCGTTTG | GCTCAGAGGG | CTACAGACTA | TGGCCAGAAC | TCATCTGTGT | ATTGCTAGAA 420  
 ACCACTTTTC | TTTCTGTGT | TGTCTTTTAA | TGTGGAACCT | GCTAGACAAAC | TGTGGAACCT 480  
 TCAAATTCAT | TTCCATTTC | ATAACCTAAT | GCAAATC

50 Seq ID NO: 504 Protein sequence  
 Protein Accession #: NP\_002398

55 1 | 11 | 21 | 31 | 41 | 51  
 MKLLMLMLA | ALLLHCYADS | GCKLLEDMEV | KTINSNDISIP | EYKELLQEFI | DSDAAAAMG 60  
 KFKQCFLNQS | HRTLKNFGLM | MHTVYDSIWC | NMKSN

60 Seq ID NO: 505 DNA sequence  
 Nucleic Acid Accession #: NM\_014791.1  
 Coding sequence: 171..2126

65 1 | 11 | 21 | 31 | 41 | 51  
 TTGGCGGGCG | GAAGCGGCCA | CAACCCGGCG | ATCGAAAAGA | TTCTTAGGAA | CGCCGTACCA 60  
 GCCGCGTCTC | TCAGGACAGC | AGGCCCTGTG | CCTTCTGTCT | GGCGCCGCTC | AGCCGTGCCC 120  
 TCCGCCCTCT | AGGTTCTTTT | TCTAATTCCT | AATAAACTTG | CAAGAGGACT | ATGAAAGATT 180  
 ATGATGAATC | TCTCAAATAT | TATGAATTAC | ATGAAACTAT | TGGACAGGTG | GGCTTTGCAA 240  
 AGGTCAAATC | TGCCCTGCCA | ATCCTTACTG | GAGAGATGGT | AGCTATAAAA | ATCATGGATA 300  
 70 AAAACACACT | AGGAGTGAT | TTGCCCGGGA | TCAAAACGGA | GATTGAGGCC | TTGAAGAACC 360  
 TGAGACATCA | GCATATATGT | CAACTCTACC | ATGTGCTAGA | GACAGCCAAC | AAAATATTCA 420  
 TGGTTCTTGA | GTACTGCCCT | GGAGGAGAGC | TGTCTGACTA | TATAATTTC | CAGGATCGCC 480  
 TGTGAGAGA | GGAGACCCGG | GTTGTCTTCC | GTCAGATAGT | ATCTGCTGTT | GCTTATGTGC 540  
 ACAGCCAGGG | CTATGCTCAC | AGGGACCTCA | AGCCAGAAAA | TTTGCTGTTT | GATGAATATC 600  
 75 ATAAATTAAA | GCTGATTGAC | TTTGGTCTCT | GTGCAAAACC | CAAGGGTAAC | AAGGATTACC 660  
 ATCTACAGAC | ATGCTGTGGG | AGTCTGGCTT | ATGCAGCACC | TGAGTTAATA | CAAGGCAAT 720  
 CATATCTTGG | ATCAGAGGCA | GATGTTTGGG | GCATGGGCAT | ACTGTTATAT | GTTCTTATGT 780  
 GTGATTTTCT | ACCATTGAT | GATGATAATG | TAATGGCTTT | ATACAAGAAG | ATTATGAGAG 840  
 80 GAAAATATGA | TGTTCCTCAAG | TGGCTCTCTC | CCAGTAGCAT | TCTGCTTCTT | CAACAAATGC 900  
 TGCAGGTGGA | CCCAAAGAAA | CGGATTTCTA | TGAATAATCT | ATTGAACCAT | CCCTGGATCA 960  
 TGCAAGATTA | CAACTATCCT | GTTGAGTGGC | AAAGCAAGAA | TCCTTTTATT | CACCTCGATG 1020  
 ATGATTGCGT | AACAGAACTT | TCTGTACATC | ACAGAAACAA | CAGGCAACAA | ATGGAGGATT 1080  
 TAAATTCAC | GTGGCAGTAT | GATCACCTCA | CGGCTACCTA | TCTTCTGCTT | CTAGCCCAAG 1140  
 AGGCTCGGGG | AAAACCAAGT | CGTTTAAGGC | TTTCTTCTTT | CTCCTGTGGA | CAAGCCAGTG 1200  
 CTACCCCAT | CACAGACATC | AAGTCAATA | ATTGGAGTCT | GGAAGATGTG | ACCGCAAGTG 1260

5  
 10  
 15  
 20

```

ATAAAAAATTA TGTGGCGGGA TTAATAGACT ATGATTGGTG TGAAGATGAT TTATCAACAG 1320
GTGCTGCTAC TCCCCGAACA TCACAGTTTA CCAAGTACTG GACAGAATCA AATGGGGTGG 1380
AATCTAAATC ATTAACITCCA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAAG 1440
AAAATGTATA TACTCCTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTTCTTGAGC 1500
CAAAGACTCC AGTTAATAAG AACCAGCATA AGAGAGAAAT ACTCACTACG CCAAATCGTT 1560
ACACTACACC CTCAAAGACT AGAAACCACT GCCTGAAAGA AACTCCAATT AAAATACCAG 1620
TAAATTCAAC AGGAACAGAC AAGTTAATGA CAGGTGTCAT TAGCCCTGAG AGGCGGTGCC 1680
GCTCAGTGGG ATTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAAA AGAAAGGGAG 1740
CCAAAGTGTT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA 1800
GCAAAAGGAA GGGTTCTGCC AGAGACGGGC CCAGAAGACT AAAGCTTCAC TATAATGTGA 1860
CTACAACATG ATTAGTGAAT CCAGATCAAC TGTGTAATGA AATAATGTCT ATTCTTCCAA 1920
AGAAGCATGT TGACTTTGTA CAAAAGGGTT ATACACTGAA GTGTCAAACA CAGTCAGATT 1980
TTGGGAAAGT GACAATGCAA TTTGAATTAG AAGTGTGCCA GCTTCAAAAA CCGCATGTGG 2040
TGGGTATCAG GAGGCAGCGG CTTAAGGGCG ATGCCTGGGT TTACAAAAGA TTAGTGGAAG 2100
ACATCCTATC TAGCTGCAAG GTATAATTGA TGGATTCTTC CATCCTGCCG GATGAGTGTG 2160
GGTGTGATAC AGCCTACATA AAGACTGTTA TGATCGCTTT GATTTTAAAG TTCATTGGAA 2220
CTACCAACTT GTTCTCTAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAACAACAAA 2280
GATATTATTT TGTGTATGAA TCTAAATCAA GCCCATCTGT CATTATGTTA CTGTCTTTTT 2340
TAATCATGTG GTTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG 2400
AATGTAAGCT CTTAACTATG TCTCTTTGTA ATGTGTAATT TCTTCTGAA ATAAACCAT 2460
TTGTGAATAT
  
```

Seq ID NO: 506 Protein sequence  
Protein Accession #: NP\_055606.1

25  
 30  
 35  
 40

```

1 11 21 31 41 51
| | | | |
MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA 60
LKNLRHQHIC QLYHVLETAN KIFMVLEYCP GGELEFDYIIS QDRLESEETR VVFRQIVSAV 120
AYVHSQGYAH RDLKPENILF DEYHKLKID FGLCAKPKGN KDYHLQTCGG SLAYAAPELI 180
QKKSYLESEA DVWSMGILLY VLMCGFLPFD DDNMALYK KMRGKYDVPK WLSFSSILL 240
QQMLQVDPKK RISMKNLLNH PWIMQDYNYP VEWQSKNPFH HLDDDCVTEL SVHHRNNRQT 300
MEDLISLWQY DHLTATYLLL LAKKARGKPV RLRLSSFSCG QASATPFTDI KSNNWSLEDV 360
TASDKNYVAG LIDYDWCEDD LSTGAATPRT SQFTKYWTES NGVESKSLTP ALCRTTPANKL 420
KNKENVYTPK SAVKNBEEYFM FPEPKTPVNK NQHKREILT PNRYTTPSKA RNQCLKETPI 480
KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV 540
LTRSKRKGSA RDGPRRLKLH YNVTTTRLVN PDQLLNEIMS ILPKKHVDFV QKGYTLKCQT 600
QSDFGKVTMQ FELEVCQLQK PDVVGIRRRQ LKGDWVYKR LVEDILSSCK V
  
```

Seq ID NO: 507 DNA sequence  
Nucleic Acid Accession #: NM\_000582  
Coding sequence: 88..990

45  
 50  
 55  
 60  
 65  
 70

```

1 11 21 31 41 51
| | | | |
GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
AACGCCGACC AAGGAAACTT CACTACCATG AGAATTGCAG TGATTGTGCT TTGCCTCCTA 120
GGCATCACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAAGAGCAG 180
CTTTACAACA AATACCAGGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240
CAGAAATCTCC TAGCCCCACA GACCCCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCACATG 300
GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360
AAGCACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420
TCTGATGAAT CTGATGAAC TGTCACTGAT TTCTCCACGG ACCTGCCAGC AACCGAAGTT 480
TTCACCTCCG TTTGCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGTTTAT 540
GGACTGAGGT CAAAATCTAA GAAAGTTTCG AGACCTGACA TCCAGTACCC TGATGCTACA 600
GACGAGGACA TCACCTCACA CATGGAAAGC GAGGAGTTGA ATGGTGCATA CAAGGCCATC 660
CCCGTTGGCC AGGACCTGAA CGCGCCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT 720
GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780
TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATGTA TAGTCAGGAA 840
CTTTCCAAAG TCAGCCGTGA ATTCCACAGC CATGAATTC ACAGCCATGA AGATATGCTG 900
GTTGTAGACC CCAAAGTAA GGAAGAAGAT AAACACCTGA AATTTCTGAT TTCTCATGAA 960
TTAGATAGTG CATCTTCTGA GGTCAATTAA AAGGAGAAAA AATACAATTT CTCACCTTGC 1020
ATTTAGTCAA AAGAAAAAAT GCTTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT 1080
CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA 1140
ATTAGTTTAT TTTGTGGCTT CATGGAAACT CCCTGTAAAC TAAAAGCTTC AGGGTTATGT 1200
CTATGTTTAT TCTATAGAAG AAATGCAAAC TATCACTGTA TTTTAATATT TGTATTTCTC 1260
TCATGAATAG AAATTTATGT AGAAGCAAAC AAAATACTTT TACCCACTTA AAAAGAGAAT 1320
ATAACATTTT ATGTCACTAT AATCTTTTGT TTTTAAAGTT AGTGTATATT TTGTTGTGAT 1380
TATCTTTTGT TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGGTGTC 1440
AATTGCTTAT TTGTTTCCCA ACGGTTGTCC AGCAATTAAT AAAACATAAC CTTTTTACT 1500
GCCTAAAAAA AAAAAAATAA AAAA
  
```

Seq ID NO: 508 Protein sequence  
Protein Accession #: NP\_000573

75  
 80

```

1 11 21 31 41 51
| | | | |
MRIAVICFCL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ QONLLAPQTL 60
PSKSNESHSH MDDMDEDDDD DHVDSQDSID SNDSDDVDDT DDSHQSDSH HSDSDDELVT 120
DFPFDLPATE VFTPVVPTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYPA TDEDITSHME 180
SEELNGAYKA IPVAGDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
NEHSDVIDSQ ELSKVSREFH SHEFHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN
  
```

Seq ID NO: 509 DNA sequence  
Nucleic Acid Accession #: AB051390.1  
Coding sequence: 34..2457

5	1	11	21	31	41	51	
	AGCGGCCGCG	GCACAAAGTT	GGGGGCCGCG	AAGATGAGGC	TGTCCCCGCG	GCCCCCTGAAG	60
	CTGAGCCGGA	CTCCGGCACT	GCTGGCCCTG	GCGCTGCCCC	TGGCCGCGCG	GCTGGCCCTTC	120
10	TCCGACGAGA	CCCTGGACAA	AGTGCCCAAG	TCAGAGGGCT	ACTGCAGCCG	TATCTGCGC	180
	GCCAGGGCA	CGCGGCGCGA	GGGCTACACC	GAGTTACGCC	TCCGCGTGGA	GGGCGACCCC	240
	GACTTCTACA	AGCCGGGAAC	CAGCTACCGC	GTAACACTTT	CAGCTGCTCC	TCCCTCCTAC	300
	TTCAGAGGAT	TCACATTAAT	TGCCCTCAGA	GAGAACAGAG	AGGGTGATAA	GGAAGAAGAC	360
	CATGCTGGGA	CCTTCCAGAT	CATAGACGAA	GAAGAACTC	AGTTTATGAG	CAATTGCCCT	420
15	GTTCAGTCA	CTGAAAGCAC	TCCACGGAGG	AGGACCCGGA	TCCAGGTGTT	TTGGATAGCA	480
	CCACCAGCGG	GAACAGGCTG	CGTGATTCTG	AAGGCCAGCA	TCGTACAAAA	ACGCATTATT	540
	TATTTTCAAG	ATGAGGGCTC	TCTGACCAAG	AAACTTTGTG	AACAAGATTG	CACATTTGAT	600
	GGGGTGACTG	ACAAACCCAT	CTTAGACTGC	TGTGCCTGCG	GAAGTCCCAA	GTACAGACTC	660
	ACATTTTATG	GGAATTGGTC	CGAGAAGACA	CACCCAAAGG	ATTACCCTCG	TCGGGCCAAC	720
20	CACGTGCTCG	CGATCATCGG	AGGATCCAC	TCCAAGAATT	ATGTACTGTG	GGAATATGGA	780
	GGATATGCCA	GCGAAGGCGT	CAAACAAGTT	GCAGAATTGG	GCTCACCCGT	GAAATATGAG	840
	GAAGAAATTC	GACAACAGAG	TGATGAGGTC	CTCACCGTCA	TCAAAGCCAA	AGCCCAATGG	900
	CCAGCCTGGC	AGCCTCTCAA	CGTGAGAGCA	GCACCTTCAG	CTGAATTTTC	CGTGACAGCA	960
	ACGCGCCATT	TAATGTCTTT	CCTGACCATG	ATGGGCCCTA	GTCCCGACTG	GAACGTAGGC	1020
25	TTATCTGCGA	AAGATCTGTG	CACCAAGGAA	TGTGGCTGGG	TCCAGAAGGT	GGTGCAAGAC	1080
	CTGATTCCCT	GGGACGCTGG	CACCGACAGC	GGGGTGACCT	ATGAGTCACC	CAACAAACCC	1140
	ACCATTCCCT	AGGAGAAAT	CCGGCCCTTG	ACCAGCCTGG	ACCATCTCA	GAGTCCCTTC	1200
	TATGACCCAG	AGGGTGGGTC	CATCACTCAA	GTAGCCAGAG	TTGTCATCGA	GAGAAATCGCA	1260
	CGGAAGGGTG	AACAATGCAA	TATTTGTACCT	GACAAATGTC	ATGATATTGT	AGCTGACCTG	1320
30	GCTCCAGAA	AGAAAGATGA	AGATGACACC	CCTGAAACCT	GCATCTACTC	CAACTGGTCC	1380
	CCATGTTCCG	CTTCGAGCTC	CTCCACCTGT	GACAAAGGCA	AGAGGATGCG	ACAGCGCATG	1440
	CTGAAAGCAC	AGCTGGACCT	CAGCGTCCCC	TGCCCTGACA	CCCAGGACTT	CCAGCCCTGC	1500
	ATGGGCCCTG	GCTGCACTGA	CGAAGACGGC	TCCACCTGCA	CCATGTCCGA	GTGGATCACC	1560
	TGGTCCGCTT	CGAGCATCTC	CTCGCGCATG	GGCATGAGGT	CCCGGGAGAG	GTATGTGAAG	1620
35	CAGTTCCCGG	AGGACGGCTC	CGTGTGCACG	CTGCCCACTG	AGGAAACGGA	GAAGTGACAG	1680
	GTCAACGAGG	AGTGCTCTCC	CAGCAGCTGC	CTGATGACCG	AGTGGGGCGA	GTGGGACGAG	1740
	TGCAGCGCCA	CCTGCGGCAT	GGGCATGAAG	AAGCGGCACC	GCATGATCAA	GATGAACCCC	1800
	GCAGATGGCT	CCATGTGCAA	AGCCGAGACA	TCACAGGCAG	AGAAGTGCA	GATGCCAGAG	1860
	TGCCACACCA	TCCCATGCTT	GCTGTCCCCA	TGGTCCGAGT	GGAGTGACTG	CAGCGTGACC	1920
40	TGCGGGAAGG	GCAATGCGAA	CCGACAGCGG	ATGCTCAAGT	CTCTGGCAGA	ACTTGGAGAC	1980
	TGCAATGAGG	ATCTGGAGCA	GGTGAGGAAG	TGCATGCTCC	CTGAATGCCC	CATTGACTGT	2040
	GAGCTCACCG	AGTGGTCCCC	TGTGTCGGAA	TGTAACAAGT	CATGTGGGAA	AGGCCACGTG	2100
	ATTGCAACCC	GGATGTGCAA	AATGGAGCCT	CAGTTTGGAG	GTGCACCCCTG	CCAGAGACT	2160
	GTGCAGCGAA	AAAAGTGCCG	CATCCGAAAA	TGCCCTTGAA	ATCCATCCAT	CCAAAAGCTA	2220
45	CGCTGGAGGG	AGGCCCGAGA	GAGCCGGCGG	AGTGAGCAGC	TGAAGGAAGA	GTCTGAAGGG	2280
	GAGCAGTTCC	CAGGTTGTAG	GATGCGCCCA	TGGACGGCCT	GGTCAGAAATG	CACCAACTG	2340
	TGCGGAGGTG	GAATTACAGA	ACGTTACATG	ACTGTAAAGA	AGAGATTCAA	AAGCTCCCGA	2400
	TTTACCAGCT	GCAAAGACAA	GAAGGAGATC	AGAGCATGCA	ATGTTCTATC	TTGTTAGCAA	2460
	GGGTACGAGT	TCCCCAGGGC	TGCACCTTAG	ATTCAGAGT	CACCAATGGC	TGGATTATTT	2520
50	GCTTGTTTAA	GACAATTTAA	ATTGTGTACG	CTAGTTTTC	TTTTTGCACT	GTGGTTTCGCC	2580
	CAGTAGTCTT	GTGGATGCCA	GAGACATCCT	TTCTGAATAC	TTCTTGATGG	GTACAGGCTG	2640
	AGTGGGGCGC	CCTCACCTTC	AGCCAGCCTC	TTCTGTCAGA	GGAGTAGTGT	CAGCCACCTT	2700
	GTACTAAGCT	GAACATGTGC	CCTCTGGAGC	TTCCACCTGG	CCAGGGAGGA	CGGAGACTTT	2760
	GIACCTACTC	ACATCTGGAG	GCAACCATGT	CTGGAAGTGA	CTATGCGCTGA	GTCCCAAGGT	2820
55	CGCGGAGGTA	GGAAACATTC	ACAGATGAAG	ACAGCAGATT	CCCCACATTC	TCACTTTTGG	2880
	CCTGTTCAAT	GAACACATTT	TTTGCCCATC	TCTTCTTAGT	GGAACCTTTAG	GTCTCTTTTC	2940
	AAGTCTCCTC	AGTCATCAAT	AGTTCTCTGG	GAAGAACAGA	GCTGGTAGAC	TTGAAGAGGA	3000
	GCATTGATGT	TGGGTGGGCT	TTGTTCTTTC	ACTGAGAAAT	TCCGAATACA	TTTGCTCTAC	3060
	CCCTGATATT	GGTTCCTGAT	GCCCCCCCAA	CAAAAATAAA	TAAATAAATT	ATGGCTGCTT	3120
60	TATTTAAATA	TAAGGTAGCT	AGTTTTTACA	CCTGAGATAA	ATAATAAGCT	TAGAGTGTAT	3180
	TTTTCCCTTG	CTTTTGGGGG	TTGAGAGGAG	TATGTACAAT	TCTTCTGGGA	AGCCAGCCTT	3240
	CTGAACCTTT	TGTTACTAAA	TCCTTATTGG	AACCAAGACA	AAGGAAGCAA	AATTGGTCTC	3300
	TTTAGAGACC	AATTTGCCTA	AATTTTAAAA	TCTTCTTACA	CACATCTAGA	CGTTCAAGTT	3360
	TGCAAAATCAG	TTTTTAGCAA	GAAACATTTT	TTGCTATACA	AACATTTTGC	TAAGTCTGCC	3420
65	CAAAGCCCCC	CCAATGCATT	CCTTCAACAA	AATACAATCT	CTGTACTTTA	AAGTTATTTT	3480
	AGTCATGAAA	TTTTTATATG	AGAGAGAAAA	AGTTACCGAG	ACAGAAAAACA	AATCTAAGGG	3540
	AAAGGAATAT	TATGGGATTA	AGCTGAGCAA	GCAATTCTGG	TGGAAAAGTCA	AACCTGTCTG	3600
	TGCTCCACAC	CAGGGCTGTG	GTCCCTCCAG	ACATGCATAG	GAATGGCCAC	AGGTTTACAC	3660
	TGCTTTCCCA	GCAATTATAA	GCACACCAGA	TTGAGGGAGA	CTGACCAACA	AGGATAGTGT	3720
70	TAAAAGGACA	TTTTTCTCAGT	TGGGTCCATC	AGCAGTTTTT	CTTCTGCAAT	TTATTGTTGA	3780
	AAACTATTGT	TTCAATTTCT	CTTTTATAGG	CCTTATTACT	GCTTAATCCA	AATGTGTACC	3840
	ATTGGTGAGA	CACATACAAT	GCTCTGAATA	CACTACGAAT	TTGTATTAAA	CACATCAGAA	3900
	TATTTCCAAA	TACAACATAG	TATAGTCTTG	AATATGTACT	TTTAACACAA	GAGAGACTAT	3960
	TCAATAAAAA	CTCACTGGGT	CTTTTATGTC	TTTAAGCTAA	GTAAGTGTTC	AGAAGGTTCT	4020
75	TTTTTATATT	GTCCCTCCAC	TCCATCATTT	TCAATAAAAG	ATAGGGCTTT	TGCTCCCTTG	4080
	TTCTTGGAGG	GACCATTAAT	ACATCTCTGA	ACTACCTTTG	TATCCAACAT	GTTTAAATTC	4140
	CTTAAATGAA	TGCTTTTCTC	CCAAAAAAGG	CACAATATAA	AGAAACACAA	GATTTAATTA	4200
	TTTTTCTACT	TGGGGGGAAA	AAAGTCTCTA	TGTAGAAGCA	CCCACTTTTG	CAATGTTGTT	4260
	CTAAGCTATC	TATCTAACTC	TCAGCCCATG	ATAAGTTTCC	TTAAGCTGGT	GATTCTTAAT	4320
	CAAGGACAAG	CCACCTAGT	GTCTCATGTT	TGTATTGGT	CCCAAGTTGG	TACATTTTAA	4380
80	AATCTTGATT	TTGGAGACTT	AAAACAGGT	TAATGGCTAA	GAATGGGTAA	CATGACTCTT	4440
	GTGGGATTGT	TATTTTGTGT	TTGCAATGGG	GAATTTATAA	GAAGCATCAA	GTCTCTTTCT	4500
	TACCAAGCTG	TTGTTAGGTG	GTTTATAGTT	CTTTTGGCTA	ACAAATCATT	TTGGAAATAA	4560
	AGATTTTTTA	CTACAAAAAT	G				

Seq ID NO: 510 Protein sequence  
Protein Accession #: BAB18461.1

```

5 1      11      21      31      41      51
   |      |      |      |      |      |
MRLSPAPLKL SRTPALLALA LPLAALAFS DETLDKVPKS EGYCSRILRA QGTRREGYTE    60
FSLRVEGDPD FYKPGTSYRV TLSAAPPSTF RGFTLIALRE NREGDKBEDH AGTFQIIDEE    120
ETQFMSNCPV AVTESTPRRR TRIQVFWIAP PAGTGCVILK ASIVQKRIIY FQDEGSLTKK    180
LCEQDSTFDG VTDKPIILDCC ACGTAKYRLT FYGNWSEKTH PKDYPRRANH WSAIIGGSHS    240
KNYVLWEYGG YASEGVKQVA ELGSPVKMEE EIRQSSDEVL TVIKAKAQWP AWQPLNVRAA    300
PSAEFSVDRT RHLMSFLTMM GPSPDMNVGL SAEDLCTKEC GWVQKVVDL IPWDAGTDSG    360
VTYESPNKPT IPQEKIRPLT SLDHPQSPFY DPEGGSITQV ARVVIERTAR KGEQCNIVPD    420
NVDDIVADLA PEEKDEDDTP ETCIYSNWSP WSACSSSTCD KGRMRQRML KAQLDLSVPC    480
PDTQDFQPCM GPGCSDDEDS TCTMSEWITW SPCISCSMG MRSRERYVKQ FPEDGVSCTL    540
PTEETEKCTV NEECSPSSCL MTEWGEWDEC SATCGMGMKK RHRMIKMNP DGSMDKAETS    600
QAEKCMPEEC HTIPCLLSFW SEWSDCSVTC GKGMRTQRQM LKSLAELGDC NEDLEQVEKC    660
MLPECPIDCE LTEWSQWSEC NKSCGKHVHI RTRMIQMEPQ FGGAPCPETV QRKKCRIRKC    720
LRNPSIQKLR WREARESRRS EQLKESEGE QFPGCRM RPW TAWSECTKLC GGGIQERYMT    780
VKKRFKSSQF TSCKDKKEIR ACNVHPC

```

Seq ID NO: 511 DNA sequence  
Nucleic Acid Accession #: NM\_003108.1  
Coding sequence: 76..1401

```

25 1      11      21      31      41      51
   |      |      |      |      |      |
GGGGTGGGAG GGGGAGGGGG ACCTCCGCAC GAGACCCAGC GGCCCGGGTT GGAGCGTCCA    60
GCCCTGCAAC GGATCATGGT GCAGCAGGCG GAGAGCTTGG AAGCGGAGAG CAACCTGCCC    120
CGGGAGGCGC TGGACACGGA GGAGGGCGAA TTCATGGCTT GCAGCCCGGT GGCCCTGGAC    180
GAGAGCGACC CAGACTGGTG CAAGACGCGC TCGGGGCACA TCAAGCGGCC GATGAACGCG    240
TTCATGGTAT GGTCCAAGAT CGAACGCGAG AAGATCATGG AGCAGTCTCC GGACATGCAC    300
AAGCCCGAGA TCTCCAAGAG GCTGGGCAAG CGCTGAAAA TGCTGAAGGA CAGCGAGAAG    360
ATCCCGTTCA TCCGGGAGGC GGAGCGGCTG CGGCTCAAGC ACATGGCCGA CTACCCCGAC    420
TACAAGTACC GGCCCGGGA AAGACCCAAA ATGGACCCCT CGGCCAAGCC CAGCGCCAGC    480
CAGAGCCGAG AGAAGAGCGC GGCCGCGGCG GCGCGGCGGG GCGCGGCGGG AGGCGCGGGC    540
GGTGCCAAGA CCTCCAAGGG CTCCAGCAAG AAATGCGGCA AGCTCAAGGC CCCCGCGGCC    600
GCGGGCGCCA AGGCGGGGCG GGGCAAGGCG GCCCAGTCCG GGGACTACGG GGGCGCGGGC    660
GACGACTACG TGCTGGGCGC CCTGCGCGTG AGCGGCTCGG GCGGCGGCGG CGCGGGCAAG    720
ACGGTCAAGT GCGTGTCTCT GGATGAGGAC GACGACGACG ACGACGACGA CGACGAGCTG    780
CAGCTGCAGA TCAACAGGA GCCGACGAG GAGGACGAGG AACCACCGCA CCAGCAGCTC    840
CTGCAGCCGC CGGGGAGGCA GCCGTCGAG CTGCTGAGAC GCTACAACGT CGCCAAAGTG    900
CCCGCAGGCC CTACGCTGAG CAGCTCGGCG GAGTCCCCCG AGGGAGCGAG CCTCTACGAC    960
GAGGTGCGGG CCGGCGCGAC CTGCGGCGCC GGGGCGGCGA GCGGCTCTA CTACAGCTTC    1020
AAGAACATCA CCAAGCAGCA CCCGCCGCGC CTGCGCGAGC CCGCGCTGTC GCCCGCGTCC    1080
TCGCGCTCGG TGCTCCACCTC CTGCTCCAGC AGCAGCGGCA GCAGCAGCGG CAGCAGCGGC    1140
GAGGACGCGG ACGACCTGAT GTTCGACCTG AGCTTGAATT TCTCTCAAAG CGCGCACAGC    1200
GCCAGCGAGC AGCAGCTGGG GGGCGGCGCG GCGGCGGCGA ACCTGTCCCT GTGCTGTGGT    1260
GATAAGGATT TGGATTCTGT CAGCGAGGCG AGCCTGGGCT CCCACTTCGA GTTCCCCGAC    1320
TACTGCAGCG CGGAGCTGAG CGAGATGATC GCGGGGGACT GGCTGGAGGC GAACTTCTCC    1380
GACCTGGTGT TCACATATTG AAAGGCGCCC GCTGCTCGCT CTTTCTCTCG GAGGGTGCAG    1440
AGCTGGGTTT CTGTGGAGGA AGTTGTAGTG GTGATGATGA TGATGATGAT AATGATGATG    1500
ATGATGGTGG TGTTGATGGT GCGGTGGTA GGGTGGAGGG GAGAGAAGAA GATGCTGATG    1560
ATATTGATAA GATGTCGTGA CGCAAAGAAA TTGAAAACA TGATGAAAAT TTTGGTGGAG    1620
TTAAAGTGAA ATAGTAGTAT TTTAAACATT TTTCTGTGCC TTTTGTGTC CCCCCTCCCT    1680
TCTTTATCG TGCTCTCAAG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCCAA    1740
AAAATGTGTT TTTGTAAATTA CTATTTCTTT TTCTGAAAT TCGTGATTGC AACAAAGGCA    1800
GAGGGGGCGG CGCGGCGGAG GGGAGGTAGG ACCCGCTCCG GAAGGCGCTG TTTGAAGCTT    1860
GTCGGTCTTT GAAGTCTGGA AGACGTCTGC AGAGGACCCCT TTTGGCAGCA CAACTGTTAC    1920
TCTAGGAGAT TGGTGGAGAT ATTTTTTTTT CTTAAGAGAA CTTAAGAAGC TGGTGATTTT    1980
TTTTTAACAA AAAAAGGG

```

Seq ID NO: 512 Protein sequence  
Protein Accession #: NP\_003099.1

```

65 1      11      21      31      41      51
   |      |      |      |      |      |
MVQQAESLEA ESNLPREALD TEEGEFMACS PVALDESDPD WCKTASGHIK RPMNAFMVWS    60
KIERRKIMEQ SPD MHNAEIS KRLGKRWKML KDSEKIPFIR EAERLR LKHM ADYPDYKYRP    120
RKKPKMPDPS KPSASQSPK SAAGGGGSSA GGGAGGAKTS KGSSKKCGKL KAPAAAGAKA    180
GAGKAAQSGD YGGAGDDYVL GSLRVSSGGG GGAGKTVKCV FLDEDDDDDD DDELQLQIK    240
QEPDEEDEEP PHQQLLPFG QPSSQLLRRY NVAKVPASPT LSSSAESPEG ASLYDEVVRAG    300
ATSGAGGGSR LYYSFKNIT QHPPLAQPA LSPASSRSVS TSSSSSSGSS SGSSGEDADD    360
LMFDLSLNFQ QSAHSASEQQ LGGGAAGNLL SLSLVDKDLD SFSEGSLSGH FEFPDYCTPE    420
LSEMIAGDWL EANFSDLVFT Y

```

Seq ID NO: 513 DNA sequence  
Nucleic Acid Accession #: CAT Cluster

```

80 1      11      21      31      41      51
   |      |      |      |      |      |
GGTCGACCTA AATCTGATAA CTGGCTTATT ATGTAATTTA TTGGTGTTAT TATAGTAGAG    60
ATTGGTAATC TACAGTAAGA TTTTCAGTTA GGATTTGAGA TTATGATAAT AACTAATAGA    120
ATATTTCTAA ATTGGAATTA GAAGATTGTT GTATGACAGA GAGTCAGGAC TTGCCATTGG    180

```

GCAAACATCA AAGTCATTGT TTGGTGTGTA ATAGTACAAA ATCATCTTGC TTAACAGAGA 240  
 AAGGATATCT GTTGTCTCCC AATGAAACAA TTTTCTTGAA ATAGAGGGCC CAGAATTGGT 300  
 CTCTGACAAAT TAATAAGAC ATCAAAGATA GCAAAATGAT TTTATATATCT TAGGGCCAAAT 360  
 ACTACCAATT TAATAATTAA AACAAGTTCT GGTGAGCTCT GAACTTGGCA GAATTGGTGG 420  
 CAACATAGAC TTTGGATTTT CCAAAATCCC CACATAAAAC AAAGGGGATC AACTAGATAG 480  
 AAAAACCAGA AACCTTTGGA AATATCTGTT TAAAAAATAA AAAAAGTCGA CGCGGGCC

Seq ID NO: 514 DNA sequence

Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51  
 | | | | |  
 GGAGCCACAG TGAAAGTCAA GAATGTCAGT GATTCACAT TTAATATCTA CATTTTGGCA 60  
 GGGCAGTTAC TCTTTTGTAG TATAACATTG AGCTGATAGC ACATAGTGTA GACAAGTGAA 120  
 TACAGGATTC TCTGGGTGTG ATTCCCAGAA GTCTGGAGGT CATTTGGATA TTTGTGGGCC 180  
 CTTGGCTTCA CTCTGACTTG TGTGACACAT AAAAATTGTG ATGAAATGTC CTATAGATGT 240  
 CCTGCAGGTC TTAAGAAGAAC CTTTCCAAAC TATGAAACAG CCCAGCAGCA CTGAGTTAGA 300  
 GGTAATTTCT GAACCCCTGA AACTATAAAC TATTCTAACT GCACATAGAA TTGGCAAGTA 360  
 GCATTCTATG TCTATGAACA GTATGTCTTT TCTATATAAC AGAGAAAATC TTTTAAAGCA 420  
 AACTACTCAG TTTAAAACCT AATTCTTCTC ATAATCTCAG TACTTTTGAA TGAAGACATA 480  
 TCAATGCAAC AGTACACTCT TATTGAGGCA TTTGAAAGAA AGAATTCGAG ATCTAGTTTG 540  
 TATCAGATAT TATAAATTAG TATGGTTTAG TCTTTGTCTAT GAAATTTCTAC TTAATTTTGG 600  
 GACTATAGGT TTAAGAATGT AAGCAGAAGT TCTGCACCAA TCAGAATAAG CTACATTATG 660  
 CTTGAGTGAC AACTACTGTA ATGACAAAAT ATCAGTGGCT TAATACAATG GTTTTCTCT 720  
 CATACCTTGT CATAAAGAGT CAGCAAGGAC CCTGCTCATT ATGGTCCCTC AGGGACCCAG 780  
 GGTTGTGGGA AGCTCCACCA TTTTAGATAG CTCCTTCAA AGTCAGCCAT CTTTGGCAGT 840  
 CCATGTCCCC CAACAGGCTG GCAAAATTG GCTCTGATG GCTTCAAGGA TTGAGCATCG 900  
 GGCAGTTTAA ATGCTTTCAA CATGGAAGT GGACACCGGC CACTCCCACT CACATCCCTT 960  
 GGGCCAGAAC TAGGTCACTG GGCCCGGACC TAACTTCGGA GGGTTGGGGA ATTGTAATTC 1020  
 CTCATGTAC CCAAAGTGGG GAGAAGCCAG ATACTGAGAA ACATCAATAA TGGCTAACAG 1080  
 AAATCCATTC TACCATTCCC TTTGCTTAA GTGAAAAGAT GAGTACTTTC ATCAATTTGT 1140  
 AAATCTACT TTTGAAGTAA ATCTGGTAG CTGTCATGGG GGCTGGATT CCAGAAGGCC 1200  
 ATATGTAATT TGGGAATGAC ATTCACTTAA GCTCATAGAA TATCATTATT TGATGTAAAA 1260  
 TGCCCTCAT TGAATACAG GACCAAAATG CACTAACCA AAAACCCCCC TCCCCACGGG 1320  
 GCCCGGGTCC CTAATTTCCC TCCATCCCTT TAAATGAGGC ATTCTATGAT TTGGAATGGA 1380  
 AGCCCAAGTT TAGTCGTAAG AATTTTACTT AATTCAAGAA TTATTTCTAC TGAATATGTG 1440  
 CCAGTTCTGA AAGGAATGCA AAGTCAAAAT TTGCATCTTC TTTGCTCAAG GGCCTTTAGA 1500  
 TGTAACAACA CAGACATGAT ACAAGGCTGA CAATGACATT ATGATTAAAT TATGTTAAAC 1560  
 AACTTATTA ATTGTGAATC AAAAAAAAT TATGTTCTTT ATTTTATGGT TTTGCATAGT 1620  
 CTTGACTCAC TGCCTACATA CCCCTCTTGT TCCTCAGTTC TTATCCCTGA TTTCTTACAG 1680  
 GATGGCTTAA GACAGCTGTA GATGTTTTTA TTTAGCAAAA AAAAAAATAA AAAAGTCGAC 1740  
 GCGGCCGCGA ATTTAGTAG

Seq ID NO: 515 DNA sequence

Nucleic Acid Accession #: NM\_012427

Coding sequence: 43..924

1 11 21 31 41 51  
 | | | | |  
 CTTGTGGTTC CTCTCTACTT GGGGAAATCA GGTGCAGCGG CCATGGCTAC AGCAAGACCC 60  
 CCCTGGATGT GGGTGTCTCTG TGCTCTGATC ACAGCCTTGC TTCTGGGGGT CACAGAGCAT 120  
 GTTCTCGCCA ACAATGATGT TTCCTGTGAC CACCCCTCTA ACACCGTGCC CTCTGGGAGC 180  
 AACCCAGGACC TGGGAGCTGG GGCCGGGGAA GACGCCCGGT CGGATGACAG CAGCAGCCGC 240  
 ATCATCAATG GATCCGACTG CGATATGCAC ACCCAGCCGT GGCAGGCCGC GCTGTTGCTA 300  
 AGGCCCAACC AGCTCTACTG CGGGGCGGTG TTGGTGCATC CACAGTGGCT GCTCACGGCC 360  
 GCCCATGCA GAAAGAAAGT TTTCAAGATC CGTCTCGGCC ACTACTCCCT GTCAACAGTT 420  
 TATGAATCTG GGCAGCAGAT GTTCCAGGGG GTCAAATCCA TCCCCCACC TGGCTACTCC 480  
 CACCCTGGCC ACTCTAACGA CCTCATGCTC ATCAAATGCA ACAGAAGAAT TCGTCCCACT 540  
 AAAGATGTCA GACCCATCAA CGTCTCCTCT CATTGTCCCT CTGCTGGGAC AAAAGTGCTT 600  
 GTGTCTGGCT GGGGACAAAC CAAGAGCCCC CAAGTGCACT TCCCTAAGGT CCTCCAGTGC 660  
 TTGAATATCA GCGTGCTAAG TCAGAAAAGG TGCGAGGATG CTTACCCGAG ACAGATAGAT 720  
 GACACCATGT TCTGCGCCGG TGACAAAGCA GGTAGAGACT CCTGCCAGGG TGATTCTGGG 780  
 GGGCCTGTGG TCTGCAATGG CTCCTGTCAG GGAATCGTGT CCTGGGGAGA TTACCCCTGT 840  
 GCCCGGCCCA ACAGACCGGG TGTCTACACG AACCTCTGCA AGTTCAACAA GTGGATCCAG 900  
 GAAACCATCC AGGCCAACTC CTGAGTCAAT CCAGGACTCA GCACACCGGC ATCCCCACCT 960  
 GCTGCAGGGA CAGCCCTGAC ACTCCTTTCA GACCCTCATT CCTTCCAGGA GATGTTGAGA 1020  
 ATGTTTATCT TCCAGCCCAT TGACCCCATG TCTCCTGGAC TCAGGGTCTG CTTCCCCCAC 1080  
 ATTGGGCTGA CCGTGTCTCT CTAGTTGAAC CCTGGGAACA ATTTCCAAAA CTGTCCAGGG 1140  
 CGGGGGTTC GTCTCAATCT CCCTGGGGCA CTTTCATCCT CAAGCTCAGG GCCCATCCCT 1200  
 TCTCTGCAGC TCTGACCCAA ATTTAGTCCC AGAAATAAAC TGAGAAGTGG AAAAAAATAA

Seq ID NO: 516 Protein sequence

Protein Accession #: NP\_036559

1 11 21 31 41 51  
 | | | | |  
 MATARPPPMW VLCALITALL LGVTEHVLN NDVSCDHPSN TVPSGSNQDL GAGAGEDARS 60  
 DDSSSRING SDCHMHTQFW QAALLLRPNQ LYCGAVLVHP QWLLTAHCR KKVFRVRLGH 120  
 YSLSPVYESG QQMFQGVKSI PHPGYSHPGH SNDLMLIKLN RRIRPTKDVR PINVSSHCP 180  
 AGTKCLVSGW GTTKSPQVHF PKVLQCLNIS VLSQKRCEDA YPRQIDDTMF CAGDKAGRDS 240  
 CQDGGGPPV CNGSLQGLVS WGDYPCARP RPQVYTNLCK FTKWIQETIQ ANS



Seq ID NO: 517 DNA sequence  
Nucleic Acid Accession #: NM\_001719  
Coding sequence: 123..1418

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
      CTGCCACCTG GGGCCGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
10     CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCTGTGCG CTCTGGGCAC 180
      CCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
      GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
      CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
      CCATGTTTAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
      GCCAGGGCTT CTCCTACCCC TACAAGCCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
15     GCCTGCAAGA TAGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
      TGGAAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
      TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
      ACATCCGGGA ACGCTTTCAG AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
      AGCACTTGGG CAGGAATTCG GATCTCTTCC TGCTCGACAG CCGTACCCTC TGGGCCTCGG 780
20     AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACCAGCAA CCACTGGGTG GTCAATCCGC 840
      GGCACAACCT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
      AGTTGGCGGG CTTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGTTGGCTT 960
      TCTTCAAGGC CACGAGGTTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA 1020
25     GCCAGAACC GTCGAAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
      AGAACAGCAG CAGCGACGAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
      GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAGG CTACGCCGCC TACTACTGTG 1200
      AGGGGGAGTG TGCCCTCCCT CTGAATCTCT ACATGAACGC CACCAACCCAC GCCATCGTGC 1260
      AGACGCTGGT CCACTTCATC AACCCGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCACGC 1320
      AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
30     ACAGAAACAT GGTGTTCGGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCCT 1440
      TTGGGGCCAA GTTTTCTCG ATCCTCCAT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
      CTGCCTTTTG TGAGACCTTC CCTCCCTAT CCCCAACTTT AAAGTGTGA GAGTATTAGG 1560
      AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
      TCCTACAAGC TGTGCAAGCA AACCTAGCA GGAAAAAACA ACAACGCATA AAGAAAAATG 1680
35     CCGGGGCCAG GTCATGGCT GGGAAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
      TTATGAGCGC TACCAAGCCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
      GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
      CAATAAACG AATGAATG

```

Seq ID NO: 518 Protein sequence  
Protein Accession #: NP\_001710

```

45     1      11      21      31      41      51
      |      |      |      |      |      |
      MHVRSRLAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQE RREMQREILS 60
      ILGLPHRPRP HLQGHNSAP MFMLDLYNAM AVEEGGPGG QGFSYPYKAV FSTQGPPLAS 120
      LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHRFRFDL SKIPEGEAVT AAEFRYKYD 180
      IRERFDNETF RISVYQLQE HLGRESLFL LDSRTLWASE EGWLVDITA TSNHWVNP 240
      HNLGLQLSVE TLDQGSINPK LAGLGRHGP QNKQPFMVA FKATEVHFRS IRSTGSKQRS 300
50     QNRSKTFKNG EALRMANVAK NSSSDQKQAC KHELYVSFR DLGWQDWIIA PEGYAAYYCE 360
      GECAPPLNSY MNATNHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
      RNMVVRACGC H

```

Seq ID NO: 519 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 264..782

```

60     1      11      21      31      41      51
      |      |      |      |      |      |
      CCCTGCTCCA GTCACACCCG GAAGCTGACT GGTCCACGCA CAGCTGAAGC ATGAGGAAAC 60
      TCATCGCGGG ACTAATTTC CTTAAATTT AGACTTGACAG AGTAAGGACT TCAACTGACC 120
      TTCCTCAGAC TGAGAACTGT TTCCAGTATA TACATCAAGT CACTGAGATC TCCAGCACCC 180
      TGCCGGTGGC ACTACTGAGA GACGAGGTGC CAGGGTGGTT CCTGAAAGTG CCTGAGCCCC 240
      AACTTATCAG CAAGGAGCTC ATCATGCTGA CAGAAGTCAT GGAGGTCTGG CATGGCTTAG 300
65     TGATCGCGGT GGTGTCCTC TTCTGTCAGG CTGCTTCCT CACCGCCATC AACTACCTGC 360
      TCAGCAGGCA CATGGCCAC AAGAGTGAAC AGATACTGAA AGCGGCCAGT CTCAGGTTTC 420
      CCAGGCCAG CCCTGGCCAC CATCATCCAC CTGCTGTCAA AGAGATGAAG GAGACTCAGA 480
      CAGAGAGAGA CATCCCAATG TCTGATTCCC TTACAGGCA TGACAGCGAC ACACCCTCAG 540
      ATAGCTTGA TAGCTCTGC AGTTCGCCTC CTGCCTGCCA GGCCACAGAG GATGTGGATT 600
70     ACACACAAGT CGTCTTTCT GACCTGGAG AACTAAAAA TGACTCCCCG CTGGACTATG 660
      AGAACATAAA GGAATATCAA GATTATGTA ATGTCAATCC AGAAAGACAC AAGCCAGTT 720
      TCTGGTATT TGTCAACCT GCTCTGTCTG AGCCAGCGGA ATATGATCAA GTGGCCATGT 780
      GAATTCCAAA TATTTTAAAT GGGGTCCAGT TCTCTATGGA TTCTTACATT TAATTTGTAG 840
75     GGAATGCCA TTTTCCCCC TTAACAAGG CATGGGGCTC ACAAGTCTAT GGAGACAGGC 900
      CAAAAGAAAT GTGGAGAAGA AAAGTATGTA ATACACAGAG GTCCTCAAGA CCCATGGACT 960
      CCTGTCTGT ACCCAAAAAA GCTGTTCGTT CCTCAAAAAA AAAACAAGG CTTGGCTGGG 1020
      AAAACAGGCC AATGCCCCG CAAGAAAGGT TGAGATCAGA TGTTAGGAAG AACTTTCAGG 1080
      TAAAGTATGA GAACTATGGA GTCCATCAGC AGAGATAGTA GTGAAGTCTC TCCCAGGGA 1140
80     AAATTTTAAA AAGGTTGAA CAGCTGTTGT AGAGTTCTAT TTGGCAATCT CATGGTTAAA 1200
      TGACTTCCCT TTGAGCTCTT TAATTATTGG CAATAAACAA CTCTTTAAA AGTTTAAAAT 1260
      AAAATAGCAA CCACCACCA

```

Seq ID NO: 520 Protein sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
 5 MLTEVMEVWH GLVIAVVSFL LQACFLTAIN YLLSRHMAHK SEQILKAASL QVPRPSPGHH 60  
 HPPAVKEMKE QTERTDIPMS DSLYRHSDST PSDSLDSSCS SPPACQATED VDYTVVFSFSD 120  
 PGELEKNDSP L DYENIKEITD YVNVNPERHK PSFWYFVNPA LSEPAEYDQV AM

Seq ID NO: 521 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 107..328

1 11 21 31 41 51  
 15 CTGCTCTGTC TGAGCCAGCG GAATATGATC AAGTGGCCAT GTGAATTCCA AATATTTTAA 60  
 ATGGGGTCCA GTTCTCTATG GATTCTTACA TTTAATTTGT AGGGAAATGC CATTTTTCCC 120  
 CCTTAAACAA GGCATGGGCG TCACAAGTCT ATGGAGACAG GCCAAAAAGA ATGTGGAGAA 180  
 GAAACTGAT AAATACACAG AGGTCTCTCA GACCCATGGA CTCTCTGCT GTACCCAAAA 240  
 AAGCTGTTTC TCCCTCAAAA ACAAAAACAA GGCTTGGCTG GGAAACACAG CCAATGCCCC 300  
 20 GGCAAGAAAG GTTGAGATCA GATGTTAGGA AGAACTTTCA GGTAAAGTAT GAGAACTATG 360  
 GAGTCCATCA GCAGAGATAG TAGTGAAGTC TCTCCACAGG GAAAATTTTA AAAAGGTTGA 420  
 ATCAGCTGTT GTAGAGTTCT ATTTGGCAAT CTCATGGTTA AATGACTTCC CTTTGAGCTC 480  
 TTTAATTATT GGCAATAAAC AACTTCTTTA AAAGTTTAA ATAAATAGC AACCACCACC 540  
 A

Seq ID NO: 522 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
 30 MPFFPLKQGM GLTSLWRQAK KNVEKTKDKY TEVLKTHGLL VCTQKSCSFL KNKNKAWLGK 60  
 QANAPARKVE IRC

Seq ID NO: 523 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 211..1895

1 11 21 31 41 51  
 40 GGATCTGAGG GGCGCCAGT CACTTCTCTC ACGTTCTCGT GCTGGGCGGG AGGAGCGGAT 60  
 GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTTT TTGGGTCGGA 120  
 GAGGAATTAT CTGATAAAAT TCCTGGGTTA ATATTTTAA AAACGGAGAG TTTTFAAAAA 180  
 TGATTTTTTT CCTCGAAAA TGACCTTTTT ATGCTTCGAA GCAGTTTGTC AACCAGCATA 240  
 GTGCTTTTTT TTTTCTCTTC TTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG 300  
 45 CACAGGTTCC TTGAACAGCT GGATTCTGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360  
 CTGTGTCTGA AAGCGAAAGT ACAATGTGAA CTCAACATCA CAGCTCAACT CCAGGAGGGA 420  
 GAAGGTAATT GTTTCCTCTG ATGGGATGGA CTCATTGTTT GGCCAGAGG AACAGTGGGG 480  
 AAAATATCGG CTGTTCCATG CCTCTCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540  
 50 TTCCGACACT GTAACCCCAA TGGAAACATGG GATTTTATGC ACAGCTTAAA TAAACATGG 600  
 GCCAATTATT CAGACTGCCT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660  
 TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCCTTG 720  
 CCTGTGGCTA TTCTCATCAT TGGTTACTTC AGACGATTGC ATTGCACTAG GAACTATATC 780  
 CACATGCACT TATTTGTGTC TTTCTATGCT AGAGCTACAA GCATCTTTGT CAAAGACAGA 840  
 GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900  
 55 CAAAATTTCCA TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT 960  
 GTTGTGATGT TTATTTACTT CCTGGCTACA AATTATTATT GGATCCTGGT GGAAGGTCTC 1020  
 TACCTGCATA ATCTCATCTT TGTGGCTTTC TTTTCGGACA CCAAAATACCT GTGGGGCTTC 1080  
 ATCTTGATAG GCTGGGGGTT TCCAGCAGCA TTTGTTGCAG CATGGGCTGT GGCACGAGCA 1140  
 ACTCTGGCTG ATGCGAGGTG CTGGGAACCT AGTGCTGGAG ACATCAAGTG GATTTATCAA 1200  
 60 GCACCGATCT TAGCAGCTAT TGGGCTGAAT TTTATTCTGT TTCTGAATAC GGTTAGAGTT 1260  
 CTAGCTACCA AAATCTGGGA GACCAATGCA GTTGGGCATG ACACAAGGAA GCAATACAGG 1320  
 AAACCTGGCCA AATCGACACT GGTCTGGTCT CTAGTCTTTG GAGTGCATTA CATCGTGTTC 1380  
 GTATGCCTGC CTCACCTCTT CACTGGGCTC GGGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440  
 TTCTTCAACT CTTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500  
 65 GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGTGGAATC TCTCCGTGGA CTGGAAGAAG 1560  
 ACACCGCCAT GTGGCAGCGC CAGATGCGGC TCAGTGCTCA CCACCGTGAC GCACAGCACC 1620  
 AGCAGCCAGT CACAGGTGGC GGCACGACCA CGCATGGTGC TTATCTCTGG CAAAGCTGCC 1680  
 AAGATCGCCA GCAGACAGCC TGACAGCCAC ATCACTTTAC CTGGCTATGT CTGGAGTAAC 1740  
 TCAGAGCAGG ACTGCTGCC ACACCTTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800  
 70 CAGGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGAATCTAA CCCAGACACT 1860  
 GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

Seq ID NO: 524 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51  
 75 MLRSSLSLSI VLFSSFSST INESSSRKR HRFLEQLDSD GTITIEBQIV LVLKAKVQCE 60  
 LNITAQLEQG EGNCFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCNPNGTW 120  
 80 DFMHSLNKTW ANYSDCLRFL QPDISIGKQE FFERLYVMT VGYISIFGSL AVAILIIGYF 180  
 RRLHCTRYNI HMFIFVSFML RATSIFVKDR VVHAHIGVKE LESLIMQDDP QNSIEATSVD 240  
 KSQYIGCKIA VVMFIYFLAT NYWILVEGL YLHNLIFVAF FSDTKYLWGF ILIGWGFPA 300  
 FVAAWAVARA TLADARCWEL SAGDIKWIYQ APILAAIGLN FILPLNTRVR LATKIWTNA 360  
 VGHDTRKQYR KLAKSTLVLV LVFVGHYIVF VCLPHSFTGL GWEIRMHCEL FFNSFQGFV 420  
 SIIYCYCNQE VQAEVKMKWS RWNLSVDWKR TPPCGSRRCG SVLTVTVTST SSQSQAAS 480

RMVLISGKAA KIASRQPDSDH ITPGYVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKP 540  
SRPMESNPDT EGCGQETEDV L

Seq ID NO: 525 DNA sequence  
Nucleic Acid Accession #: NM\_005048  
Coding sequence: 143..1795

```

1      11      21      31      41      51
|      |      |      |      |      |
10  GGCCGGTGGC CCGGGCCCGA CCACCCAGC TCGCGTCTGT TACTGGCCAC AAGTTTGCTC 60
    TGGGCCAGCC AAGTTGGCAA CTTGGAAGCT TCTCCCGGGC TCTGGAGGAG GGTCCCTGCT 120
    TCTTCTTACA GCCGTTCCGG GCATGGCCGG GCTGGGGGCG TCGCTCCACG TCTGGGGTTG 180
    GCTAATGTCT GGCAGCTGCC TCCTGGCCAG AGCCAGCTGT GATTCTGATG GCACCATTAC 240
    TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
15  AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTCCCTGAA TGGGATGGAC TCATTGTGTG 360
    GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCATGCT CCTCTTATA TTTATGACTT 420
    CAACCATAAA GGAGTTGCTT TCCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480
    CAGCTTAAAT AAAACATGGG CCAATTATTC AGACTGCCTT CGCTTCTGTC AGCCAGATAT 540
    CAGCATAGGA AAGCAAGAA TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
20  CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCAT GGTACTTCA GACGATTGCA 660
    TTGCACTAGG AACTATATCC ACATGCACCT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720
    CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
    AATAATGCAG GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCACAATA 840
    TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATG 900
25  GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTCTT TTTCCGACAC 960
    CAAATACCTG TGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGCAGC 1020
    ATGGGCTGTG GCACAGACCA CTCTGGCTGA TGCAGAGTGC TGGGAACTTA GTGCTGGAGA 1080
    CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATTCTGTT 1140
    TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCATGA 1200
30  CACAAGGAAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCTTGCTCC TAGTCTTTGG 1260
    AGTGCAATTAC ATCGTGTTCG TATGCCTGCC TCACTCCTTC ACTGGGCTCG GGTGGGAGAT 1320
    CCGCATGCAC TGTGAGCTCT TCTTCAACTC CTTTCAGGGT TTCTTTGTGT CTATCATCTA 1380
    CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGAATCT 1440
35  CTCGTTGGAC TGGAAAGGA CACCGCCATG TGGCAGCCGC AGATGCGGCT CAGTGCTCAC 1500
    CACCGTGAGC CACAGACCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGTCT 1560
    TATCTCTGGC AAAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACTTTACC 1620
    TGGCTATGTC TGGAGTAAC TCAAGCAGGA CTGCTGCCA CACTCTTCC ACGAGGAGAC 1680
    CAAGGAAGAT AGTGGGAGGC AGGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740
    GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAAACT GAGGATGTTT TCTGAATGGA 1800
40  CATTTGTGGC TGACTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860
    ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT 1920
    TTTTAGGCTC CATGAATTGG CTCCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAT 1980
    GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCTTC TAAATTAATG TATGGTATT 2040
    GCTCTGTGAT TGTTCATTTT TTTCTGTAC TTTTGGGTAG AAAAAAGATT CAATTGCTTG 2100
45  GCTGTAGCTT TCTCTCATAT ATATCACCTT AAATATAATG AAGATCTTTT AGTGTGTATC 2160
    ATTTTCTTTT TAGAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220
    ATTTATTTT CCTGTGCTAG GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280
    GATCTAAGAA CAGTACTCTG CTGGAATAAT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340
    TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAAG AATATTTCAC 2400
50  ACATCCCTTC TTTGAATGAG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460
    TTCTTTGTAA ACCATGTGAT GTGGAAGAGT TTCTCTAGTT AGTGAGCTTG TGTCTGCAA 2520
    TTGATTTTGT TTGTAAGTGA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTCCTTG 2580
    TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAATAATTT GTTTTAAAAA 2640
    T

```

Seq ID NO: 526 Protein sequence  
Protein Accession #: NP\_005039

```

1      11      21      31      41      51
|      |      |      |      |      |
60  MAGLGASLHV WGLWMLGSCL LARAQLDSGD TITIEEQIVL VLKAKVQCEL NITAOEQEGE 60
    GNCFFPEWDGL ICWPRGTGK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSLNKTWA 120
    NYSCLRLRFLQ PDISIGKQEF FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH 180
    MHLEFVSFMLR ATSFVFKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSVDK SQYIGCKIAV 240
65  VMFIYFLATN YYWILVEGLY LHNLIFFVAF SDTKYLWGF I LIGWGFPAF VAAWAVARAT 300
    LADARCWELS AGDIKWIIQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK 360
    LAKSTLVLVL VFGVHYIVFV CLPHSFTGLG WEIRMHCELF FNSFQGFVVS ILYCYCNGEV 420
    QAEVKMWSR WNLVDWKRT PPCGSRRCS VLTTVTHTS SQSQVAASR MVLISGKAAK 480
70  IASRQPDSDH ITPGYVWSN SEQDCLPHSF HEETKEDSGR QGDDILMEKPS RPMESNPDE 540
    GCQGETEDVL

```

Seq ID NO: 527 DNA sequence  
Nucleic Acid Accession #: XM\_036683  
Coding sequence: 38..3655

```

1      11      21      31      41      51
|      |      |      |      |      |
75  GCTTTGCCCA GTAGTTGGAA AGTGAAGTCT ACTCGTGATG GTTCTCCTGT CACTTTGGTT 60
    GATAGCAGCC GCTCTGGTAG AGGTTAGGAC TTCAGCTGAT GGACAAGCTG GTAATGAAGA 120
    AATGGTGCAA ATAGATTTAC CAATAAAGAG ATATAGAGAG TATGAGCTGG TGACTCCAGT 180
    CAGCAAAAT ATAGAAAGAC GCTATCTCTC CCATACCTCT TCTGCGAGTC AAAAAAGAG 240
    GTCAGCGAGG GACGTGTCTT CCAACCCTGA GCAGTTGTTC TTTAATATCA CGGCATTGTTG 300
    AAAAGATTTT CATCTGCGAC TAAAGCCCAA CACTCAACTA GTAGCTCCTG GGGCTGTTGT 360
80  GGAGTGGCAT GAGACATCTC TGGTGCCTGG GAATATAACC GATCCCATTA ACAACCATCA 420

```

	ACCAGGAAGT	GCTACGTATA	GAATCCGGAA	AACAGAGCCT	TTGCAGACTA	ACTGTGCTTA	480
	TGTTGGTGAC	ATCGTGGACA	TTCCAGGAAC	CTCTGTTGCC	ATCAGCAACT	GTGATGGTCT	540
	GGCTGGGAATG	ATAAAAGTG	ATAATGAAGA	GTATTTCATT	GAACCCCTGG	AAAGAGGTAA	600
5	ACAGATGGAG	GAAGAAAAAG	GAAGGATTCA	TGTTGTCTAC	AAGAGATCAG	CTGTAGAACA	660
	GGCTCCCATTA	GACATGTCCA	AAGACTTCCA	CTACAGAGAG	TCGGACCTGG	AAGGCCCTTGA	720
	TGATCTAGGT	ACTGTTTATG	GCAACATCCA	CCAGCAGCTG	AATGAAACAA	TGAGACGCCG	780
	CAGACACGCG	GGAGAAAACG	ATTACAATAT	CGAGGTACTG	CTGGGAGTGG	ATGACTCTGT	840
	GGTCCGTTTC	CATGGCAAAG	AGCACGTCCA	AAACTACCTC	CTGACCCCTAA	TGAACATTGT	900
10	GAATGAAATT	TACCATGATG	AGTCCCTCGG	AGTGCATATA	AATGTGGTCC	TGGTGC GCAT	960
	GATAATGCTG	GGATATGCAA	AGTCCATCAG	CCTCATAGAA	AGGGGAAACC	CATCCAGAAG	1020
	CTTGAGGAAT	GTGTGTCTGT	GGGCGTCCCA	ACAGCAAAGA	TCTGATCTCA	ACCACCTCTGA	1080
	ACACCATGAC	CATGCAATTT	TTTTAACCCAG	GCAAGACTTT	GGACCTGCTG	GAATGCAAGG	1140
	ATATGCTCCA	GTACCCGGCA	TGTGTCATCC	AGTGAGAAGT	TGTACCCCTGA	ATCATGAGGA	1200
15	TGGTTTTTCA	TCTGCTTTTG	TAGTAGCCCA	TGAAACGGGC	CATGTGTTGG	GAATGGAGCA	1260
	TGATGGACAA	GGCAACAGT	GTGGTGATGA	GACTGCTATG	GGAAAGTGTCA	TGGCTCCCTT	1320
	GGTACAAGCA	GCATTCCATC	GTTACCACTG	GTCCCGATGC	AGTGGTCAAG	AACTGAAAAG	1380
	ATATATCCAT	TCCTATGACT	GTCTCCTTGA	TGACCCCTTT	GATCATGATT	GGCCTAAACT	1440
	CCGAGAACTT	CCTGGAATCA	ATTATTCTAT	GGATGAGCAA	TGTCGTTTTG	ATTTTGGTGT	1500
20	TGGCTATAAA	ATGTGCACCG	CGTTCGGAAC	CTTTGACCCA	TGTAACACAG	TGTGGTGTAG	1560
	CCATCCTGAT	AATCCCTACT	TTTGTAAAG	TAAAGAGGGA	CCTCCACTTG	ATGGGACTGA	1620
	ATGTGCTGCT	GGAAAATGGT	GCTATAAGGG	TCATTGCGATG	TGGAAGAATG	CTAATCAGCA	1680
	AAAAACAAGT	GGCAATTTGG	GGTCATGGAC	TAAATTTGGC	TCCTGTTCTC	GGACATGTGG	1740
	AACTGGTGT	CGTTTCAGAA	CACGCCAGTG	CAATAATCCC	ATGCCCATCA	ATGGTGGTGA	1800
25	GGATTGTCTC	GGTGTAAATT	TTGAGTACCA	GCTTTGTAA	ACAGAGAAT	GCCAAAAACA	1860
	CTTTGAGGAC	TTGAGAGCAC	AGCAGTGTCA	GCAGCGAAAC	TCCCACTTTG	AATACCAGAA	1920
	TACCAAAACAC	CACCTGGTTG	CATATGAACA	TCCCTGACCC	AAGAAAAGAT	GCCACCTTTA	1980
	CTGTGAGTCC	AAGGAGACTG	GAGATGTTGC	TTACATGAAA	CAACTGGTGC	ATGATGGAAC	2040
	GCACGTCTCT	TACAAAGATC	CATATAGCAT	ATGTGTGCGA	GGAGAGTGTG	TGAAAGTGGG	2100
30	CTGTGATAAA	GAAATTTGGT	CTAATAAGGT	TGAGGATAAG	TGTGGTGTCT	GTGGAGGAGA	2160
	TAAATCCCCAC	TGCCGAACCG	TGAAGGGGAC	ATTTACCAGA	ACTCCAGGGA	AGCTTGGGTA	2220
	CCTTAAGATG	TTTGATATAC	CCCCTGGGGC	TAGACATGTG	TTAATCCAAG	AAGACGAGGC	2280
	TTCTCCTCAT	ATTCTTGCTA	TTAAGAACCA	GGCTACAGGC	CATTATATTT	TAAATGGCAA	2340
	AGGGGAGGAA	GCCAAGTCGC	GGACCTTCAT	AGATCTTGGT	GTGGAGTGGG	ATTATAACAT	2400
35	TGAAGATGAC	ATTGAAAGTC	TTACACCCGA	TGGACCTTTA	CATGATCCTG	TTATTGTTTT	2460
	GATTATACCT	CAAGAAAATG	ATACCCGCTC	TAGCCCTGAC	TATAAGTACA	TCATCCATGA	2520
	AGACTCTGTA	CCTACAATCA	ACAGCAACAA	TGTCATCCAG	GAAGAATTAG	ATACTTTTGA	2580
	GTGGGCTTTG	AAGAGCTGGT	CTCAGTGTTC	CAAACCTGT	GGTGGAGGTT	TCCAGTACAC	2640
	TAAATATGGA	TGCCGTAGGA	AAAGTGATAA	TAAATTTGGT	CATCGCAGCT	TCTGTGAGGC	2700
40	CAACAAAAAG	CCGAAAACCT	TTAGACGAAT	GTGCAATATT	CAAGAGTGTG	CACATCCACT	2760
	CTGGGTAGCA	GAAGAAATGG	AACACTGCAC	CAAAACCTGT	GGAAGTTCTG	GCTATCAGCT	2820
	TCGCACTGTA	CGCTGCCTTC	AGCCACTCCT	TGATGGCACC	AACCGCTCTG	TGCACAGCAA	2880
	ATACTGCATG	GGTGACCGTC	CCGAGAGCCG	CCGGCCCTGT	AACAGAGTGC	CCTGCCCTGC	2940
	ACAGTGGAAA	ACAGGACCTT	GGAGTGAAGT	TTCACTGACC	TGCGGTGAAG	GAACGGAGGT	3000
45	GAGGAGGTC	CTCTGCAGGG	CTGGGGACCA	CTGTGATGGT	GAAAAGCCTG	AGTCGGTCAG	3060
	AGCCTGTCAA	CTGCCCTCCT	GTAATGATGA	ACCATGTTTG	GGAGACAAGT	CCATATTCTG	3120
	TCAAATGGAA	GTGTTGGCAC	GATACTGCTC	CATACCAGGT	TATAACAAGT	TATGTTGTGA	3180
	GTCTGCGAGC	AAGCGCAGTA	GCACCTGCCC	ACCACCATAC	CTTCTAGAAG	CTGCTGAAAC	3240
	TCATGATGAT	GTCACTCTTA	ACCCTAGTGA	CCTCCCTAGA	TCTCTAGTGA	TGCCTACATC	3300
50	TTTGGTTTCT	TATCATTTCAG	AGACCCCTGC	AAAGAAGATG	TCTTTGAGTA	GCATCTCTTC	3360
	AGTGGGAGGT	CCAAATGCAT	ATGCTGCTTT	CAGGCCAAAC	AGTAAACCTG	ATGGTGCTAA	3420
	TTTACGCCAG	AGGAGTGCTC	AGCAAGCAGG	AAGTAAGACT	GTGAGACTGG	TCACCGTACC	3480
	ATCCTCCCCA	CCGAAACCTG	CAGTTCCAGT	TCACAAATGG	CTGCTGCTTC	CTGCTGCTTC	3540
	CTTCTTTGCA	GCCAGTGATT	CAATAGGTGC	TTCTTCTCAG	GCAAGAACCT	CAAAGAAAGA	3600
55	TGGAAAGATC	ATTGACAACA	GACGTCCGAC	AAGATCATCC	ACCTTAGAAA	GATGAGAAAG	3660
	TGAACCAAAA	AGGCTAGAAA	CCAGAGGAAA	ACCTGGACAA	CCTCTCTCTT	CCCATGGTGC	3720
	ATATGCTTGT	TTAAAGTGGG	AATCTCTATA	GATCGTCAGC	TCAATTTTATC	TGTAAATGGA	3780
	AGAACAGAAA	GTGCTGGCTC	ACTTCTAGT	TGCTTTCATC	CTCCTTTTGT	TCTGCATTGA	3840
	CTCATTTACC	AGAATTTCAT	GGAGAGAAAT	ACCAAGATT	ATTACAAAAG	AAAAATATGT	3900
60	TGCTAAGATT	GTGTGTGTCG	CTCTCTGAAG	CAGAAAAGGG	ACTGGAACCA	ATTGTGCATA	3960
	TCAGCTGACT	TTTGTGTTGT	TTTAGAAAAG	TTACAGTAAA	AATTAAAAAG	AGATAACCAAT	4020
	GGTTTACACT	TTAACAAGAA	ATTTTGGATA	TGGAACAAAG	AATTCTTAGA	CTGTATTTCC	4080
	TATTTATCTA	TATTAGAAAT	ATTGTATGAG	CAAATTTGCA	GCTGTTGTGT	AAATACTGTA	4140
65	TATTGCAAAA	ATCAGTATTA	TTTTAAGAGA	TGTGTTCTCA	AATGATTGTT	TACTATATTA	4200
	CATTCTGGA	TGTTCTAGGT	GCCTGTCTGT	GAGTATTGCC	TTGTTTGACA	TTCTATAGGT	4260
	TAAATTTCAA	AGCAGAGTAT	TACAAAAGAG	AAGTTAGAAT	TACAGCTACT	GACAATATAA	4320
	AGGGTTTTGT	TGAATCAACA	ATGTGATACG	TAAATTTATG	AAAAAGAAAA	GAAACACAAA	4380
	AGCTATAGAT	ATACAGATAT	CAGCTTACCT	ATTGCCTTCT	ATACTTATAA	TTTAAAGGAT	4440
70	TGGTGTCTTA	GTACACTTGT	GGTCACAGGG	ATCAACGAAT	AGTAAATAAT	GAACCTCGTC	4500
	AAGACAAAAC	TGAAACCCCT	TTTCCAGGAC	CTCAGTAGGC	ACCGTTGAGG	TGTCCTTTGT	4560
	TTTTGTGTGT	GTGTGTTCTT	TTTTAATTTT	CGCATTGTTG	ACAGATACAA	ACAGTTATAC	4620
	TCAATGTACT	GTAATAATCG	CAAGGAAAAA	AGTTTGGGGA	TAACTTATTT	GTATGTTGGT	4680
	AGCTGAGAAA	AATATCATCA	GTCTAGAAAT	GATATTTGAG	TATAGTAGAG	CTTTGGGGCT	4740
75	TTGAAGGCAG	TGTTCAAGAA	GCATATGTCG	ATGGTTGAGA	TATTTATTTT	CCATATGGTT	4800
	CATGTTCAAA	TGTTTCAAC	CACAAATGAT	CTGACTGCAA	TAATGTGCTA	ATAATTTATG	4860
	TCAGTAGTCA	CCTTGCTCAC	AGCAAAGCCA	GAAATGCTCT	CTCCAGGGAG	TAGATGTAAA	4920
	GTACTGTAGC	ATAGAATTCA	GAACCTGAAGA	TATTTATTAA	AAGTTGATT	TTTTTCTGTG	4980
	ATAGTATTTT	TATGTACTAA	ATATTACAC	TAAATATCAAT	TACATATTTT	GGTAAACTAG	5040
80	AGAGACATAA	TTAGAGATGC	ATGCTTTGTT	CTGTGCATAG	AGACCTTTAA	GCAAACTACT	5100
	ACAGCCAACCT	CAAAAGCTAA	AACTGAACAA	ATTTGATGTT	ATGCAACAT	CTTGCAATTT	5160
	TAGTAGTTGA	TATTAAAGTT	ATGACTTGT	TCCCTTCAAG	GAAACATTAA	ATTGTATGGA	5220
	CTCAGCTAGC	TGTTTCAAGT	AATTGTGAAT	TAGAAACATT	TTTAAAGTT	TTTGAAAGAG	5280
	ATAAGTGCAAT	CATGAATTAC	ATGTACATGA	GAGGAGATAG	TGATATCAGC	ATAATGATTT	5340
	TGAGGTGAGT	ACCTGAGCTG	TCTAAAAATA	TATTATACAA	ACTAAATGT	AGATGAATTA	5400
	ACCTCTCAAA	GCACAGAATG	TGCAAGAAGT	TTTGCAATTT	AATCGTTGTA	AACTAACAGC	5460

TTAAGCTATT GACTCTATAC CTCTAAAGAA TTGCTGCTAC TTTGTGCAAG AACTTTGAAG 5520  
 GTCAAAATAG GCAAAATCCA GATAGTAAAA CAATCCCTAA GCCTTAAGTC TTTTITTTTTT 5580  
 CCTAAAAATT CCATAGAAAT AAAATTCTCT CTAGTTTACT TGTGTGTGCA TACATCTCAT 5640  
 CCACAGGGGA AGATAAGAT GGTACACAAA ACAGTTTCCA TAAAGATGTA CATATTCAAT 5700  
 ATACTTCTGA CCTTTGGGCT TTCTTTTCTA CTAAGCTAAA AATTCCTTTT TATCAAAGTG 5760  
 TACACTACTG ATGCTGTTTG TTGACTGAG AGCACGTACC AATAAAAATG TTAACAAAAT 5820  
 AT

Seq ID NO: 528 Protein sequence  
 Protein Accession #: XP\_036683

1 11 21 31 41 51  
 | | | | |  
 15 MVLLSLWLIA AALVEVRTSA DGQAGNEEMV QIDLPIKRYR EYELVTPVST NLEGRYLSHT 60  
 LSASHKKRSA RDVSSNPEQL FFNITAFGKD FHLRLKPNTQ LVAPGAVVEW HETSLVPGNI 120  
 TDPINNHPQG SATYRIKTE PLQTNCAVVG DIVDIPGTSV AINSNCDGLAG MIKSDNDEEYF 180  
 IEPLERKQKM EEEKGRTHVV YKRSAVEQAP IDMSKDFHYR ESDLEGLDDL GTVYGNHQQ 240  
 LNETMRRRRR AGENDYNIEV LLGVDDSVVR FHGKEHVQNY LLTLMNIVNE IYHDESLGVH 300  
 INVVLVRMIM LGYAKSISLI ERGNPSRSLE NVCRWASQQQ RSDLNHSEHH DHAIFLTRQD 360  
 20 FGPAQMGGYA PVTGMCHPVR SCTLNHEDGF SSAFVVAHET GHVLGMEHDG QGNRCGDETA 420  
 MGSVMAPLVQ AATHRYHWSR CSGQELKRYI HSYDCLLDDP FDHDPWKLPE LPGINYSMDE 480  
 QCRPFDGVGY KMCTAFRTFD PCKQLWCSHP DNPYFCKTKK GPPLDGTBECAG AGKWCYKGHC 540  
 MWKNANQQKQ DGNWGSWTKF GSCSRTCTGT VRFRTQCNM PMPINGGQDC PGVNFYQLC 600  
 NTECQKHFE DFRAGQCCQR NSHFYQNTK HHWLPYEHDP PKKRCHLYCQ SKETGDVAYM 660  
 25 KQLVHDGTHC SYKDPYSICV RGECKVKGCD KEIGSNKVED KCGVCGGDNH HCRTVKGTFT 720  
 RTPRKLGYLK MFDIPPGRAR VLIQDEEASP HILAIKNQAT GHYILNGKGE EAKSRTFIDL 780  
 GVEWDYNIED DIESLHTDGP LHDPVIVLII PQENDTRSSL TYKYIHEDS VPTINSNNVI 840  
 QEELDTFEWA LKSNWSQCSKP CGGGFYQYTKY GCRKSDNKM VHRSFCEANK KPKPIRMCN 900  
 IQECTHPLWV AEWEHCCTKT CGSSGYQLRT VRCLQPLLDG TNRSVHSKYC MGDREPSRRP 960  
 30 CNRVPCPAQW KTGFWSECSV TCGEGTEVRQ VLRAGDHCD GEKPEVRAC QLPCCNDEPC 1020  
 LGDKSIFCQM EVLARYCSIP GYNKLCCESC SKRSTLPPP YLLEAAETHD DVISNPDLP 1080  
 RSLVMPSTSLV PYHSETPAKK MSLSSISSVG GPNAYAAFRP NSKPDGANLR QRSAGQAGSK 1140  
 TVRLVTVPS PPTKRVLHSS ASQMAAAFF AASDSIGASS QARTSKKD GK IIDNRRPTRS 1200  
 STLER

Seq ID NO: 529 DNA sequence  
 Nucleic Acid Accession #: NM\_002774  
 Coding sequence: 246..980

1 11 21 31 41 51  
 | | | | |  
 40 AGGCGGACAA AGCCCGATTG TTCCTGGGCG CTTTCCCAT CGCGCCTGGG CCTGCTCCCC 60  
 AGCCCGGGGG AGGGCGGGGG GCCAGTGTGG TGACACACGC TGTAGCTGTC TCCCGGGCTG 120  
 GCTGGCTCGC TCTCTCCTGG GGACACAGAG GTCGGCAGGC AGCACACAGA GGGACCTACG 180  
 45 GGCACTGTGT CCTTCCCCCG ACTCAAGAAAT CCCCGGAGGC CCGGAGGCCT GCAGCAGGAG 240  
 CGGCCATGAA GAAGTGTGAT GTGGTGCTGA GTCTGATTGC TGCAGCCTGG GCAGAGGAGC 300  
 AGAATAAGTT GGTGCTATGGC GGACCCCTGG ACAAGACATC TCACCCCTAC CAAGCTGCCC 360  
 TCTACACCTC GGGCCACTTG CTCTGTGGTG GGGTCTTAT CCATCCACTG TGGGTCTCTCA 420  
 CAGCTGCCCA CTGCAAAAAA CCGAATCTTC AGGTCTTCTT GGGGAAGCAT AACCTTCGGC 480  
 50 AAAGGGAGAG TTCCAGGAG CAGAGTCTTG TTGTCCGGGC TGTGATCCAC CCTGACTATG 540  
 ATGCCGCCAG CCATGACCAG GACATCATGC TGTGTGCGCT GGCACGCCCA GCCAACTCT 600  
 CTGAATCAT CCAGCCCTT CCCCTGGAGA GGGACTGCTC AGCCCAACCC ACCAGCTGCC 660  
 ACATCTGGG CTGGGGCAGG ACAGCAGATG GTGATTCTCC TGACACCATC CAGTGTGCAT 720  
 ACATCCACCT GGTGTCCCTG GAGGAGTGTG AGCATGCCTA CCCTGGCCAG ATCACCAGCA 780  
 55 ACATGTTGTG TGCTGGGGAT GAGAAGTACG GGAAGGATTC CTGCCAGGGT GATTCTGGGG 840  
 GTCCGCTGCT ATGTGGAGAC CACCTCCGAG GCCTTGTGTC ATGGGGTAAC ATCCCTGTG 900  
 GATCAAAGGA GAAGCCAGGA GTCTACACCA ACGTCTGCAG ATACACGAAC TGGATCCAAA 960  
 AAACCATTC A GGCAGAGTGA CCCTGACATG TGACATCTAC CTCCCGACCT ACCACCCAC 1020  
 TGGCTGGTTC CAGAACGCTC CTCACCTAGA CCTGCTCTCC CCTCTCTCTC TGCCAGCTC 1080  
 60 TGACCTGAT GCTTAATAAA CGCAGCGACG TGAGGGTCTC GATTCTCCCT GGTTTTACCC 1140  
 CAGCTCCATC CTGTCATCAC TGGGGAGGAC GTGATGAGTG AGGACTTGGG TCCTCGGTCT 1200  
 TACCCCCACC ACTAAGAGAA TACAGGAAAA TCCCTTCTAG GCATCTCTC TCCCAACCC 1260  
 TTCCACACGT TTGATTCTCT CTGTCAGAGG CCCAGCCACG TGTCTGGAAT CCCAGCTCCG 1320  
 CTGCTTACTG TCGGTGTCCC CTGGGATGT ACCTTTCTTC ACTGCAGATT TCTCACTGT 1380  
 65 AAGATGAAGA TAAGGATGAT ACAGTCTCCA TCAGGCAGTG GCTGTTGGAA AGATTTAAGA 1440  
 TTTACACCT ATGACATACA TGGGATAGCA CCTGGGCCGC CATGCACTCA ATAAAGAAATG 1500  
 TATTTT

Seq ID NO: 530 Protein sequence  
 Protein Accession #: NP\_002765

1 11 21 31 41 51  
 | | | | |  
 75 MKKLMVLSL IAAAWAEFQN KLVHGGPCDK TSHPYQAALY TSGHLLCGGV LIHPLWVLT 60  
 AHCKKPNLQV FLGKHNLRQR ESSQEQQSVV RAVIHDPYDA ASHDQDIMLL RLARPALKSE 120  
 LIQPLPLERD CSANTTSCHI LGWKTADGD FPDITQCAIY HLVSREECEH AYPGQITQNM 180  
 LCAGDEKYGK DSCQGDGGP LVCGDHLRGL VSWGNI PCGS KEKPGVYTNV CRYTNWIKT 240  
 IQAK

Seq ID NO: 531 DNA sequence  
 Nucleic Acid Accession #: NM\_012152  
 Coding sequence: 43..1104

1 11 21 31 41 51

5  
10  
15  
20

CTTCTTTTAA	TTTCTTTCTA	GGATGTTTAC	TTCTTCTCCA	CAATGAATGA	GTGTCACTAT	60
GACAAGCACA	TGGACTTTTT	TTATAATAGG	AGCAACACTG	ATACTGTCTG	TGACTGGACA	120
GGAAACAAAG	TTGTGATTGT	TTTGTGTGTT	GGGACGTTTT	TCTGCCTGTT	TATTTTTTTT	180
TCTAATTCTC	TGGTCATCGC	GGCAGTGATC	AAAAACAGAA	AATTTTCATT	CCCCCTCTAC	240
TACCTGTGGG	CTAATTTAGC	TGCTGCCGAT	TTCTTCGCTG	GAATTGCCTA	TGTATTCTCT	300
ATGTTTAAAC	CAGGCCAGT	TTCAAAAAC	TTGACTGTCA	ACCGCTGGTT	TCTCCGTCAG	360
GGGCTTCTGG	ACAGTAGCTT	GACTGCTTCC	CTCACCACCT	TGCTGGTTAT	CGCCGTGGAG	420
AGGCACATGT	CAATCATGAG	GATGCGGGTC	CATAGCAACC	TGACCAAAAA	GAGGGTGACA	480
CTGCTCATTT	TGCTTGTCTG	GGCCATCGCC	ATTTTTATGG	GGGCGGTCCC	CACACTGGGC	540
TGGAATTGCC	TCTGCAACAT	CTCTGCCTGC	TCTTCCCTGG	CCCCCATTTA	CAGCAGGAGT	600
TACCTTGTTT	TCTGGACAGT	GTCACACCTC	ATGGCCTTCC	TCATCATGGT	TGTGGTGATC	660
CTGCGGATCT	ACGTGTACGT	CAAGAGGAAA	ACCAACGTCT	TGTCTCCGCA	TACAAGTGGG	720
TCCATCAGCC	GCCGGAGGAC	ACCCATGAAG	CTAATGAAGA	CGGTGATGAC	TGTCTTAGGG	780
GCGTTTGTGG	TATGCTGGAC	CCCGGGCCTG	GTGGTTCTGC	TCCTCGACGG	CCTGAAGTGC	840
AGGCAGTGTG	GCGTGCAGCA	TGTGAAAAGG	TGGTTCCTGC	TGCTGGCGCT	GCTCAACTCC	900
GTCTGTAACC	CCATCATCTA	CTCTACAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
ATGATCTGCT	GCTTCTCTCA	GGAGAACCAC	GAGAGGCGTC	CCTCTCGCAT	CCCTCCACA	1020
GTCTCAGCA	GGAGTGACAC	AGGCAGCCAG	TACATAGAGG	ATAGTATTAG	CAAAGGTGCA	1080
GTCTGCAATA	AAAGCACTTC	CTAAACTCTG	GATGCCTCTC	GGCCACCCCA	GGTGATGACT	1140
GTCTTAGG						

Seq ID NO: 532 Protein sequence

Protein Accession #: NP\_036284

25  
30  
35

1	11	21	31	41	51	
MNECHYDKHM	DDFYNRSNTD	TVDDWTGTLK	VIVLCVGTFF	CLFIFFSNLS	VIAAVIKNRK	60
FHFPPFYLLA	NLAAADFFAG	IAYVFLMFNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
LVIIVERHMS	IMRMVRHSNL	TKKRVTLLIL	LWVAIAIFMG	AVPTLGNWCL	CNISACSSLA	180
PIYSRSYLVF	WTVSNLMAFL	IMVVYLRIY	VYVKRKTINV	SPHTSGSISR	RRTPMKLMKT	240
VMTVLGAFVV	CWTPGLVVL	LDGLNCRQCG	VQHVKRWFLL	LALLNSVVP	IISYKDEDM	300
YGTMKMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK	STS	

Seq ID NO: 533 DNA sequence

Nucleic Acid Accession #: NM\_002821

Coding sequence: 150..3362

40  
45  
50  
55  
60  
65  
70  
75  
80

1	11	21	31	41	51	
AACTCCCGCC	TCGGGACGCC	TCGGGGTCGG	GCTCCGGCTG	CGGCTGCTGC	TGCGGCGCCC	60
GCGCTCCGGT	GCGTCCGCCT	CCTGTGCCCG	CCGCGGAGCA	GTCTGCGGCC	CGCCGTGCGC	120
CCTCAGCTCC	TTTTCTGTAG	CCGCGCGCGA	TGGGAGCTGC	CGCGGGATCC	CCGCGCCAGAC	180
CCGCGCGGTT	GCCTCTGTCT	AGCGTCTCTG	TGCTGCCGCT	GCTGGGCGGT	ACCCAGACAG	240
CCATTGTCTT	CATCAAGCAG	CCGTCTCTCC	AGGATGCACT	GCAGGGGCGC	CGGCGCTGTC	300
TTGCTGTGTA	GGTTGAGGCT	CCGGGCCCCG	TACATGTGTA	CTGGCTGTCT	GATGGGGCCC	360
CTGTCCAGGA	CACGGAGCGG	CGTTTCGCCC	AGGGCAGCAG	CCTGAGCTTT	GCAGCTGTGG	420
ACCGGCTGCA	GGACTCTGGC	ACCTTCCAGT	GTGTGGCTCG	GGATGATGTC	ACTGGAGAAG	480
AAGCCCGCAG	TGCCAAGGCC	TCCTTCAACA	TCAAATGGAT	TGAGGCAGGT	CCTGTGGTCC	540
TGAAGCATCC	AGCCTCGGAA	GCTGAGATCC	AGCCACAGAC	CCAGGTCACA	CTTCGTGTC	600
ACATTGATGG	GCACCTCTCG	CCCACTTACC	AATGGTTCGG	AGATGGGACC	CCCTTTCTCT	660
ATGGTCAGAG	CAACCAACAC	GTCAAGCAGA	AGGAGCGGAA	CCTGACGCTC	CGGCCAGCTG	720
GTCTCAGACA	TAGTGGGCTG	TATTCCTGCT	GCGCCACAG	TGCTTTTGGC	CAGGCTTGCA	780
GCAGCCAGAA	CTTCACCTTG	AGCATTGCTG	ATGAAAGCTT	TGCCAGGGTG	GTGCTGGCAC	840
CCCAAGAGCT	GGTAGTGGAG	AGGTATGAGG	AGGCCATGTT	CCATTGCCAG	TTCTCAGCCC	900
AGCCACCCCC	GAGCCTGCAG	TGGCTCTTTG	AGGATGAGAC	TCCCATCACT	AACCCGAGTC	960
GCCCCCACA	CCTCCGCAGA	GCCACAGTGT	TTGCCAACGG	GTCTCTGCTG	CTGACCCAGG	1020
TCCGCGCCAG	CAATGCAGGG	ATCTACCGCT	GCATTGGCCA	GGGCGAGAGG	GGCCACCCA	1080
TCATCTTGGA	AGCCACACTT	CACCTAGCAG	AGATTGAAGA	CATGCCGCTA	TTTGAGCCAC	1140
GGGTGTTTAC	AGCTTGGCAG	GAGGAGCGTG	TGACCTGCCT	TCCCCCAAG	GGTCTGCCAG	1200
AGCCACAGCT	GTGGTGGGAG	CACGCGGGAG	TCCGGCTGCC	CACCCATGGC	AGGGTCTACC	1260
AGAAGGGCCA	CGAGCTGGTG	TTGGCCAATA	TTGCTGAAAG	TGATGCTGGT	GTCTACACCT	1320
GCCACGCGGC	CAACCTGGCT	GGTCAGCGGA	GACAGGATGT	CAACATCACT	GTGGCCACTG	1380
TGCCCTCTCT	GCTGAAGAAC	CCCCAAGACA	GCCAGCTGGA	GGAGGGCAAA	CCCGGCTACT	1440
TGGATTGCCT	GACCCAGGCG	ACACCAAAAC	CTACAGTTGT	CTGGTACAGA	AACCAGATGC	1500
TCATCTCAGA	GGACTCACGG	TTCGAGGTCT	TCAAGAATGG	GACCTTGCGC	ATCAACAGCG	1560
TGGAGGTGTA	TGATGGGACA	TGGTACC GTT	GTATGAGCAG	CACCCAGGCC	GGCAGCATCG	1620
AGGCGCRAAG	CCGTGTCCAA	GTGCTGGAAA	AGCTCAAGTT	CACACCACCA	CCCCAGCCAC	1680
AGCAGTG CAT	GGAGTTTGAC	AAGGAGGCCA	CGGTGCCCTG	TTCAAGCCACA	GGCCGAGAGA	1740
AGCCCACTAT	TAAGTGGGAA	CGGGCAGATG	GGAGCAGCCT	CCAGAGTGGG	GTGACAGACA	1800
ACGCTGGGAC	CCTGCATTTT	GCCC GGTTGA	CTCGAGATGA	CGCTGGCAAC	TACACTTGCA	1860
TTGCTCCAA	CGGGCCGAG	GGCCAGATTC	GTGCCCATGT	CCAGCTCACT	GTGGCAGTTT	1920
TTATCACCTT	CAAGTGGAAA	CCAGAGCGTA	CGACTGTGTA	CCAGGGCCAC	ACAGCCCTAC	1980
TGCAGTGCAG	GGCCAGGGG	GACCCCAAGC	CGCTGATTCA	GTGAAAGGC	AAGGACCGCA	2040
TCCTGGACCC	CACCAAGCTG	GGACCCAGGA	TGCACATCTT	CCAGAATGGC	TCCCTGGTGA	2100
TCCATGACGT	GGCCCTGAG	GACTCAGGCC	GCTACACCTG	CATTGCAGGC	AACAGCTGCA	2160
ACATCAAGCA	CACGAGGCGC	CCCCTCTATG	TCGTGGACAA	GCCTGTGCCG	GAGGAGTCGG	2220
AGGGCCCTGG	CAGCCCTCCC	CCCTACAAGA	TGATCCAGAC	CATTGGGTTG	TCGGTGGGTG	2280
CCGCTGTGGC	CTACATCAAT	GCCGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
AAGCCAAGCG	GCTGCAGAA	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCCTCAACG	2400
GAGGGCCTTT	GCAGAAACGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
GCTTGGGCTC	CGGCCCGCGG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
TCCCACGGTC	TAGCCTGCAG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
TCCTGGCAAA	GGCTCAGGGC	TTGGAGGAGG	GAGTGGCAGA	GACCTTGTA	CTTGTGAAGA	2640

5  
10  
15  
20  
25

```

GCCTGCAGAC GAAGGATGAG CAGCAGCAGC TGGACTTCCG GAGGGAGTTG GAGATGTTTG 2700
GGAAGCTGAA CCACGCCAAC GTGGTGCGGC TCCTGGGGCT GTGCCGGGAG GCTGAGCCCC 2760
ACTACATGGT GCTGGAATAT GTGGATCTGG GAGACCTCAA GCAGTTCCTG AGGATTTCCA 2820
AGAGCAAGGA TGAAAAATTG AAGTCACAGC CCCTCAGCAC CAAGCAGAAG GTGGCCCTAT 2880
GCACCCAGGT AGCCTCGGGC ATGGAGCACC TGTCACACAA CCGCTTTGTG CATAAGGACT 2940
TGGCTGCGCG TAACCTGCCTG GTCAGTGCCC AGAGACAAGT GAAGGTGTCT GCCCTGGGCC 3000
TCAGCAAGGA TGTGTACAAC AGTGAGTACT ACCACTTCCG CCAGGCCTGG GTGCCGCTGC 3060
GCTGGATGTC CCCCAGAGCC ATCCTGGAGG GTGACTTCTC TACCAAGTCT GATGTCTGGG 3120
CCTTCGGTGT GCTGATGTGG GAAGTGTTTA CACATGGAGA GATGCCCAT GGTGGGCAGG 3180
CAGATGATGA AGTACTGGCA GATTTGCAGG CTGGGAAGGC TAGACTTCCT CAGCCCGAGG 3240
GCTGCCCTTC CAAACTCTAT CGGCTGATGC AGCGCTGCTG GGCCCTCAGC CCCAAGGACC 3300
GGCCCTCCTT CAGTGAGATT GCCAGCGCCC TGGGAGACAG CACCGTGGAC AGCAAGCCGT 3360
GAGGAGGGAG CCGCTCAGG ATGGCTGGG CAGGGGAGGA CATCTCTAGA GGAAGCCTCA 3420
CAGCATGATG GGCAAGATCC CTGTCTCTCT GGGCCCTGAG GTGCCCTAGT GCAACAGGCA 3480
TTGCTGAGGT CTGAGCAGGG CCTGGCCTTT CTCTCTCTC CTCACCTCA TCCTTTGGGA 3540
GGCTGACTTG GACCCAACT GGGCGACTAG GGCTTTGAGC TGGGCAGTTT CCCCTGCCAC 3600
CTCTTCCTCT ATCAGGGACA GTGTGGGTGC CACAGGTAA CCAATTTCT GGCCTTCAAC 3660
TTCTCCCTT GACCGGGTCC AACTCTGCCA CTCATCTGCC AACTTTGCC GTGGGAGGCT 3720
AGGCTTGGGA AGCTTGGGT TTGTGGGGAG TTCTTAATA TTCTCAAGT CTGGGCACAC 3780
AGGGTTAATG AGTCTCTTGC CCACTGGTCC ACTTGGGGT CTAGACCAGG ATTATAGAGG 3840
ACACAGCAAG TGAGTCTCTC CCACTCTGGG CTTGTGCACA CTGACCAGA CCCACGTCTT 3900
CCCCACCTT CTCTCTTTC CTCATCTTAA GTGCCCTGGA GATGAAGGAG TTTTCAGGAG 3960
CTTTTGACAC TATATAAACC GCCCTTTTGT TATGACCAC GGGCGGCTT TATATGTAAT 4020
TGCAGCGTGG GGTGGGTGGG CATGGGAGGT AGGGGTGGGC CCTGGAGATG AGGAGGGTGG 4080
GCCATCCTTA CCCCACTT TTATTGTTGT CGTTTTTGT TGTGTTTGT TTTTGTGTTT 4140
TGTTTTTGT TTTACACTCG CTGCTCTCAA TAAATAAGCC TTTTTTA

```

Seq ID NO: 534 Protein sequence  
Protein Accession #: NP\_002812

30  
35  
40  
45  
50

```

1 11 21 31 41 51
MGAARGSPAR PRRLLPLLSVL LLPLLGGTQT AIVFIKQPSS QDALQRRAL LRCEVEAPGP 60
VHVYLLDGA PVQDTERRFA QGSSLSFAAV DRLQDSGTFQ CVARDVVTGE EARSANASFN 120
IKWIEAGPVV LKHPASEAEI PQQTQVTLRC HIDGHPRTY QWFRDGTPLS DQGSNHTVSS 180
KERNLTLRPA GPEHSGLYSC CAHSAFGQAC SQONFTLSIA DESFARVLA PQDVVVARVE 240
EAMFHCQFSA QPPPSLQWLF EDETPITNRS RPPHLRRATV FANGSLLLTQ VRPRNAGIYR 300
CIGQQQRGPP ILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPPKGLP EPSVWWEHAG 360
VRLPTHGRVY GKHLNHLVLAN IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKKPQD 420
SQLEEGKPGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEVYDGTWYR 480
CMSSTPAGSI EAQARVQVLE KLKFTPPPQP QQCMFEDKEA TVPCSATGRE KPTIKWERAD 540
GSSLPEWVTD NAGTLHFARV TRDDAGNYTC IASNGPQQGI RAHVQLTVAV FITFKVEPER 600
TTYVQGHYAL LQCEAQGDPK PLIQWKGDNR ILDPKLGPR MHIFQNGSLV IHDVAPEDSG 660
RYTCIAGNSC NIKHTEAPLY VVDKPVPEES EGGSPPPYK MIQTIGLSVG AAVAYIIAIVL 720
GLMFYCKKRC KAKRLQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780
KRHSTSDKM HFRSSLPQIT TLGKSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ 840
LDFRRELEMF GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLKQFLRIS KSKDEKLKSQ 900
PLSTKQKVAL CTQVALGMEH LSNRNFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960
YHFRQAWVPL RWSPEAILE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEVILADLQ 1020
AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDSKP

```

Seq ID NO: 535 DNA sequence  
Nucleic Acid Accession #: NM\_013952  
Coding sequence: 161..1357

55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
TTCAGAAGGA GGAGAGACAC CGGGCCCAGG GCACCCTCGC GGGCGGGCGG ACCCAAGCAG 60
TGAGGGCCTG CAGCCGGCCG GCCAGGGCAG CGGCAGGCGC GGCCCGGACC TACGGGAGGA 120
AGCCCCGAGC CCTCGGGCGG CTGCGAGCGA CTCCCCGGCG ATGCCTCACA ACTCCATCAG 180
ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG AGGGGCCCTT GTGAATGGCA GACCTCTGCC 240
GGAAGTGGTC CGCCAGCGCA TCGTAGACCT GGCCACCAG GGTGTAAGGC CCTGCACAT 300
CTCTCGCCAG CTCGCGCTCA GCCATGGCTG CGTCAGCAAG ATCCTTGGCA GGTACTACGA 360
GACTGGCAGC ATCCGGCCTG GAGTGATAGG GGGCTCCAAG CCCAAGGTGG CCAACCCCAA 420
GGTGGTGGAG AAGATTGGGG ACTACAAACG CCAGAACCTT ACCATGTTTG CCTGGGAGAT 480
CCGAGACCGG CTCCTGGCTG AGGGCGTCTG TGACAATGAC ACTGTGCCCA GTGTCAGCTC 540
CATTAATAGA ATCATCCGGA CCAAGAGTGA GCAACCATTC AACCTCCCTA TGGACAGCTG 600
CGTGGCCACC AAGTCCCTGA GTCCCGGACA CACGCTGATC CCCAGCTCAG CTGTAACCTC 660
CCCGGAGTCA CCCAGTGGG ATTCCTGGG CTCCACCTAC TCCATCAATG GGCTCCTGGG 720
CATCGCTCAG CCTGGCAGCG ACAAGAGGAA AATGGATGAG AGTGATCAGG ATAGCTGCCG 780
ACTAAGCATT GACTCACAGA GCAGCAGCAG CGGACCCCGA AAGCACCTTC GCACGGATGC 840
CTTCAGCCAG CACCACCTCG AGCCGCTCGA GTGCCCATTT GAGCGGCAGC ACTACCCAGA 900
GGCCTATGCC TCCCCAGGC ACACCAAAGG CGAGCAGGGC CTCTACCCGC TGCCCTTGCT 960
CAACAGCACC CTGGACGACG GGAAGGCCAC CCTGACCCCT TCCAACACGC CACTGGGGCG 1020
CAACCTCTCG ACTCACGACA CCTACCCCGT GGTGGCAGCT CCGCCCTTTT GGATCTGCAG 1080
CAAGTCTGGT CCGGGGTCCC GCCCTTCAAT GCCTTTCCCC ATGCTGCCTC CGTGTACGGG 1140
CAGTTACGGG GCCAGGCCCT CCTCTCAGGG CGAGAGATGG TGGGGCCAC GCTGCCCGGA 1200
TACCCACCCG AACTCCCAAC CAGCGGACAG GGCAGCTATG CCTCCTGTC CATCGCAGGC 1260
ATGGTGGCAG GAAGTGAATA CTCTGGCAAT GCCTATGGCC ACACCCCTA CTCCTCTAC 1320
AGCGAGGCCT GGGGCTTCCC CAACTCCAGC TTGCTGAGTT CCCCATATTA TTACAGTTCC 1380
ACATCAAGGC CGAGTGACCC GCCCACTT GCCACGGCCT TTGACCATCT GTAGTTGCCA 1440
TGGGACAGT G

```

Seq ID NO: 536 Protein sequence  
Protein Accession #: NP\_039246

```

5      1      11      21      31      41      51
|      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK    60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND    120
TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY    180
SINGLLGIAQ PGSDKRKMDD SDQDSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF    240
10    ERQHYPEAYA SPSHTKGEQG LYPLPLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAA    300
PPFWICSKSA PGSRPSMPFP MLPPCTGSSR ARPSSQGERW WGRPCPDTHP TSPPADRAAM    360
PPLPSQAWWQ EVNTLAMPMA TPPTPTPTARP GASPTPAC

```

Seq ID NO: 537 DNA sequence  
Nucleic Acid Accession #: NM\_003466.1  
Coding sequence: 11..1363

```

20      1      11      21      31      41      51
|      |      |      |      |      |
GAATTCGGCG ATGCCTCACA ACTCCATCAG ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG    60
AGGGGCCTTT GTGAATGGCA GACCTCTGCC GGAAGTGGTC CGCCAGCGCA TCGTAGACCT    120
GGCCACCACAG GGTGTAAGGC CCTGCGACAT CTCTCGCCAG CTCGCGCTCA GCCATGGTTG    180
CGTCAGCAAG ATCCTTGCCA GGTACTACGA GACTGGCAGC ATCCGGCCTG GAGTGATAGG    240
GGGCTCCAAG CCAGAGGTGG CCACCCCAA GGTGGTGGAG AAGATTGGGG ACTACAAACG    300
25    CCAGAACCTT ACCATGTTTG CCTGGGAGAT CCGAGACCGG CTCTGGCTG AGGGCGTCTG    360
TGACAATGAC ACTGTGCCCA GTGTGAGCTC CATTAAATAGA ATCATCCGGA CCAAAGTGCA    420
GCAACCATTTC AACCTCCCTA TGGACAGCTG CGTGGCCACC AAGTCCCTGA GTCCCGGACA    480
CACGCTGATC CCCAGCTCAG CTGTAACCTC CCGGAGTCA CCCCAGTCCG ATTCCCTGGG    540
30    CTCCACCTAC TCCATCAATG GGCTCCTGGG CATCGCTCAG CCTGGCAGCG ACAAGAGGAA    600
AATGGATGAC AGTGATCAGG ATAGCTGCCG ACTAAGCATT GACTCACAGA GCAGCAGCAG    660
CGGACCCCGA AAGCACTTTC GCACGGATGC CTTCAGCCAG CACCACCTCG AGCCGCTCGA    720
GTGCCCATTT GAGCGGCAGC ACTACCCAGA GGCTATGCC TCCCCCAGCC ACACCAAAGG    780
CGAGCAGGGC CTCTACCCGC TGCCCTTGCT CAACAGCACC CTGGACGACG GGAAGGCCAC    840
35    CTTGACCCCT TCCAACACGC CACTGGGGCG CAACCTCTCG ACTCACCAGA CCTACCCCGT    900
GGTGGCAGAT CCTCACTCAC CCTTCGCCAT AAAGCAGGAA ACCCCCGAGG TGTCCAGTTC    960
TAGCTCCACC CTTCTCTCTT TATCTAGCTC CGCCTTTTGG GATCTGCAGC AAGTCGGCTC    1020
CGGGGTCCCG CCCTTCAATG CCTTTCCCA TGCTGCCTCC GTGTACGGGC AGTTTACGGG    1080
CCAGGCCCTC CTCTCAGGGC GAGAGATGGT GGGGCCACG CTGCCCGGAT ACCCACCCA    1140
40    CATCCCCACC AGCGGACAGG GCAGCTATGC CTCTCTGCC ATCGCAGGCA TGGTGGCAGG    1200
AAGTGAATAC TCTGGCAATG CCTATGGCCA CACCCCTTAC TCCTCTACA GCGAGGCTG    1260
GCGCTTCCCC AACTCCAGCT TGCTGAGTTC CCCATATTAT TACAGTTCCA CATCAAGGCC    1320
GAGTGACACG CCCACACTG CCACGGCCTT TGACCATCTG TAGTTGAAGC TT

```

Seq ID NO: 538 Protein sequence  
Protein Accession #: NP\_003457

```

50      1      11      21      31      41      51
|      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK    60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND    120
TVPSVSSINR IIRTKVQQPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY    180
SINGLLGIAQ PGSDKRKMDD SDQDSCRLSI DSQSSSSGPR KHLRTDAFSQ HHLEPLECPF    240
55    ERQHYPEAYA SPSHTKGEQG LYPLPLNST LDDGKATLTP SNTPLGRNLS THQTYPVVAD    300
PHSPFAIKQE TPVSSSSST PSSLSSSAFL DLQQVGSQVVP PFNAFPHAAS VYQQTGQAL    360
LSGREMVGPT LPGYPPHPT SQGGSYASSA IAGMVAGSEY SGNAYGHTPY SSYSEAWRFP    420
NSSLSSPFY YSSTSRPSAP PTTATAFDHL

```

Seq ID NO: 539 DNA sequence  
Nucleic Acid Accession #: NM\_006799  
Coding sequence: 19..963

```

65      1      11      21      31      41      51
|      |      |      |      |      |
GCCGCGGGAG AGGAGGCCAT GGGCGCGCGC GGGCGCGTGC TGCTGGCGCT GCTGCTGGCT    60
CGGGCTGGAC TCAGGAAGCC GGAGTCGAG GAGGCGGCGC CGTTATCAGG ACCATGCGGC    120
CGACGGGTCA TCACGTCGCG CATCGTGGGT GGAGAGGACG CCGAACTCGG GCGTTGGCCG    180
TGGCAGGGGA GCCTGCGCCT GTGGGATTCC CACGTATGCG GAGTGAGCCT GCTCAGCCAC    240
CGCTGGGCAC TCACGGCGGC GCACTGCTTT GAAACCTATA GTGACCTTAG TGATCCCTCC    300
GGGTGGATGG TCCAGTTTGG CCAGCTGACT TCCATGCCAT CCTTCTGGAG CCTGCAGGCC    360
70    TACTACACCC GTTACTTCGT ATCGAATATC TATCTGAGCC CTCGCTACCT GGGGAATTCA    420
CCCTATGACA TTGCTCTGGT GAAGCTGTCT GCACCTGTCA CCTACACTAA ACACATCCAG    480
CCCATCTGTC TCCAGGCCTC CACATTGAG TTTGAGAACC GGACAGACTG CTGGGTGACT    540
GGCTGGGGGT ACATCAAAGA GGATGAGGCA CTGCCATCTC CCCACACCTC CCAGGAAGTT    600
75    CAGGTGCGCA TCATAACAA CTCTATGTGC AACCACCTCT TCCTCAAGTA CAGTTTCCGC    660
AAGGACATCT TTGGAGACAT GGTTTGTGCT GGCAATGCCC AAGGCGGGAA GGATGCCCTG    720
TTCGGTGACT CAGGTGGACC CTTGGCCTGT AACAAGAATG GACTGTGGTA TCAGATTGGA    780
GTCGTGAGCT GGGGAGTGGG CTGTGGTGGG CCCAATCGGC CCGGTGTCTA CACCAATATC    840
AGCCACCCTT TTGAGTGGAT CCAGAAGCTG ATGGCCCGA GTGGCATGTC CCAGCCAGAC    900
80    CCTCTCTGGC CGCTACTCTT TTCCCTCTT CTCTGGGCTC TCCCACTCCT GGGGCCGGTC    960
TGAGCCTACC TGAGCCCATG CAGCTGGGG CCACTGCCAA GTCAGGCCCT GGTTCCTCTC    1020
TGCTTGTITT GGTAAATAAC ACATTCAGT TGATGCCCTG CAGGGCATTC TTCAAA

```

Seq ID NO: 540 Protein sequence  
Protein Accession #: NP\_006790



```

1      11      21      31      41      51
|      |      |      |      |      |
5  MGARGALLLA LLLARAGLRK PESQEAAPLS GPCRRRVITS RIVGGEDAEI GRWPWQGSRLR 60
   LWDSHVCVGS LLSHRWALTA AHCFTYSDL SDPSGWMVQF GQLTSMPSFW SLQAYYTRYF 120
   VSNLYLSPRY LGNSPYDIAL VKLSAPVYTF KHIQPICLQA STFEFENRTD CWVTGWGYIK 180
   EDEALPSPHT LQEVQVAIIN NSMCNHLFLK YSFRKDIFGD MVCAGNAQGG KDACFGDSSG 240
   PLACNKNLW YQIGVVSWGVC GCGRPNRPGV YTNISHHFEW IQKLMAQSGM SQPDPSPWPLL 300
   FFPLLWALPL LGPV

```

Seq ID NO: 541 DNA sequence  
Nucleic Acid Accession #: NM\_014344  
Coding sequence: 131..1444

```

15 1      11      21      31      41      51
   |      |      |      |      |      |
   GCGGCCGCGA TGGGGCCGAA GCGCCCCGAAG CCCCAGGAGCC CACAAACTGC CGGGCCCGCC 60
   TCGCCGCGCG GACCCGGGTG CCTGGGCTCG GCTTGAAGCG GCGGCGGCGC ACCGGCACAG 120
   CCGCGGGAGC ATGGGCAGGA GGATGCGGGG CGCCGCGGCC ACCGCGGGGC TCTGGCTGCT 180
20 GCGCTGTGGC TCGTGTCTGG CGCTGTGGGG AGGGCTCTCT CCGCCGCGGA CCGAGCTGCC 240
   CGCCTCCCGG CCGCCCGAAG ACCGACTCCC ACGGCGCCCG GCCCGGAGCG GCGGCCCGCG 300
   GCCCGCGCCT CGCTTCCCTC TGCCCCCGCC CCTGGCGTGG GACGCGCGCG GCGGCTCCCT 360
   GAAAACTTTC CGGGCGCTGC TCACCCCTGGC GGCCGCGCGC GACGCGCCGC CCGGCGAGTC 420
   CCGGAGCGAG CCCAGGTGGC ACGTGTGAGC CAGGCGAGCC CGGCGGAGG AGAGCGCCGC 480
25 GGTGCACGGG GCGCTCTTCT GGAGCCGCGG CCTGGAGGAG CAGGTGCCCC CGGGCTTTTC 540
   GGAGGCCCAG GCGGCGGCGT GGCTGGAGGC GGCTCGCGGC GCCCGGATGG TGGCCCTGGA 600
   GCGCGGGGGT TGCGGGCGCA GCTCCAAACCG ACTGGCCCGT TTTGCCGACG GCACCCGCGC 660
   CTGCGTGCGC TACGGCATCA ACCCGGAGCA GATTCAAGGC GAGGCCCTGT CTTACTATCT 720
   GGCGCGCCTG CTGGCCCTCC AGCGCCACGT GCCCGCGCTG GCATCTGGCTC GGTGAGGCG 780
30 TCGGGGCGCG CAGTGGGCGC AGGTGCAGGA GGAGCTGCGC GCTGCGCACT GGACCGAGGG 840
   CAGCGTGTGT AGCCTGCACAC GCTGGCTGCC CAACCTCACG GACGTGTGTG TGCCCGCGCC 900
   CTGCGCTGCG GAGGACGCGC GTCTGCGCCC CCTCCGGGAT GCCGGGGGTG AGCTGGCCAA 960
   CCTCAGCCAG GCGGAGCTGG TGGACCTAGT ACAATGGACC GACTTAATCC TTTTCGACTA 1020
35 CCTGACGGCC AACTTCGACC GGCTCGTAAG CAACCTCTTC AGCCTGCAGT GGGACCCGCG 1080
   CGTCATGCAG CGTGCCACCA GCAACCTGCA CCGCGGTCCG GCGCGGGCGC TGGTCTTTCT 1140
   GGACAATGAG GCGGCTTGG TGACGCGCTA CCGGCTAGCA GGCATGTGGG ACAAGTATAA 1200
   CGAGCCGCTG TTGCAGTCAG TGTGCGTGT CCGCGAGCGG ACCGCGCGGC GCGTCTGGA 1260
   GCTGCACCGC GGACAGGAGC CCGCGGCGCG GCTGCTGCGC CTCTACCGGC GCCACGAGCC 1320
40 TCGCTTCCCG GAGCTGGCCG CCTTGCAGA CCCCACGCT CAGCTGTAC AGCGCCGCT 1380
   CGACTTCTCT GCCAAGCACA TTTTGCACGT TAAGGCCAAG TACGCGCGCC GGTCTGGGAC 1440
   TTAGTGTAC CCGGAGGAAA AGAGAGAGAT CTGGGGCTGG GGTATGGATG ATGGGGGGA 1500
   GGGCGGTGCG CTCTGCCACT GTCAGGGACC AGCGGCCCAA CGCCACCCG CAAAGGTGTC 1560
   TAAAACTTC AGCTTTTCAC CCACCTGCCC CTTTCTTTCA ATCCACGCT GTTCTCTTC 1620
45 AAAGTTCTGG GAGGACGAAC TCACCGAGGC GAGAAGTGTA ACATCTCTC CACCCAGCTT 1680
   ATAAAGGAT TCTTTACTGT GCCAGCACGG GGATTGGATC CGAAGAACT GGCTACTGGG 1740
   GTTTGGCCCC CGAGTGGCCG TCCCTGTGGG AGATGCACCC CATTTCTGGG CCCCCTCAT 1800
   TCCCTTCCG AAAAAGGAAA ACTTGCCTTT GAGCCGTTGA GCTAATTCTG CAATTTTCTA 1860
   CCAAACAGAG CCGTGGTGGC CCGCGAGCAG GGCTGTGACA TTGGCTGTGT GAGCCCTTC 1920
50 CTGTGTTCTC CCGTGTTCAG AGCGCGCGA TGGTGAGATC ACTGTTCCAA GCAGGGGGAG 1980
   GGCTCGCGAT AGGACAAAGA GAGCAGGACC TCCAGACTCT GGGGAGCCCT GCAGACCTTG 2040
   ACAATTGTC TGACTCATTC CTGACCTCTT GTCATTTTGG CCTGAAGGCT ACAAAATCAG 2100
   GGTCACTGT ATGCACTAAG TCAAAATG AATTTCTTCC TCCCTCTCGC AACCGACCAA 2160
   AATTTTGACA ACGATGATGT TCACCAAGAG GAAAAAATA TCAGTTTAT GCACTTTAT 2220
55 TTGTTTGTAT TTTCAATTTT TATTAAGAAA AAATTTTAT TTACAGAAT TACCTTCTCT 2280
   GTATATATGT GCATAAAGTG TGGTGTAAAT ATACTAAACA AACTTATAT TCAATAAAG 2340
   GGAGTTTAAA ATTTAAAAA AAAAAA

```

Seq ID NO: 542 Protein sequence  
Protein Accession #: NP\_055159

```

60 1      11      21      31      41      51
   |      |      |      |      |      |
   MGRMRGAAA TAGLWLLALG SLLALWGLL PPRTELPASR PPEDRLPRRP ARSGGPAPAP 60
   RFPLPPPLAW DARGGSLKTF RALLTLAAGA DGPPRQSRSE PRWHVSARQP RPEESAAVHG 120
65 GVFWSRGLEE QVPPGFSEAQ AAAWLEAARG ARMVALERGG CGRSSNRLAR FADGTRACVR 180
   YGINPEIQIG EALSYYLARI LGLQRHVPPL ALARVEARGA QWAQVQELR AAHWTEGSVV 240
   SLTRWLPNLT DVVVPAPWRS EDGRLRPLRD AGGELANLSQ AELVDLVQWT DLILFDYLT 300
   NFDRLVSNLF SLQWDPRVMQ RATSNLHRGP GGALVFLDNE AGLVHGYYRVA GMWDKYNEPL 360
70 LQSVCFRER TARRVLELHR GQDAAARLLR LYRRHEPRFP ELAALADPHA QLLQRRDLDFL 420
   AKHILHCKAK YGRRSQT

```

Seq ID NO: 543 DNA sequence  
Nucleic Acid Accession #: XM\_007652.4  
Coding sequence: 1..1290

```

75 1      11      21      31      41      51
   |      |      |      |      |      |
   ATGCCCGGCT CTGGCGCGTG GAAGCGCCTC AAATCTATGC TAAGGAAGGA TGATGCGCCG 60
80 CTGTTTTTAA ATGACACCAG CGCCTTTGAC TTCTCGGATG AGGCGGGGGA CGAGGGGCTT 120
   TCTCGGTTCA ACAAACTTCG AGTTGTGGTG GCCGATGACG GTTCCGAAGC CCGGAAAGG 180
   CCTGTAAACG GGGCGCAACC GACCCTCCAG GCCGACGATG ATTCTTACT GGACCAAGAC 240
   TTACTTTTGA CCAACAGTCA GCTGAGTTTG AAGGTGGACT CCTGTGACAA CTGCACGAAA 300
   CAGAGAGAGA TACTGAAGCA GAGAAAGGTG AAAGCCAGGT TGACCATTCG TGCCGTTCTG 360
   TACTTGCTTT TCATGATTGG AGAACTGTA GGTGGATACA TTGCAATAG CCTAGCAATC 420

```

5 ATGACAGATG CACTTCATAT GTTAACTGAC CTAAGCGCCA TCATACTCAC CCTGCTTGCT 480  
 TTGTGGCTAT CATCAAAATC ACCAACCAAA AGATTACCTT TTGGATTICA TCGCTTAGAG 540  
 GTTTTGTGAG CTATGATTAG TGTGCTGTTG GTGTATATAC TTATGGGATT CCTCTTATAT 600  
 GAAGCTGTGC AAAGAACTAT CCATATGAAC TATGAAATAA ATGGAGATAT AATGCTCATC 660  
 ACCGCAGCTG TTGGAGTTGC AGTTAATGTA ATAATGGGGT TTCTGTTGAA CCAGTCTGGT 720  
 CACCGTCACT CCCATTCCCA CTCCTCGCCT TCAATTTCCC CTACCAGAGG TTCTGGGTGT 780  
 GAACGTAACC ATGGGCAGGA TAGCCTGGCA GTGAGAGCTG CATTTGTACA TGCTTTGGGA 840  
 GATTTGGTAC AGAGTGTGG TGTGCTAATA GCTGCATACA TCATACGATT CAAGCCAGAA 900  
 10 TACAAGATTG CTGATCCCAT CTGTACATAC GTATTTTCAT TACTTGTGGC TTTTACAACA 960  
 TTTTGAATCA TATGGGATAC AGTAGTTATA ATACTAGAAG GTGTGCCAAG CCATTTGAAT 1020  
 GTAGACTATA TCAAGAAGC CTTGATGAAA ATAGAAGATG TATATTAGT CGAAGATTTA 1080  
 AATATCTGGT CTCTCACTTC AGGAAAATCT ACTGCCATAG TTCACATACA GCTAATTCCT 1140  
 GGAAGTTTCA CTAAATGGGA GGAAGTACAG TCCAAAGCAA ACCATTTATT ATTGAACACA 1200  
 15 TTTGGCATGT ATAGATGTAC TATTAGCTT CAGAGTTACA GGCAAGAAGT GGACAGAACT 1260  
 TGTGCAAAAT GTCAGAGTTC TAGTCCCTGA

Seq ID NO: 544 Protein sequence  
 Protein Accession #: XP\_007652.1

20 1 11 21 31 41 51  
 | | | | |  
 MAGSGAWKRL KSMRLKDDAP LFLNDTSAPD FSDEAGDEGL SRFNKLRRVV ADDGSEAPER 60  
 PVNGAHPFLQ ADDDSLDDQD LPLTNSQLSL KVDSCDNCSK QREILKQRKV KARLTIAAVL 120  
 25 YLLFMIGELV GGYIANSLAI MTDALHMLTD LSAILITLLA LWLSSKSPK RFTFGPHRLE 180  
 VLSAMISVLL VYILMGFLLY EAVQRTIHMN YEINGDIMLI TAAVGVAVNV IMGFLNQSG 240  
 HRHSHSHSLP SNSPTRGSGC ERNHGQDSL A VRAAFVHALG DLVQSVGVLI AAYIIRFKPE 300  
 YKIADPICTY VPSLLVAFIT FRIIWDTVVI ILEGVPSHLN VDYIKEALMK IEDVYSVEDL 360  
 NIWSLTSGKS TAIVHIQLIP GSSSKWEEVQ SKANHLLNT PGMRYCTIQL QSYRQEVDR 420  
 CANCQSSSP

Seq ID NO: 545 DNA sequence  
 Nucleic Acid Accession #: AB037765.1  
 Coding sequence: 1..2478

35 1 11 21 31 41 51  
 | | | | |  
 ATGTTTTCCG GCTTCAATGT CTTTAGAGTT GGGATCTCTT TTGTCATAAT GTGCATTTT 60  
 TACATGCCAA CAGTAACTC TTTACCAGAA CTGAGTCCTC AGAAATATTT TAGTACATG 120  
 40 CAACCAGGAA AAGCCTCTTT AGCTTATTTT TGTCAAGCTG ATTCCCCAAG AACATCTGTA 180  
 TTTCTTGAAG AACTGAATGA GGCTGTTAGA CCTCTGCAGG ACTATGGAAT TTCAGTTGCC 240  
 AAGGTTAATT GTGTCAAAGA AGAAATATCA AGATACTGTG GAAAAGAAAA GGATTGTATG 300  
 AAAGCATATT TATTCAGGG CAACATATTG CTCAGAGAAAT TCCCTACTGA CACCTGTGTT 360  
 GATGTGAATG CCATTTGCGC CCATGTTCTC TTTGCTCTTC TTTTATGTA AGTGAATAT 420  
 45 ATTACCAACC TGAAGACCT TCAGAACATA GAAAATGCTC TGAAGGAAA AGCAATATT 480  
 ATATTCTCAT ATGTAAGAGC CATTGGAATA CCAGAGCACA GAGCAGTCAT GGAAGCCGCT 540  
 TTTGTGTATG GGACTACATA CCAATTTGTC TTAACCACAG AAATGCCCC TTTGGAAAGT 600  
 ATTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT TTCATGTGAA ACTAGTCTTG 660  
 GACTTGACCC AGCAATGTAG AAGAACAATA ATGGAACAGC CATTGACTAC ACTGAACATT 720  
 50 CACCTGTTTA TTAAGACAAT GAAAGCACCT CTGTTGACTG AAGTTGCTGA AGATCCTCAA 780  
 CAAGTTTCAA CTGTCCATCT CCAACTGGGC TTACTACTGG TTTTATTTGT TAGCCAACAG 840  
 GCTACTTATG AAGCTGATAG AAGAACTGCA GAATGGGTTG CTGCGCTCT TCTGGGAAAA 900  
 GCAGGAGTTC TACTCTGTT AAGGGACTCT TTGGAAGTGA ACATTCTCA AGATGCTAAT 960  
 GTGGTCTTCA AAAGAGCAGA AGAGGGAGTT CCAGTGAAT TTTTGGTATT ACATGATGTT 1020  
 55 GATTTAATAA TATCTCATGT GGAAAATAAT ATGCACATTG AGGAAATACA AGAAGATGAA 1080  
 GACAAATGACA TGGAAAGTCC AGATATAGAT GTTCAGGATG ATGAAGTGGC AGAAACTGTT 1140  
 TTCAGAGATA GGAAGAGAAA ATTACCTTTG GAACCTACAG TGAACATAAC AGAAGAAACA 1200  
 TTTAATGCAA CAGTGATGGC TTCTGACAGC ATAGTACTCT TCTATGCTGG TTGGCAAGCA 1260  
 GTATCCATGG CATTTTGTGA ATCCTATATT GATGTGGCAG TTAAACTGAA AGGCACATCT 1320  
 60 ACTATGCTTC TTACTAGAAT AAAGTGTGCA GATTGGTCTG ATGTATGTAC TAAGCAAAAT 1380  
 GTTACTGAAT TTCTATCAT AAAGATGTAC AAGAAAGGCG AGAACCAGT ATCTTATGCT 1440  
 GGAATGTAG GAAACGAAGA TCTCCTAAAA TTTATCCAGC TCAACAGGAT TTCATATCCA 1500  
 GTGAATATAA CATCGATCCA AGAAGCAGAA GAATATTTAA GTGGGAATT ATATAAAGAC 1560  
 CTCACTTGT ATTCTAGTGT GTCAGTATTG GGACTATTTA GTCCAACCAT GAAAACAGCA 1620  
 65 AAAGAAGATT TTAGTGAAGC AGGAACTAC CTAAAAGGAT ATGTTATCAC TGGAAATTTAT 1680  
 TCTGAAGAAG ATGTTTTGCT ACTGTCAACC AAATATGCTG CAAGTCTTCC AGCCCTGCTG 1740  
 CTTGCCAGAC ACACAGAAGG CAAAATAGAG AGCATCCAC TAGCTAGCAC ACATGCACAA 1800  
 GACATAGTTC AAATAATAAC AGATGCACTA CTGGAATGT TTCCGGAAAT CACTGTGGAA 1860  
 70 AATCTTCCCA GTTATTTTCA ACTTCAGAAA CCATTATTGA TTTTGTTCAG TGATGGCACT 1920  
 GTAAATCCTC AGTATAAAAA AGCAATATTG AACTGGTAA AGCAGAAATA CTTGGATTCA 1980  
 TTTACTCCAT CCTGGTTTAA TCTAAAGAAT ACTCCAGTGG GGAGAGGAAT CTTGAGGGCA 2040  
 TATTTGTATC CTCTGCTTCC CCTTCTCTT CTCTTTTGG TGAATCTGCA TTCAGGTGGC 2100  
 CAAGTATTTG CATTTCTTTC AGACCAGGCT ATAATTGAAG AAAACCTTGT ATTGTGGCTG 2160  
 75 AAGAAATTAG AATCGGCACT AGAAAATCAT ATCACAATTT TACCTGCTCA AGAATGGAAA 2220  
 CCTCTCTTTC CAGCTTATGA TTTTCTAAGT ATGATAGATG CCGCAACATC TCAACGTGGC 2280  
 ACTAGGAAAG TTCCCAAGTG TATGAAAGAA ACAGATGTGC AGGAGAATGA TAAGGAACAA 2340  
 CATGAAGATA AATCGGCACT CAGAAAAGAA CCGATTGAAA CTCTGAGAAT AAAGCATTTG 2400  
 80 AATAGAAGTA ATTGGTTTAA AGAAGCAGAA AAATCATTTA GACGTGATAA AGAGTTAGGA 2460  
 TGCTCAAAAG TGAACATA

Seq ID NO: 546 Protein sequence  
 Protein Accession #: BAA92582.1

1 11 21 31 41 51  
 | | | | |

MFSGFNVFRV GISFVIMCIF YMPTVNSLPE LSPQKYFSTL QPGKASLAYF CQADSPTS SV 60  
 FLEELNEAVR PLQDYGISVA KVNVCKEEIS RYCGKEKDL M KAYLFKGNIL LREFPTDTLF 120  
 DVNAIVAHVL FALLFSEVKY ITNLEDLQNI ENALGKANI IFSYVRAIGI PEHRAVMEAA 180  
 FVYGTTYQFV LTTEIALLES IGSEDVEYAH LYFFHCKLVL DLTQQCRRTL MEQPLTTLNI 240  
 HLFIKTMKAP LLEVAEDPQ QVSTVHLQLG LPLVFIVSQQ ATYEADRRTA EWWAVRLLGK 300  
 AGVLLLLRDS LEVNI PQDAN VVFKRAEEGV PVEFLVLHDV DLIISHVENN MHIEEIQEDE 360  
 DNDMEGPDID VQDDEVAETV FRDRKRKLPL ELTVELTEET FNATVMASDS IVLFYAGWQA 420  
 VSMAPLQSYI DVAVKLKGT S TMLLRINCA DWSDVCTKQN VTEFPIIKMY KKGEPVSVYA 480  
 GMLGTEDLLK FIQLNRISYP VNITSIQEAE EYLSGELYKD LILYSSVSVL GLFSPITMKA 540  
 KEDFSEAGNY LKGYVITGIY SEEDVLLST KYAASLPALL LARHTEGKIE SIPLASTHAQ 600  
 DIVQIITDAL LEMFPEITVE NLPSYFRLQK PLLILFSDGT VNPQYKAIL TLVKQKYLDS 660  
 FTFCWNLNKN TPVGRGILRA YFDPLPPLPL LVLVNLHSGG QVFAFPSDQA IIEENLVLWL 720  
 KKLEAGLENH TILPADEWK PPLPAYDFLS MIDAATSQRG TRKVPKCMKE TDVQENDKEQ 780  
 HEDKSAVRKE PIETLRKHK NRSNWFKEAE KSFRDRKELG CSKVN

Seq ID NO: 547 DNA sequence  
 Nucleic Acid Accession #: NM\_033102.1  
 Coding sequence: 1..1662

1 11 21 31 41 51  
 | | | | |  
 ATGGTCCAGA GGCTGTGGGT GAGCCGCGCTG CTGCGGCACC GGAAAGCCCA GCTCTTGCTG 60  
 GTCAACCTGC TAACCTTTGG CCTGGAGGTG TGTTTGGCCG CAGGCATCAC CTATGTGCCG 120  
 CCTCTGCTGC TGGAGTGGG GGTAGAGGAG AAGTTTATGA CCATGGTGCT GGGCATTTGT 180  
 CCAGTGCTGG GCCTGGTCTG TGTCCCGCTC CTAGGCTCAG CCAGTGACCA CTGGCGTGGA 240  
 CGCTATGGCC GCCGCGCGCC CTTTCACTGG GCACTGTCTT TGGGCATCCT GCTGAGCCTC 300  
 TTTCTCATCC CAAGGGCCGG CTGGCTAGCA GGGCTGCTGT GCCCGGATCC CAGGCCCTTC 360  
 GAGCTGGCAC TGCTCATCCT GGGCGTGGGG CTGCTGGACT TCTGTGGCCA GGTGTGCTTC 420  
 ACTCCACTGG AGGCCCTGCT CTCTGACCTC TTCCGGGACC CGGACCACTG TCGCCAGGCC 480  
 TACTCTGTCT ATGCTTTCAT GATCAGTCTT GGGGGCTGCC TGGGTACCT CTGCTGCTGC 540  
 ATTGACTGGG ACACCTGATC CCTGGCCCCC TACCTGGGCA CCCAGGAGGA GTGCCCTCTT 600  
 GGCCTGCTCA CCTCATCTT CTTCACCTGC GTAGCAGCCA CACTGCTGGT GGTGAGGAG 660  
 GCAGCGCTGG GCCCCACCGA GCCAGCAGAA GGGCTGTCCG CCCCTCTCTT GTGCCCCAC 720  
 TGCTGTCCAT GCCGGGCGCG CTTGGCTTTC CGGAACCTGG GCGCCCTGCT TCCCGGCTG 780  
 CACGAGCTGT GCTGCCGCAT GCCCGCAGC CTGCGCGGGC TCTTCGTGGC TGAGCTGTGC 840  
 AGCTGGATGG CACTCATGAC CTTACGCTG TTTTACACGG ATTTCTGTGG CGAGGGGCTG 900  
 TACCAGGGCG TGCCAGAGC TGAGCCGGGC ACCGAGGCCG GGAGACACTA TGATGAAGGC 960  
 GTTCGGATGG GCAGCTGGG GCTGTCTCTG CAGTGCGCCA TCTCCCTGGT CTTCTCTCTG 1020  
 GTCATGGACC GGCCTGTGCA GCGATTCCGG ACTCGAGCAG TCTATTGGC CAGTGTGGCA 1080  
 GCTTTCCCTG TGCTGCCGG TGCCACATGC CTGTCCACA GTGTGCCGT GGTGACAGCT 1140  
 TCAGCCGCC TCACCGGGT CACCTTCTCA GCCCTGCAGA TCCTGCCCTA CACTGCGCC 1200  
 TCCTCTTACC ACCGGGAGAA GCAGGTGTTT CTGCCCAAT ACCGAGGGGA CACTGGAGGT 1260  
 GCTAGCAGT AGGACAGCT GATGACCAGC TTCTGCCAG GCCTAAGCC TGGAGCTCCC 1320  
 TTCCCTAATG GACACGTGGG TGTGGAGGC AGTGGCCTGC TCCACCTCC ACCCGGCTC 1380  
 TGCGGGGCT CTGCTGTGA TGTCTCCGTA CGTGTGGTGG TGGGTGAGCC CACCGAGGCC 1440  
 AGGGTGTGTC CGGGCCGGGG CATCTGCTG GACCTCGCCA TCCTGGATAG TGCTTCTCTG 1500  
 CTGTCCAGG TGCCCGCATC CTTGTTATG GGCTCCATTG TCCAGCTCAG CCAGTCTGTC 1560  
 ACTGCCTATA TGTGTCTGC CGCAGGCTG GGTCTGGTCG CCATTACTT TGCTACACAG 1620  
 GTAGTATTG ACAAGAGCGA CTTGGCCAAA TACTCAGCGT GA

Seq ID NO: 548 Protein sequence  
 Protein Accession #: NP\_149093.1

1 11 21 31 41 51  
 | | | | |  
 MVQRLWVSRL LRHRKAQLLL VNLTFGLEV CLAAGITYVP PLLLEVGVVEE KFMTMVLGIG 60  
 PVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILSL FLIPRAGWLA GLLCPDRPL 120  
 ELALLILGVG LLDGCGQVCF TPLEALLSDL FRDPDHCRQA YSVYAFMISL GGCLGYLLPA 180  
 IDWDTALAP YLGTQEECLF GLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH 240  
 CCPCRARLAF RNLGALLPRL HQLCCRMPT LRLFLVAELC SWMALMTFTL FYTDFVGEGL 300  
 YQGVPRAEFG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRF TRAVYLASVA 360  
 AFPVAAGATC LSHSVAVVTA SAALTGTFTS ALQILPYTLA SLYHREKQVF LPKYRGDTGG 420  
 ASSEDSLMTS FLPGPKPGAP FPNHVGAGG SGLLPPPPAL CGASACDVSV RVVVGEPTEA 480  
 RVVPGRIGICL DLAILDLSAFL LSQVAPSLFM GSIVQLSQSV TAYMVSAGL GLVAIYFATQ 540  
 VVFDKSLAK YSA

Seq ID NO: 549 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1389

1 11 21 31 41 51  
 | | | | |  
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGAGA GAGATTAGA TGACAGAGAA 60  
 ACCCTTGTTC CTGAACATGA GTATAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120  
 GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGT 180  
 GGGTTTCTCT TGGGAATATT GCTTTATTC TGGGTTTCAT ATGTACGGA CTTTCCCTT 240  
 GTTTTATGTA TAAAGGAGG GGCCCTCTCT GGAACAGATA CCTACCAGTC TTTGGTCAAT 300  
 AAAACTTTCG GCTTTCAGG GTATCTGCTC CTCTCTGTTT TTAGTTTTC GTATCCTTTT 360  
 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAGT TTTTCAAGA 420  
 ATCCAGAGG TTGATCCTGA AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTC 480  
 ACAGTTACCT TTAATCTGCC TTTATCCTTG TACCGAAATA TAGCAAGCT TGGAAAGGTC 540  
 TCCCTCATCT CTACAGGTTT AACAACTCTG ATTCTGGAA TTGTAATGGC AAGGGCAATT 600  
 TCACTGGGTC CACGATATCC AAAACAGAA GACGCTGGG TATTGCAAA GCCCAATGCC 660  
 ATTCAGCGCG TCGGGTTTAT GTCTTTTGCA TTTATTTGCC ACCATACTC CTTCTTAGTT 720

TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780  
 GTGATTCTCG TATTTATCTG TATATCTTTT GCTACATGTG GATACTTGAC ATTTACTGGC 840  
 TTCACCCAAAG GGGACTTAT TGAATAATTAC TGCAGAAATG ATGACCTGGT AACATTGGGA 900  
 AGATTTTGGT ATGGGTGTAC TGTCAATTTG ACATACCCTA TGGAAATGCTT TGTGACAAGA 960  
 GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTCAT CGGTTTTCCA CATTGTTGTA 1020  
 ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATTG TGATTGATTG CCTCGGGATA 1080  
 GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCCTCA TTTTATCAT TCCATCAGCC 1140  
 TGTTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200  
 ATGCTTCCCA TCGGTGCTGT GGTGATGGTT TTTGGATTCT TCATGGCTAT TACAAATACT 1260  
 CAAGACTGCA CCAATGGGCA GGAAATGTTT TACTGCTTTC CTGACAATTT CTCTCTCACA 1320  
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTAAA TATTAGTATC 1380  
 TTTCAATGA

Seq ID NO: 550 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 MG YQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIIGSGI IGLPYSMKQA 60  
 GFPLGILLLF WVS YVTD FSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPF 120  
 IAMISYNIIA GDTLSKVQFQ IPGVDPENVF IGRHFIIGLS TVTFTLPLSL YRNIKALGKV 180  
 SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKPNA IQAVGVMSFA FICHHSNFLV 240  
 YSSLEEPTVA KWSRLIHMSI VISVFICIFF ATCGYLTFTG FTQGDLFENY CRNDDLVTFFG 300  
 RFCYGVTVIL TYPMCEFVTR EVIANVFFGG NLSGVFHIVV TVMVITVATL VSLIDCLGI 360  
 VLELNGVLCA TPLIFIIPSA CYLKLSEEPH THSDKIMSCV MLPIGAVVMV FGFVMAITNT 420  
 QDCTHGQEMF YCFPDNFSLT NTSSEHVQQT TQLSTLNISI FQ

Seq ID NO: 551 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1284

1 11 21 31 41 51  
 | | | | |  
 ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CCGCCGCAGA GAGGATTGCC TTATTCAATG 60  
 AAGCAAGCTG GGTTCCTTTT GGGAAATATTG CTTTATTCTT GGGTTTCATA TGTACAGAC 120  
 TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180  
 TTGGTCAATA AAACCTTTCGG CTTTCCAGGG TATCTGTCTC TCTCTGTCTC TCAGTTTTTG 240  
 TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300  
 TTTCAAAGAA TCCCAGGAGT TGATCCTGAA AACGTGTTTA TTGGTCGCCA CTTCAATTAT 360  
 GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACCGAAATAT AGCAAAGCTT 420  
 GGAAAGGTCT CCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGAAT TGTAAATGGCA 480  
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAG 540  
 CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTTGCCA CCATAACTCC 600  
 TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660  
 ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATCTTTTG CTACATGTGG ATACTTGACA 720  
 TTTACTGGCT TCACCCAAGG GGACTTATTT GAAAATTACT GCAGAAATGA TGACCTGGTA 780  
 ACATTTGGAA GATTTTGTTA TGGTGTCACT GTCATTTTGA CATACCTAT GGAATGCTTT 840  
 GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTTCATC GGTTTTCCAC 900  
 ATTGTGTAA CAGTGTAGGT CATCACTGTA GCCACGCTTG TGTATTGCT GATTGATTGC 960  
 CTCGGGATAG TTCTAGAACT CAATGGTGTG CTCGTGTCAA CTCCTTCAT TTTTATCATT 1020  
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080  
 TCTGTGTGTA TGCTTCCCAT TGGTGTCTGT GTGATGGTTT TTGGATTCTG CATGGCTATT 1140  
 ACAATACTC AAGACTGCAC CCATGGGCGAG GAAATGTTCT ACTGCTTCC TGACAATTTT 1200  
 TCTCTCACA ATACTCAGA GTCCTCATGT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260  
 ATTAGTATCT TTAACACTCGA GTAA

Seq ID NO: 552 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 MG YQRQEPVI PPQRGLPYSM KQAGFPLGIL LFWVSYVTD FSLVLLIKGG ALSGDTYQS 60  
 LVNKTGFFPG YLLSVLQFL YPFIAMISYN ILAGDTLSKV QRIPGVDP E NVFGRHFII 120  
 GLSTVFTFLP LSLYRNIAKL GKVS LISTGL TLLILGIVMA RAISLGPHIP KTEDAWVFAK 180  
 PNAIQAVGVM SFAFICHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240  
 FTGFTQGDLE ENYCRNDDL V TFRFCYGV T VILTYPMCE F VTREVIANVF FGGNLSVVFH 300  
 IVVTVMVITV ATLVSLLIDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360  
 SCVMLPIGAV VMVFGFVMAI TNTQDCTHQ EMFYCFPDNF SLTNTSESHV QTTQLSTLN 420  
 ISIFQLE

Seq ID NO: 553 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1203

1 11 21 31 41 51  
 | | | | |  
 ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CCGCCGCAGT TTTCCTTGT TTTATTGATA 60  
 AAAGGAGGGG CCTCTCTGG AACAGATACC TACCACTCTT TGGTCAATAA AACTTTCGGC 120  
 TTTCCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180  
 AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TTCAAAGAAT CCCAGGAGTT 240  
 GATCCTGAAA ACGTGTATT TGGTCGCCAC TTCAATTATT GACTTTCCAC AGTTACCTTT 300  
 ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGCTCT CCTCATCTCT 360  
 ACAGGTTTAA CAACTCTGAT TCTTGAATT GTAATGGCAA GGGCAATTC ACTGGGTCCA 420  
 CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAGC CCAATGCCAT TCAAGCGGTC 480

GGGGTTATGT CTTTTCGATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCCTTA 540  
 GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCATCGT GATTTCGTGA 600  
 TTTATCTGTA TATTCCTTGC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660  
 GACTTATTGG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTGGGAAG ATTTTGTAT 720  
 GGTGTCACTG TCATTTTGAC ATACCCCTATG GAATGCTTTG TGACAAGAGA GGTAATTGCC 780  
 AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTTCCACA TTGTGTAAAC AGTGATGGTC 840  
 ATCACTGTAG CCACGCTTGT GTCATTGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC 900  
 AATGGTGTGC TCTGTGCAAC TCCCTCATTT TTTATCATTC CATCAGCCTG TTATCTGAAA 960  
 CTGTCTGAAG AACCAAGGAC ACATCCGAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020  
 GGTGCTGTGG TGATGGTTTT TGGATTGCTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080  
 CATGGGCAGG AAATGTTCTA CTGCTTTCCT GACAATTTCT CTCTCACAAA TACCTCAGAG 1140  
 TCTCATGTTC AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200  
 TAA

Seq ID NO: 554 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYPFIAMI 60  
 SYNIIAGDTL SKVFQRIQGV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSILIS 120  
 TGLTTLILGI VMAAISLGP HIPKTEDAWV FAKPNAIQAV GVMSFAFICH HNSFLVYSSL 180  
 EEPTVAKWSR LIHMSIVISV FICIFFATCG YLTFTGFTQG DLFENYCRND DLVTFGRFCY 240  
 GVTVILTYPM ECFVTREVIA NVFFGGNLSV VEHIVVTVMV ITVATLVSLI IDCLGIVLEL 300  
 NGVLCATPLI FIIPSACYLK LSEEPRTSHD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360  
 HQEMFYCFP DNFSLTNTSE SHVQTTQLS TLNISIFQLE

Seq ID NO: 555 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1140

1 11 21 31 41 51  
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCAGG TCAATAAAAC TTTCGGCTTT 60  
 CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120  
 TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180  
 CCTGAAAACG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTCCACAGT TACCTTTACT 240  
 CTGCCCTTAT CCTGTACCG AAATATAGCA AAGCTTGGAA AGGTCCTCCCT CATCTCTACA 300  
 GGTTTAACAA CTCTGATTCT TGGAAATTGA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360  
 ATACCAAAAC CAGAAGACGC TTGGGTATTT GCAAGCCCA ATGCCATTCA AGCGGTCCGG 420  
 GTTATGTCTT TTGCATTTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480  
 GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540  
 ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600  
 TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660  
 GTCACGTGTA TTTTGACATA CCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720  
 GTGTTTTTTG TGGGAATCTT TTCATCGGTT TTCCACATTG TTGTACAGT GATGGTCATC 780  
 ACTGTAGCCA CGCTTGCTGC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840  
 GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCATTCAT CAGCCTGTTA TCTGAACTG 900  
 TCTGAAGAAC CAAGGACACA CTCGATAAG ATTATGTCTT GTGTCATGCT TCCCATTTGT 960  
 GCTGTGGTGA TGGTTTTTGG ATTCGTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020  
 GGGCAGGAAA TGTTCTACTG CTTTCCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT 1080  
 CATGTTTCTG AGACAACACA ACTTTCTACT TTAAATATTA GTATCTTTCA ACTCGAGTAA

Seq ID NO: 556 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MGYQRQEPVI PPQVKNKTFG FPGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIQGV 60  
 PENVFIGRHF IIGLSTVTFI LPLSLYRNI KLKGVSLIST GLTTLILGIV MARAISLGP 120  
 IPKTEDAWVF AKPNAIQAVG VMSFAFICH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180  
 ICIFPATCGY LTFTGTGQGD LFNENYCRND LVTGFRFCY VTVILTYPME CFVTREVIAN 240  
 VFFGGNLSV FHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL 300  
 SEEPRTSHDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES 360  
 HVQTTQLST LNISIFQLE

Seq ID NO: 557 DNA sequence  
 Nucleic Acid Accession #: XM\_057188.1  
 Coding sequence: 769..4269

1 11 21 31 41 51  
 ATGGGATGTC CTCTCCCTCT CACTCTGGGC TTCTGTCCCA CTCTATCTT AGTGTCAATC 60  
 CTCGCCCAAG TCTGTGTCCC TCTCTCTCCC CTAAATCTCT GGCCCTCCTT TTCTGAGTTC 120  
 CTGCCCTTGC CCCAATCTCT TGGTTTTTGC ATCCCCCTCT GCCCCTTGCC TCAGTCAAGT 180  
 CTCCCTGTGC TGTCTCTCTC CCCCCGGCCC GGACCTCTGC ACCCCCCAGG TCGCTGTCCC 240  
 TCTGTCCCTT TATCGCGGCC TGGGACCCGC CCTCTCCCG CCTCCCGCTT TGGCGTCTCC 300  
 AAGACTCCCT GCCCCCCAGA CCTCGCCCG CCCCAGGCTA GGCTGGAAAG TGGAGGATCC 360  
 GGTGTGCTCT GGGCGGGTCT GGAAGCAGAG CCGGCGGAGG GAGCGCCGGG GCCCTGGGCT 420  
 GCAGGAGGTT CGGCGGGCCG CGGCAGCATG GTGGTGCCGG AGAAGGAGCA GAGCTGGATC 480  
 CCCAAGATCT TCAAGAAGAA GACCTGCACG ACGTTCATAG TTGACTCCAC AGATCCGGGG 540  
 GATGGGGTCT CGCTCTATATG CCCAGGCTGT TCTCAAATCT CTGGGCTCAA GCAGTCCCTC 600  
 TGCCTTGAC TCCCAAAGTG CTGGATTGT GCCCAGCCGT CCTTGAAGTT TTGCTCAGAA 660  
 GAGCAAATCT TCTGGGAAGT AGCTGCAGGT GTTGAAGTA GCTGCAGGGG AACTAGGGGA 720

5 TTCAAGGATG GAGCTGAAAT GGGTGAACGG ACAAAGTCGG TAAACTGAAT GGAGGATGCC 780  
 TTGGGGGCGAG CCGTGGTGAC CGTGTGGGAC AGCGATGCAC ACACCCACGGA GAAGCCACACC 840  
 GATGCGCTACG GAGAGCTGGA CTTACACGGG GCCGGCCGCA AGCACAGCAA TTTCCTCCGG 900  
 CTCTCTGACC GAACGGATCC AGCTGCAGTT TATAGTCTGG TCACACGCAC ATGGGGCTTC 960  
 10 CGTGCCCCGA ACCTGGTGGT GTCACTGCTG GGGGGATCGG GGGGGCCCGT CCTCCAGACC 1020  
 TTGGTGCAGG ACCTGCTGCG TCGTGGGCTG GTGCGGGCTG CCCAGAGCAC AGGAGCCTGG 1080  
 ATTGTCACTG GGGGTCTGCA CACGGGCATC GGCCGGCATG TTGGTGTGGC TGTACGGGAC 1140  
 CATCAGATGG CCAGCACTGG GGGCACCAGG GTGGTGGCCA TGGGTGTGGC CCCCTGGGGT 1200  
 TGGGTCCGGA ATAGAGACAC CCTCATCAAC CCCAAGGGCT CGTTCCTGC GAGGTACCGG 1260  
 TGGCGCGGTG ACCCGGAGGA CGGGGTCCAG TTTCCCTGG ACTACAACTA CTCGGCCTTC 1320  
 TTCTTGGTGG ACACAGGCAC ACACGGCTGC CTGGGGGGCG AGAACCGCTT CCCTTGGCG 1380  
 CTGGAGTCTT ACATCTCACA GCAGAAGACG GCGTGGGAG GGAATGGAAT TGACATCCCT 1440  
 15 GTCTGCTCC TCCTGATTGA TGGTGTAGAG AAGATGTTGA CGCGAATAGA GAACGCCACC 1500  
 CAGGCTCAGC TCCCATGTCT CCTCGTGGCT GGTCTAGGGG GAGCTGCGGA CTGCCTGGCG 1560  
 GAGACCTGAG AAGACACTCT GGGCCAGGG AGTGGGGGAG CCAGGCAAGG CGAAGCCCGA 1620  
 GATCGAATCA GGGTCTTCTT TCCCAAAGGG GACCTTGAGG TCCTGACAGC CCAGGTGGAG 1680  
 AGGATTATGA CCCGGAAGGA GCTCCTGACA GTCTATTCTT CTAGGATGG GTCTGAGGAA 1740  
 TTTGAGACCA TAGTTTGAAG GGCCTTGGT AGGCCTGTG GAGCTGCGGA GGCCTCAGCC 1800  
 20 TACCTGGATG AGCTGCTGTT GGTGTGGCT TGAACCCGCG TGGACATTGC CCAGAGTGAA 1860  
 CTCTTTGCGG GGGACATCCA ATGGCGGTCC TTCCATCTCG AAGCTTCCCT CATGGACGCC 1920  
 CTGCTGAATG ACCGGCTGGA GTTCGTGCGC TTGCTCATTT CCCACGGCT CAGCCTGGGC 1980  
 CACTTCTCGA CCCCAGATGG CCTGGCCCAA CTCTACAGCG CGGCGCCCTC CAACTCGCTC 2040  
 ATCCGCAACC TTTTGGACCA GCGCTCCAC AGCGCAGGCA CCAAGCCCTC AGCCCTAAAA 2100  
 25 GGGGGAGCTG CGGAGCTCCG GCGCCCTGAC GTGGGGCATG TGCTGAGGAT GCTGCTGGGG 2160  
 AAGATGTGCG CGCCGAGTA CCCCTCGGG GCGCCTCGGG ACCCTCACCC AGGCCAGGGC 2220  
 TTCGGGGAGA GCATGTATCT GCTCTCGGAC AAGGCCACCT CGCGCTCTC GCTGGATGCT 2280  
 GGGCTCGGGC AGGCCCCCTG GAGCGACCTG CTCTTTTGGG CACTGTGTCT GAACAGGGCA 2340  
 CAGATGGCCA TGTACTCTG GAGATGGGT TCCAATGCAG TTTCTCAGC TCTTGGGGCC 2400  
 30 TGTTTGCTGC TCCGGGTGAT GGCACGCTG GAGCCTGACG CTGAGGAGGC AGCACGGAGG 2460  
 AAAGACCTGG CGTTCAGTT TGAGGGGATG GGCCTTGACC TCTTTGGCGA GTGCTATCGC 2520  
 AGCAGTGAGG TGAGGGCTGC CCGCTCTCTC CTCCGCTGCT GCGCGCTCTG GGGGGATGCC 2580  
 ACTTGCTCC AGCTGGCCAT GCAAGCTGAC GCGCGTGCTT TCTTTGCCCA GGATGGGGTA 2640  
 35 CAGTCTCTGC TGACACAGAA GTGGTGGGA GATATGGCCA GCACTACACC CATCTGGGCC 2700  
 CTGTTCTCG CTTCTTTTG CCCTCCACTC ATCTACACCC GCCTCATCAC CTTCAGGAAA 2760  
 TCAGAAGAGG AGCCACACG GAGGAGGATA GAGTTTGACA TGGATAGTGT CATTAAATGGG 2820  
 GAAGGGCTG TCGGGACGGC GACCCAGCC GAGAAGACGC CGCTGGGGGT CCGCGCCAG 2880  
 TCGGGCCGTC CGGGTGTGTC GGGGGCCGC TGCGGGGGGC GCGGTGCTT ACGCCGCTGG 2940  
 40 TTCCACTTCT GGGGCGCGCC GGTGACCATC TTCATGGGCA ACGTGGTCAG CTACCTGCTG 3000  
 TTCTGCTGTC TTTTCTCGCG GGTGCTGCTC GTGGATTTC AGCCGCGGCC CCGCGCTCC 3060  
 CTGGAGCTGC TGCTCTATT CTGGCTTTC ACGCTGCTGT GCGAGGAAC GCGCCAGGGC 3120  
 CTGAGCGGAG GCGGGGGCAG CCTCGCAGC GGGGGCCCG GGCCTGGCCA TGCTCACTG 3180  
 AGCCAGCGCC TGCGCTCTA CCTCGCCGAC AGCTGGAACC AGTGCAGCT AGTGGCTCTC 3240  
 45 ACCTGCTTCC TCCTGGGCT GGGCTGCCG CTGACCCCG GTTTGTACCA CCTGGGCCGC 3300  
 ACTGTCTCT GCATCGACT CATGTTTTC ACGGTGCGGC TGCTTCACAT CTTACGGTC 3360  
 AACAAACAGC TGGGGCCCAA GATCGTCATC GTGAGCAAGA TGATGAAGGA CGTGTCTTTC 3420  
 50 TTCTCTTCT TCCTCGGCT GTGGTGGTA GCCTATGGCG TGGCCACGGA GGGGCTCCTG 3480  
 AGGCCACGGG ACAGTGACT CCCAAGTATC CTGCGCCGCG TCTTCTACCG TCCCTACCTG 3540  
 CAGATCTTCG GGCAGATTCC CCAGGAGGAC ATGGACGTGG CCCTCATGGA GCACAGCAAC 3600  
 TGCTGCTCG AGCCCGGCTT CTGGGCACAC CCTCTGGGG CCCAGGCGGG CACTTGCCTG 3660  
 TCCAGTATG CCAACTGGCT GGTGGTGTG CTCTCTGTC TCTTCTGCT CGTGGCCAAC 3720  
 ATCCTGCTGG TCAACTTGCT CATTGCCATG TTCAGTTACA CATTGGGCAA AGTACAGGGC 3780  
 55 AACAGCGATC TCTACTGGAA GCGCGAGCGT TACCCCTCA TCCGGGAATT CCACTCTCGG 3840  
 CCGCGCTGG CCGCCCTTAT TATCGTCATC TCCCACTTGC GCCTCCTGCT CAGGCAATTG 3900  
 TGACGGGAC CCGCGAGCCC CCAGCGTCC TCCCGGCCCC TCGAGCATTT CCGGGTTTAC 3960  
 CTTTCTAAGG AAGCCGAGCG GAAGCTGCTA ACGTGGGAAT CGGTGCATAA GGAGAACTTT 4020  
 CTGCTGGCAC GCGCTAGGGA CAAGCGGGAG AGCGACTCCG AGCGCTGAA GCGCACGTC 4080  
 CAGAAGGTGG ACTTGGCACT GAAACAGCTG GGACACATCC GCGAGTACGA ACAGCGCTG 4140  
 60 AAAGTGTGAG AGCGGGAGGT CCAGCAGTGT AGCCCGCTCC TGGGGTGGGT GGCCGAGGCC 4200  
 CTGAGCCGCT CTGCTTGTCT GCGCCAGGT GGGCCGCCAC CCCCTGACCT GCCTGGGTCC 4260  
 AAAGACTGAG CCTGCTGCTG GACTTCAAG GAGAAGCCCC CACAGGGGAT TTTGCTCCTA 4320  
 GAGTAAGGCT CATCTGGGCC TCGGCCCCCG CACCTGGTGG CCTTGTCTT GAGGTGAGCC 4380  
 CCATGTCCAT CTGGGGCACT GTCAGGACCA CTTTGGGAG TGTCATCCTT ACAAACCACA 4440  
 65 GCATGCCCCG CTCTCCCGA AACCACTCCC AGCCTGGGAG GATCAAGGCC TGGATCCCGG 4500  
 GCGGTATCC ATCTGAGGCG TGCAGGGTCC TTGGGGTAAC AGGGACCACA GACCCTCAC 4560  
 CACTCACAGA TTCTCACAC TGGGGAAATA AAGCCATTTC AGAGGAAAAA AAAAAAAA 4620  
 AAAAAAAAAA AAAAAAAAAA A

Seq ID NO: 558 Protein sequence  
 Protein Accession #: XP\_057188.1

70 1 11 21 31 41 51  
 MEDAFGAADV TVWDSDAHT EKPTDAYGEL DFTGAGRKHS NFLRLSDRT PAAVYSLVTR 60  
 75 TWGFRAENLV VSVLGGSGGP VLQTLWQDLL RRLGLVRAAQ TGAWIVTGGL HTGIGHRVGV 120  
 AVRDRHQMAST GGTKVVMAMG APWGVVRNRD TLINPKGSFP ARYRWRGDPE DGVQFPLDYN 180  
 YSAFFLVDDG THGCLGGENR FLRLLESYIS QKQTVGGGT IDIPVLLLI DGDEKMLTRI 240  
 ENATQAQLPC LNVAGSGGAA DCLAETLED T LAPSGGARQ GEARDIRRF FPKGDLVLQ 300  
 AQVERIMTRK ELLTVYSSED GSEEFETIVL KALVKACGSS EASAYLDEL L LAVAWNVRDI 360  
 80 AQSELRGDI QWRSFHLEAS LMDALLNDRP EFVRLISHG LSLGHFLTPM RLAQLYSAAP 420  
 SNLIRNLLD QASHSAGTKA PALKGGAAEL RPPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480  
 PGQGFESMY LLSDKATSPL SLDAGLQAP WSDLLWALL LNRAQMAMYF WEMGSNAVSS 540  
 ALGACLLLRV MARLEPAEE AARRKDLAFK FEGMGVDLFG ECVRSSEVRA ARLLLRRCPL 600  
 WGDATCLQLA MQADARAFQ QDGVQSLLTQ KWWGDMASTT PIWALVAF CPPLIXTRLI 660  
 TFRKSEEP REELEFDMDS VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGRCGGRRC 720

LRRWFHFWGA PVTIFMGNVV SYLLFLLLF S RVLLVDFQPA PPGSLELLLY FWAFTLLCEE 780  
 LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLLTPGLY 840  
 HLGRITVLICID FMVFTVRLHL IFTVNKQLGP KIVIVSKMMK DVFFFLFFLG VWLVAYGVAT 900  
 EGLLRPRDSF PFSILRRVFY RPYLQIFGQI PQEDMDVALM BHSNCSSEFG FWAHPFGAQA 960  
 GTCVSQYANW LVVLLLVIFL LVANILLVNL LIAMFSYTFG KVQNSDLYW KAQRVRLIRE 1020  
 FHSRPAALAPP FIVISHRLRL LRQLCRRPRS PQPSSPALEH FRVYLSKEAE RKLLTWESVH 1080  
 KENFLARAR DKRESDSERL KRTSQKVDLA LKQLGHIREY BQRLKVLERE VQQCSRVLGW 1140  
 VAEALSRSAL LPPGGPPPPD LFGSKD

Seq ID NO: 559 DNA sequence  
 Nucleic Acid Accession #: NM\_006853.1  
 Coding sequence: 26..874

1 11 21 31 41 51  
 AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTGCGGG ACTGGAAGTC 60  
 ATCGGGCAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCCTCCC CCCTCCAGGC 120  
 CATGAGGATT CTGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGGAGAGAC 180  
 CAGGATCATC AAGGGGTTTC AGTGCAAGCC TCACTCCCAG CCCTGGCAGG CAGCCCTGTT 240  
 CGAGAAGACG CGGCTACTCT GTGGGGCGAC GCTCATCGCC CCCAGATGGC TCCTGACAGC 300  
 AGCCCACTGC CTCAAGCCCC GCTACATAGT TCACCTGGGG CAGCACAAAC TCCAGAAGGA 360  
 GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCCTTC CCCCACCCCG GCTTCAACAA 420  
 CAGCCTCCCC AACAAAGACC ACCGCAATGA CATCATGCTG GTGAAGATGG CATCGCCAGT 480  
 CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCCTCA CGCTGTGTCA CTGCTGGCAC 540  
 CAGCTGCCTC ATTTCCGGGT GGGGCAGCAC GTCCAGCCCC CAGTTACGCC TGCCTCACAC 600  
 CTTCGATGTC GCCAACATCA CCATCATTGA GCACCAGAAG TGTGAGAACG CCTACCCCGG 660  
 CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAAGAA GGGGGCAAGG ACTCCTGCCA 720  
 GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCAGTCTCTT CAAGGCATTA TCTCCTGGGG 780  
 CCAGGATCCG TGTGCGATCA CCCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAAAATATGT 840  
 GGACTGGATC CAGGAGACGA TGAAGAACAA TTAGACTGGA CCCACCCACC ACAGCCCATC 900  
 ACCCTCCATT TCCACTTGGT GTTTGGTTCC TGTTCACCTC GTTAATAAGA AACCTAAGC 960  
 CAAGACCCCT TACGAAATTT CTTTGGGCTT CCTGGACTAC AGGAGATGCT GTCACCTAAT 1020  
 AATCAACCTG GGGTTCCGAA TCAGTGAGAC CTGGATTCAA ATCTGCTT GAAATATTGT 1080  
 GACTCTGGGA ATGACAACAC CTGGTTTGTG CTCTGTTGTA TCCCCAGCCC CAAAGACAGC 1140  
 TCCTGGCCAT ATATCAAGGT TTCAATAAAT ATTTGCTAAA TGAGTG

Seq ID NO: 560 Protein sequence  
 Protein Accession #: NP\_006844.1

1 11 21 31 41 51  
 MRILQLILLA LATGLVGGET RIIKGFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA 60  
 AHCLKPRYIV HLGQHNLOKE EGCEQTRTAT ESFPHPGFNN SLPNKDHRND IMLVKMASPV 120  
 SITWAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIE HQKCNAYPG 180  
 NITDTMVCAS VQEGGKDSQC GDSGGPLVCN QSLQGIISWG QDPCAIRKP GYITKVCKYV 240  
 DWIQETMKNN

Seq ID NO: 561 DNA sequence  
 Nucleic Acid Accession #: AY046419.1  
 Coding sequence: 1..1743

1 11 21 31 41 51  
 ATGTTTACCT TCCTGTCATC TGTCAGTCTGCT GCTGTCAAGT GCCTCCTGGT GGGTTATGAA 60  
 CTGCGGATCA TCTCTGGGGC TCTTCTTCAG ATCAAAACCT TATTAGCCCT GAGCTGCCAT 120  
 GAGCAGGAAA TGGTTGTGAG CTCCTCTGTC ATTTGGAGCCC TCCTTGCCCTC ACTCACCGGA 180  
 GGGGTCCTGA TAGACAGATA TGGAGAAGAG ACAGCAATCA TCTGTGCATC CTGCCTGCTT 240  
 GGACTCGGAA GCTTAGTCTT GATCCTCAGT TTATCCTACA CGGTTCTTAT AGTGGGACGC 300  
 ATTGCCATAG GGGTTTCCAT CTCCTCTCTT TCCATTGCCA CTGTGTGTTA CATCGCAGAG 360  
 ATTGCTCCTC AACACAGAAG AGGCCTTCTT GTGTCACTGA ATGAGCTGAT GATTGTGATC 420  
 GGCATTCTTT CTGCCTATAT TTCAAATTAC GCATTTGCCA ATGTTTCCA TGGCTGGAAG 480  
 TACATGTTTG GTCTGTGAT TCCCTTGGA GTTTTGCAAG CAATTGCAAT GTATTTTCTT 540  
 CCTCCAAGCC CTCGGTTTCT GGTGATGAAA GGACAAGAGG GAGCTGCTAG CAAGGTTCTT 600  
 GGAAGGTTAA GAGCAGTCTC AGATACAACCT GAGGAACCTA CTGTGATCAA ATCCTCCCTG 660  
 AAAGATGAAT ATCAGTACAG TTTTGGGAT CTGTTTCGTT CAAAAGACAA CATGCGGACC 720  
 CGAATAATAG TAGGACTAAC ACTAGTATTT TTTGTACAAA TCACTGGCCA ACCAAACATA 780  
 TTGTTCTATG CATCAACTGT TTTGAAGTCA GTTGGATTTC AAAGCAATGA GGCAGCTAGC 840  
 CTCGCCTCCA CTGGGGTTGG AGTCGTCAAG GTCATTAGCA CCATCCCTGC CACTCTTCTT 900  
 GTAGACCATG TGGGCAGCAA AACATTCTCT TGCAATTGGT CCTCTGTGAT GGCAGCTTCG 960  
 TTGGTGACCA TGGGCATCGT AAATCTCAAC ATCCACATGA ACTTCACCCA TATCTGCAGA 1020  
 AGCCACAATT CTATCAACCA GTCCTTGGAT GAGTCTGTGA TTTATGGACC AGGAAACCTG 1080  
 TCAACCAACA ACAATACTCT CAGAGACCAC TTCAAAGGGA TTTCTTCCCA TAGCAGAAGC 1140  
 TCACTCATGC CCGTGAAGAA TGATGTGGAT AAGAGAGGGG AGACGACCTC AGCATCCTTG 1200  
 CTAATGCTG GATTAAGCCA CACTGAATAC CAGATAGTCA CAGACCTTGG GGCAGTCCCA 1260  
 GCTTTTGTGA AATGGCTGTC CTTAGCCAGC TTGCTTGTTT ATGTTGCTGC TTTTCAATT 1320  
 GGTCTAGGAC CAATGCCCTG GCTGGTGCTC AGCGAGATCT TTCCTGGTGG GATCAGAGGA 1380  
 CGAGCCATGG CTTTAACTTC TAGCATGAAC TGGGGCATCA ATCTCCTCAT CTCGCTGACA 1440  
 TTTTGAAGT TAACTGATCT TATTGGCTG CCAATGGGTG GCTTTATATA TACAATCATG 1500  
 AGTCTAGCAT CCCTGCTTTT TGTGTTATG TTTATACCTG AGACAAAGGG ATGCTCTTTG 1560  
 GAACAAATAT CAATGGAGCT AGCAAAAGTG AACTATGTGA AAAACAACAT TTGTTTATG 1620  
 AGTCATCACC AAGAAGAAAT AGTGCCRAAA CAGCCTCAAA AAGAAAACC CCAGGAGCAG 1680  
 CTCTTGAGT GTAACAAGCT GTGTGGTAGG GGCCAATCCA GGCAGCTTTC TCCAGAGACC 1740  
 TAA

Seq ID NO: 562 Protein sequence  
Protein Accession #: AAL02327.1

```

5      1      11      21      31      41      51
|      |      |      |      |      |
MFTFLSSVTA AVSGLLVGYE LGIISGALLQ IKTLALLSCH EQEMVSSSLV IGALLASLTG 60
GVLLIDRYGRR TAILLSSCLL GLGSLVLILS LSYTVLIVGR IAIGVSISSL SIATCVYIAE 120
IAPQHRRLGL VSLNELMIVI GILSAYISNY AFANVFHGWK YMFGLVPLG VLQAIAMYFL 180
PPSPRFLVMK GQEGAASKVL GRRLRALSDDT EELTVIKSSL KDEYQYSFWD LFRSKDNMRT 240
10    RIMIGLTLVF FVQITGQPNL LFYASTVLKS VGFQSNAAAS LASTGVGVVK VISTIPATLL 300
VDHVGSKTFL CIGSSVMAAS LVTMGIVNLN IHMNFTHICR SHNSINQSLD ESVIYGPGLN 360
STNNNTLRDH FKGISHSRS SLMPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDVP 420
AFLKWLSLAS LLVYVAAPSI GLGPMPLVL SEIFPGGIRG RAMALTSSMN WGINLLISLT 480
15    FLTVDLIGL PWVCFIYTIM SLASLLFVVM FIPETKGC SL EQISMELAKV NYVKNNICFM 540
SHHQEELVFK QPQRKRPQEQ LLECNKLCGR QQSRLSPET

```

Seq ID NO: 563 DNA sequence  
Nucleic Acid Accession #: XM\_059466.1  
Coding sequence: 1..894

```

20      1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGCCGC GGGCGCTCGT CACGGCGCTC AGCCTCGGCC TCAGCCTGTG TCCCTGGGG 60
CTGCTCGTCA CGGCCATCTT CACCGACCAC TGGTACGAGA CCGACCCCGG GCGCCACAAG 120
25    GAGAGCTGCG AGCGCAGCCG CGCGGGCGCC GACCCCCCGG ACCAGAAGAA CCGCCTGATG 180
CGCTGTGCGC ACCTGCCGCT GCGGGACTCG CCCCCTGCTG GCGGCCGGCT GCTCCCGGGC 240
GCCCGGGGGC GCGCGGACCC CGAGTCTCTG CGCTCGCTCC TGGGGCTCGG CCGGCTGGAC 300
GCCGAGTGGC GCGCGCCCTT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
CTGGGCATCG ACCGGGACAT CGACACCCCT ATCCTGAAAG GTATTGCGCA GCGATGCACG 420
30    GCCATCAAGT ACCACTTTTC TCAGCCCATC CGCTTGCAGG ACATTCTTTC TAATTTAACC 480
AAGACATACG AGCAAGATGA GTGGCACCTG CTTCATTTAA GAAGAATCAC TGCTGGCTTC 540
CTCGGCATGG CCGTAGCCCT CTCTCTCTGC GGCTGCATTG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACGTGGCT GGAATCTGTG TCCTCATGAC AGGGATATT 660
35    TGCACCATTT CCTCTGTAC TTATGCCGCC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCTGCC TGTCTGATGT GAACATGGTT ACAGCTGGTC CATCTTTTGC 780
GCCTGGTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCGC TTATCCGTTT 840
ATTAGCCGGA CCAAGATTGC ACAGCTAAAG TCTGGCAGAG ACTCCACGGT ATGA

```

Seq ID NO: 564 Protein sequence  
Protein Accession #: XP\_059466.1

```

40      1      11      21      31      41      51
|      |      |      |      |      |
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DPPDQKNRLM 60
45    PLSHLPLRDS PPLGRRLLP GPGRADPEW RSLGLGLGLD AECGRPLFAT YSGLWRKCYF 120
LGIDRDIDTL ILKGIAQRCT AIKYHFSQPI RLRNIPFNLT KTIQDEWHL LHLRRITAGF 180
LGMMAVLLC GCTVATVSSF WEESLTQHVA GLLFLMTGIF CTISLCTYAA SISYDLNRLP 240
KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

```

Seq ID NO: 565 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..3315

```

55      1      11      21      31      41      51
|      |      |      |      |      |
ATGTCCTTTC GGGCAGCCAG GCTCAGCATG AGGAACAGAA GGAATGACAC TCTGGACAGC 60
ACCCGGACCC TGTACTCCAG CGCGTCTCGG AGCACAGACT TGTCTTACAG TGAAGCGCAG 120
TTGGTGAATT TTATTCAAGC AAATTTTAAG AAACGAGAAT GTGTCTTCTT TACCAAAGAT 180
60    TCCAAGGCCA CGGAGAATGT GTGCAAGTGT GGCTATGCCC AGAGCCAGCA CATGGAAGGC 240
ACCCAGATCA ACCAAAGTGA GAAATGGAAC TACAAGAAAC ACACCAAGGA ATTTCTTACC 300
GACGCCTTTG GGGATATTCG GTTTGAGACA CTGGGGAAGA AAGGGAAGTA TATACGCTCG 360
TCCTGCGACA CGACGCGGGA AATCCTTTAC GAGCTGCTGA CCCAGCACTG GCACCTGAAA 420
ACACCCAACC TGGTCATTTT TGTGACCGGG GCGGCCAAGA ACTTCGCCCT GAAGCCGCGC 480
ATGCGCAAGA TCTTCAGCCG GCTCATCTAC ATCGCGCAGT CCAAGAGTGC TTGGATTCTC 540
65    ACGGAGGCA CCCATTATGG CCTGATGAAG TACATCGGGG AGGTGCTGAG AGATAACACC 600
ATCAGCAGGA GTTCAGAGGA GAATATTGTG GCCATTGGCA TAGCAGCTTG GGCATGGTTC 660
TCCAACCGGG ACACCTCAT CAGGAATTGC GATGCTGAGG GCTATTTTTC AGCCAGTAC 720
CTTATGGATG ACTTCACAAG AGATCCACTG TATATCTTGG ACAACAACCA CACACATTG 780
CTGCTCGTGG ACAATGGCTG TCATGGACAT CCCACTGTG AAGCAAAGCT CCGGAATCAG 840
70    CTAGAGAAGT ATATCTCTGA GCGCACTATT CAAGATTCCA ACTATGGTGG CAAGATCCCC 900
ATTGTGTGTT TTGCCCAAGG AGGTGGAAAA GAGACTTTGA AAGCCATCAA TACCTCCATC 960
AAAAATAAAA TTCCTTGTGT GGTGTGGGAA GGCTCGGGCC AGATCGCTGA TGTGATCGCT 1020
AGCCTGGTGG AGGTGGAGGA TGCCCTGACA TCTTCTGCGG TCAAGGAGAA GCTGGTGC GC 1080
TTTTTACCCC GCACGGTGTG CCGGCTGCCT GAGGAGGAGA CTGAGAGTTG GATCAAATGG 1140
75    CTCAAAGAAA TTCTCGAATG TTCTCACCTA TTAACAGTTA TTAATATGGA AGAAGCTGGG 1200
GATGAAATGG TGAGCAATGC CATCTCCTAC GCTCTATACA AAGCCTTCAG CACCAAGTGG 1260
CAAGACAAGG ATAATGGGAA TGGGCAGCTG AAGCTTCTGC TGGAGTGGAA CCAGCTGGAC 1320
TTAGCCAATG ATGATCTTTT CACCAATGAC CGCGATGGG AGTCTGCTGA CCTTCAAGAA 1380
GTCATGTTTA CGGCTCTCAT AAAGGACAGA CCCAAGTTTG TCCGCTCTT TCTGGAGAAT 1440
GGCTTGAACC TACGGAAGTT TCTCACCAT GATGCTCTCA CTGAATCTT CTCCAACCAC 1500
80    TTCAGCACGC TTGTGTACCG GAATCTGCAG ATCGCCAAGA ATTCTATATA TGATGCCCTC 1560
CTCAGCTTTG TCTGGAATCT GGTGCGAAC TTCGGAAGAG GCTTCCGGAA GGAAGACAGA 1620
AATGCCGGGG ACGAGATGGA CATAGAATC CACGACGTGT CTCCTATTAC TCGGCACCCC 1680
CTGCAAGCTC TCTTCATCTG GGCCATTCTT CAGAATAAGA AGGAATCTC CAAAGTCATT 1740

```



TGGGAGCAGA CCAGGGGGCTG CACTCTGGCA GCCCTGGGAG CCAGCAAGCT TCTGAAGACT 1800  
 CTGGGCCAAG TGAAGAACGA CATCAATGCT GCTGGGGAGT CCGAGGAGCT GGCTAATGAG 1860  
 TACGAGACCC GGGCTGTGTA GCTGTTCAC T GAGTGTACCA GCAGCGATGA AGACTTGGCA 1920  
 GAACAGCTGC TGGTCTATTC CTGTGAAGCT TGGGGTGGAA GCAACTGTCT GGAGCTGGCG 1980  
 GTGGAGGCCA CAGACCAGCA TTTCATCGCC CAGCCTGGGG TCCAGAATTT TCTTTCTAAG 2040  
 CAATGGTATG GAGAGATTTC CCGAGACACC AAGAACTGGA AGATTATCCT GTGTCTGTTT 2100  
 ATTATACCCT TGGTGGGCTG TGGCTTTGTA TCATTAGGA AGAAACCTGT CGACAAGCAC 2160  
 AAGAAGCTGC TTTGGTACTA TGTGGCGTTC TTCACCTCCG CTTTCGTGGT CTTCTCCTGG 2220  
 AATGTGGTCT TCTACATCGC CTTCTCTCTG CTGTTTGCC T ACCTGCTGCT CATGGATTTC 2280  
 CATTTCGGTG CACACCCCCG CAGCTGGTCT CTGTACTCGC TGGTCTTTGT CCTCTTCTGT 2340  
 GATGAAGTGA GACAGTGGTA CGTAAATGGG GTGAATTATT TTACTGACCT GTGGAATGTG 2400  
 ATGGACACGC TGGGGCTTTT TTACTTCATA GCAGGAATTG TATTTTCGGT CCACCTCTCT 2460  
 AATAAAAGCT CTTTGTATTC TGGACGAGTC ATTTTCTGTC TGGACTACAT TATTTTCACT 2520  
 CTAAGATTGA TCCACATTTT TACTGTAAGC AGAAACTTAG GACCCAAGAT TATAATGCTG 2580  
 CAGAGGATGC TGGTGAAGAA GTTCTTCTTC CTGTTCTCT TGGCGGTGTG GATGGTGGCC 2640  
 TTTGGCGTGG CCAGGCAAGG GATCCTTAGG CAGAATGAGC AGCGCTGGAG GTGGATATTC 2700  
 CGTTCGGTCA TCTACGAGCC CTACCTGGCC ATGTTTCGGC AGGTGCCAG TGACGTGGAT 2760  
 GGTACCACGT ATGACTTTGC CCACTGCACC TTCACTGGGA ATGAGTCCAA GCCACTGTGT 2820  
 GTGGAGCTGA ATGAGCACAA CCTGCCCGG TCCCGGAGT GGATCACCAT CCCCTGGTGT 2880  
 TGCATCTACA TGGTTATCCA CAACATCCTG CTGGTCAACC TGCTGGTCCG CATGTTTGGC 2940  
 TACACGGTGG GCACCGTCCA GGAGAACAA T GACCAGGTCT GGAAGTTCCA GAGGTACTTC 3000  
 CTGGTGCAGG AGTACTGCAG CCGCCTCAAT ATCCCCCTCC CCTTCATCGT CTTCTGCTTAC 3060  
 TTCTACATGG TGGTGAAGAA GTGCTTCAAG TGTGTCTGCA AGGAGAAAAA CATGGAGTCT 3120  
 TCTGTCTGCT GTTTCAAAAA TGAAGACAA T GAGACTCTGG CATGGAGGGG TGTCTATGAAG 3180  
 GAAACTACC TTGTCAAGAT CAACACAAA GCCAACGACA CCTCAGAGGA AATGAGGCAT 3240  
 CGATTTAGAC AACTGGATAC AAAGCTTAAT GATCTCAAGG GTCTTCGAA AGAGATTGCT 3300  
 AATAAAATCA AATGA

Seq ID NO: 566 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MSFRAARLSM RNRNRDILDS TRTLYSSASR STDLSYSED LVNFIQANFK KRECVFETKD 60  
 SKATENVCKC GYAQSQHMEG TQINQSEKWN YKHTKEFPT DAFGDIQFET LGKKGKYLRL 120  
 SCDTDAEILY ELLTQHWHLK TPNLVISVTG GAKNFALKPR MRKIFSRLLY IAQSKGAWIL 180  
 TGGTHYGLMK YIGEVVRDNT ISRSSSEENIV AIGIAAWGMV SNRDTLIRNC DABGYFLAQY 240  
 LMDDFTRDPL YILDNNHNLH LLVDNGCHGH PTVEAKLRNQ LEKYISERTI QDSNYGGKIP 300  
 IVCFAQGGGK ETLKAINTSI KNKIPCVVVE GSGQIADVIA SLVEVEDALT SSAVKEKLVR 360  
 FLPRTVSRRLP EETESWIKW LKEILECSHL LTVIKMEEAG DEIVSNAISY ALYKAFSTSE 420  
 QDKDNWNGQL KLLLEWNLQD LANDEIFTND RRWESADLQE VMFTALIKDR PKFVRLFLEN 480  
 GLNLRKFLTH DVLTELFNSH FSTLVYRNLO IAKNSYNDAL LTFVWKLVAN FRRGFRKEDR 540  
 NGRDEMDIEL HDVSPITRHP LQALFIWAIL QNKKELSKVI WEQTRGCTLA ALGASKLLKT 600  
 LAKVNDINA AGESEELANE YETRAVELFT ECYSSDEDLA EQLLVYSCEA WGGSNCLLELA 660  
 VEATDQHRIA QPGVQNFLSK QWYGEISRDT KNWKIILCLF IIPLVGCGFV SFRKKPVDKH 720  
 KKLWYYVAF FTSPPVVFWS NVVFIYIAFL LFAFVLLMDF HSPVHPPELV LYSLVFVLFC 780  
 DEVRQVYVNG VNYFTDIWNV MDPLGLFYFI AGIVFRLHSS NKSSLYSGRV IFCLDYIIFT 840  
 LRLHIIFTVS RNLGPKIIML QRLMIDVFFF LFLFAVWMVA FGVARQGILR QNEQRWRWIF 900  
 RSVIYEPYLA MFGQVPSDVD GTTYDFAHCT FTGNESKPLC VELDEHNLP RPEWITIPLV 960  
 CIYMLSTNIL LVNLLVAMFG YTVGTQENN DQVWKQRYF LVQEYCSRLN IPFFPIVFAY 1020  
 FYMVVKKCFK CCCKEKNMES SVCCFKNEDN ETLAWEGVMK ENYLVKINTK ANDTSEMRH 1080  
 RFRQLDTKLN DLKGLLEKIA NKIK

Seq ID NO: 567 DNA sequence  
 Nucleic Acid Accession #: NM\_006911.1  
 Coding sequence: 1..558

1 11 21 31 41 51  
 ATGCCTCGCC TGTCTTGTG CCACCTGCTA GAATCTGTG TACTACTGAA CCAATTTTCC 60  
 AGAGCAGTCG CGGCCAAATG GAAGGACGAT GTTATTAAAT TATGCGGCGG CGAATTAGTT 120  
 CGCGGCGAGA TTGCCATTG CCGCATGAGC ACCTGGAGCA AAAGGTCTCT GAGCCAGGAA 180  
 GATGCTCCTC AGACACCTAG ACCAGTGGCA GAAATTGTAC CATCCTTCAT CAACAAAGAT 240  
 ACAGAAACTA TAATTATCAT GTTGAATTTC ATTGCTAATT TGCCACCGGA GCTGAAGGCA 300  
 GCCCTATCTG AGAGGCAACC ATCATTACCA GAGCTACAGC AGTATGTACC TGCAATTAAG 360  
 GATTCCAATC TTAGCTTTGA AGAATTTAAG AAACCTATTC GCAATAGGCA AAGTGAAGCC 420  
 GCAGACAGCA ATCCTTCAGA ATTAATAATC TTAGGCTTGG ATACTCATTC TCAAAAAAAG 480  
 AGACGACCCT ACGTGGCACT GTTTGAGAAA TGTTCCTTAA TTGGTTGTAC CAAAAGGTCT 540  
 CTGTCTAAAT ATTGCTGA

Seq ID NO: 568 Protein sequence  
 Protein Accession #: NP\_008842.1

1 11 21 31 41 51  
 MPRLFLFHLH EFCLLLNQFS RAVAAKWKDD VIKLCGRELV RAQIAICGMS TWSKRSLSQE 60  
 DAPQTRPPIA EIVPSPIKND TETIIIMLEF IANLPPELKA ALSERQPSLP ELQQYVPALK 120  
 DSNLSPFEFK KLIRNRQSEA ADSNPSELKY LGLDTHSQKK RRPYVALFEK CCLIGCTKRS 180  
 LAKYC

Seq ID NO: 569 DNA sequence  
 Nucleic Acid Accession #: XM\_036453.1

Coding sequence: 1..3978

1 11 21 31 41 51  
 5 ATGCTGCCCC TGTACCAGGA GGTGAAGCCC AACCCGCTGC AGGACGCGAA CCTCTGCTCA 60  
 CGCGTGTCT TCTGGTGGCT CAATCCCTTG TTTAAATTTG GCCATAAACG GAGATTAGAG 120  
 GAAGATGATA TGTATTACAGT GCTGCCAGAA GACCGCTCAC AGCACCTTGG AGAGGAGTTG 180  
 CAAGGGTTCT GGGATAAAGA AGTTTTAAGA GCTGAGAATG ACGCACAGAA GCCTTCTTTA 240  
 10 ACAAGAGCAA TCATAAAGTG TTACTGGAAA TCTTATTTAG TTTTGGGAAT TTTTACGTTA 300  
 ATTGAGGAAA GTGCCAAAGT AATCCAGCCC ATATTTTGGG GAAAAATTAT TAATTATTTT 360  
 GAAAAATTATG ATCCCATGGA TTCTGTGGCT TTGAACACAG CGTACGCCCTA TGCCACGGTG 420  
 CTGACTTTTT GCACGCTCAT TTTGGCTATA CTGCATCACT TATATTTTTA TCACGTTTCA 480  
 TGTGCTGGGA TGAGGTTACG AGTAGCCATG TGCCATATGA TTTATCGGAA GGCACCTTCG 540  
 15 CTTAGTAACA TGGCCATGGG GAAGACAACC ACAGGCCAGA TAGTCAATCT GCTGTCCAAT 600  
 GATGTGAACA AGTTTGATCA GGTGACAGTG TTCTTACACT TCCTGTGGGC AGGACCACTG 660  
 CAGCGCATCG CAGTGACTGC CCTACTCTGG ATGGAGATAG GAATATCGTG CCTGTCTGGG 720  
 ATGGCAGTTG TAATCATTTT CCTGCCCTTG CAAAGCTGTT TTTGGGAAGT GTTCTCATCA 780  
 CTGAGGAGTA AAATGCAAC TTTCACGGAT GCCAGGATCA GGACCATGAA TGAAGTTATA 840  
 ACTGGTATAA GGATAATAAA AATGTACGCC TGGGAAAAGT CATTTTCAAA TCTTATTACC 900  
 20 AATTGAGAA AGAAGAGAT TTCCAAGATT CTGAGAAAGT CCTGCCCTAG GGGGATGAAT 960  
 TTGGCTTCGT TTTTCAGTGC AAGCAAAATC ATCGTGTGTT TGACCTTCAC CACCTACGTG 1020  
 CTCCTCGGCA GTGTGATCAC AGCCAGCCGC GTGTTCTGTTG CAGTGACGCT GTATGGGGCT 1080  
 GTGCGGCTGA CGGTACCCCT CTTCTTCCCC TCAGCCATTG AGAGGGTGTG AGAGGCAATC 1140  
 25 GTACAGCATCC GAAGAATCCA GACCTTTTGT CTACTTGATG AGATATCACA GCGCAACCGT 1200  
 CAGCTGCCGT CAGATGTTAA AAAGATGGTG CATGTGCAGG ATTTTACTGC TTTTGGGAT 1260  
 AAGGCATCAG AGACCCCAAC TCTACAAGGC CTTTCCTTTA CTGTGAGACC TGGCGAATTG 1320  
 TTAGCTGTGG TCGGCCCGCT GGGAGCAGGG AAGTCATCAC TGTTAAGTGC CGTGCTCGGG 1380  
 GAATTGGCCC CAAGTACCGG GCTGGTCAGC GTGCATGGAA GAATTGCTTA TGTGTCTCAG 1440  
 30 CAGCCCTGGG TGTCTCGGG AACTCTGAGG AGTAATATTT TATTGGGAA GAAATACGAA 1500  
 AAGGAACGAT ATGAAAAGT CATAAAGGCT TGTGCTCTGA AAAAGGATTT ACAGCTGTTG 1560  
 GAGGATGGTG ATCTGACTGT GATAGGAGAT CGGGGAACCA CGCTGAGTGG AGGGCAGAAA 1620  
 GCACGGGTAA ACCTTGCAAG AGCAGTGTAT CAAGATGCTG ACATCTATCT CCTGGACGAT 1680  
 CCTCTCAGTG CAGTAGTGC GGAAGTTAGC AGACACTTGT TCGAAGCTGT TATTGTCAA 1740  
 35 ATTTTGCATG AGAAGATCAC AATTTTAGTG ACTCATCAGT TGCAGTACCT CAAAGCTGCA 1800  
 AGTCAGATTC TGATATTGAA AGATGGTAAA ATGGTGCAGA AGGGGACTTA CACTGAGTTC 1860  
 CTAAAACTCG GTATAGATTT TGGCTCCCTT TTAAGAAGG ATAATGAGGA AAGTGAACAA 1920  
 CCTCCAGTTC CAGGAACCTC CACACTAAGG AATCGTACCT TCTCAGAGTC TTCGGTTTGG 1980  
 TCTCAACAAT CTTCTAGACC CTCCTTGAAA GATGGTGCTC TGGAGAGCCA AGATACAGAG 2040  
 40 AATGTCCAGT TTACCATATC AGAGGAGAAC CGTTCGAAAG GAAAAGTTGG TTTTCAGGCC 2100  
 TATAAGAAAT ACTTCAGAGC TGGTGCTCAC TGGATTGTCT TCATTTTCTT TATTTCTCTA 2160  
 AACACTGCAG CTCAGGTTGC CTATGTGCTT CAAGATTGGT GGCTTTCATA CTGGGCAAC 2220  
 AAACAAGTA TGCTAAATGT CACTGTAAAT GGAGGAGGAA ATGTAACCGA GAAGCTAGAT 2280  
 CTTAACTGGT ACTTAGGAAT TTATTCAGGT TTAAGTGTAG CTACCGTTCT TTTTGGCATA 2340  
 45 GCAAGATCTC TATTGGTATT CTACGTCTTT GTTAACTCTT CACAAACTTT GCACAACAAA 2400  
 ATGTTTGAAT CAATTTCTGAA AGCTCCGGTA TTATTTCTTG ATAGAAATCC AATAGGAAGA 2460  
 ATTTTAAATC GTTTCTCAA AGACATTGGA CACTTGGATG ATTTGCTGCC GCTGACGTTT 2520  
 TTAGATTTC TCCAGACATT GCTACAAGTG GTTGGTGTGG TCTCTGTGGC TGTGGCCGTG 2580  
 50 ATTCCTTGGA TCGCAATACC CTTGGTTCCT CTTGGAATCA TTTTCATTTT TCTTCGGCGA 2640  
 TATTTTGGG AAACGTCAAG AGATGTGAAG CGCCTGGAAT CTACAACTCG GAGTCCAGTG 2700  
 TTTTCCCACT TGTCATCTTC TCTCCAGGGG CTCTGGACCA TCCGGGCATA CAAAGCAGAA 2760  
 GAGAGGTGTC AGGAACTGTT TGATGCACAC CAGGATTTAC ATTGAGAGGC TTGGTTCTTG 2820  
 TTTTGTACAA CGTCCCGCTG GTTCGCGCTC CGTCTGGATG CCATCTGTGC CATGTTTGTG 2880  
 55 ATCATCGTGT CCTTTGGGCT CCTGATTCTG GCAAAAACCTC TGGATGCCGG GCAGGTTGGT 2940  
 TTGGCAGTGT CCTATGCCCT CACGCTCATG GCGATGTTTC AGTGGTGTG TCGACAAAGT 3000  
 GCTGAAGTTG AGAATATGAT GATCTCAGTA GAAAGGGTCA TTGAATACAC AGACCTTGAA 3060  
 AAAGAGACAC CTTGGGAATA TCAGAAACGC CCACCAACAG CCTGGCCCCA TGAAGGAGTG 3120  
 ATAATCTTTG ACAATGTGAA CTTATGTAC AGTCCAGGTG GGCCTCTGGT ACTGAAGCAT 3180  
 CTGACAGCAC TCATTAATC ACAAGAAAAG GTTGGCATTG TGGGAAGAAC CGGAGCTGGA 3240  
 60 AAAAGTTCCC TCATCTCAGC CCTTTTGTAGA TTGTGAGAAC CCGAAGGTAA AATTGAGATT 3300  
 GATAAGATCT TGACAACTGA AATTGGACTT CACGATTTAA GGAAGAAAAT GTCAATCATA 3360  
 CCTCAGGAAC CTGTTTGTGT CACTGGAACA ATGAGGAAAA ACCTGGAATCC CTTTAATGAG 3420  
 CACACGGATG AGGAACTGTG GAATGCCTTA CAAGAGGTAC AACTTAAAGA AACCATTGAA 3480  
 GATCTTCTCTG GTAAATGGA TACTGAATTA GCAGAATCAG GATCCAATTT TAGTGTGGA 3540  
 65 CAAAGACAAC TGGTGTGCC TTGCCAGGCA ATTCTCAGGA AAAATCAGAT ATTGATTATT 3600  
 GATGAAGCGA CGGCAATAGT GGATCCAAGA ACTGATGAGT TAATACAAAA AAAATCCGG 3660  
 GAGAAATTG CCCACTGCAC CGTGTAAACC ATTGCACACA GATTGAACAC CATTATTGAC 3720  
 AGCGACAAGA TAATGTTTGT AGATTACAGA AGACTGAAAG AATATGATGA GCCGTATGTT 3780  
 TTGCTGCAAA ATAAAGAGAG CCTATTTTAC AAGATGGTGC AACAACTGGG CAAGGCAGAA 3840  
 70 GCCCGTGGCC TCACTGAAAC AGCAAAACAG GTATACTTCA AAAGAAATTA TCCACATATT 3900  
 GGTCACTAG ACCACATGGT TACAAACACT TCCAATGGAC AGCCCTCGAC CTTAACTATT 3960  
 TTCGAGACAG CACTGTGA

Seq ID NO: 570 Protein sequence  
 Protein Accession #: XP\_036453.1

1 11 21 31 41 51  
 80 MLPVYQEVKP NPLQDANLCS RVFFWNLNPL FKIGHKRRLE EDDMYSVLPE DRSQHLGEEL 60  
 QGFWDKEVLR AENDAQKPSL TRAIKICYWK SYLVLGIFTL IEESAKVIQ IFLGKIINYF 120  
 ENYDPMDSVA INTAYAYATV LTFCTLILAI LHHLYFYHVQ CAGMRLRVAM CHMIYRKALR 180  
 LSNMAMGKTT TQIIVNLLSN DVNKFQDQTV FLHFLWAGPL QAIIVTALLW MEIGISCLAG 240  
 MAVLIILLPL QSCFGLFSS LRSKTATFTD ARIRTMNEVI TGIRIKMYA WEKSFSNLIT 300  
 NLRKKBEISKI LRSSCLRGMN LASFFSASKI IVFVTFTTYV LLGSVITASR VFVAVTLYGA 360

VRLTDTLFFP SAIERVSEAI VSIRRIQTFL LLDEISQRNR QLPSDGKKMV HVQDFTAFWD 420  
 KASEPTTLQG LSFTVRPGLG LAVVGPVGAG KSSLSSAVLG ELAPSHGLVS VHGRYAYVSQ 480  
 QPWVFSGLTR SNILFGKKYE KERYEKVIKA CALKKDLQLL EDGDLTVIGD RGTTLGGGQK 540  
 ARVNLARAVY QDADTYLLDD PLSAVDAEVS RHLFELCICQ ILHEKITILV THQLQYLKAA 600  
 SQILILKDKG MVQKGTYTEF LKSGIDFGSL LKKDNEESEQ PPVPGTPTLR NRTFSESSVW 660  
 SQSSRRPSLK DGALESQDTE NVPVTLSEEN RSEGGVGFQA YKNYFRAGAH WIVFIFLILL 720  
 NTAAQVAVYL QDWLSYWAN KQSMNLNVTN GGGNVTEKLD LNWYLGIVSG LTVATVLFGI 780  
 ARSLLVFFYL VNSSQTLHNK MFESILKAPV LFFDRNPGR ILNRFSDIG HLDDLLPLTF 840  
 LDFIQTLLOV GVVSVAVAV IPWIAIPLVP LGIIFIFLRR YFLETSRDVK RLESTRSPV 900  
 FSHLSSSLQG LWTIRAYKAE ERCQELFDAH QDLHSEAWFL FLTTSRFAV RLDACAMFV 960  
 IIVAFGSLIL AKTLDAQVQG LALSIALTLM GMFQWCVRQS AEVENMMISV ERVIEYTDLE 1020  
 KEAPWEYQKR PPPAWPHEGV IIFDNVNFMY SPGGPLVLKH LTALIKSQEK VGIVGRTGAG 1080  
 KSSLISALFR LSEPEGKIWI DKILTTEIGL HDLRKKMSII PQEPVLFTGT MRKNLDPFNE 1140  
 HTDEELWNAL QEVQLKETIE DLPKMDTEL AESGSNFSVG QRQLVCLARA ILRKNQILII 1200  
 DEATANVDPR TDELIQKKIR EKFAHCTVLT IAHLNLTIID SDKIMVLDGS RLKEYDEPYV 1260  
 LLQNKESLFY KMQVQLGKAE AALTTETAKQ VYFKRNYPHI GHTDHMTNT SNGQPSTLTI 1320  
 FETAL

Seq ID NO: 571 DNA sequence  
 Nucleic Acid Accession #: AF07120  
 Coding sequence: 116..4093

	1	11	21	31	41	51	
25	GGACAGGCGT	GGCGGCCGGA	GCCCCAGCAT	CCCTGCTTGA	GGTCCAGGAG	CGGAGCCCGC	60
	GGCCACCGCC	GCCTGATCAG	CGCGACCCCG	GCCCGCGCCC	GCCCCGCCCC	GCAAGATGCT	120
	GCCCGTGTAC	CAGGAGGTGA	AGCCCAACCC	GCTGCAGGAC	GCGAACATCT	GCTCACGCGT	180
	GTTCCTCTGG	TGGCTCAATC	CCTTGTTTAA	AATTGGCCAT	AAACGGAGAT	TAGAGGAAGA	240
30	TGATATGTAT	TCAGTGCTGC	CAGAAGACCG	CTCACAGCAC	CTTGGAGAGG	AGTTGCAAGG	300
	GTTCCTGGAT	AAAGAAGTTT	TAAGAGCTGA	GAATGACGCA	CAGAAGCCTT	CTTTAACAAG	360
	AGCAATCATA	AAGTGTCTACT	GGAAATCTTA	TTTAGTTTGG	GGAATTTTAA	CGTTAATTTA	420
	GGAAGTGGCC	AAAGTAATCC	AGCCCATATT	TTTGGGAAAA	ATTATTAAAT	ATTTTGAATA	480
	TTATGATCCC	ATGGATTCTG	TGGCTTTGAA	CACAGCGTAC	GCCTATGCCA	CGGTGCTGAC	540
35	TTTTTGCACG	CTCATTTTGG	CTATACTGCA	TCACCTATAT	TTTTATCACG	TTCACTGTGC	600
	TGGGATGAGG	TTACGAGTAG	CCATGTGCCA	TATGATTAT	CGGAAGGCAC	TTCTGCTTAG	660
	TAACATGGCC	ATGGGGAAGA	CAACCACAGG	CCAGATAGTC	AATCTGCTGT	CCAATGATGT	720
	GAACAAAGTT	GATCAGGTGA	CAGTGTCTCT	ACACTTCTCT	TGGGCGAGGAC	CACTGCAGGC	780
	GATCGCAGTG	ACTGCCCTAC	TCTGGATGGA	GATAGGAATA	TCGTGCTCTG	CTGGGATGGC	840
40	AGTTCTAATC	ATTCTCTCTG	CCTTGCAAAG	CTGTTTGGG	AAGTTGTCT	CATCACTGAG	900
	GAGTAAACT	GCAACTTTCA	CGGATGCCAG	GATCAGGACC	ATGAATGAAG	TTATAACTGG	960
	TATAAGGATA	ATAAAAATGT	ACGCCTGGGA	AAAGTCATTT	TCAAATCTTA	TTACCAATTT	1020
	GAGAAAGAG	GAGATTTTGA	AGATTCTGAG	AAGTTCTGTC	CTCAGGAGGA	TGAATTTGGC	1080
	TTCTGTTTTT	AGTCAAGCA	AAATCATCGT	GTGTTGTACC	TTCAACCACT	ACGTGCTCCT	1140
	CGGCAGTGTG	ATCAGACGCA	GCCGCGTGT	CGTGGCAGTG	ACGCTGTATG	GGGCTGTGCG	1200
45	GCTGACGTTT	ACCTCTTCTT	TCCCCTCAGC	CATTGAGAGG	GTGTCAGAGG	CAATCGTCAG	1260
	CATCCGAAGA	ATCCAGACCT	TTTTGCTACT	TGATGAGATA	TCACAGCGCA	ACCGTCAGCT	1320
	GCCGTGACAT	GGTAAAGA	TGGTGATGT	GCAGGATTTT	ACTGCTTTT	GGGATAAGCG	1380
	ATCAGAGACC	CCAATCTTAC	AAGGCCTTTC	CTTTACTGTC	AGACTGGCG	AATGTGTAGC	1440
50	TGTGGTGGGC	CCCCGGGAG	CAGGGAAGTC	ATCACTGTTA	AGTGCCGTGC	TCGGGGAATT	1500
	GGCCCCAAGT	CACGGGCTGG	TCAGCGTGCA	TGGAAGAATT	GCCTATGTGT	CTCAGCAGCC	1560
	CTGGGTGTTC	TCGGGAACCT	TGAGGAGTAA	TATTTTATTT	GGGAAGAAAT	ATGAAAAGGA	1620
	ACGATATGAA	AAAGTCATAG	AGGCTTGTGC	TCTGAAAAAG	GATTACAGC	TGTTGGAGGA	1680
	TGGTGATCTG	ACTGTGATAG	GAGATCGGGG	AACCACGCTG	AGTGGAGGGC	AGAAAGCAGC	1740
55	GGTAAACCTT	GCAAGAGCAG	TGTATCAAGA	TGCTGACATC	TATCTCCTGG	ACGATCCTCT	1800
	CAGTGCAGTA	GATGCGGAAG	TAGCAGACA	CTGTGTTGAA	CTGTGTATTT	GTCAAATTTT	1860
	GCATGAGAAG	ATCACAATTT	TAGTGACTCA	TCAGTTGCAG	TACCTCAAAG	CTGCAAGTCA	1920
	GATTCTGATA	TTGAAAGATG	GTAAGATGGT	GCAGAAGGGG	ACTTACACTG	AGTTCTCTAA	1980
	ATCTGATATA	GATTTTGGCT	CCCTTTTAAA	GAAGGATAAT	GAGGAAAGTG	AACAACCTCC	2040
	AGTTCCAGGA	ACTCCACAC	TAAGGAATCG	TACCTTCTCA	GAGTCTTCGG	TTTGGTCTCA	2100
60	ACCAATCTCT	AGACCTCCT	TGAAAGATGG	TGCTCTGGAG	AGCCAAGATA	CAGAGAATGT	2160
	CCCGATTACA	CTATCAGAGG	AGAACCGTTC	TGAAGGAAAA	GTTGGTTTTC	AGGCTATATA	2220
	GAATTACTTC	AGAGCTGGTG	CTCACTGGAT	TGCTTTCATT	TTCTTATTC	TCCTAAACAC	2280
	TGCAGCTCAG	GTTGCCTATG	TGCTTCAAGA	TTGGTGGCTT	TCATACTGGG	CAACAAACA	2340
	AAGTATGCTA	AATGTCACTG	TAAATGGAGG	AGGAAATGTA	ACCGAGAAGC	TAGATCTTAA	2400
65	CTGGTACTTA	GGAATTTAAT	CAGGTTTAAC	TGTAGCTACC	GTTCTTTTTC	GCATAGCAAG	2460
	ATCTCTATTG	GTATTTCTACG	TCCTTGTATA	CTCTTACAAA	ACTTTGCACA	ACAAAATGTT	2520
	TGAGTCAATT	CTGAAAGCTC	CGGTATTATT	CTTTGATAGA	AATCCAATAG	GAAGAATTTT	2580
	AAATCGTTTT	TCCAAGACA	TTGGACACTT	GGATGATTTC	CTGCCGCTGA	CGTTTTTAGA	2640
	TTTCATCCAG	ACATTGCTAC	AAGTGGTTGG	TGTGGTCTCT	GTGGCTGTGG	CCGTGATTCC	2700
70	TTGGATCGCA	ATACCCCTGG	TTCCCTTGG	AATCATTTTC	ATTTTCTTTC	GGCGATATTT	2760
	TTTGAAGACG	TCAAGAGATG	TGAAGCGCCT	GGAATCTACA	ACTCGGAGTC	CAGTGTTTTC	2820
	CCACTTGTCA	TCTTCTCTCC	AGGGGCTCTG	GACCATCCGG	GCATACAAAG	CAGAAGAGAG	2880
	GTGTCAGGAA	CTGTTTGATG	CACACCAGGA	TTTACATTCA	GAGGCTTGGT	TCTTGTTTTT	2940
	GACAAAGTCC	CGCTGGTTCC	CGTCCGCTCT	GGATGCCATC	TGTGCCATGT	TTGTCATCAT	3000
75	CGTTCGCTTT	GGGTCCCTGA	TTCTGGCAAA	AACCTCTGGT	GCCGGGCGAG	TTGGTTTGGC	3060
	ACTGTCTCAT	GCCTCTCAGC	TCATGGGGAT	GTTCAGTGG	TGTGTTTCAG	AAAGTGCTGA	3120
	AGTTGAGAAT	ATGATGATCT	CAGTAGAAG	GGTCATTGAA	TACACAGACC	TTGAAAAGAA	3180
	AGCACCTTGG	GAATATCAGA	AACGCCACCC	ACCAGCCTGG	CCCCATGAAG	GAGTGATAAT	3240
	CTTTGACAA	GTGAACCTCA	TGTACAGTCC	AGGTGGGCTC	CTGGTACTGA	AGCATCTGAC	3300
80	AGCATCATCT	AAATCACAAG	AAAAGGTTGG	CATTGTGGGA	AGAACCGGAG	CTGGAAAAAG	3360
	TTCCCTCATT	TCAGCCCTTT	TTAGATTGTC	AGAACCCGAA	GGTAAATTTT	GGATTGATAA	3420
	GATCTTGACA	ACTGAAATTT	GACTTCACGA	TTTAAGGAAG	AAAATGTCAA	TCATACCTCA	3480
	GGAAACCTGTT	TTGTTCACTG	GAACAATGAG	GAAAAACCTG	GATCCCTTTA	AGGAGCACAC	3540
	GGATGAGGAA	CTGTGGAATG	CCTTACAAGA	GGTACAACTT	AAAGAAACCA	TTGAAGATCT	3600

TCCTGGTAAA ATGGAATCTG AATTAGCAGA ATCAGGATCC AATTTTAGTG TTGGACAAAG 3660  
 ACAACTGGTG TGCCTTGCCA GGGCAATTCT CAGGAAAAAT CAGATATTGA TTATTGATGA 3720  
 AGCGACGGCA AATGTGGATC CAAGAACTGA TGAGTTAATA CAAAAAATAA TCCGGGAGAA 3780  
 ATTTGCCACG TGCACCGTGC TAACCATTCG ACACAGATG AACACCATTA TTGACAGCGA 3840  
 CAAGATAATG GTTTTAGATT CAGGAAGACT GAAAGAATAT GATGAGCCGT ATGTTTGTCT 3900  
 GCAAAATAAA GAGAGCCTAT TTTACAAGAT GGTGCAACAA CTGGGCAAGG CAGAAGCCGC 3960  
 TGCCCTCACT GAAACAGCAA AACAGGTATA CTTCAAAAGA AATTATCCAC ATATTGGTCA 4020  
 CACTGACCAC ATGGTTACAA ACACCTCCAA TGGACAGCCC TCGACCTTAA CTATTTTCGA 4080  
 GACAGCACTG TGAATCCAAC CAAAATGTCA AGTCCGTTCC GAAGGCATTT TCCACTAGTT 4140  
 TTTGGACTAT GTAAACCACA TTGTACTTTT TTTTACTTTG GCAACAAATA TTTATACATA 4200  
 CAAGATGCTA GTTCATTGTA ATATTTCTCC C

Seq ID NO: 572 Protein sequence  
 Protein Accession #: AAC27076.1

1 11 21 31 41 51  
 | | | | |  
 MLPVYQEVKP NPLQDANICS RVFFFWLNLPL FKIGHKRRLE EDDMYSVLPE DRSQHLGEEL 60  
 QGFWDKEVLR AENDAQKPSL TRAIKCYWK SYLVLGIFTL IEESAKVIQF IFLGKIINYF 120  
 ENYDPMDSVA LNTAYAYATV LTFCTLILAI LHHLYFYHVQ CAGMRLRVAM CHMIYRKALR 180  
 LSNMAMGKTT TGQIVNLLSN DVNKFQDQTV FLHFLWAGPL QAIIVTALLW MEIGISCLAG 240  
 MAVLIILLPL QSCFGLFSS LRSKTATFTD ARIRTMNEVI TGIRIIKMYA WEKSFSNLIT 300  
 NLRKKEISKI LRSSCLRGMN LASFFSASKI IVFVTFTTYV LLGSVITASR VFAVATLYGA 360  
 VRLTVTLFFP SAIERVSEAI VSIRRIQTFL LLDEISQRNR QLPDGGKMMV HVQDFTAFWD 420  
 KASEPTLQGL LSFTVRPGEL LAVVGPVGAG KSSLLSAVLG ELAPSHGLVS VHGRYAVVSQ 480  
 QPWVFSGTLR SNILFGKKYE KERYEKVIA CALKKDLQLL EDGDLTVIGD RGTTLSSGQK 540  
 ARVNLARAVY QDADIYLLD PLSAVDAEVS RHLFELCICQ ILHEKITILV THQLQYLKAA 600  
 SQILILKDKG MVQKGLTYTFE LKSGIDFGSL LKKNDEESQ PPVPGTPTLR NRTFSESSVW 660  
 SQSSSRPSLK DGALESQDTE NVPVTLSEEN RSEGVGFOA YKNYFRAGAH WIVFIFLILL 720  
 NTAAQVAYVL QDWLWLYWAN QKSMNLVTVN GGGNVTEKLD LNWYLGIVSG LTVATVLPFI 780  
 ARSLLVFVYL VNSSQTLHNK MFESILKAPV LFFDRNPIGR ILNRFKDIG HLDLPLPLTF 840  
 LDFIQTLQV VGVVSVAVAV IPWIAIPLVP LGIIFIFLRR YFLETSRDVK RLESTRSPV 900  
 FSHLSSSLQG LWTIRAYKAE ERCQELFDAH QDLHSEAWFL FLTTSRWFAV RLDAICAMFV 960  
 IIVAFGSLIL AKTLIDAGVQG LALSIALTLM GMFQWCVRQS AEVENMMISV ERVIEYTDLE 1020  
 KEAPWEYQKR PPPAWPHEGV IIFDNVNFMY SPGGPLVLKH LTALIKSQEK VGIVGRTGAG 1080  
 KSSLISALFR LSEPEGKIWI DKILTTEIGL HDLRKKMSII PQEPVLFTGT MRKNLDPFKE 1140  
 HTDEELWNAL QEVQLKETIE DLPKGMDEL AESGSNFSVG QRQLVCLARA ILRKNQILII 1200  
 DEATANVDPR TDELIQKIR EKFAHCTVLT IAHLRLNTIID SDKIMVLDSE RLKEYDEPYV 1260  
 LLQNKESLFY KMVQQLGKAE AALTTETAKQ VYFKRNYPHI GHTDHMTNT SNGQPSTLTI 1320  
 FETAL

Seq ID NO: 573 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1365

1 11 21 31 41 51  
 | | | | |  
 ATGGAATCAA TCTCTATGAT GGGGAAGCCCT AAGAGCCTTA GTGAAACTTG TTTACCTAAT 60  
 GGCATAAATG GTATCAAAGA TGCAAGGAAG GTCACGTAG GTGTGATTGG AAGTGGAGAT 120  
 TTTGCCAAAT CCTTGACCAT TCGACTTATT AGATGCGGCT ATCATGTGGT CATAGGAAGT 180  
 AGAAATCCTA AGTTGTCTTC TGAATTTTCT CCTCATGTGG TAGATGTCAC TCATCATGAA 240  
 GATGCTCTCA CAAAAACAAA TATAATATTT GTTGCTATAC ACAGAGAACA TTATACCTCC 300  
 CTGTGGGACC TGAGACATCT GCTGTGGGT AAAATCCTGA TTGATGTGAG CAATAACATG 360  
 AGGATAAACC AGTACCAGA ATCCAATGCT GAATATTTGG CTTTATTATT CCCAGATTCT 420  
 TTGATTGTCA AAGGATTAA TGTGTCTCA GCTTGGGCAC TTCAGTTAGG ACCTAAGGAT 480  
 GCCAGCCGGC AGGTTTATAT ATGCAGCAAC AATATTCAAG CGCGACAACA GGTATTGAA 540  
 CTTGCCCGCC AGTTGGAATT CATTCCTATT GACTTGGGAT CCTTATCATC AGCCAGAGAG 600  
 ATTGAAAATT TACCCCTACG ACTCTTTACT CTCTGGAGAG GGCCAGTGGT GGTAGCTATA 660  
 AGCTTGGCCA CATTTTCTTT CCTTTATTCC TTTGTCAGAG ATGTGATTCA TCCATATGCT 720  
 AGAAACCAAC AGAGTGACTT TTACAAAATT CCTATAGAGA TTGTGAATAA AACCTTACCT 780  
 ATAGTTGCCA TTACTTTGCT CTCCTAGTA TACCTCGCAG GTCTCTGGC AGCTGCTTAT 840  
 CAACTTTATT ACGGCACCAA GTATAGGAGA TTTCCACCTT GGTGGAAC CTGTTACAG 900  
 TGTAGAAAAC AGCTTGATT ACTAAGTTT TTCTTCGCTA TGGTCCATGT TGCCTACAGC 960  
 CTCTGCTTAC CGATGAGAAG GTCAGAGAGA TATTTGTTTC TCAACATGGC TTATCAGCAG 1020  
 GTTCATGCAA ATATTGAAAA CTCTTGAAT GAGGAAGAAG TTTGGAGAAT TGAATGTAT 1080  
 ATCTCCTTTG GCATAATGAG CCTTGGCTTA CTTTCCCTCC TGGCAGTCAC TTCTATCCCT 1140  
 TCAGTGAGCA ATGCTTTAAA CTGGAGAGAA TTCAGTTTAA TTCAGTCTAC ACTTGGATAT 1200  
 GTCGCTCTGC TCATAAGTAC TTTCCATGTT TTAATTTATG GATGGAACG AGCTTTTGAG 1260  
 GAAGAGTACT ACAGATTTTA TACACCACCA AACTTTGTTT TTGCTCTGT TTTGCCCTCA 1320  
 ATTGTAATTC TGGATCTTTT GCAGCTTTGC AGATACCCAG ACTGA

Seq ID NO: 574 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 MESISMGGSP KSLSETCLPN GINGIKDARK VTGVIGSGD FAKSLTIRLI RCGYHVIVGS 60  
 RNPKFASEFP PHVVDVTHHE DALTKNIIIF VAIHREHYTS LWDLRHLLVG KILIDVSNM 120  
 RINQYPSNA EYLASFPPDS LIVKGFNVVS AWALQLGPKD ASRQVYICSN NIQARQQVIE 180  
 LARQLNFIPI DLGSLSSARE IENLPLRLFT LWRGPVVVAI SLATFFFLYS FVRDVIHPYA 240  
 RNQSDIFYKI PEIVNKTLP IVAITLLSLV YLAGLLAAAY QLYYGTQYRR FPPWLETWLQ 300  
 CRKQLGLLSF FFAFVHVAYS LCLPMRRSER YLFLNMAYQQ VHANIENSWN BEEVWRIEMY 360  
 ISFGIMSLGL LSLLAVTSIP SVSNALNWRE FSFIQSTLGY VALLISTFHV LIYGWKRAFE 420  
 BEYRYFTFP NFVLAIVLPS IVILDLLQLC RYPD

Seq ID NO: 575 DNA sequence  
Nucleic Acid Accession #: NM\_001873.1  
Coding sequence: 3..1721

5  
10  
15  
20  
25  
30  
35  
40  
45  
50

1	11	21	31	41	51	
AAATGGCGTG	CCCGTCTCTC	CGCCGGCCCC	CTGCCTCGCA	GTGGTTTCTC	CTGCAGCTCC	60
CCTGGGCTCC	GCGGCCAGTA	GTGCAGCCCG	TGGAGCCGCG	GCTTTGCCCG	TCTCCTCTGG	120
GTGGCCCCAG	TGCGCGGGCT	GACACTCAT	CAGCCGGGGA	AGGTGAGGCG	AGTAGAGGCT	180
GGTGCAGAAC	TGCGCGCCCC	CAGCAGCGCC	GGCGGGCTAA	GCCACAGGGC	GGGCAGACAA	240
AAGAGGCCGC	CGCGGTAGGA	AGGCACGGCC	GGCGGGCGCG	GAGCGCAGCG	ATGGCCGGGC	300
GAGGGGGCAG	CGCGGTGCTG	GCTCTGTGCG	GGGCACTGGC	TGCCTGCGGG	TGGCTCCTGG	360
GCGCCGAAGC	CAGGAGCCCC	GGGGCGCCCG	CGCGGGGCAT	GAGGCGGCGC	CGGCGGCTGC	420
AGCAAGAGGA	CGGCATCTCC	TTCAGTACC	ACCCTACCC	CGAGCTGCGC	GAGGCGCTCG	480
TGTCCGTGTG	GCTGCAGTGC	ACCGCCATCA	GCAGGATTTA	CACGGTGGGG	CGCAGCTTCG	540
AGGGCCGGGA	GCTCCTGGTC	ATCGAGCTGT	CCGACAACCC	TGGCGTCCAT	GAGCCTGGTG	600
AGCTGAATT	AAAATACATT	GGGAATATGC	ATGGGAATGA	GGCTGTTGGA	CGAGAACTGC	660
TCATTTTCTT	GGCCAGTAC	CTATGCAACG	AATACCAGAA	GGGGAACGAG	ACAATTGTCA	720
ACCTGATCCA	CAGTACCCGC	ATTCACATCA	TGCCTTCCCT	GAACCCAGAT	GGCTTTGAGA	780
AGGCAGCGTC	TCAGCCTGGT	GAACTCAAGG	ACTGGTTTGT	GGGTCGAAGC	AATGCCCAGG	840
GAATAGATCT	GAACCGGAAC	TTTCCAGACC	TGGATAGGAT	AGTGTACGTG	AATGAGAAAG	900
AAGGTGGTCC	AAATAATCAT	CTGTTGAAAA	ATATGAAGAA	AATTGTGGAT	CAAAACACAA	960
AGCTTGCTCC	TGAGACCAAG	GCTGTCAATC	ATTGGATTAT	GGATATTCCCT	TTTGTGCTTT	1020
CTGCCAATCT	CCATGGAGGA	GACCTTGTGG	CCAATTATCC	ATATGATGAG	ACGCGGAGTG	1080
GTAGTGCTCA	CGAATACAGC	TCCTCCCCAG	ATGACGCCAT	TTTCCAAAGC	TTGGCCCGGG	1140
CATACTCTTC	TTTCAACCCG	GCCATGTCTG	ACCCCAATCG	GCCACCATGT	CGCAAGAAATG	1200
ATGATGACAG	CAGCTTTGTA	GATGGAACCA	CCAACGGTGG	TGCTTGGTAC	AGCGTACCTG	1260
GAGGGATGCA	AGACTTCAAT	TACCTTAGCA	GCAACTGTTT	TGAGATCACC	GTGGAGCTTA	1320
GCTGTGAGAA	GTTCACCACT	GAAGAGACTC	TGAAGACCTA	CTGGGAGGAT	AACAAAAACT	1380
CCCTCATTAG	CTACCTTTAG	CAGATACACC	GAGGAGTTAA	AGGATTGTCT	CGAGACCTTC	1440
AAGGTAACCC	AATTGCGAAT	GCCACCATCT	CCGTGGAAGG	AATAGACCAC	GATGTTACAT	1500
CCGCAAAAGG	TGGTGATTAC	TGGAGATTGC	TTATACCTGG	AAACTATAAA	CTTACAGCCT	1560
CAGCTCCAGG	CTATCTGGCA	ATAACAAAGA	AAGTGGCAGT	TCCTTACAGC	CCTGCTGCTG	1620
GGGTTGATTT	TGAAGTGGAG	TCATTTTCTG	AAAGGAAAGA	AGAGGAGAAG	GAAGAAATGA	1680
TGGAATGGTG	GAAATGATG	TCAGAAACTT	TAAATTTTTA	AAAAGGCTTC	TAGTTAGCTG	1740
CTTTAAATCT	ATCTATATAA	TGTAGTATGA	TGTAATGTGG	TCTTTTTTTT	AGATTTTGTG	1800
CAGTTAATAC	TTAACAATGA	TTTATTTTTT	AATCATTTAA	ATATTAATCA	ACTTTCCTTA	1860
AAATAAATAG	CCCTCTTAGG	AAAAATATAA	GAACTTGATA	TATTTTCATC	TCTTATATAG	1920
TATTCATTTT	CCTACCTATA	TTACACAAAA	AAGTATAGAA	AAGATTAAAG	TAATTTTGCC	1980
ATCCTAGGCT	AAAATGCAAT	ATTCTCGGTA	TTATTTACAA	TGCAGAATTT	TTTGAGTAAT	2040
TCTAGCTTTC	AAAAATTAGT	GAAGTTCTTT	TACTGTAATT	GGTGACAATG	TCACATAATG	2100
AATGCTATTG	AAAAGGTAA	CAGATACAGC	TCGGAGTTGT	GAGCACTCTA	CTGCAAGACT	2160
TAAATAGTTC	AGTATAAATT	GTCGTTTTTT	TCTTGTGCTG	ACTAACTATA	AGCATGATCT	2220
TGTTAATGCA	TTTTTGATGG	GAAGAAAAGG	TACATGTTTA	CAAAGAGGTT	TTATGAAAAG	2280
AATAAAAAAT	GACTTCTTGC	TTGTACATAT	AGGAGCAATA	CTATTATATT	ATGTAGTCCG	2340
TTAACACTAC	TTAAAGTATT	AGGGTTTTCT	CTTGGTTGTA	GAGTGGCCCA	GAATTGCATT	2400
CTGAATGAAT	AAAGGTTAAA	AAAAATCCCC	CAGTGAAAAA	AAA		

Seq ID NO: 576 Protein sequence  
Protein Accession #: NP\_001864.1

55  
60  
65

1	11	21	31	41	51	
MAGRGSALL	ALCGALAACG	WLLGAEAEQEP	GAPAAAGMRRR	RRLQEDGIS	FEYHRYPELR	60
EALVSVWLQC	TAISRIYTVG	RSFEGRELLV	IELSDNPGVH	EPGEPEFKYI	GNMHGNEAVG	120
RELLIFLAQY	LCNEYQKNGE	TIVNLIHSTR	IHIMPSLNP	GFEKAASQPG	ELKDWFVGRS	180
NAQGDILNRR	FPDLRIYVY	NEKEGGPNNH	LLKNMKIIVD	QNTKLAPETK	AVIHWIMDIP	240
FVLSANLHGG	DLVANYPYDE	TRSGSAHEYS	SSPDDAIFQS	LARAYSSFNP	AMSDPNRPPC	300
RKNDSSSFF	DTTNGGAWY	SVPGMQDEFN	YLSNCFEIT	VELSCEKFPF	EETLKYWED	360
NKNSLISYLE	QIHRGVKGFV	RDLQGNPIAN	ATISVEGIDH	DVTSKDGIDY	WRLLIPGNYK	420
LTASAPGYLA	ITKKVAVPYS	PAAGVDFELE	SFSEKKEEEK	EELMEWKKMM	SETLNF	

Seq ID NO: 577 DNA sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..933

70  
75  
80

1	11	21	31	41	51	
ATGTGCAGCA	ATGGACGGTG	CATCCCGGGC	GCCTGGCAGT	GTGACGGGCT	GCCTGACTGC	60
TTGCAACAAG	GTGATGAGAA	GGAGTGCCCC	AAGGCTAAGT	CGAAATGTGG	CCCGACCTTC	120
TTCCCTGTGT	CCAGCGGCAT	CCATTGCATC	ATTGGTTCGT	TCCCGTGCAA	TGGGTTTGAG	180
GACTGTCCCG	ATGGCAGCGA	TGAAGAGAAC	TGCACAGCAA	ACCCTCTGCT	TTGCTCCACC	240
GCCCCGTACC	ACTGCAAGAA	CGGCCCTCTG	ATTGACAAGA	GCTTCATCTG	CGATGGACAG	300
AATAACTGTC	AAGACAACAG	TGATGAGGAA	AGCTGTGAAA	GTTCTCAAGA	ACCCGGCAGT	360
GGGCAAGTGT	TTGTGACTTC	AGAGAACCAA	CTTGTGTATT	ACCCAGCAT	CACCTATGCC	420
ATCATCGGCA	GTCCTGTCAT	TTTGTGCTG	GTGGTGGCCC	TGCTGGCACT	GGTCTTGAC	480
CACGACGGCA	AGCGGAACAA	CCTCATGACG	CTGCCCGTGC	ACCGGCTGCA	GCACCCTGTG	540
CTGCTGTCCC	GCTCTGGTGT	CCTGGACCC	CCCCACCAT	GCAACGTGAC	CTACAACGTC	600
AATAATGGCA	TCCAGTATGT	GGCCAGCCAG	GCGGAGCAGA	ATGCGTCGGA	AGTAGGCTCC	660
CAACCTCTCT	ACTCCGAGGC	CTTGCTGGAC	CAGAGGCTTG	CGTGGTATGA	CCTTCTCCA	720
CCGCCCTACT	CTTCTGACAC	GGAATCTCTG	AACCAAGCCG	ACCTGCCCCC	CTACCGCTCC	780
CGGTCCGGGA	GTGCCAACAG	TGCCAGCTCC	CAGGCAGCCA	GCAGCTCTCT	GAGCGTGGAA	840
GACACGAGCC	ACAGCCCGGG	GCAGCCTGGC	CCCCAGGAGG	GCATGCTGTA	GCCCCAGGAC	900

TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 578 Protein sequence  
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MCSNGRCIPG	AWQCDGLPDC	FDKSDEKECP	KAKSKCGPTF	PPCASGIHCI	IGRFRNGFE	60
DCPDGSDENQ	CTANPLLCST	ARYHCKNGLC	IDKSFICDGQ	NNCQDNSDEE	SCESSQEPGS	120
GQVFTVSENQ	LVVYPSITYA	IIGSSVIFVL	VVALLALVLH	HQRKRNNLMT	LPVHRLQHPV	180
LLSRLVVLHD	PHHCNVTYNV	NNGIQYVASQ	AEQNASEVGS	PPSYSEALLD	QRPAWYDLFP	240
PPYSSDTESL	NQADLPYPYRS	RSGSANSASS	QAASSLLSVE	DTSHSPGQPG	PQEGTAEPRD	300
SEPSQGTEEV						

Seq ID NO: 579 DNA sequence  
Nucleic Acid Accession #: AF179274.1  
Coding sequence: 1..1125

1	11	21	31	41	51	
ATGGTGCTGT	GGGAGTCCCC	GCGGCAGTGC	AGCAGCTGGA	CACCTTTCGA	GGGCTTTTGC	60
TGGCTGCTGC	TGCTGCCCCG	CATGCTACTC	ATCGTAGCCC	GCCCGGTGAA	GCTCGCTGCT	120
TTCCCTACCT	CCTTAAGTGA	CTGCCAAACG	CCCACCGGCT	GGAATTGCTC	TGGTTATGAT	180
GACAGAGAAA	ATGATCTCTT	CCTCTGTGAC	ACCAACACCT	GTAATTTTGA	TGGGGAATGT	240
TTAAGAATTG	GAGACACTGT	GACTTGCGTC	TGTCAGTTCA	AGTGCAACAA	TGACTATGTG	300
CCTGTGTGTG	GCTCCAATGG	GGAGAGCTAC	CAGAATGAGT	GTTACCTGCG	ACAGGCTGCA	360
TGCAAAACAGC	AGAGTGAGAT	ACTTGTGGTG	TCAGAAGGAT	CATGTGCCAC	AGATGCAGGA	420
TCAGGATCTG	GAGATGGAGT	CCATGAAGGC	TCTGGAGAAA	CTAGTCAAAA	GGAGACATCC	480
ACCTGTGATA	TTTGCCAGTT	TGGTGACGAA	TGTGACGAAG	ATGCCGAGGA	TGTCCTGGTG	540
GTGTGTAATA	TTGACTGTTC	TCAAAACCAAC	TTCAATCCCC	TCTGCGCTTC	TGATGGGAAA	600
TCTTATGATA	ATGCATGCCA	AATCAAAGAA	GCATCGTGTC	AGAAACAGGA	GAAAATTGAA	660
GTCATGTCTT	TGGGTCGATG	TCAAGATAAC	ACAACCTACAA	CTACTAAGTC	TGAAGATGGG	720
CATTATGCAA	GAACAGATTA	TGCAGAGAAT	GCTAACAAAT	TAGAAGAAAG	TGCCAGAGAA	780
CACCACATAC	CTTGTCCCGA	ACATTACAA	GGCTTCTGCA	TGCATGGGAA	GTGTGAGCAT	840
TCTATCAATA	TGCAGGAGCC	ATCTTGCAAG	TGTGATGCTG	GTTTACTTGG	ACAACACTGT	900
GAAAAAAGG	ACTACAGTGT	TCTATACGTT	GTTCCCGGTC	CTGTACGATT	TCAGTATGTC	960
TTAATCGCAG	CTGTGATTGG	AACAATTGAG	ATTGCTGTCA	TCTGTGTGGT	GGTCTCTGTC	1020
ATCACAGGA	AATGCCCCAG	AAGCAACAGA	ATTCACAGAC	AGAAGCAAAA	TACAGGGCAC	1080
TACAGTTCAG	ACAATACAAC	AAGAGCGTCC	ACGAGGTTAA	TCTGA		

Seq ID NO: 580 Protein sequence  
Protein Accession #: NP\_057276.2

1	11	21	31	41	51	
MVLWESPRQC	SSWTLCEGFC	WLLLLPVMML	IVARPVKLAA	FPTSLSDCQT	PTGWNCSGYD	60
DRENDLFLCD	TNTCKFDGEC	LRIGDTVTCV	CQFKCNNDYV	PVCGSNGESY	QNECYLRQAA	120
CKQQSEILVV	SEGSCATDAG	SGSGDGVHEG	SGETSQKETS	TCDICQFGAE	CDEDAEDVWC	180
VCNIDCSQTN	FNPLCASDGG	SYDNACQIKE	ASCQKQEKIE	VMSLGRQCDN	TTTTTKSEDG	240
HYARTDYAEN	ANKLEESARE	HHI PCPEHYN	GFCMHGKCEH	SINMQEPSCR	CDAGYTQGH	300
EKKDYSVLVY	VPGEVRFQYV	LIAAVIGTIQ	IAVICVVVLC	ITRKCPRSNR	IHRQKQNTGH	360
YSSDNTTRAS	TRLI					

Seq ID NO: 581 DNA sequence  
Nucleic Acid Accession #: S78203.1  
Coding sequence: 1..2190

1	11	21	31	41	51	
ATGAATCCTT	TCCAGAAAAA	TGAGTCCAAG	GAAACTCTTT	TTTACCTGT	CTCCATTGAA	60
GAGGTACCAC	CTCGACCACC	TAGCCCTCCA	AAGAAGCCAT	CTCCGACAAT	CTGTGGCTCC	120
AACATATCCAC	TGAGCATTGC	CTTCATTGTG	GTGAATGAAT	TCTGCGAGCG	CTTTCTCTAT	180
TATGGAATGA	AAGCTGTGCT	GATCCTGTAT	TTCCTGTATT	TCCTGCACTG	GAATGAAGAT	240
ACCTCCACAT	CTATATACCA	TGCCTTCAGC	AGCCTCTGTT	ATTTTACTCC	CATCCTGGGA	300
GCAGCCATTG	CTGACTCGTG	GTTGGGAAAA	TTCAAGACAA	TCATCTATCT	CTCCTTGGTG	360
TATGTGCTTG	GCCATGTGAT	CAAGTCCTTG	GGTGCCCTTAC	CAATACTGGG	AGGACAAGTG	420
GTACACACAG	TCCTATCATT	GATCGGCCTG	AGTCTAATAG	CTTTGGGGAC	AGGAGGCATC	480
AAACCCTGTG	TGGCAGCTTT	TGGTGGAGAC	CAGTTTGAAG	AAAAACATGC	AGAGGAACGG	540
ACTAGATACT	TCTCAGTCTT	CTACCTGTCC	ATCAATGCAG	GGAGCTTGAT	TTCTACATTT	600
ATCACACCCA	TGCTGAGAGG	AGATGTGCAA	TGTTTTGGAG	AAGACTGCTA	TGCATTGGCT	660
TTTGGAGTTC	CAGGACTGCT	CATGTAATT	GCACTTGTTG	TGTTTGCAAT	GGGAAGCAAA	720
ATATACAATA	AACCAACCCC	TGAAGGAAAC	ATAGTGGCTC	AAGTTTTCAA	ATGTATCTGG	780
TTTGTCTATT	CCAATCGTTT	CAAGAACCGT	TCTGGAGACA	TTCCAAGCG	ACAGCACTGG	840
CTAGACTGGG	CAGCTGAGAA	ATATCCAAG	CAGCTCATT	TGGATGTAAA	GGCACTGACC	900
AGGGTACTAT	TCCTTTATAT	CCCATTGCC	ATGTTCTGGG	CTCTTTTGA	TCAGCAGGGT	960
TCAGGATGGA	CTTTGCAAGC	CATCAGGATG	AATAGGAATT	TGGGGTTTTT	TGTGCTTCAG	1020
CCGACACAGA	TGCAGGTTCT	AAATCCCTTT	CTGGTCTTTA	TCTTCATCCC	GTTGTTTGAC	1080
TTTGTCTATT	ATCGTCTGGT	CTCCAAGTGT	GGAATTAAC	TCTCATCACT	TAGGAAAAATG	1140
GCTGTTGGTA	TGATCCTAGC	GTGCCCTGGCA	TTTGCACTTG	CGGCAGCTGT	AGAGATAAAA	1200
ATAAATGAAA	TGGCCCCCAG	CCAGTCAGGT	CCCCAGGAGG	TTTTCTTACA	AGTCTTGAAT	1260
CTGGCAGATG	ATGAGGTGAA	GGTGACAGTG	GTGGGAAATG	AAAACAATTC	TCTGTTGATA	1320
GAGTCCATCA	AATCCTTTCA	GAAAACACCA	CACATTTC	AACCTGCACCT	GAAAACAAAA	1380
AGCCAGGATT	TTCACTTCCA	CCTGAAATAT	CACAAATTTG	CTCTCTACAC	TGAGCATTCT	1440
GTGCAGGAGA	AGAACTGGTA	CAGTCTTGTC	ATTCGTGAAG	ATGGGAACAG	TATCTCCAGC	1500

ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGGT 1560  
 AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT 1620  
 GAAGACTATG GTGTGTCTGC TTATAGAAGT GTGCAAGAG GAGAATACCC TGCACTGCAC 1680  
 TGTAGAACAG AAGATAAGAA CTTTCTCTCG AATTGGGTC TTCTAGACTT TGGTGCAGCA 1740  
 TATCTGTTTG TTATTAATAA TAACACCAAT CAGGGTCTTC AGGCCTGGAA GATTGAAGAC 1800  
 ATTCCAGCCA AAAAAATGTC CATTGCGTGG CAGCTACAC AATATGCCCT GGTACAGCT 1860  
 GGGGAGGTCA TGTTCTCTGT CACAGGTCTT GAGTTTTCTT ATTCTCAGGC TCCCTCTAGC 1920  
 ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCGTG 1980  
 CTTGTTGTGG CACAGTCTAG TGGCCTGGTA CAGTGGGCGG AATTCATTTT GTTTTCCTCG 2040  
 CTCCTGCTGG TGATCTGCCT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAAG 2100  
 ACAGAGGATA TGCGGGGTCC AGCAGATAAG CACATTCCTC ACATCCAGGG GAACATGATC 2160  
 AAACTAGAGA CCAAGAAGAC AAAACTCTGA

Seq ID NO: 582 Protein sequence  
 Protein Accession #: AAB34388.1

1 11 21 31 41 51  
 | | | | |  
 MNPFQKNESK ETLFSPVSIE EVPPRPPSPK KKPSPITICGS NYPLSIAFIV VNEFCERFSY 60  
 YGMAVAVLILY FLYFLHWNED TSTSIYHAFS SLCYFTPIILG AAIADSWLKG FKTIYLSLV 120  
 YVLGHVILKSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFGGD QFEEKHAEER 180  
 TRYFSVFYLS INAGSLISTF ITPMLRGDVQ CFGEDCYALA FGVPGLLMVI ALVVVFAMGSK 240  
 IYNKPPPEGN IVAQVFKCIW FAISNRFKNR SGDIPKQHW LDWAAEKYPK QLIMDVKALT 300  
 RVLYLYIPLP MFALLDQGG SRWTLQAIMR NRNLGFFVLQ PDQMQLVLPF LVLIFIPLED 360  
 FVIYRLVSKG GINFSRLKRM AVGMILACLA FAVAAAVEIK INEMAPAQSG PQEVFLQVLN 420  
 LADDEVKVTV VGNENNSLLI ESIKSFQKTP HYSKLHLKTK SQDFHFLKY HNLSLYTEHS 480  
 VQEKWYSLV IREDGNSISS MMVKDTESEK TNGMTTVRFV NTLHKDVNIS LSTDTSLNVG 540  
 EYGVSAVRT VQRGYPAHV CRTEDKNFSL NLGLLDFGAA YLFVITNNTN QGLQAWKIED 600  
 IPANKMSIAW QLPQYALVTA GEVMSVSVGL EFSYSQAPSS MKSVLQAALW LTIAGVNIIV 660  
 LVVAQFSLV QWAEFILFSC LLLVICLIFS IMGYVYPVK TEDMRGPADK HIPHIQGNMI 720  
 KLETKKTKL

Seq ID NO: 583 DNA sequence  
 Nucleic Acid Accession #: NM\_032642.1  
 Coding sequence: 184..1263

1 11 21 31 41 51  
 | | | | |  
 GACCATTAGC AGGCACCCAG GCCTGTCTTT GGCTCGGAAA CGGTGGCCCC CAATGTAGCC 60  
 TAGTTTGAAC CTAGGAATCTG CAGGACCAGA GAGATTCCAC TGGAGCCTGA TGGACGGGTG 120  
 ACAGAGGGAA CCCTACTCTG GAAACTGTCA GTCCACGGGC ACTGGGGAGG GCTGAGGCGG 180  
 ACCATGCCCA GCCTGCTGCT GCTGTTCACG GCTGCTCTGC TGTCCAGCTG GGCTCAGCTT 240  
 CTGACAGACG CCAACTCTGT GTGGTCATTA GCTTTGAACC CGGTGCAGAG ACCCGAGATG 300  
 TTTATCATCG GTGCCACGCC CGTGTGCAGT CAGCTTCCCG GGCTCTCCCC TGGCCAGAGG 360  
 AAGCTGTGCC AATTGTACCA GGAGCACATG GCCTACATAG GGGAGGGAGC CAAGACTGGC 420  
 ATCAAGGAAT GCCAGACCA GTTCCGGCAG CGGCGGTGGA ATTGCAGCAC AGCGGACAAAC 480  
 GCATCTGTCT TTGGGAGAGT CATGCAGATA GGCAGCCGAG AGACCGCCTT CACCCACGCG 540  
 GTGAGCGCCG CGGGCGTGGT CAACGCCATC AGCCGGGCGT GCCGCGAGGG CGAGCTCTCC 600  
 ACCTGCGGCT GCAGCCGGAC GCGCGGGGCC AAGGACCTGC CCCGGGACTG GCTGTGGGGC 660  
 GGCTGTGGGG ACAACGTGGA GTACGGCTAC CGCTTCGCCA AGGAGTTTGT GGATGCCCGG 720  
 GAGCGAGAGA AGAATTTTGC CAAAGGATCA GAGGAGCAGG GCCGGGTGCT CATGAACCTG 780  
 CAAAACAACG AGGCCGGTGC CAGGGCTGTG TATAAGATGG CAGACGTAGC CTGCAATATG 840  
 CACGGCGTCT CGGGGTCTGT CAGCCTCAAG ACCTGCTGGC TGCAGCTGGC CGAGTTCCGC 900  
 AAGTTCGGAG ACCGGCTGAA GGAGAAGTAC GACAGCGCGG CCGCATGCGC CGTACCCGCG 960  
 AAGGGCCGGC TGGAGCTGGT CAACAGCCGC TTCACCCAGC CCACCCCGGA GGACCTGGTC 1020  
 TATGTGGACC CCAGCCCGCA CTACTGCCTG CGCAACGAGA GCACGGGCTC CCTGGGCACG 1080  
 CAGGGCCGCT TCTGCAACAA GACCTCGGAG GGCATGGATG GCTGTGAGCT CATGTGCTGC 1140  
 GGGCGTGGCT ACAACAGTAT CAAGAGCGTG CAGGTGGAGC GCTGCCATCG CAAGTTCAC 1200  
 TGGTGTCTGT TCGTCAAGTG TAAGAAGTGC ACGGAGATCG TGGACCAGTA CATCTGTAAA 1260  
 TAGCCCGGAG GGCCTGCTCC CGGCCCCCC TGCACCTGCG CTCACAAAGG TCTATATTAT 1320  
 ATAAATCTAT ATAAATCTAT TTTATATTG TATAAGTAAA TGGGTGGGTG CTATACAATG 1380  
 GAAAGATGAA AATGGAAAGG AAGAGCTTAT TTAAGAGACG CTGGAGATCT CTGAGGAGTG 1440  
 GACTTTGCTG GTTCTCTCTT CTTGTTGGGT GGGAGACAGG GCTTTTCTC TCCCTCTGGC 1500  
 GAGGACTCTC AGGATGTAGG GACTTGGAAA TATTTACTGT CTGTCCACCA CGGCCCTGGG 1560  
 GAGGAGGTT GTGGTTGGAT GGAGGAGATG ATCTTGTCTG GAAGTCTAGA GTCTTTGTTG 1620  
 GTTAGAGGAC TGCCCTGTAT CCTGGCCACT AGGCCAAGAG GCCCTATGAA GGTGGCGGGA 1680  
 ACTCAGCTTC AACCTCGATG TCTTCAGGGT CTTGTCCAGA ATGTAGATGG GTTCCGTAAG 1740  
 AGGCCCTGGT CTCTCTTACT CTTTCATCCA CGTGCACTTG TCGGCGCATCT GCAGTTTACA 1800  
 GGAACGGCTC CTTCCTTAAA ATGAGAAGTC CAAGGTCTAT TCTGGCCAG TGACCACAGA 1860  
 GAGATCTGCA CCTCCCGGAC TTCAGGCTGT CTTTCCAGC GAGAATTCTT CATCCTCCAC 1920  
 GGTTCACTAG CTCTACCTG AAGAGGAAAG GGGGCCATTT GACCTGACAT GTCAGGAAAG 1980  
 CCCTAAACTG AATGTTTGGC CTGGGCTGCG AGAAGCCAGG GTGCATGACC AGGCTGCGTG 2040  
 GACGTTATAC TGTCTTCCCC CACCCCGGGG GAGGGGAAGC TTGAGCTGCT GCTGTCACTC 2100  
 CTCCACCGAG GGAGGCTCA CAAACACAG GACGCTGCAA CGGGTCAGGC TGGCGGGCCC 2160  
 GGCGTGTCA TCATCTCTGC CCCAGGTGTA CGGTTTCTCT CTGACATTAA ATGCCCTTCA 2220  
 TGGAAAAAAA AAAAAGAAAA AAAAAAAA AA

Seq ID NO: 584 Protein sequence  
 Protein Accession #: NP\_116031.1

1 11 21 31 41 51  
 | | | | |  
 MPSSLLLFTH ALLSSWAQLL TDANSWWSLA LNPVQRPMEF IIGAQPVCSSQ LPGLSPGQK 60  
 LCQLYQEHMA YIGEGAKTGI KECQHQFRQR RWNCTADNA SVFGRVMQIG SRETAFTHAV 120

SAAGVVNAIS RACREGELST CGCSRTARPK DLPRDNLWGG CGDNVEYGYR FAKEFVDARE 180  
 REKNFAKGSE EQGRVLMNLQ NNEAGRRAVY KMADVACKCH GVSQSGCSLKT CWLQLAEPRK 240  
 VGDRLEKEKYD SAAAMRVTRK GRLELVNSRF TQPTPEDLVY VDFSPDYCLR NESTGSLGTQ 300  
 GRLCNKTSSEG MDGCELMCCG RGYNQFKSVQ VERCHCKFHW CCFVRCKKCT EIVDQYICK

Seq ID NO: 585 DNA sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1479

1 11 21 31 41 51  
 | | | | | |  
 ATGGCTTTGA ACTCAGGGTC ACCACCAGCT ATTGGACCTT ACTATGAAAA CCATGGATAC 60  
 CAACCGGAAA ACCCTATCC CGCACAGCCC ACTGTGGTCC CCACTGTCTA CGAGGTGCAT 120  
 CCGGCTCAGT ACTACCCGTC CCCCGTGCCC CAGTACGCCC CGAGGGTCTT GACGCAGGCT 180  
 TCCAACCCCG TCGTCTGCAC GCAGCCCAAA TCCCCATCCG GGACAGTGTG CACCTCAAAG 240  
 ACTAAGAAAG CACTGTGCAT CACCTTGACC CTGGGGACCT TCCTCGTGGG AGCTGCGCTG 300  
 GCCGCTGGCC TACTCTGGAA GTTCATGGGC AGCAAGTGCT CCAACTCTGG GATAGAGTGC 360  
 GACTCCTCAG GTACCTGCAT CAACCCCTCT AACTGGTGTG ATGGCGTGTG ACACTGCCCC 420  
 GGGCGGGAGG ACAGAAATCG GTGTGTTTCG CTCTACGGAC CAAACTTCAT CCTTCAGGTG 480  
 TACTCATCTC AGAGGAAGTC CTGGCACCTT GTGTGCCAAG ACGACTGGAA CGAGAACTAC 540  
 GGGCGGGCGG CTTGCAGGGA CATGGGTAT AAGAATAATT TTTACTCTAG CCAAGGAATA 600  
 GTGGATGACA CGGGATCCAC CAGCTTTATG AACTGAACA CAAGTGCCGG CAATGTCGAT 660  
 ATCTATAAAA AACTGTACCA CAGTGATGCC TGTTCCTCAA AAGCAGTGGT TTCTTTACGC 720  
 TGTATAGCCT CGGGGGTCAA CTTGAACTCA AGCCCGCAGA GCAGGATCGT GGGCGGCGAG 780  
 AGCGCGCTCC GGGGGGCTG GCCCTGGCAG GTCAAGCTGC ACGTCCAGAA CGTCCACGTG 840  
 TGGGAGGCT CCATCATCAC CCCCGAGTGG ATCGTGACAG CCGCCCACTG CGTGGAAAAA 900  
 CCTCTTAACA ATCCATGGCA TTGGACGGCA TTTGCGGGGA TTTTGAGACA ATCTTTTCATG 960  
 TTCTATGGAG CCGGATACCA AGTAGAAAAA GTGATTCTC ATCCAAATTA TGACTCCAAG 1020  
 ACCAAGAAAC ATGACATTGC GCTGATGAAG CTGCAGAACG CTCTGACTTT CAACGACCTA 1080  
 GTGAAACCCAG TGTGCTCTGC CAACCCAGGC ATGATGCTGC AGCCAGAACA GCTCTGCTGG 1140  
 ATTTCCGGGT GGGGGGCCAC CGAGGAGAAA GGAAGACCT CAGAAAGTGT GAACGCTGCC 1200  
 AAGGTGCTTC TCATTGAGAC ACAGAGATGC AACAGCAGAT ATGCTCTATG CAACCTGATC 1260  
 ACACCAAGCA TGATCTGTGC CGGCTTCTTG CAGGGGAACG TCGATTCTTG CCAGGGTGAC 1320  
 AGTGGAGGGC CTCTGTGCAT TTCGAAGAAC AATATCTGGT GGCTGATAGG GGATACAAGC 1380  
 TGGGGTTCTG GCTGTGCCAA AGCTTACAGA CCAGGAGTGT ACGGGAATGT GATGGTATTC 1440  
 ACGGACTGGA TTTATCGACA AATGAGGGCA GACGGCTAA

Seq ID NO: 586 Protein sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | | |  
 MALNSGSPPA IGPIYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTA 60  
 SNPVVCTQPK SPSTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120  
 DSSGTCINPS NWCDGVSHCP GGEDENRCVR LYGNPFIQV YSSQRKSWHP VCQDDWNENY 180  
 GRAACRDMGY KNNFYSSQGI VDDSGSTSM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240  
 CIACGVNLNS SRQSRIVGGE SALPGANFWQ VSLHVQNVHV CGGSIITPEW IVTAAHCVEK 300  
 PLNNPWHWTA FAMILRQSFY FYGAGYQVEK VISHPNYDSK TKNNIDIALMK LQKPLTFNDL 360  
 VKPVCLPNPG MMQLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLIIETQRC NSRYVYDNL 420  
 TPAMICAGFL QGNVDSQGD SGGPLVTSKN NIWWLIGDTS WSGGCAKAYR PGVYGVNMVF 480  
 TDWIYRQMRA DG

Seq ID NO: 587 DNA sequence  
 Nucleic Acid Accession #: NM\_005656.1  
 Coding sequence: 57..1535

1 11 21 31 41 51  
 | | | | | |  
 GTCATATTGA ACATTCACAGA TACCTATCAT TACTCGATGC TGTGATAAC AGCAAGATGG 60  
 CTTTGAATC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAATAACCAT GGATACCAAC 120  
 CGGAAAAACC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG 180  
 CTCAGTACTA CCCGTCCTCC GTGCCCCAGT ACGCCCCGAG GGTCTTGACG CAGGCTTCCA 240  
 ACCCCGTCGT CTGCACGAG CCCAATCCC CATCCGGGAC AGTGTGCACC TCAAAGACTA 300  
 AGAAAGCACT GTGCATCACC TTGACCTGG GACCTTCCT CGTGGGAGCT GCGCTGGCCG 360  
 CTGGCCTACT CTGGAAGTTC ATGGGCAGCA AGTGCTCCAA CTCTGGGATA GAGTGCAGCT 420  
 CCTCAGGTAC CTGCATCAAC CCCTCTAAT GGTGTGATGG CGTGTACAC TGCCCCGGCG 480  
 GGGAGGACGA GAATCGGTGT GTTCGCTCT ACGGACCAA CTTCATCCTT CAGATGTACT 540  
 CATCTCAGAG GAAGTCTTGG CACCCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600  
 GGGCGGCTG CAGGGACATG GGCTATAAGA ATAATTTTCT CTCTAGCCAA GGAATAGTGG 660  
 ATGACAGCGG ATCCACACAG TTTATGAAAC TGAACACAAG TGCCGGCAAT GTCGATATCT 720  
 ATAAAAAAT GTACCACAGT GATGCCTGTT CTTCAAAAGC AGTGGTTTCT TTAGCTGTGT 780  
 TAGCCTGCGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG 840  
 CGCTCCCGGG GCGCTGGCCC TGGCAGGTCA GCCTGCACGT CCAGAACGTC CAGCTGTGCG 900  
 GAGGCTCCAT CATCACCCCG GAGTGGATCG TGACAGCCGC CCACTGCGTG GAAAAACCTC 960  
 TTAACAATCC ATGGCATTTG ACGGCATTG CGGGGATTTT GAGACAATCT TTCTATGTTCT 1020  
 ATGGAGCCGG ATACCAAGTA CAAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA 1080  
 AGAACATGA CATTCGCTG ATGAAGCTGC AGAAGCCTCT GACTTTCAAC GACCTAGTGA 1140  
 AACCAAGTGT TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACAGCTC TGCTGGATTT 1200  
 CCGGGTGGGG GGCCACCCAG GAGAAAGGGA AGACCTCAGA AGTGTGAAC GCTGCCAAGG 1260  
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAAC CTGATCACAC 1320  
 CAGCCATGAT CTGTGCCGGC TTCCTGCAGG GGAACGTCGA TTCTTGCCAG GGTGACAGTG 1380  
 GAGGCGCTCT GGTCACTTCG AACACAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440  
 GTTCTGGCTG TGCACAAAGT TACAGACCAG GAGTGACGG GAATGTGATG GTATTACGG 1500  
 ACTGGATTTA TCGACAAATG AAGGCAACCG GCTAATCCAC ATGGTCTTCG TCCTTGACGT 1560



CGTTTTACAA GAAACAATG GGGCTGGTTT TGCTTCCCCG TGCATGATTT ACTCTTAGAG 1620  
 ATGATTACAGA GGTCACTTCA TTTTATTAA ACAGTGAAC TGTCTGGCTT TGGCACTCTC 1680  
 TGCACATCTG TGCAGGCTGC AGTGGCTCCC CTGCCACGCC TGTCTCTCCT AACCCCTTGT 1740  
 5 CCGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGGAAGAGG 1800  
 GTTGGAGGCT GCCCCATTG AGATCTTCTT GCTGAGTCCT TTCCAGGGGC CAATTTTGGG 1860  
 TGAGCATGGA GCTGTCACTT CTGAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920  
 GGAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTTGGTAGTG 1980  
 TCCCCAGCCT ACTTCACAAG GGGATTTTGC TGATGGGTTC TTAGAGCCTT AGCAGCCCTG 2040  
 10 GATGGTGGCC AGAAATAAAG GGACCAGCCC TTCATGGGTG GTGACGTGGT AGTCACTTGT 2100  
 AAGGGGAACA GAAACATTTT TGTCTTATG GGGTGAGAA ATAGACAGTG CCCTTGGTGC 2160  
 GAGGGAAGCA ATTGAAAAGG AACTTGCCCT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220  
 CATTTGGGTGG GGCCTCTGGG AGGGAGACTC AGCCTTCTCT CTCATCTCTC CTGACCCTGC 2280  
 TCCTAGCACC CTGGAGAGTG AATGCCCTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340  
 15 ATGTCGGCCT CTTGAGCCT GATAGTCATT GGAATTTAG GTCCATGGG GAAATCAAGG 2400  
 ATGCTCAGTT TAAGGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460  
 CTGAGTTCAA AGCCATCTT

Seq ID NO: 588 Protein sequence  
 Protein Accession #: NP\_005647.1

1 11 21 31 41 51  
 MALNSGSPPA IGPYYENHGY OPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTOA 60  
 25 SNPVVCTQPK SPSGTVCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120  
 DSSGTCINPS NWCDGVSHCP GGEDENRCVR LYGPNNFILQM YSSQRKSWHP VCQDDWNENY 180  
 GRAACRDMGY KNNFYSSQGI VDDSGSTSEFM KLNSTAGNVD IYKKLYHSDA CSSKAVVSLR 240  
 CLACGVNLSN SRQSRIVGGE SALPGAWPQV VSLHVQNVHV CGGSIITPEW IVTAAHCVKE 300  
 PLNNPWHHTA FAGILRQSFM FYGAGYQVQK VISHPNYDSK TKNNIDIALMK LQKPLTFNDL 360  
 30 VKPVCLPNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLETQRC NSRVVYDNL 420  
 TPAMICAGFL QGNVDSQCQD SGGPLVTSNN NIWWLIGDTS WSGSCAKAYR PGVYGNVMVF 480  
 TDWIYRQMK NG

Seq ID NO: 589 DNA sequence  
 Nucleic Acid Accession #: NM\_001935.1  
 Coding sequence: 1..2301

1 11 21 31 41 51  
 40 ATGAAGACAC CGTGAAGATG TCTTCTGGGA CTGCTGGGTG CTGCTGCGCT TGTCAACATC 60  
 ATCACCGTGC CCGTGGTTCT GCTGAACAAA GGCACAGATG ATGCTACAGC TGACAGTCGC 120  
 AAAAATTACA CTCTAACTGA TTACTTAAAA AATACTTATA GACTGAAGTT ATACTCCTTA 180  
 AGATGGATTG CAGATCATGA ATATCTCTAC AAACAAGAAA ATAATATCTT GGTATTCAAT 240  
 GCTGAATATG GAAACAGCTC AGTTTTCTTG GAGAACAGTA CATTTGATGA GTTTGGACAT 300  
 45 TCTATCAATG ATTATTTCAAT ATCTCTCTGAT GGGCAGTTTA TTCTCTAGA ATACAACATC 360  
 GTGAAGCAAT GGAGGCATTG CTACACAGCT TCATATGACA TTTATGATTT AAATAAAAGG 420  
 CAGCTGATTA CAGAAGAGAG GATTCCAAAC AACACACAGT GGGTCACATG GTCACCAGTG 480  
 GGTCATAAAT TGGCATATGT TTGGAACAAT GACATTTATG TTAATAATGA ACCAAATTGA 540  
 CCAAGTTACA GAATCATATG GACGGGAAA GAAGATATAA TATATAATGG AATAACTGAC 600  
 TGGGTTTATG AAGAGGAAGT CTTCAGTGCC TACTCTGCTC TGTGGTGGTC TCCAAACGGC 660  
 50 ACTTTTTTAG CATATGCCA ATTTAACGAC ACAGAAGTCC CACTTATTGA ATACTCCTTC 720  
 TACTCTGATG AGTCACTGCA GTACCCAAAG ACTGTACGGG TTCCATATCC AAAGGCAGGA 780  
 GCTGTGAATC CAACTGTAAA GTTCTTTGTT GTAAATACAG ACTCTCTCAG CTCAGTCACC 840  
 AATGCAACTT CCATACAAAT CACTGCTCCT GCTTCTATGT TGATAGGGGA TCACTACTTG 900  
 TGTGATGTGA CATGGGCAAC ACAAGAAAGA ATTTCTTTGC AGTGGCTCAG GAGGATTTCAG 960  
 55 AACTATTCCG TCATGGATAT TTGTGACTAT GATGAATCCA GTGGAAGATG GAACTGCTTA 1020  
 GTGGCAGGCG AACACATTGA AATGAGTACT ACTGGCTGGG TTGGAAGATT TAGGCCCTCA 1080  
 GAACCTCAT TTACCCTTGA TGGTAATAGC TTCTACAAGA TCATCAGCAA TGAAGAAGGT 1140  
 TACAGACACA TTTGCTATTT CCAAATAGAT AAAAAAGACT GCACATTTAT TACAAAAGGC 1200  
 60 ACCTGGGAAG TCATCGGGAT AGAAGCTCTA ACCAGTGATT ATCTATACTA CATTAGTAAT 1260  
 GAATATAAAG GAATGCCAGG AGGAAGGAAT CTTTATAAAA TCCAACCTAG CGACTATACA 1320  
 AAAGTGACAT GCCTCAGTTG TGAGCTGAAT CCGGAAAGGT GTCAGTACTA TTCTGTGTCA 1380  
 TTCAGTAAAG AGGCGAAGTA TTATCAGCTG AGATGTTCCG GTCCTGGTCT GCCCTCTAT 1440  
 ACTCTACACA GCAGCGTGAA TGATAAAGGG CTGAGAGTCC TGGAAAGACA TTCAGCTTTG 1500  
 65 GATAAAATGC TGCAGATGT CCAGATGCCC TCCAAAAAAC TGGACTTCAT TATTTTGAAT 1560  
 GAAACAAAAT TTTGGTATCA GATGATCTTG CCTCCTCATT TTGATAAATC CAAGAAATAT 1620  
 CCTCTACTAT TAGATGTGTA TGCAGGCCCA TGTAGTCAAA AAGCAGACAC TGTCTTCAGA 1680  
 CTGAACCTGG CCCTTACCT TGCAAGCACA GAAACATTA TAGTAGCTAG CTTTGTATGGC 1740  
 70 AGAGGAAGTG GTTACCAAGG AGATAAGATC ATGCATGCAA TCAACAGAAG ACTGGGAACA 1800  
 TTTGAAGTTG AAGATCAAAT TGAAGCAGCC AGACAATTTT CAAAATGGG ATTTGTGGAC 1860  
 AACAAACGAA TTGCAATTTG GGGCTGGTCA TATGGAGGGT ACGTAACCTC AATGGTCTCTG 1920  
 GGATCGGGAA GTGGCGTGT CAAGTGTGGA ATAGCCGTGG CGCCTGTATC CCGGTGGGAG 1980  
 TACTATGACT CAGTGTACAC AGAACGTTAC ATGGGTCTCC CAACTCCAGA AGACAACCTT 2040  
 GACCATTA CAATTTCAAC AGTCATGAGC AGAGCTGAAA ATTTTAAACA AGTTGAGTAC 2100  
 75 CTCCTTATTC ATGGAACAGC AGATGATAAC GTTCACTTTC AGCAGTCAGC TCAGATCTCC 2160  
 AAAGCCCTGG TCGATGTTGG AGTGGATTTC CAGGCAATGT GGTATACTGA TGAAGACCAT 2220  
 GGAATAGCTA CGAGCAGAG ACACCAACAT ATATATACCC ACATGAGCCA CTTCAATAAA 2280  
 CAATGTTTCT CTTTACCTTA G

Seq ID NO: 590 Protein sequence  
 Protein Accession #: NP\_001926.1

1 11 21 31 41 51  
 MKTPWKILLG LLGAAALVTI ITVPVLLNKG GTDDATADSR KTYTLTDYLK NTYRLKLYSL 60

RWISDHEYLY KQENNILVFN AEYGNSSVFL ENSTFDEFHG SINDYSISPD GQFILLEYN 120  
 VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVTWSPV GHKLAYVWNN DIYVKIEPNL 180  
 PSYRITWTKG EDIIYNGITD WYVEEVFSA YSALWWSPNG TFLAYAQFND TEVPLIEYSF 240  
 YSDESLQYPK TVRVYPYKAG AVNPTVKFFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300  
 CDVTWATQER ISLQWLRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGWVGRFRPS 360  
 EPHTFLDGNS FYKIIISNEEG YRHICYFQID KKDCTFITKG TWEVIGIEAL TSDYLYYISN 420  
 EYKGMPPGGRN LYKIQLSDYT KVTCLSCSELN PERCQYYSVS FSKEAKYYQL RCSGPGLPLY 480  
 TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKKLDFIILN ETKFWYQML PPHFDKSKKY 540  
 PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIVASFDG RSGSYQGDKI MHAINRRLGT 600  
 FEVEDQIEAA RQFSKMGFVD NKRIAIWGS YGGYVTSMLV GSGSGVFKCG IAVAPVSRWE 660  
 YYDSVYTERY MGLPTPEDNL DHYRNSTVMS RAENFKQVEY LLIHGTADDN VHFQQAQIS 720  
 KALVDVGVD FQAMWYTDDEH GIASSTAQH IYTHMSHFIF QCFSLP

Seq ID NO: 591 DNA sequence

Nucleic Acid Accession #: NM\_016077.1

Coding sequence: 128..667

1 11 21 31 41 51  
 | | | | |  
 TCGCTTTGTG ATTCTTGATC CGGAACCTTG TCACCCAGGA ACCCCGGAAG AGGTAGCTCA 60  
 CGCGATAGAA ACGTGTTCGC TTGCCAGAA GAAGGGAAGG CGCGAGTGAG GAAAGGAGGT 120  
 ACTGTAGATG CCTCCAAAT CTTGGTTAT GGAATATTG GCTCATCCA GTACACTCGG 180  
 CTTGGCTGTT GGAGTTGCTT GTGGCATGTG CTTGGGCTGG AGCCTTCGAG TATGCTTTGG 240  
 GATGCTCCCC AAAAGCAAGA CGAGCAAGAC ACACACAGAT ACTGAAAGTG AAGCAAGCAT 300  
 CTTGGGAGAC AGCGGGGAGT ACAAGATGAT TCTTGTGGTT CGAAATGACT TAAAGATGGG 360  
 AAAAGGGAAA GTGGCTGCC AGTGCTCTCA TGCTGCTGTT TCAGCTTACA AGCAGATTCA 420  
 AAGAAGAAAT CTTGAAATGC TCAAACAATG GGAATACTGT GCCAGCCCA AGGTGGTGGT 480  
 CAAAGCTCCT GATGAAGAAA CCTGTATTGC ATTATTGGCC CATGCAAAA TGCTGGGACT 540  
 GACTGTAAGT TTAATTCAAG ATGCTGGACG TACTCAGATT GCACCAGGCT CTCAACTGT 600  
 CCTAGGGATT GGGCCAGGAC CAGCAGACCT AATTGACAAA GTCACCTGGT ACCTAAACT 660  
 TTACTAGGTG GACTTTGATA TGACAACAAC CCCTCCATCA CAAGTGTGTT AAGCCTGTCA 720  
 GATTCTAACA ACAAAGCTG AATTTCTTCA CCAACTTAA ATGTTCTTGA GATGAAATA 780  
 AAACCTATTC CCATGTCTA AAAAA

Seq ID NO: 592 Protein sequence

Protein Accession #: NP\_057161.1

1 11 21 31 41 51  
 | | | | |  
 MPSKSLVMEY LAHPSTLGLA VGVACGMCLG WSLRVCFGML PKSKTSKTHT DTESEASILG 60  
 DSGEYKMLIV VRNDLKMKGK KVAAQCASHA VSAYKQIQR NPMLKQWEY CGQPKVVKVA 120  
 PDEETLIAL AHAKMLGLTV SLIQDAGRTQ IAPGSQTVLG IGPGPADLID KVTGHLKLY

Seq ID NO: 593 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..1896

1 11 21 31 41 51  
 | | | | |  
 ATGCGCGCCG TGCCGCTGCC CGCCCCGCTC CTGCGCTGCG TGCTGCTCGC GCTCCTGGCC 60  
 GCTCCGCGCG CCCGCGCCAG CAGAGCCGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120  
 CGCGAGTCGC GGCACCCGCC CGGCCCCGGG CCCGGGAACA CCACCCGTT TGGGTCTGGG 180  
 GCGGCGGGCG GCAGCGGCAG CTCACGCTCC AACAGCAGTG GCGACGCTT GGTGACCCGC 240  
 ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAGGCAG CCGTGATCGT GCGCTTCGCC 300  
 TTTACACCCC TCCTCATCGC CTGCGCTGCTG CTGCGCTGCT TCAGGTGCGG AAAGAGGTGA 360  
 AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCAGTGGG AATGGCGCCA 420  
 CTAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480  
 TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCTT 540  
 GTGCCCCACC CCTTCATCCT CGACATTGAC CTTCCAGCAA GATGCACTGG AAGGCCTGAT 600  
 GGTGGAATCA GACCTGGTAA AACCTGTTT CAGCCTGGT GGCATCCTGT GGAAGTTGG 660  
 TCAGTGCACA CTTGGGTTGT GAAGGACTGG ACCTGGAAGC CCTCTGCGT CGGAGGTGTT 720  
 GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTC AGGCATCTGC 780  
 TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCACCACAA TGGAGTTGCT TCTGCCACCC 840  
 TTTGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGTTTTCG ACAACTGCAG 900  
 CTGAATCTCA TGGAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGTCTCATCT 960  
 GCCAGGTGCT TGCCACTGGT CTTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020  
 CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTACAC ACAAACTATG 1080  
 AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGGCCAGC GGGGCACCTT TTGTGAAGAC 1140  
 AGAGCAGTGA CTAAGTTTCT CCAGGTTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200  
 GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260  
 ACCCATCTCT TCAGTTGGC TCGTTAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320  
 AGGGTGTTC GCGCTCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380  
 TGCCTTTTGG TTTTGAAGAT TCTGTTGAGG CGCATCCTC ACCTTGACCT CTTCTACAAA 1440  
 ATCTGTCTCC CTTGCTGTGC CGTGGAAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500  
 FTCTTGTGCT CATTTGAGCA GAGCCCAACA AAGGCAGCTG CTGCCACCGG GGAGCCTGTC 1560  
 AAACAGGGCG CAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620  
 GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCAGCTGA GGATGTCACT 1680  
 CACCTGGAG GAGACTTGA TGGGGTGGCA AATTTCTATT TGGAGGAAGA GGGTTTCCAG 1740  
 GATGGCAGAT GCCAGAAGAT GGTCTGTGAT TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800  
 TGTGAGAGGC TCACAGTTTC CCATCACTTC TCAGGCCATT CCAAGTCTTG GTCTTCTCTT 1860  
 TCCCCCGCAG AGCCCTGTGT TCTGTCCAGG CCTGA

Seq ID NO: 594 Protein sequence

Protein Accession #: FGENESH predicted

```

1      11      21      31      41      51
|      |      |      |      |      |
5  MRVAPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPPGPG PGNTTRFGSG 60
AAGSGSSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF AFTLLIACLL LRVFRSGKRL 120
KTRKYDIIT TPAERVMAP LNEDEDEDED STVFDIKYRV SLPAALRRQL PGQTLTLTVP 180
VPPPFILDID LPARCSGRPD GGIRPGKTCF PAWWHPVESW SAATWGVKDW TWKPSCVGGV 240
ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPP FGHFPKVPPT STPHGFRQLQ 300
10 LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAESDLPN PWWHFSATGS PIKTLYTQTM 360
STLGLDVFCE AGQRGTFCE RAVTKVLQGS SFSKQLRWKP ALESGFPHHL RLLRECPPLS 420
THPVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAAGPEV KRGPSGQLTR HTPCPGWGITH 540
ANLQTIPTDQ GQEGPREDVT HPGGDLGVA NFYLEEEGFQ DGRQCQKMLM SEEGPPSLTG 600
15 CERLTGSHHF SSHSKSWFL SPRQPLFLSR P

```

Seq ID NO: 595 DNA sequence  
Nucleic Acid Accession #: NM\_021614.1  
Coding sequence: 1..1740

```

20 1      11      21      31      41      51
|      |      |      |      |      |
ATGAGCAGCT GCAGGTACAA CGGGGGCGTC ATGCGGCCGC TCAGCAACTT GAGCGCGTCC 60
CGCCGGAACC TGCAGAGAT GGACTCAGAG GCGCAGCCCC TGCCAGCCCC CGCGTCTGTC 120
GGAGGAGGTG CCGCGCGCTC CTCGCCGTCT GCAGCCGCTG CCGCCGCCGC CGCTGTTTCG 180
25 TCCTCAGCCC CCGAGATCGT GGTGTCTAAG CCCGAGCACA ACAACTCCAA CAACCTGGCG 240
CTCTATGGAA CCGCGCGCGG AGGCAGCACT GGAGGAGGCG GCGCGGTGG CCGGAGCGGG 300
CACGGCAGCA GCAGTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAAG 360
CTGGGCCACC GCGCGCCCTT GTTCGAAAAG CGCAAGCGGC TCAGCGACTA CGCGCTCATC 420
30 TTCGCGATGT TCGGCATCGT GGTCTATGTC ATCAGACCG AGCTGTCTGT GGGCGCTAC 480
GACAAGGCGT CGCTGTATTC CTTAGCTCTG AAATGCCTTA TCAGTCTCTC CACGATCATC 540
CTGCTCGGTC TGATCATCGT GTACCACGCC AGGGAATAAC AGTTGTTTAT GGTGGACAAT 600
GGAGCAGATG ACTGGAGATA AGCCATGACT TATGAGCGTA TTTTCTTCAT CTGCTTGGAA 660
35 ATACTGGTGT GTGCTATTCA TCCCATACCT GGAATTATA CATTACATG GACGGCCCGC 720
CTTGCCCTTCT CCTATGCCCC ATCCACAACC ACCGCTGATG TGGATATTAT TTTATCTATA 780
CCAATGTTCT TAAAGCTATA TCTGATTGCC AGAGTCATGC TTTTACATAG CAAACTTTTC 840
ACTGATGCTT CCTCTAGAAA CATTGGAGCA CTTAATAAGA TAAACTTCAA TACACGTTTT 900
GTTATGAAGA CTTTATGAC TATATGCCCA GGAACGTGAC TCTTGGTTTT TAGTATCTCA 960
TTATGGATAA TTGCCGATG GACTGTCCGA GCTTGTGAAA GGTACCATGA TCAACAGGAT 1020
40 GTTACTAGCA ACTTCTTGG AGCGATGTGG TTGATATCAA TAACTTTTCT CTCCATTGGT 1080
TATGGTGACA TGGTACCTAA CACATACTGT GGAAAGGAG TCTGCTTACT TACTGGAATT 1140
ATGGGTGCTG GTTGACAGC CTTGGTGTA GCTGTAGTGG CAAGGAAGCT AGAAGTTACC 1200
AAAGCAGAAA AACACGTGCA CAATTTCATG ATGGATACTC AGCTGACTAA AAGACTAAAA 1260
AATGCAGCTG CCAATGTACT CAGGGAAACA TGGCTAATTT ACAAATAATC AAAGCTAGTG 1320
45 AAAAAAGATG ATCATGAAA AGTAAGAAAA CATCAACGAA AATTCTGCA AGCTATTTCAT 1380
CAATTAAGAA GTGTAATAAT GGAGCAGAGG AACTGAATG ACCAAGCAAA CACTTTGGTG 1440
GACTTGGCAA AGACCCAGAA CATCATGTAT GATATGATTT CTGACTTAAA CGAAAGGAGT 1500
GAAGACTTCG AGAAGAGGAT TGTACCCTG GAAACAAAAC TAGAGACTTT GATTGGTAGC 1560
ATCCACGCCC TCCCTGGGCT CATAAGCCAG ACCATCAGGC AGCAGCAGAG AGATTTCATT 1620
50 GAGGCTCAGA TGGAGAGCTA CGACAAGCAC GTCACTTACA ATGCTGAGCG GTCCCGTCC 1680
TCGTCCAGGA GCGCGCGTCT CTCTCCACA GCACCACCAA CTTTCATCAGA GAGTAGCTAG

```

Seq ID NO: 596 Protein sequence  
Protein Accession #: NP\_067627.1

```

55 1      11      21      31      41      51
|      |      |      |      |      |
MSSCRYNGGV MRPLSNLSAS RRLNHEMDSE AQPLQPPASV GGGGASSPS AAAAAAAVS 60
SSAPEIVSVK PEHNNSNNLA LYGTGGGGST GGGGGGGSG HGSSSGTKSS KKKNQNIYK 120
60 LGHRRALFEK RKRLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII 180
LLGLIIVYHA REIQLFMVDI GADDWRIAMT YERIFFICLE ILVCAIHIP GNYTFTWTAR 240
LAFSYPSTT TADVDIILSI PMFLRLYLIA RVMLLHSLKF TDASSRSIGA LNKINFNTRF 300
VMKTLMTICP GTVLLVFSIS LWIIAAWTVR ACERYHDQOD VTSNFLGAMW LISITFLSIG 360
YGDMVPNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHNF MDTQLTKRVK 420
65 NAAANVLRET WLIYKNTKLV KKIDHAKVRK HQRKFLQAIH QLRSVKMEQR KLNDQANTLV 480
DLAKTQNIY DMISDLNERS EDFEKRIVTL ETKLETIGS IHALPGLISQ TIRQQQRDFI 540
EAQMESYDKH VTYNASRSR SSRRRRSSST APPTSSESS

```

Seq ID NO: 597 DNA sequence  
Nucleic Acid Accession #: NM\_016029.1  
Coding sequence: 228..1097

```

70 1      11      21      31      41      51
|      |      |      |      |      |
CTGCGATCCC GCAGGGCAGC GACGCGACTC TGGTGCGGGC CGTCTTCTTC CCCCCGAGCT 60
75 GGGCGTGGCG GCGCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGCGC 120
TGCTCCTGCT CTTGGTGCAG CTGCTGCGCT TCCTGAGGGC TGACGGCGAC CTGACGCTAC 180
TATGGGCCGA GTGGCAGGGA CGACGCCAGC AATGGGAGCT GACTGATATG GTGGTGTGGG 240
TGACTGGAGC CTCGAGTGGA ATTGGTGAGG AGCTGGCTTA CCAAGTTGCT AAAGTAGGAG 300
80 TTTCTCTTGT GCTGTAGACC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC 360
TAGAGAAATG CAATTTAAAA GAAAAAGATA TACTTGTGTT GCCCTTGAC CTGACCGACA 420
CTGGTTCCCA TGAAGCGGCT ACCAAAGCTG TTCTCCAGGA GTTTGGTAGA ATCGACATTC 480
TGGTCAACAA TGGTGAATG TCCACGCTT CTCTGTGCAT GGATACCAGC TTGGATGTCT 540
ACAGAAAGCT AATAGAGCTT AACTACTTAG GGACGGTGTC CTTGACAAAA TGTGTTCTGC 600
CTCACATGAT CGAGAGGAAG CAAGGAAAGA TTGTTACTGT GAATAGCATC CTGGGTATCA 660

```

TATCTGTACC TCTTTCATT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGTTTTTTTA 720  
 ATGGCCTTCG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCAG 780  
 GACCTGTGCA ATCAAAATAT GTGGAGAATT CCTAGCTGG AGAAGTCACA AAGACTATAG 840  
 GCAATAATGG AGACCACTCC CACAAGATGA CAACAGTCG TTGTGTGCGG CTGATGTTAA 900  
 TCAGCATGGC CAATGATTTG AAAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA 960  
 CATATTTGTG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAAG ATGGGGAAGA 1020  
 AAAGGATTGA GAACCTTAAG AGTGGTGTGG ATGCAGACTC TTCTTATTTT AAAATCTTTA 1080  
 AGACAAAACA TGA CTGAAAA GAGCACCTGT ACTTTTCAAG CCACTGGAGG GAGAAATGGA 1140  
 AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200  
 ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260  
 AGATTGCCAT GAATCTTGCA AA

Seq ID NO: 598 Protein sequence  
 Protein Accession #: NP\_057113.1

1 11 21 31 41 51  
 | | | | |  
 MNWELLWLVL VLLALLLLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MVVWVTGASS 60  
 GIGELAYQL SKLGVSLVLS ARRVELERV KRRCLENGNL KEKDILVLP DLTDTSHEA 120  
 ATKAVLQEFQ RIDILVNNNG MSQSLCMDT SLDVYRKLE LNYLGTSLT KCVLPHEMER 180  
 KQKIVTVNS ILGIISVPLS IGYCASKHAL RGFNGLRTE LATYPGIIVS NICPGPVQSN 240  
 IVENSLAGEV TKTIGNNGDQ SHKMTTSCRV RLMLISMAND LKEVWISEQP FLLVTVLWQY 300  
 MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD

Seq ID NO: 599 DNA sequence  
 Nucleic Acid Accession #: NM\_000793.2  
 Coding sequence: 401..1222

1 11 21 31 41 51  
 | | | | |  
 GCCTGCAGAG AGAGGCACCT TGCACCAAG AGAGATAGCA AGAAGGGAAA GACAGAGAGT 60  
 GAGAAAAAAG AGGAGTCAGT CGCTCCTGGG GAAGGGAGAG AGTGAGACTG GGAGAAAGAG 120  
 AAGCACAGAA AGTGTGTGTA AAACGGAGTA AAGAAAGAAA AAAAAAAC TACCCTTAAA 180  
 GCACATTTAA AAAAAAATAA CTCTGGCAAT TCAAGAAAGA AACAGGCTAC GTTTAAAGAG 240  
 CATAGAGACA ATGAAAGGCT AAAGAAAATT TTAATACTCT TGCCACAGTC TCATAGGTGC 300  
 TTGGAAATGA AAGTAGAACT GCCTGTCTTT AACGGACTCT GACAGAGAGG GTGAAGGGGA 360  
 ACCAGAGCGC ACAAGGGAAC TGACTCAGGA GGCAGAGAAG ATGGGCATCC TCAGCGTAGA 420  
 CTTGCTGATC ACACTGCAAA TTCTGCCAGT TTTTCTCTCC AACTGCCTCT TCCTGGCTCT 480  
 CTATGACTCG GTCATTCTGC TCAAGCACGT GGTGCTGCTG TTGAGCCGCT CCAAGTCCAC 540  
 TCGCGGAGAG TGGCGGCGCA TGCTGACCTC AGAGGGACTG CGCTGCGTCT GGAAGAGCTT 600  
 CCTCTCGAT GCCTACAAAC AGGTGAAATT GGGTGAGGAT GCCCCCAATT CCACTGTGGT 660  
 GCATGTCTCC AGTACAGAAG GAGGTGACAA CAGTGGCAAT GGTACCCAGG AGAAGATAGC 720  
 TGAGGGAGCC ACATGCCACCT TTCTTGACTT TGCCAGCCCT GAGCGCCAC TAGTGGTCAA 780  
 CTTTGGCTCA GCCACTTAC CTCTTTTAC GAGCCAGCTG CCAGCCTTCC GCAAACTGGT 840  
 GGAAGAGTTC TCCTCAGTGG CTGACTTCCT GCTGGTCTAC ATTGATGAGG CTCATCCATC 900  
 AGATGGCTGG GCGATACCGG GGGACTCCTC TTTGTCTTTT GAGGTGAAGA AGCACCAGAA 960  
 CCAGGAAGAT CGATGTGCAG CAGCCAGCA GCTTCTGGAG CGTTTCTCT TGCCGCCCAA 1020  
 GTGCCGAGTT GTGGCTGACC GCATGGACAA TAACGCCAAC ATAGCTTACG GGGTAGCCTT 1080  
 TGAACGTGTG TGCATTGTGC AGAGACAGAA AATTGCTTAT CTGGGAGGAA AGGCCCCCTT 1140  
 CTCCTACAAC CTTCAAGAAG TCCGGCATTG GCTGGAGAAG AATTTCAGCA AGAGATGAAA 1200  
 GAAAACTAGA TTAGCTGTTT AAAGGTATGA TTATAAGAGA GCTTATTGTT TTAATAAGTT 1260  
 ATATAAAGGC AAGGAATATA AGAATGAAT CCATATTCA ACAGAGCCCT ATTGGCTTAC 1320  
 TGAAGAGACA GAGTTTATCT ATCGAAGAA CATGAATCTC TAACAGCTCC ATACTTCTTT 1380  
 CACTACTCAA ATGGCATTGG GCTGAGTAAG TAACCATATC ACCTCTCTTC TTAGTAAAAA 1440  
 GCCCTATGTG AAAAGATCCC AAGATGGAGA GGAAGAAACG CTAATTCAGC ATGTGTTTCA 1500  
 TCTGCATTGA GAAGGAACCTG ATACATCTGA TGCATGCTTT GAGACCAGAA GAAAGACTT 1560  
 ACCTGAATAA TTACTACATT AGGGAAGCTA CTGTCTACGT TAAGATAAAG GGTATTGCCT 1620  
 TGGCTCTATT TGGCATGGAT GGAGCCAGT TGGAAAAATC CCAATATTA CAACAAGTCC 1680  
 TTGAACCAG GCCATGTGGT TAGACGTTGG TGTTAAGGTT AGACCTTATG TTAGAGTCAT 1740  
 TTCTGATGTT CCAGCTTCTA GCCATGTAGT GCTCTCAGTC TTCATACCCC AGAAATTATT 1800  
 GGTATATTGG TAGATACCGA GAATGATCCC TCAGTCTGAG AGGTAGAAAT GATCATCTGT 1860  
 AATCTGAGGG TTAATTTCCTA GGCAGGTGGA GAGAGTGTA AAAAAGAAAT GAAATTGACA 1920  
 AGCTAGGAAA GAGGAGGCAG AAAGATTGG AAAATTCACA GAGTTTCACC CTTAAGCTGT 1980  
 AGAGAGTGGG TCACATTTGT TAGCCACGGA AACATAGAAA CATACACAAG GCCAGAAAAA 2040  
 GAAGAAGGAG CTCACTAAA AGTGGCATAG AGAATACACA TATAAAACA ATATATTGT 2100  
 CATATGCTCC TAGAGAGGAG AAAGGGGTGA TTGAAGAAA AAAAAATACT TAAATATTG 2160  
 TAATTGTGAG GGGTTTCTTT TGGAAATAAT TACTTTTGAA CCATGTATGT GGTATGTATA 2220  
 TTTTCAGTGG GTTAATTATA CCCCATGATA CCTATTAAAG GAAACCAGT GGGTCTGGTG 2280  
 GTGCTGGTCT TTCTCTCCCC ATCTCTACAA TTTCTATGTG GCCCAAGTCA TTCTTAATCT 2340  
 TGGTCTCTAT AGCAGTGTTC TCTCTGAATG CTGAGCTGAA GAAATTATAC GTACATACAC 2400  
 ACATACATAC ATACATACAA ATATATGTAT ATATATTCTC AGCTGCTGCG GGAGGTAGGT 2460  
 ACCATGGCCA TTCAGCACAG CCTTGATTTC CTCCCAAAGT AGGTGAGCTA TAGTGAAGAA 2520  
 TAGGTGCAAA CAAACAAGCT TACTTCCATT GCAAAATAGA AGAAGAGGAA GTTAGAGATA 2580  
 ATTCTGATCA ATCAATTTGG AGGCTTTGTT ATAAGGCAAC CCCCAGTATA TCATGGAATT 2640  
 TCCATTGACA TTTGAATTTG GACTTGGATC TTCCCTTGGT CCCATTAGCT GAGGTTTATG 2700  
 AATCTAAAGT CCCATAGATA TATGATTATA ATGCTATTTT AAAAAATATA TATATAAAT 2760  
 ATTTTCTTCT TTTTAAATA GACACTATAG TTTTACCCAT AAGTAATATT TAAAGATTAT 2820  
 AGCTCCAAA AGAATGGACC AACCCTTTC GTATCATAAT TTCTTTTGGT TAAATATGAG 2880  
 ACTATTATGA AATCATAGTA TATGATTGTA TTTAAAGGTA CAATCAAAGG ATCTTTTGTG 2940  
 CATTCCATTA ATAACCTGAT AAAAAATAAA TAAATGGAT AGAAAAAAC TAAAGTTGAA 3000  
 AATACATTCT TAAACTGATT GTCTGAAATG AGAAAAAGAG GAGAACTAGG TGTGCAAGAA 3060  
 CCAACGTTAT TTTATTTTAT TTTTAAATG GGAGCAACAT ATCAGTCTGT TCACCAGCTG 3120  
 GTATATTGTG TAAATATTAA AGCTCCATTG GGACTGATTT TTCATGGCAA CATCAGCTTT 3180  
 CTAATGTCTCT AAATCTTATA AAAACCAACC ACAGAAGAAC AAAGCAAATT TCATTATCTA 3240

5 ATGAGTTGCT GGAAAAATCAT ATTGAGAATA ATTATTTTCAG ATTCCTCAGT TGTAACTTC 3300  
 TACATTTCAAG GGCTTATCTC TGCCCCCATT GATTTTAAAC CTCAAAATGG TGTGAGATTT 3360  
 ACTGTGGAAC CCTAAGACGAG TAAAATAAAA AACCTGGTTG CAGCACATTC ACCTGTTGT 3420  
 CCTTAAATTT CCCCTTTTTT CTCTATGTAC GATAAAGTAA CAGTATGTCA GATAAGCCGG 3480  
 TGGGGGGATG AGATTAGGCT GAGGCAGTGC TAGTCAACTG GGGGAAAAGG ATGATGGAAA 3540  
 AATCACCAGG TTGTGCTATA TTTTAAAGA AGGAGGTCGT TTATGTGTGC AGACAATTCT 3600  
 CCCTGAGGTT AGCCCAATGG AGAAATGAAG CAGAGGAAGG AAACATAGAA AGACATGGGC 3660  
 10 TATCAGGGAG GAAGATGTTT AATAGAACAT GCAAGAATTT CTGGAAGAAA GGCTGTGGAA 3720  
 GGGCCCAATGG AGAAAATGAA TGGACAAAGC TCAGGAATCC CTACGCTATG TAGAATGTTT 3780  
 TTGGTGTAT CAGGGTTAAG CCCTGTAATT ATGTAACCTA TTTATCGCAA CATGAATTTT 3840  
 TATGATTTCT TGTGATGTAT TCTTTTATGA AATTAACAAG AACTCATTAT TTTGAGGTAG 3900  
 AGGAAAATCA ATGCTTTATC TGATATGCTG AGAAATTATT AGATTGCCAA TACTCATGTG 3960  
 CGTTTCATGT GTTTTATAAG GTTTGTTCCT TTGAAGAATT GTAGTTCTTA GTCCACAGG 4020  
 15 GAAATGTGTA TCTATTATA TATCATAGTA TAAATCTATG ATATATTTAT ATCATATATA 4080  
 AAAGTCTGAG TCTCTTTCT TAGTCCCTAA TCATGTTTCT CCCATAGGCT GTGTTTACAT 4140  
 GGAGCTATCG GTTTAGCCTT TTAAGCTTCA TTAGCTTGTC TATTATTGAA ATAGTTTCCA 4200  
 AGAAAATTTA GATATTATCA TAACATCTGG GTCTACTCAA ACACTTATG TTTGAAAGAC 4260  
 TTATGCTTG GACCTATCAA AAACCTGACT TATTTATTGC TTAGTGAAAA TACTAGTGGG 4320  
 20 ATCAACAATG ATTTTCTTGA ATGGGCATGA ATGGAGATGC CCGCACAGTA ATGTAGAAAT 4380  
 GTTTCATACA GCTATTAATA TGTAACAGAC CTCCTTAGAG GCAGATTAGT AACTGTTTCT 4440  
 ACTTTGTATA GCTAAGTGAC AGTCACCTAA CTTACATGAC TTTCTTTTTT CACATTGGGT 4500  
 CTCTGGTCTT GTGTCTTAC CTCAATTATA GCACGTCTCC TTGATTTTGT GTAGTATCAA 4560  
 CTCCGAGTG TCTCTTCTAG TTAAGTTCTT CTCCGTTAA CCAGGAAGTG CTTATTCTCT 4620  
 25 CATCACAGTG GGAAGAATAG CCTATTGTCT TTCATTTTGC CTGAGTGTAT TTTACTATTT 4680  
 GGGCTCTGAA ATAAAAATTA TGAATATATG TGAGGTCACA TGTGGTGTCT GCCTTGCTGC 4740  
 ATAAAAATTT AGGAGGGCAG GTTAGGAGAC AGTTATGTAT GGCCTTTCGG GAAAATTCAA 4800  
 AGGGTGGGAT TACAAGGGTG TTCTCAGGC ATGCCCTAT GGGCCCTATG TGAAGCAAG 4860  
 AGAATTGAC TGATTACAG GACTTCTCTT TATGTCAATC TTAAGAGGAT GGATGAATCT 4920  
 30 GGACATTTGT TCCACCCGAC CTCTGACTGA TGGTTTGGAA AATAACTTTA ATTAGGATCA 4980  
 TATGACCATT GAAAAAGGAA AAATGTAGAC TCTGACTTCC GTCCCACTGA AGGATTAATG 5040  
 AAAACCTTTA CTAGCATTTA GAGCTTTTCA GAACATCCCC ACTGTCATGT GTCTCAGCAG 5100  
 TGGAGACTGC AAGTAAGGCT TTTAATTTTA GGAGGTTTTT TTTTTTTTTT TTTTTTCCCC 5160  
 TAAATGGTAT GGCCAAAAGT CAGAGTTAAA ATATATATAG TTAGATTCCA ACTTCCTCCT 5220  
 35 TCACCTAAA AATAGAATCC AAACCCACTC TTCATATATG CTCCAGAAAT GGGGCTTAAG 5280  
 TACCAATCTC TGCTTTGCAA TGGGCACAAT CTGGTGCATG TCCTGAGGCT CTCTAAGAAA 5340  
 AGAGAGGATC TAGGATGGGA GAGCTAGAAA GTTGCTAACT GGAAGAACA AGGCCCTGAG 5400  
 GGGTTGGTCT ACCAATCTGG GAAGATTGTA AAACAACTT CTCGCACTG AAGGAAGGCT 5460  
 GAAGGCTGCT GCAAGTCATT GAGTGACTTT AGGATGAGCA AAACATTGGG CCACTTCCTA 5520  
 40 ATGCCCTATG TGTATAGTAC CAGAAGCAAG GTCTCAGACT TAACAGACCC AGCTCTGTTC 5580  
 CRAAGTGAGT CTGAACCAAT AGAAGCAAA CATGTGCAGA TATCCAAACA AGACTGCTCA 5640  
 TGCAAGTCGG GGTCTGCTAC CCGTCTTAGG CAGCAACAGC AGAGCTCCAG GGAGCTTATT 5700  
 CAATATTATC TGAGACTTCG AAGACCCAGC AGATGTTTAA TGAAGTCACT ATTTTGGCTC 5760  
 AAACCCCTCA CTCTCTCCCC TCCCTCAAA AAGCCACAG GTAAACACAT AAATGAAAGA 5820  
 45 AACCACAGA AGGGGATGGG AAATAAGAA AATTCTCTCA AGACTTCTCC AGGCCCATGT 5880  
 CACTGGTCAG CGTGGTTTTT ATGTGTATTA GGATTGGGGG ATGTGAAGAA ATAAGTATCC 5940  
 AGTACTTTAT AACCAGGCA ATTAATGAT ATTGGGGTAG GGAATGTTGG CCAGTTTGT 6000  
 TTAGTTTTCG CATCACTAGT TCACCCAGAC CTCACCTAGC CCAGTAAT CGGGCGCCCC 6060  
 50 GAAGAGGGAG ACAGAGATGT GCCAGAGTTG ACCCAGTGTG CGGATGATAA CTAAGTACGA 6120  
 AAGAGTCATC GACCTCAGTT AGTGGTTGGA TGTAGTCACA TTAGTTTGGC TCTCCCCATC 6180  
 TTTGTCTCCC TGGCAAGGAG AATATGCGGG ACATGATGCT AAGAGCCCTG GGTAAATGTG 6240  
 GTGAGAAATG ACACGCTGAT ATGCTACACA TATGTGCTTC TCAGTTGCAG AAAATGAACT 6300  
 GCTTTGGGAG ATTATCAGTA GAAAGAGTGT TATCATATTG GTGCTGAGT CTATGTGTGC 6360  
 55 TTATACAATT TGTCTTGTGA TTTTAATAAA CTTTGAATAA AAGAATAAAA AAAAAAATAA 6420  
 AAAAAAATAA

Seq ID NO: 600 Protein sequence  
 Protein Accession #: NP\_000784.2

60 1 11 21 31 41 51  
 MGILSVLLLI TLQILPVFFS NCLFLALYDS VILLKHVVLL LSRKSKSTRGE WRRMLTSEGL 60  
 RCVWKSFLLD AYKQVKLGED APNSSVVHVS STEGGDNNGN GTQEKIAEGA TCHLLDFASP 120  
 ERPLVVNFGS ATUPPFTSQL PAFRKLVEEF SSVADFLIVY IDEAHPSDGW AIPGDSLSLF 180  
 65 EVKKHQHQED RCAAQQLLE RFSLPQCRV VADRMDNNAN IAYGVAFERV CIVQRQKIAY 240  
 LGGKGPFSYN LQEVHRHLEK NFSKRUKKTR LAG

Seq ID NO: 601 DNA sequence  
 Nucleic Acid Accession #: NM\_005233.1  
 Coding sequence: 101..3052

70 1 11 21 31 41 51  
 CCATGGATGG TAACCTCTCC AGCAATCAGA GCGCTCCCCC TCACATCAGT GGCATGCTTC 60  
 75 ATGGAGATAT GCTCCTCTCA CTGCCCTCTG CACCAGCAAC ATGGATTGTC AGCTCTCCAT 120  
 CCTCTCTCTT CTCAGCTGCT CTGTTCTCGA CAGCTTCGGG GAACGTGATTC CGCAGCCTTC 180  
 CAATGAAGTC AATCTACTGG ATTCAAAAAC AATTCAAGGG GAGCTGGGCT GGATCTCTTA 240  
 TCCATCAAT GGGTGGGAG AGATCAGTGG TGTGGATGAA CATTACACAC CCATCAGGAC 300  
 TTACCAGGTG TGCAATGTCA TGGACCACAG TCAAAACAAT TGGCTGAGAA CAAACTGGGT 360  
 80 CCCAGGAAC TCAGCTCAGA AGATTATGT GGAGCTCAAG TTCCTCTAC GAGACTGCAA 420  
 TAGCATTCCTA TTGGTTTATG GAACTTGCAA GGAGACATTC AACCTGTACT ACATGGAGTC 480  
 TGATGATGAT CTTGGGGTGA AATTCGAGA GCATCAGTTT ACAAAGATTG ACACCATTCG 540  
 AGCTGATGAA AGTTTCACTC AAATGGATCT TGGGGACCGT ATTCTGAAGC TCAACACTGA 600  
 GATTAGAGAA GTAGTGCTTG TCAACAAGAA GGGATTTTAT TTGGCATTTT AAGATGTTGG 660  
 TGCTTGTGTT GCCTTGGTGT CTGTGAGAGT ATACTTCAAA AAGTGCCCAT TTACAGTGAA 720

GAATCTGGCT ATGTTTCCAG ACACGGTACC CATGGACTCC CAGTCCCTGG TGGAGGTTAG 780  
 AGGGTCTTGT GTCAACAAAT CTAAGGAGGA AGATCCTCCA AGGATGTACT GCAGTACAGA 840  
 AGGCCGAATGG CTGTGATCCA TTGGCAAGTG TTCTTGCAAT GCTGGCTATG AAGAAAGAGG 900  
 TTTTATGTGC CAAGCTTGTC GACCAGGTTT CTACAAGGCA TTGGATGGTA ATATGAAGTG 960  
 5 TGCTAAGTGC CCGCCTCACA GTTCTACTCA GGAAGATGGT TCAATGAAC TGCAGGTGTGA 1020  
 GAATAATTAC TTCCGGGCGAG ACAAGACCC TCCATCCATG GCTTGATCCC GACCTCCATC 1080  
 TTCACCAAGA AATGTTATCT CTAATATAAA CGAGACCTCA GTTATCCTGG ACTGGAGTTG 1140  
 GCCCCGAGAC ACAGGAGGCC GGAAGATGT TACCTTCAAC ATCATATGTA AAAAATGTGG 1200  
 10 GTGGAATATA AAACAGTGTG AGCCATGCAG CCCAAATGTC CGCTTCTCTC CTCGACAGTT 1260  
 TGGACTCACC AACACCCAGG TGACAGTGAC AGACCTTCTG GCACATACTA ACTACACCTT 1320  
 TGAGATTGAT GCCGTTAATG GGGTGTGAGA GCTGAGCTCC CCACCAAGAC AGTTTGTCTG 1380  
 GGTCAGCATC ACAACTAATC AGGCTGCTCC ATCACCTGTC CTGACGATTA AGAAAGATCG 1440  
 GACCTCCAGA AATAGCATCT CTTTGTCTCT GCAAGAACCT GAACATCTTA ATGGGATCAT 1500  
 15 ATTGGACTAC GAGGTCAAAT ACTATGAAA GCAGGAACAA GAAACAAGTT ATACCATCTT 1560  
 GAGGGCAAGA GGCACAAATG TTACCATCAG TAGCCTCAAG CTGACACTA TATACGTATT 1620  
 CCAATCCCA GCCCGAACAG CCGCTGGATA TGGGACGAAC AGCCGCAAGT TTGAGTTTGA 1680  
 AACTAGTCCA GACTCTTTCT CCATCTCTGG TGAAAGTAGC CAAGTGGTCA TGATCGCCAT 1740  
 TTAGCGGCA GTAGCAATTA TTCTCCTCAC TGTGTCTATC TATGTTTTGA TTGGGAGGTT 1800  
 CTGTGGCTAT AAGTCAAAAC ATGGGGCAGA TGAAAAAGA CTTCAATTTG GCAATGGGCA 1860  
 20 TTTAAACATT CAGGTTCTCA GGACTTATGT TGACCCACAT ACATATGAAG ACCCTACCCA 1920  
 AGCTGTTTCT GAGTTTGCCA AGGAATTGGA TGCCACCAAC ATATCCATTG ATAAAGTTGT 1980  
 TGGAGCAGGT GAATTTGGAG AGGTGTGCAG TGGTCGCTTA AAACCTCTCT CAAAAAAGA 2040  
 GATTTTCAAGT GCCATTAAAA CCTGAAAGT TGGCTACACA GAAAAGCAGA GGAGAGACTT 2100  
 25 CTTGGGAGAA GCAGCATTA TGGGACAGTT TGACCCACCC AATATCATTC GACTGGAAGG 2160  
 AGTTGTTACC AAAAGTAAGC CAGTTATGAT TGTCACAGAA TACATGGAGA ATGTTCTCTT 2220  
 GGATAGTTTC CTACGTAAAC ACGATGCCCA GTTTACTGTC ATTACAGTAG TGGGGATGCT 2280  
 TCGAGGGATA GCATCTGGCA TGAAGTACCT GTGACAGATG GGTATGTTTC ACCGAGACCT 2340  
 CGCTGCTCGG ACATCTTGA TCAACAGTAA CTTGGTGTGT AAGGTTTCTG ATTTGCGACT 2400  
 30 TTGCGGTGTC CTGGAGGATG ACCCAGAAGC TGCTTATACA ACAAGAGGAG GGAAGATCCC 2460  
 AATCAGGTGG ACATCACCAG AAGCTATAGC CTACCCGAAG TTCACGTCAG CCAGCGATGT 2520  
 ATGGAGTTAT GGGATTATTC TCTGGGAGGT GATGTCTTAT GGAGAGAGAC CATACTGGGA 2580  
 GATGTCCAAT CAGGATGTAA TTAAAGCTGT AGATGAGGGC TATCGACTGC CACCCCCCAT 2640  
 GGACTGCCCA GCTGCCCTGT ATCAGCTGAT GCTGGACTGC TGGCAGAAAG ACAGGAACAA 2700  
 35 CAGACCCCAAG TTTGAGCAGA TTGTTAGTAT TCTGGACAAG CTTATCCGGA ATCCCAGCAG 2760  
 CCTGAAGATC ATCACCAGTG CAGCCGCAAG GCCATCAAAC CTTCTTCTGG ACCAAAGCAA 2820  
 TGTGGATATC TCTACCTTCC GCACAACAGG TGACTGGCTT AATGGGTGCC GGACAGCACA 2880  
 CTGCAAGGAA ATCTTCACGG GCGTGGAGTA CAGTTCTTGT GACACAATAG CCAAGATTTC 2940  
 CACAGATGAC ATGAAAAAGG TTGGTGTGAC CGTGGTTGGG CCACAGAAGA AGATCATCAG 3000  
 40 TAGCATTAAG GCTCTAGAAA CGCAATCAAA GAATGGCCCA GTTCCCGTGT AAAGCAGCAG 3060  
 GGAAGTGCTT CTGGACGGAA GTGGTGGCTG TGGAAGGCGT CAAGTCATCC TGCAGACAGA 3120  
 CAATAATTCT GGAGATACTG GTGGAAGTT

Seq ID NO: 602 Protein sequence  
 Protein Accession #: NP\_05224.1

1 11 21 31 41 51  
 | | | | |  
 MDCQLSILL LSCSVLDSFG ELIPQPSNEV NLLDSKTIQG ELGWISYPSH GWEEISGVDE 60  
 50 HYTPRTYQV CNVMDHSQNN WLRTNWVPRN SAQKIYVELK FTLRDCNSIP LVLGTCKETF 120  
 NLYYMESDDD HGVKFREHQF TKIDTIAADE SFTQMDLGDR ILKLNTEIRE VGPVNKKGFY 180  
 LAFQDVGACV ALVSVRVYFK KCPFTVKNLA MFPDTPVMDS QSLVEVRGSC VNNKSKEEDPP 240  
 RMYCSTEGEW LVPIGKCCSN AGYEERGFMC QACRPGFYKA LDGNMKCAK PPHSSTQEDG 300  
 SMNCRCENNY FRADKDPSPM ACTRPPSPR NVISININETS VILDWSWFLD TGGRKDVTFN 360  
 55 IICKKCGWNI KQCEPCSPNV RFLPRQFGLT NTVTVTDLL AHTNYTFEID AVNGVSELSS 420  
 PPRQFAVSI TTNQAAAPSPV LTIKKDRISR NSISLSWQEP EHPNGIILDY EVKYYEKQEQ 480  
 ETSYTLRAR GTNVITISLK PDTIYVFQIR ARTAAGYGTN SRKFETSP DSFSISGESS 540  
 QVVMIAISAA VAILLLTVVI YVLIGRFGY KSKHGADEKR LHFNGNHLKL PGLRITYVDPH 600  
 TYEDPTQAVH EFAKELDATN ISIDKVVAG EFGVCSGRL KLPSKKEISV AIKTLKVGYT 660  
 60 EKQRDRFLGE ASIMQFDPH NIIRLEGVVT KSKPVMIVTE YMENGSLDSF LRKHDAQFTV 720  
 IQLVGLRGI ASGMKYLSDM GYVHRDLAAR NILINSNLVC KVSDFGLSRV LEDDPEAAYT 780  
 TRGGKIPIRW TSPEAIAYRK FTSASDVWSY GIVLWEVMSY GERPYWEMSN QDVIKAVDEG 840  
 YRLPPMDCP AALYQLMLDC WQKDRNRNRPK FEQIVSILDK LIRNPGSLKI ITSAAARPSN 900  
 LLLDQSNVDI STFRITGDWL NGVRTAHCKE IFTGVEYSSC DTIAKISTDD MKKVGVTVPV 960  
 65 PQKKIISIK ALETQSKNGP VPV

Seq ID NO: 603 DNA sequence  
 Nucleic Acid Accession #: NM\_005727.1  
 Coding sequence: 122..847

1 11 21 31 41 51  
 | | | | |  
 GCCAGGCGTC CCTCTGCCTG CCCACTCAGT GGCAACACCC GGGAGCTGTT TTGTCTTTTG 60  
 70 TGGAGCCTCA GCAGTTCCCT CTTTCAGAAC TCACTGCCAA GAGCCCTGAA CAGGAGCCAC 120  
 CATGCAGTGC TTCAGCTTCA TTAAGACCAT GATGATCCTC TTCAATTGCG TCATCTTTCT 180  
 75 GTGTGGTGCA GCCCTGTTGG CAGTGGGCAT CTGGGTGTCA ATCGATGGGG CATCTTTTCT 240  
 GAAGATCTTC GGGCCACTGT CGTCCAGTGC CATGCAGTTT GTCAACGTGG GCTACTTTCT 300  
 CATCGCAGCG GGCCTGTGCG TCTTTGCTCT TGGTTTCTCG GGCTGCTATG GTGCTAAGAC 360  
 TGAGAGCAAG TGTGCCCTCG TGACGTTCTT CTTTCATCTC CTCCTCATCT TCATTGCTGA 420  
 80 GGTTCGACGT GCTGTGGTGC CCTTGGTGTA CACCACAATG GCTGAGCACT TCCTGACGTT 480  
 GCTGTGATGT CCTGCCATCA AGAAAGATTA TGGTTCCCGA GAAGACTTCA CTCAGGTGTG 540  
 GAACACCAAC ATGAAAGGCG TCAAGTGCTG TGGCTTCACC AACTATACGG ATTTTGAGGA 600  
 CTCACCTTAC TTCAAAGAGA CAGTGCCTT TCCCCATTTC TGTTCGAATG ACAACGTCAAC 660  
 CAACACAGCC AATGAAACCT GCACCAAGCA AAGGCTCAC GACCAAAAAG TAGAGGGTTG 720  
 CTTCAATCAG CTTTGTATAG ACATCCGAAC TAATGCAGTC ACCGTGGGTG GTGTGGCAGC 780

TGGAAATTGGG GGCCTCGAGC TGGCTGCCAT GATTGTGTCC ATGTATCTGT ACTGCAATCT 840  
 ACAATAAGTC CACTTCTGCC TCTGCCACTA CTGCTGCCAC ATGGGAAC TGAAAGAGGCA 900  
 CCCTGGCAAG CAGCAGTGAT TGGGGGAGGG GACAGGATCT AACAAATGTCA CTGGGGCCAG 960  
 AATGGACCTG CCCTTTCTGC TCCAGACTTG GGGCTAGATA GGGACCACTC CTTTTAGGCG 1020  
 ATGCTGACT TTCCTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG 1080  
 GTAGCCAGTT CTGTTGCCCA TTCCCCCAGT CTATTAAACC CTTGATATGC CCCCTAGGCC 1140  
 TAGTGGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT 1200  
 AAGTGAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAACC 1260  
 TGTTACAATG TTAATAAAA

Seq ID NO: 604 Protein sequence  
 Protein Accession #: NP\_005718.1

1 11 21 31 41 51  
 | | | | |  
 MQCFSEFIKTM MIFENLLIFL CGAALLAVGI WVSIDGASFL KIFGPLSSSA MQFVNVGYFL 60  
 IAAGVVVFAL GFLGCGYAKT ESKCALVTFF FILLILIFIAE VAAAVVALVY TTMAEHFLTL 120  
 LVVPAIKKDY GSQEDFTQVW NITMKGLKCC GFTNYTDFED SPYFKENSAF PPFCCNDNVT 180  
 NTANETCTEQ KAHDQKVEGC FNQLLYDIRT NAVTVGGVAA GIGGLELAAM IVSMYLYCNL 240  
 Q

Seq ID NO: 605 DNA sequence  
 Nucleic Acid Accession #: NM\_000729.2  
 Coding sequence:

1 11 21 31 41 51  
 | | | | |  
 GGCTCAGCTG CCGGGCTGCT CCGGTTGGAA ACGCCAAGCC AGTGCCGCTC CTAATCCAAA 60  
 AGCCATGAAC AGCGGCGTGT GCCTGTGCGT GCTGATGGCG GTACTGGCGG CTGGCGCCCT 120  
 GACGCAGCCG GTGCTCCCGC CAGATCCCGC GGGCTCCGGG CTGCAGCGGG CAGAGGAGGG 180  
 GCCCGCTAGG CAGCTGAGGG TATCGCAGAG AACGGATGGC GAGTCCCGAG CGCACCTGGG 240  
 CGCCCTGCTG GCAAGATACA TCCAGCAGGC CCGGAAAGCT CCTTCTGGAC GAATGTCCAT 300  
 CGTTAAGAAG CTGCAGAAC TGGACCCAG CCACAGGATA AGTGACCGGG ACTACATGGG 360  
 CTGGATGGAT TTTGGCCGTC GCAGTGGCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420  
 GCCGCCATCA GCCCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAAAT AAGACAACAA 480  
 TCACACTCAT AACTCATTTG CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540  
 TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACACGCT CACCAGAAAT 600  
 TGTGCAAACT GAAGACAAAA CTGTTTTCTT CATCTGTGAC TCCGTGTCTG AAAATGTTGT 660  
 TATGCTATTA AAGTGATTTC ATTCTGCC

Seq ID NO: 606 Protein sequence  
 Protein Accession #: NP\_000720.1

1 11 21 31 41 51  
 | | | | |  
 MNSGVCLCVL MAVLAAGALT QPVPPADPAG SGLQRAEEAP RRQLRVVSQRT DGESERAHLGA 60  
 LLARYIQAR KAPSGRMSIV KNLQNLDPFH RISDRDYMGW MDFGRRSAEE YEYPS

Seq ID NO: 607 DNA sequence  
 Nucleic Acid Accession #: NM\_001423.1  
 Coding sequence: 219..692

1 11 21 31 41 51  
 | | | | |  
 AGCACTCTCC AGCCTCTCAC CGCAAAATTA CACACCCAG TACACCAGCA GAGGAAACTT 60  
 ATAACCTCGG GAGGCGGGTC CTTCCTCTCA GTGCGGTAC ATACTTCCAG AAGAGCGGAC 120  
 CAGGGCTGCT GCCAGCACT GCCACTCAGA GCGCCTCTGT CGCTGGGACC CTTCAGAACT 180  
 CTCTTTGCTC ACAAGTTACC AAAAAAATA GAGCCAACAT GTTGTGATTG CTGGCTGGTA 240  
 TCTTTGTGGT CCACATCGCT ACTGTTATTA TGCTATTGTT TAGCACCATT GCCAATGTCT 300  
 GGTGTGGTTT CAATACGGTA GATGCATCAG TAGGTCTTTG GAAAAACTGT ACCAACATTA 360  
 GCTGCAGTGA CAGCCTGTGA TATGCCAGTG AAGATGCCCT CAAGACAGTG CAGGCCTTCA 420  
 TGATTCTCTC TATCATCTTC TGTGTCTATG CCCTCCTGGT CTTCTGTGTC CAGCTCTTCA 480  
 CCATGGAGAA GGGAAACCGG TTCTTCTCTT CAGGGGCCAC CACACTGGTG TGCTGGCTGT 540  
 GCATCTTGT GGGGTGTGCC ATCTACACTA GTCATTATGC GAATCGTGAT GGAACGCAGT 600  
 ATCACCACGG CTATTCCTAC ATCCTGGGCT GGATCTGCTT CTGCTTCAGC TTCTCATCTG 660  
 GCGTTCTCTA TCTGGTCTG AGAAAGAAAT AAGGCCGGAC GAGTTCATGG GGATCTGGGG 720  
 GGTGGGGAGG AGGAAGCCGT TGAATCTGGG AGGGAAGTGG AGGTTGCTGT ACAGGAAAAA 780  
 CCGAGATAGG GGAGGGGGGA GGGGGAAGCA AAGGGGGGAG GTCAAATCCC AAACCATTAC 840  
 TGAGGGGATT CTCTACTGCC AAGCCCTGCG CCTGGGGAGA AAGTAGTTGG CTAGTACTTT 900  
 GATGCTCCCT TGATGGGGTC CAGAGAGCCT CCCTGCAGCC ACCAGACTTG GCCTCCAGCT 960  
 GTTCTTAGTG ACACACACTG TCTGGGGCCC CATCAGCTGC CACAACACCA GCCCCACTTC 1020  
 TGGGTTCATG ACTGAGGTCC ACAGACCTAC TGCATGAGT TAAAAATAGC GTACAAGTTC 1080  
 TGGCAAGAGC AGATACTGTC TTTGTGCTGA ATACGCTAAG CCTGGAAGCC ATCCTGCCCT 1140  
 TCTGACCCAA AGCAAAACAT CACATTCAG TCTGAAGTGC TACTGGGGG GCTTTGGCCT 1200  
 GTGAGCCATT GTCCCTCTTT GGAACAGATA TTTAGCTCTG TGAATTCTAG TGACAAAAATG 1260  
 GGAGGAGGAA AGAGAGTTTG TAAGGTCTAT CTGGTGGGTT AGCTAAACCA AGAAGGAGAC 1320  
 CTTTTCACAA TGGAAACCTT GGGGGATGGT CAGAGCCAG TCGAGACCTC ACACACGGCT 1380  
 GTCCCTCATG GAGACCTCAT GCCATGGTCT TTGCTAGGCC TCTTGTGTA AGCCAAGGCA 1440  
 GCTCTTCTGG AGTTTCTCTA AAGTCACTAG TGAACAATTC GGTGGTAAAA GTACCACACA 1500  
 AACTATGGGA TCCAAGGGGC AGTCTTGCAA CAGTGCCATG TTAGGGTTAT GTTTTTAGGA 1560  
 TTCCCTCAA TGCACTCAGT GTTCTTTTA AGTATACAAC AGGAGAGAGA TGGACATGGC 1620  
 TCATTGTAGC ACAATCCTAT TACTCTTCTT CTAACATTTT TGAGGAAGTT TTGCTAAT 1680  
 ATCAATATTG AGGATCAGG CTCTAGGCT CAGTGGTAGC TCTGGCTTAG ACACACCTG 1740  
 GAGTGATCAC CTCTGGGGA CCCTGCCTAT CCCACTTCAC AGGTGAGGCA TGGCAATTCT 1800

5 GGAAGCTGAT TAAACACAC ATAAACCAAA ACCAAACAAC AGGCCCTTGG GTGAAAGGTG 1860  
 CTATATAATT GTGAAGTATT AAGCCTACCG TATTTCAGCC ATGATAAGAA CAGAGTGCCT 1920  
 GCATTCCCGAG GAAATACAGA AATCCCATG AGATAAATAA AATATATAGT GATGGGCAGA 1980  
 TCTTTTCTTT AAAATAAAAA AGCAAAACT CTGTGTGTAC CTAGTCAGAT GGTAGACGAG 2040  
 CTGTCTGCTG CCGCAGGAGC ACCTCTATAC AGGACTTAGA AGTAGTATGT TATTCTTGGT 2100  
 TAAGCAGGCA TTGCTTTGCC CTGGAGCAGC TATTTTAAGC CATCTCAGAT TCTGTCTAAA 2160  
 GGGGTTTTTT GGAAGACGT TTTCTTTATC GCCCTGAGAA GATCTACCCC AGGGAGAATC 2220  
 TGAGACATCT TGCCTACTTT TCTTTATTAG CTTTCTCCTC ATCCATTCTT TTTATACCTT 2280  
 TCCTTTTTGG GGAGTTGTTA TGCCATGATT TTTGGTATTT ATGTAAAGG ATTATTACTA 2340  
 10 ATTCTATTTC TCTATGTTA TTCTAGTTAA GGAATGTGT AGGGCAAGCC ACCAAATTAC 2400  
 CTAGGCTGAG GTTAGAGAGA TTGGCCAGCA AAAACTGTGG GAAGATGAAC TTTGTCATTA 2460  
 TGATTTCATT ATCAGATGAT TATAGAAGGC TGTCTTAGTG CAAAAACAT ACTTACATTT 2520  
 CAGACATATC CAAAGGGAAT ACTCACATTT TGTTAAGAAG TTGAACATATG ACTGGAGTAA 2580  
 15 ACCATGTATT CCCTTATCTT TTACTTTTTT TCTGTGACAT TTATGTCTCA TGTAAATTGC 2640  
 ATTACTCTGG TGGATTGTTT TAGTACTGTA TTGGGCTTCT TCGTTAATAG ATTATTTTCA 2700  
 ATACTATAAT TGTAAATATT TTGATACAAA TGTTTATAAC TCTAGGGATA TAAAAACAGA 2760  
 TTCTGATTCC CTTCAAAAAA AAAAAA

Seq ID NO: 608 Protein sequence  
Protein Accession #: NP\_001414.1

1 11 21 31 41 51  
 25 MLVLLAGIFV VHIAIVIMLF VSTIANVWL V SNTVDASVGL WKNCTINISCS DLSLYASEDA 60  
 LKTQVAFMIL SIIFCVIALF VFVQLFTME KGNRFLLSGA TTLVCWLCIL VGVSIYTSYH 120  
 ANRDGTQYHH GSYLLGWIC FCFSLIIGVL YLVLRKK

Seq ID NO: 609 DNA sequence  
Nucleic Acid Accession #: NM\_004961.2  
Coding sequence: 55..1575

1 11 21 31 41 51  
 35 GCCAGAGCGT GAGCCGCGAC CTCCGCGCAG GTGGTCTCGC CCGTCTCCGC GGAAATGTTG 60  
 TCCAAAGTTC TTCCAGTCCCT CCTAGGCATC TTATTGATCC TCCAGTCGAG GGTCTGAGGA 120  
 CCTCAGACTG AATCAAAGAA TGAAGCCTCT TCCCGTGATG TTGCTATATG CCCCAGCCCC 180  
 CAGCCTCTGG AAAATCAGCT CCTCTCTGAG GAAACAAAGT CAACTGAGAC TGAGACTGGG 240  
 AGCAGAGTTG GCAAACTGCC AGAAGCCTCT CGCATCCTGA ACACATATCT GAGTAATTAT 300  
 40 GACCACAAAC TCGCCCTCTG CATTTGAGAG AAGCCCACTG TGGTCACTGT TGAGATCGCC 360  
 GTCACAGGCC TTGGTCTCTCT CTCTATCCTA GACATGGAAT ACACCATTTGA CATCATCTTC 420  
 TCCAGACCT GGTACGACGA ACGCCTCTGT TACAACGACA CCTTTGAGTC TCTTGTCTTG 480  
 AATGGCAATG TGGTAGGCCA GCTATGGATC CCGGACACCT TTTTATAGAA TTCTAAGAGG 540  
 ACCCAGGAGC ATGAGATCAC CATGCCCAAC CAGATGGTCC GCATCTACAA GGATGGCAAG 600  
 45 GTGTTGTACA CAATTAGGAT GACCATTGAT GCCGGATGCT CACTCCACAT GCTCAGATT 660  
 CCAATGGATT CTCACTCTTG CCTCTATCTT TTCTCTAGCT TTTCTATACC TGAGAATGAG 720  
 ATGATCTACA AGTGGGAAAA TTTCAAGCTT GAAATCAATG AGAAGAACTC CTGGAAGCTC 780  
 TTCCAGTTTG ATTTTACAGG AGTGAGCAAC AAAACTGAAA TAATCACAAC CCCAGTTGGT 840  
 GACTTCATGG TCATGACGAT TTTCTTCAAT GTGAGCAGGC GGTTTGGCTA TGTTCCTTTT 900  
 50 CAAAACATATG TCCCTTCTTC CGTGACCACG ATGCTCTCCT GGGTTTCTCT TTGGATCAAG 960  
 ACAGAGTCTG CTCAGGCCCC GACCTCTCTA GGGATCACCT CTGTTCTGAC CATGACCACG 1020  
 TTGGGACACT TTTCTCTGTA GAATTTCCCG CGTGTCTCCT ATATCACAGC CTGGGATTTT 1080  
 TATATCGCCA TCTGCTTCGT CTCTGCTTTC TGGCTCTGCT TGGAGTTTGC TGTGCTCAAC 1140  
 TTCTGATCT ACAACCAGAC AAAAGCCCAT GCTTCTCTTA AACTCCGCCA TCCTCGTATC 1200  
 55 AATAGCCGTG CCGATGCCCC TACCCGTGCA CGTTCCCGAG CCTGTGCCCC CCAACATCAG 1260  
 GAAGCTTTTG TTGTCAGAGT TGTCAACACT GAGGGAAAGT ATGGAGAGGA GCGCCCGTCT 1320  
 TGCTCAGCCC AGCAGCCCCC TAGCCAGGCT AGCCCTGAGG GTCCCCGAG CCTCTGCTCC 1380  
 AAGCTGGCCT GCTGTGAGTG GTGCAAGCCT TTTAAGAAGT ACTTCTGCAT GGTCCCCGAT 1440  
 TGTGAGGGCA GTACCTGGCA GCAGGGCCGC CTCTGCATCC ATGTCTACCG CCTGGATAAC 1500  
 TACTCGAGAG TTGTTTCTCC AGTGACTTTC TTCTTCTTCA ATGTGCTCTA CTGGCTTGT 1560  
 60 TGCCCTAAGT TGTAGGTACC AGCTGTIACC CTGTGGGGCA ACCCTCTCAG TTCCCCAGGA 1620  
 GGTCCAAGCC CCTTGCCAAG GGAGTTGGGG GAAAGCAGCA GCAGCAGCAG GAGCGACTAG 1680  
 AGTTTTCCTT GCCCCATPCC CCAACAGAAA GCTTGCAGAG GGTTTGTCTT TGCTGCCCCC 1740  
 CTCCTCTACC TGGCCCATTC ACTGAGTCTT CTCAGCAGAC CATTTCAAAT TATTAATAAA 1800  
 TGGGCCACCT CCTCTTCTT CAAGGAGCAT CCGTGATGCT CAGTGTTCAA AACCACAGCC 1860  
 65 ACTTAGTGAT CAGCTCCCTA AAACCATGCC TAAGTACAGG CGGATTAGCT ATCTTCCAAC 1920  
 AATGCTGACC ACCAGACAAT TACTGCATTT TTCCAGAAGC CCACTATTGC CTTTGTAGTG 1980  
 CTTTCGGCCC AGTTCTGGCC TCAGCCTCAA AGTGACCCGA CTAGTTGCTT GCCTATACCT 2040  
 GGCACCTCAT TAAGATGCTG GGCAGCAGTA TAACAGGAGG AAGAGATCCC TCTCCTTTGG 2100  
 70 TCAGATTATT ATGTTCTCAG TTCTCTCTCC CTGCTACCCC TTTCTCTGCA GATAGATAGA 2160  
 CACTGGCATT ATCCCTTTAG GAAGAGGGGG GGGCAGCAAG AGAGCCTATT TGGGACAGCA 2220  
 TCTCTCTCTC TCTGCTGCTG TGACATCTCC CTCTCCTTGC TGGCTCCATC TTTGCTCTGC 2280  
 ACTACCAATT CAATGCCCTT CATCCAATGG GTATCTATTT TTGTGTGTGA TTATAGTAAC 2340  
 TACTCCCTGC TTTATATGCC ACCCTCTTCC TTCTCTTTGA CCCCCTGAC TCTTCTGTGA 2400  
 75 ACTTTCCAG TGACTTCCCC TAGCCCTGAC CCAGGCACTA GGCCTTGGTG ACTTCTGGG 2460  
 GCCAAGAAAC TAAGGAAACT CGGCTTTGCA ACAGGCATTA CTCGCCATTG ATTTGGTGCC 2520  
 ACCAGGGCA CACTGTGCGA GTTCTATCAC TTGCTTGACC CTTGGACCCA TAAACCACTG 2580  
 CACTGTTATA CCGGGGCGAC TCTAACCATC ACAATCAATC AATCAAAATC CCTTAAATTT 2640  
 GTATGGCATT GGAACCTTGG CAAAGCACTT TTGACAAGTT GTGTCTGATT GGAGCTTCAT 2700  
 80 GATAGCCTTG TGACATCTTT AGGGCAGGAT TCTTATCCCC ATTTTGCGA TGAACACCT 2760  
 GAGTACAGCA TTTCTGTGGG ACTGTGGATC TCACTGGAAG CTATCCAAGA GCCCACTGTC 2820  
 ACCTTCTAGA CACATGATA GGGCTAGACA GCTCAGTTCA CCATGATTCT CTTCTGTAC 2880  
 CTCTGCTGGC ACACCACTGG CAAGGCCAG AATGGCGACC TCTCTTAGC TCAATTTCTG 2940  
 GGCCTGAGGT GCTCAGACTG CCCCCAAGAT CAAATCTCTC CTGGCTGTAG TAACCCAGTG 3000  
 GAATGAATTT GGACATGCCC CAATGCTTCT ATATGCTAAG TGAAATCTGT GTCTGAATT 3060



TGTTGGGGGG TGGATAGGGT GGGGTCTCCA TCTACTTTTT GTCACCATCA TCTGAAATGG 3120  
GGAAATATGT AAATAATAT ATCAGCAAAG CAAAAGAAA AAAAAAAA

Seq ID NO: 610 Protein sequence  
Protein Accession #: NP\_004952.1

1 11 21 31 41 51  
| | | | | |  
10 MLSKVLPLVLL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60  
TGSRVGKLPE ASRILNTILS NYDHKLRLPGI GEKPTVVTV E IAVNSLGLPLS ILDMEYITIDI 120  
IFSQTWYDER LCYNDTFESL VLNGNVVSQL WIPDTFFRNS KRTHEHEITM PNQMVRIYKD 180  
GKVLVYTRMT IDAGCSLHML RFPMDSHSCP LSFSSFSYPE NEMIIYKWENF KLEINEKNSW 240  
KLFQDFDTGV SNKTEIITTP VGDFMVTMIF FNVSRRFYV AFQNYVPSSV TTMLSWVSFW 300  
15 IKTESAPART SLGITSVLTM TTLGTFSRKN FPRVSYITAL DFYIAICFVF CFCALLEFAV 360  
LNFLIYNQTK AHASPKLRHP RINSRAHART RARSACARQ HQEAFVCQIV TTEGSDGEER 420  
PSCSAQQPPS PGSEPGPRSL CSKLACCEWC KRFKKYFCMV PDCEGSTWQQ GRLCIHVYRL 480  
DNYSRVFPV TFFFNVLVW LVCLNL

Seq ID NO: 611 DNA sequence  
Nucleic Acid Accession #: NM\_021984.1  
Coding sequence: 572..1753

1 11 21 31 41 51  
| | | | | |  
25 GCCAGAGCGT GAGCCGCGAC CTCCGCGCAG GTGGTCGCGC CGGTCTCCGC GGAAATGTTG 60  
TCCAAAGTTC TTCCAGTCCT CCTAGGCATC TTATTGATCC TCCAGTCGAG AACATGTATA 120  
CAGAGAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAT GACCACAGCG 180  
GTGTAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCTTTGT 240  
30 CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC 300  
TCAGACTGAA TCAAAAGATG AAGCCTCTTC CCGTGTATGT GTCTATGGCC CCCAGCCCCA 360  
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420  
CAGAGTTGGC AAAGTGCAG AAGCCTCTCG CATCCTGAAC ACTATCCTGA GTAATTATGA 480  
CCACAAACTG CGCCCTGGCA TTGGAGAGAA GCCCACTGTG GTCACCTGTG AGATCTCCGT 540  
35 CAACAGCCTT GGTCCCTCTCT CTATCCTAGA CATGGAATAC ACCATTGACA TCATCTTCTC 600  
CCAGACCTGG TAGCAGCAAC GCCTCTGTGA CAACGACACC TTTGAGTCTC TTGTTCTGAA 660  
TGGCAATGTG GTGAGCCGAG TATGGATCCC GGACACCTTT TTTAGGAATT CTAAGAGGAC 720  
CCACGAGCAT GAGATCACCA TGCCCAACCA GATGGTCCGC ATCTACAAGG ATGGCAAGGT 780  
GTTGTACACA ATTAGGATGA CCATTGATGC CGGATGTCTA CTCCACATGC TCAGATTTC 840  
40 AATGATTCTT GGTCTTGTCC CTCTATCTTT CTCTAGCTTT TCCTATCCTG AGAATGAGAT 900  
GATCTACAAG TGGGAAAATT TCAAGCTTGA AATCAATGAG AAGAACTCCT GGAAGCTCTT 960  
CCAGTTGGAT TTTACGAGG TGAGCAACAA AACTGAAATA ATCACAACCC CAGTTGGTGA 1020  
CTTCATGGTC ATAGACGATT TCTCAATGT GAGCAGGCGG TTTGGCTATG TTGCCTTTCA 1080  
AAACTATGTC CCTTCTTCCG TGACCAAGAT GCTCTCCTGG GTTTCCTTTT GGATCAAGAC 1140  
45 AGAGTCTGCT CAGGCCGGA CCTCTTAGG GATCACCTCT GTTCTGACCA TGACCACGTT 1200  
GGGCACCTTT TCTCGTAAGA ATTTCCCGCG TGTCTCCTAT ATCACAGCCT TGGATTCTTA 1260  
TATCGCCATC TGCTTCTGCT TCTGCTCTG CGCTCTGTTG GAGTTTGCTG TGCTCAACTT 1320  
CCTGATCTAC AACCAAGCAA AAGCCCATGC TTCTCCTAAA CTCGCCATC CTGATATCAA 1380  
TAGCCGTGCC CATGCCGTA CCCGTGCACG TTCCCGAGCC TGTGCCGCC AACATCAGGA 1440  
50 AGCTTTTGTG TGCCAGATTG TCACCACTGA GGAAGTGAT GGAGAGGAGC GCCCGTCTTG 1500  
CTCAGCCGAG CAGCCGCCCTA GCCCAGGTAG CCCTGAGGGT CCCCAGGCC TCTGCTCAA 1560  
GCTGGCCTGC TGTGAGTGGT GCAAGCGTTT TAAGAAGTAC TTCTGCTAGG TCCCGGATTG 1620  
TGAGGGCAGT ACCTGGCAGC AGGCCCGCCT CTGCATCCAT GTCTACCGCC TGGATAACTA 1680  
CTCGAGAGTT GTTTTCCGAG TGACTTTCTT CTCTTCAAT GTGCTCTACT GGCTTGTTTG 1740  
55 CCTTAACCTG TAGGTACCGT CTGGTACCTT GTGGGGCAAC CTCTCCAGTT CCCAGGAGG 1800  
TCCAAAGCCC TTGCCAAGGG AGTTGGGGGA AAGCAGCAGC AGCAGCAGGA CGCATAGAG 1860  
TTTTTCTGCG CCCATCCCC AAACAGAAGC TTGCAGAGGG TTTGCTTTG CTGCCCCCTC 1920  
60 CCCCTACCTG GCCCATTCAC TGAGTTTCT CAGCAGACCA TTTCAAATTA TTAATAAATG 1980  
GGCCACCTCC CTCTTCTTCA AGGAGCATCC GTGATGCTCA GTGTTCAAAA CCACAGCCAC 2040  
TTAGTGATCA GCTCCCTAAA ACCATGCCTA AGTACAGGCG GATTAGCTAT CTTCACAA 2100  
TGCTGACCAC CAGACAATTA CTGCATTTT CCAGAAGCCC ACTATTGCCCT TTGCAGTGCT 2160  
TTCGGCCGAG TTCTGGCCTC AGCCTCAAAG TGCACCGACT AGTTGCTTGC CTATACCTGG 2220  
CACCTCATT AAGATGCTGG CAGCAGTATA ACAGGAGGAA GAGATCCCTC TCCTTGGTGC 2280  
65 AGATTATTAT GTTCTCAGTT CTCTCTCCCT GCTACCCCTT TCTCTGCAGA TAGATAGACA 2340  
CTGGCATTAT CCCTTTAGGA AGAGGGGGGG GCAGCAAGAG AGCCTATTGG GGACAGCATT 2400  
CCTCTCTCTC TGCTCTGTG ACATCTCCCT CTCCTTGCTG GCTCCATCTT TCGTCTGCAC 2460  
TACCAATTCA ATGCCCTTCA TCCAATGGGT ATCTATTTT GTGTGTGATT ATAGTAACTA 2520  
CTCCCTGCTT TATATGCCAC CCTCTTCTT CTCTTTGACC CCTGTGACTC TTTCTGTAA 2580  
70 TTTCCGAGTG ACTTCCCTTA GCCCTGACCC AGGCACTAGG CCTTGGTGAC TTCTGGGGC 2640  
CAAGAACTA AGGAACTCG GCTTTGCAAC AGGCATTACT CGCCATTGAT TGGTCCAC 2700  
CCAGGGACA CTGTCGGAGT TCTATCACTT GCTTGACCCC TGGACCCATA AACCACTCCA 2760  
CTGTTATACC CGGGGCACTG TAACCATCAC AATCAATCAA TCAAAATTCC TTAATTTGT 2820  
ATGGCACTGG AACTTTGGCA AAGCACTTT GACAAAGTGT GTCTGATTGG AGCTTCATGA 2880  
TAGCCTTGTG ACATCTTTAG GGCAGGATTC TTATCCCAT TTTGCAGATG AAAACCTGA 2940  
75 GTCACAGATT TCTGTGGGAC TGTGGATCTC ACTGGAAGCT ATCCAAGAGC CCACTGTCAC 3000  
CTTCTAGACC ACATGATAGG GCTAGACAGC TCAGTTTACC ATGATTCTCT TCTGTACCT 3060  
CTGCTGGCAC ACCAGTGGCA AGGCCAGAA TGGCGACCTC TCTTTAGCTC AATTCTGGG 3120  
CCTGAGGTGC TCAGATGCC CCCAAGATCA AATCTCTCCT GGCTGTAGTA ACCCAGTGA 3180  
ATGAATTTGG ACATGCCCTA ATGCTTCTAT ATGCTAAGTG AAATCTGTGT CTGTAATTGT 3240  
80 TTGGGGGGTG GATAGGGTGG GGTCTCCATC TACTTTTGT CACCATCATC TGAATGGGG 3300  
AAATATGTAA ATAAATATAT CAGCAAAGC

Seq ID NO: 612 Protein sequence  
Protein Accession #: NP\_068819.1

```

1      11      21      31      41      51
|      |      |      |      |      |
MEYTIIDIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFERNRSKRT HEHEITMPNQ 60
MVR1YKDGKV LYTIIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120
5 INEKN5WKLF QLDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTM 180
LSWVSFWIKT ESAPARTSLG ITSVLMTITL GTFSRKNFPR VSYITALDFY IAIQVFCFC 240
ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE 300
GSDGEERPSC SAQPPSPSGS PEGPRSLCSK LACCEWCKRF KKYFCMVPCD EGSTWQQARL 360
10 CIHVYRLDNY SRVVPVTFE FENVLWLVC LNL

```

Seq ID NO: 613 DNA sequence  
Nucleic Acid Accession #: NM\_021987.1  
Coding sequence: 572..1657

```

15      1      11      21      31      41      51
|      |      |      |      |      |
GCCAGAGCGT GAGCCGCGAC CTCCGCGCAG GTGGTCCGCG CGGTCTCCGC GGAAATGTTG 60
TCCAAAGTTC TTCCAGTCCT CCTAGGCATC TTATTGATCC TCCAGTCGAG AACATGTATA 120
20 CAGAGAAGTG CTCAAATCAT AAGTGACAG CTGATGAGTT GTCAAAAAAT GACCACAGCG 180
GTGTAAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCTTTTGT 240
CACTGCCTCC CAGCAAAAGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGGACC 300
TCAGACTGAA TCAAAGAAATG AAGCCTCTTC CCGTGATGTT GTCTATGGCC CCCAGCCCCA 360
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420
CAGAGTTGGC AAACCTGCCA AAGCCTCTCG CATCTGAAC ACTATCCTGA GTAATTATGA 480
25 CCACAAACTG CGCCTTGGCA TTGGAGAGAA GCCCACTGTG GTCACTGTG AGATCTCCGT 540
CAACAGCCTT GGTCTCTCT CTATCCTAGA CATGGAATAC ACCATGACA TCATCTTCTC 600
CCAGACCTGG AATTCTAAGA GGACCCACGA GCATGAGATC ACCATGCCCA ACCAGATGGT 660
CCGCATCTAC AAGGATGGCA AGGTGTTGTA CACAATTAGG ATGACCATG ATGCCGGATG 720
CTCACTCCAC ATGCTCAGAT TTCCAATGGA TTCTCACTCT TGCCCTCTAT CTTTCTCTAG 780
30 CTTTCTCTAT CCTGAGAATG AGATGATCTA CAAGTGGGAA AATTTCAAGC TTGAAATCAA 840
TGAGAAGAAC TCTTGGAAAG TCTTCCAGTT TGATTTTACA GGAGTGAGCA ACAAAAGTGA 900
AATAATCACA ACCCCAGTTG GTGACTTCAT GGTCTGACG ATTTTCTTCA ATGTGAGCAG 960
GCGGTTTGGC TATGTTGGCT TTCAAACTA TGTCCCTTCT TCCGTGACCA CGATGCTCTC 1020
35 CTGGGTTTCC TTTTGGATCA AGACAGAGTC TGCTCCAGCC CGGACCTCTC TAGGGATCAC 1080
CTCTGTTCTG ACCATGACCA CGTTGGGCAC CTTTCTCTGT AAGAAATTTCC CGCGTGTCTC 1140
CTATATCACA GCCTTGGATT TCTATATCGC CATCTGCTTC GTCTTCTGCT TCTGCGCTCT 1200
GTTGGAGTTT GCTGTGCTCA ACTTCTGAT CTACAACCAG ACAAAGCCCC ATGCTTCTCC 1260
TAAACTCCGC CATCTCTGTA TCAATAGCCG TGCCCATGCC CGTACCCGTG CACGTTCCCG 1320
40 AGCCTGTGCC CGCCAACATC AGGAAGCTTT TGTGTGCCAG ATTGTCAACA CTGAGGGAAG 1380
TGATGGAGAG GAGCCGCCGT CTGTCTCAGC CCAGCAGCCC CTTAGCCGAG GTAGCCCTGA 1440
GGGTCCCGCG AGCCTCTGCT CCAAGCTGGC CTGCTGTGAG TGGTGCAAGC GTTTTAAGAA 1500
GTACTTCTGC ATGGTCCCGG ATGTGTAGGG CAGTACCTGG CAGCAGGGCC GCCTCTGCAT 1560
CCATGCTTAC CGCCTGGATA ACTACTCGAG AGTTGTTTTC CCAGTGACTT TCTTCTCTCT 1620
45 CAATGTGCTC TACTGGCTTG TTTGCCCTAA CTGTAGGTA CCAGCTGGTA CCCTGTGGGG 1680
CAACCTCTCC AGTTCCCGAG GAGGTCCAAG CCCCTTGCCA AGGGAGTTGG GGGAAAGCAG 1740
CAGCAGCAGC AGGAGCGACT AGAGTTTTTC CTGCCCCATT CCCCACACAG AAGCTTGAG 1800
AGGGTTTGTG TTTGCTGCCC CTCTCCCCCTA CTTGGCCCAT TCACTGAGTT TTCTCAGCAG 1860
ACCATTTCAA ATTAATTAATA AATGGGCCAC CTCCCTCTTC TTCAAGGAGC ATCCGTGATG 1920
50 CTCAAGTGTG AAAACCCAGC CCACTTAGTG ATCAGCTCCC TAAACCATG CCTAAGTACA 1980
GGCGGATTAG CTATCTTCCA ACAATGCTGA CCACCAGACA ATTACTGCAT TTTTCCAGAA 2040
GCCCCACTAT GCCTTTGCGG TGCTTTGCGC CCAGTTCTGG CCTCAGCCTC AAAGTGCACC 2100
GACTAGTTGC TTGCTCTATC CTGGCACCTC ATTAAGATGC TGGGCAGCAG TATAACAGGA 2160
GGAAAGAGATC CCTCTCCTTT GGTGAGATTA TTATGTTCTC AGTTCTCTCT CCCTGCTACC 2220
55 CCTTCTCTG CAGATAGATA GACACTGGCA TTATCCCTTT AGGAAGAGGG GGGGGCAGCA 2280
AGAGAGCCTA TTTGGGACAG CATTCCTCTC TCTCTGCTGC TGTGACATCT CCCTCTCCTT 2340
GCTGGCTCCA TCTTTCTGCT GCACTACCAA TTCAATGCCC TTCAATCCAAT GGGTATCTAT 2400
TTTTGTGTGT GATTATAGTA ACTACTCCCT GCTTTATATG CCACCTCTCT CTTCTCTTTT 2460
GACCCCTGTG ACTCTTTCTG TAACTTTCCC AGTGACTTCC CTTAGCCCTG ACCAGGCACT 2520
60 AGGCCTTGGT GACTTCTTGG GGCCAAAGAA CTAAGGAAAC TCGGCTTTGC AACAGGCATT 2580
ACTCGCCATT GATTGGTGCC CACCCAGGGC ACACCTGTCG AGTTCTATCA CTGTCTTGAC 2640
CCCTGGACCC ATAAACCAAGT CCACTGTTAT ACCCGGGGCA CTCTAACCAT CACAATCAAT 2700
CAATCAAAAT CCCTTAAAT TGTATGGCAC TGGAACTTTG GCAAAGCACT TTTGACAAGT 2760
TGTGTCTGAT TGGAGCTTCA TGATAGCCTT GTGACATCTT TAGGGCAGGA TTCTTATCCC 2820
GATTTTGCAG ATGAAACCCC TGAGTCACAG ATTTCTGTGG GACTGTGGAT CTCCTGGGAA 2880
65 GCTATCCAAG AGCCCACTGT CACCTTCTAG ACCACATGAT AGGGCTAGAC AGCTCAGTTC 2940
ACCATGATTG TCTTCTGTCA CCTCTGCTGG CACACCAGTG GCAAGGCCCA GAATGGCGAC 3000
CTCTCTTTAG CTCAATTTCT GGGCCTGAGG TGCTCAGACT GCCCCAAGA TCAATCTCT 3060
CCTGGCTGTA TGAACCCAGT GGAATGAATT TGGACATGCC CCAATGCTTC TATATGCTAA 3120
70 GTGAATCTG TGTCTGTAAT TTGTTGGGGG GTGGATAGGG TGGGTCTCC ATCTACTTTT 3180
TGTCACCATC ATCTGAAATG GGGAAATATG TAAATAAATA TATCAGCAAA GC

```

Seq ID NO: 614 Protein sequence  
Protein Accession #: NP\_068822.1

```

75      1      11      21      31      41      51
|      |      |      |      |      |
MEYTIIDIFS QTWNSKRTHE HEITMPNQMV RIYKDGKVLV TIRMTIDAGC SLHMLRFPMD 60
SHSCPLSFSS FSYPENEMIV KWENFKLEIN EKNSWKLQFQ DFTGVSNKTE IITTPVGDEF 120
80 VMTIFFNVSR RFGYVAFQNY VPSSVTMMLS WVSFWIKTES APARTSLGIT SVLMTMTLGT 180
FSRKNFPRVS YITALDFYIA ICFVFCFCAL LEFAVLNFLI YNQTKAHASP KLRHPRINSR 240
AHARTRARSR ACARQHQEAF VCQIVTTEGS DGEERPSCSA QPPSPSGSPE GPRSLCSKLA 300
CCEWCKRFFK YFCMVPCDEG STWQQGRLCI HVRDLNYSR VVFPVTFEFL NVLYWLVLN 360
L

```

Seq ID NO: 615 DNA sequence  
Nucleic Acid Accession #: NM\_021990.1  
Coding sequence: 1309..2490

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      GCCAGAGCGT GAGCCGCGAC CTCCGCGCAG GTGGTCGCGC CGGTCTCCGC GGAAATGTTG 60
      TCCAAAGTTC TTCCAGTCCT CCTAGGCATC TTATTGATCC TCCAGTCGAG AACATGTATA 120
10     CAGAGAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAAT GACCACAGCG 180
      GTGTAAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCCTTTGT 240
      CACTGCCTCC CAGCAAAGGC AGCACTATCC GGACTTCTAA CACCATCGGT GAGTTTCATA 300
      CCTTGGCAGA TGGCCTTTAA CATTTTGTGT TAATTCAATT ATCTTACTA ATCTTCTTCT 360
      TTTTCTTGGC TGTGGTGCAT GGCTGTGGAG CTCAGGGTGG ACTCCTGTTG GGCAGCCAGT 420
      TCCTGGATGG CTGTCTGTGG GTGGAGGACT CCTGCCCTTC CTGTTTAGAC ACCCACAAAG 480
15     GCTGCTCTTT AGCCTCCTTC CCTTCATCCC TTCCCCTGC CCCCAGTGCA ACGAGTATTA 540
      CACAACCAAC AAAACCGCAA AATATTCCCA CAATTTTCTG GTCCTCTCTG GGAGAGGCCG 600
      CTCTGGCTTT TCCTCTCAGC CCTGGCCCTC TGCCCTGCTC TCACTCCTGG TTGGTGTCTG 660
      TCAGGCTGAG TAGAGGCCAA GGCGACCAAC ACTAGGCAAA CGCGGCCAGC GCTCAGACAT 720
      AAATGCCCTC TTCATTTCAC GTGTAACATT CTTTAAAAAT CTAGGTCTTG GTTTTGTGTA 780
20     TTTTCTTTTA AATAAAGAG TGATCATAAA AGAGGGACAG CATAGAAAGT CCCCAGAGAG 840
      CAGCAAGGTT TAAAGAAAT TCACAAGCCT AATCTGTAC TGCTTTATAA TTTGCTATTA 900
      CCAGTCACAA TTTAACTAGG TTTTGTGTG AAAACTTGT TGGTTTGTCT TCTGTCCCAA 960
      GAGGCACTAG CTGGGGCCCC TACAGAGTGC AGGGCAGAGC TTCATTTTTC GTTTGAATGT 1020
      TCTAGGGTCG AGGGACCTCA GACTGAATCA AAGAATGAAG CCTCTTCCCG TGATGTTGTC 1080
25     TATGGCCCCC AGCCCCAGCC TCTGAAAAAT CAGCTCCTCT CTGAGGAAAC AAAGTCAACT 1140
      GAGACTGAGA CTGGGAGCAG AGTTGGCAAA CTGCCAGAAG CCTCTCGCAT CCGAACACT 1200
      ATCCTGAGTA ATTAGACCA CAACTGCGC CCTGGCATTG GAGAGAAGCC CACTGTGGTC 1260
      ACTGTTGAGA TCTCCGTCAA CAGCCTTGT CTCTCTCTA TCCTAGACAT GGAATACACC 1320
      ATTGACATCA TCTTCTCCCA GACCTGGTAC GACGAACGCC TCTGTTACAA CGACACCTTT 1380
30     GAGTCTCTTG TTCTGAATGG CAATGTGGTG AGCCAGCTAT GGATCCCGGA CACCTTTTTT 1440
      AGGAATTTCTA AGAGGACCCA CGAGCATGAG ATCACCATGC CCAACCAGAT GGTCCGCATC 1500
      TACAAGGATG GCAAGGTGTT GTACACAATT AGGATGACCA TTGATGCCCG ATGCTCACTC 1560
      CACATGCTCA GATTTCCAAT GGATTCCTAC TCTTGCCCTC TATCTTTCTC TAGCTTTTCC 1620
      TATCCTGAGA ATGAGATGAT CTACAAGTGG GAAAATTTCA AGCTTGAAT CAATGAGAAG 1680
35     AACTCCTGGA AGCTCTTCCA GTTTGATTTT ACAGGAGTGA GCAACAAAAC TGAAATAATC 1740
      ACAACCCAG TTGGTGCATT CATGGTCATG ACGATTTTCT TCAATGTGAG CAGGCGGTTT 1800
      GGCTATGTTG CCTTTCAAAA CTATGTCCCT TCTTCCGTGA CCACGATGCT CTCCTGGGTT 1860
      TCCTTTTGGA TCAAGACAGA GTCTGTCTCA GCCCGGACCT CTCTAGGGAT CACCTCTGTT 1920
40     CTGACCATGA CCACGTGGG CACCTTTTCT CGTAAGAAAT TCCCGCGTGT CTCCTATATC 1980
      ACAGCCTTGG ATTTCTATAT CGCCATCTGC TTCGTCTTCT GCTTCTGCGC TCTGTGGAG 2040
      TTTGCTGTGC TCAACTTCTT GATCTACAAC CAGACAAAAG CCCATGCTTC TCCTAAACTC 2100
      CGCCATCTCT GATATCAATG CCGTGCCCAT GCCCGTACCC GTGCACGTT CCGAGCCTT 2160
      GCCCGCAAC ATCAGGAAGC TTTTGTGTGC CAGATTGTCA CCACTGAGGG AAGTGATGGA 2220
45     GAGGAGCGCC CGTCTTGTCT AGCCAGCAG CCCCCTAGCC CAGGTAGCCC TGAGGGTCCC 2280
      CGCAGCCTCT GCTCCAAGCT GGCCTGCTGT GAGTGGTGCA AGCGTTTTAA GAAGTACTTC 2340
      TGCATGGTCC CCGATTGTGA GGGCAGTACC TGGCAGCAGG GCCGCTCTG CATCCATGTC 2400
      TACCGCCTGG ATAACACTAG GAGAGTTGTT TTCCAGTGA CTTTCTTCTT CTTCAATGTG 2460
      CTCTACTGGC TTGTTTGCCT TAAGTTGTAG GTACCACTG GTACCTCTGT GGGCAACCTC 2520
50     TCCAGTTCCC CAGGAGGTCC AAGCCCCTTG CCAAGGGAGT TGGGGGAAAG CAGCAGCAGC 2580
      AGCAGGAGCG ACTAGAGTTT TTCTGCCCC ATTCCCCAA CAGAAGCTTG CAGAGGGTTT 2640
      GTCTTTGCTG CCCTCTCTCC CTACCTGGCC CATTCAGTGA GTTTTCTCAG CAGACCAATT 2700
      CAAATTATTA ATAAATGGGC CACCTCCCTC TTCTTCAAG AGCATCCGTG ATGCTCAGT 2760
      TTCAAAACCA CAGCCACTTA GTGATCAGCT CCCTAAACC ATGCCCTAAGT ACAGGCGGAT 2820
55     TAGCTATCTT CCAACAATGC TGACCACCAG ACAATTACTG CATTTTCCA GAAGCCCACT 2880
      ATTGCCTTTG CAGTGCTTTT GGCCAGTTT TGGCCTCAGC CTCAAAAGTG ACCGACTAGT 2940
      TGCTTGCTTA TACCTGGCAG CTCATTAAGA TGCTGGGCAG CAGTATAACA GGAGGAAGAG 3000
      ATCCCTCTCC TTGGTGCAGA TTATTATGTT CTCAGTTCTC TCTCCCTGCT ACCCTTTCT 3060
      CTGCAGATAG ATAGACACTG GCATTATCCC TTTAGGAAGA GGGGGGGGCA GCAAGAGAGC 3120
      CTATTTGGGA CAGCATTCCT CTCTCTCTGC TGCTGTGACA TCTCCCTCTC CTGTCTGGT 3180
60     CCATCTTTCT TCTGCACTAC CAATTCAATG CCCTTCATCC AATGGGTATC TATTTTGTG 3240
      TGTGATTATA GTAACACTC CTGCTTTAT ATGCCACCCT CTCTCTCTC TTTGACCCCT 3300
      GTGACTCTTT CTGTAACCTT CCCAGTGACT TCCCCTAGCC CTGACCAGGC ACTAGGCCCT 3360
      GGTGACTTCC TGGGGCCCAAG AAACCTAAGGA AACTCGGCTT TGCAACAGGC ATTAAGCTCC 3420
65     ATTGATTGGT GCCCAACCCG GGCACACTGT CGGAGTTCTA TCACTTGCTT GACCCCTGGA 3480
      CCCATAAAC AGTCCACTGT TATACCGGG GCACTTAAC CATCACAATC AATCAATCAA 3540
      ATTCCTTTAA ATTTGTATGG CACTGGAAC TTTGGCAAAG ACTTTTGACA AGTTGTGTCT 3600
      GATTGGAGCT TCATGATAGC CTGTGTGACAT CTTTAGGGCA GGATTCCTAT CCCCATTTT 3660
      CAGATGAAAA CCCTGAGTCA CAGATTTCTG TGGGACTGTG GATCTCACTG GAAGCTATCC 3720
70     AAGAGCCAC TGTCACCTTC TAGACCACAT GATAGGGCTA GACAGCTCAG TTCACCATGA 3780
      TTCTCTTCTG TCACCTCTG TGGCACACCA GTGGCAAGGC CCAAGATGGC GACCTCTCTT 3840
      TAGCTCAATT TCTGGGGCTG AGGTGCTCAG ACTGCCCCA AGATCAAATC TCTCCTGGCT 3900
      GTAGTAACCC AGTGGAATGA ATTTGGACAT GCCCAATGC TTCTATATGC TAAGTGAAAT 3960
      CTGTGCTGT AATTGTGTGG GGGTGGGTC TCCATCTACT TTTTGTCAAC 4020
75     ATCATCTGAA ATGGGGAAAT ATGTAATAA ATATATCAGC AAAGC

```

Seq ID NO: 616 Protein sequence  
Protein Accession #: NP\_068830.1

```

80     1      11      21      31      41      51
      |      |      |      |      |      |
      MEYTDIIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFRNSKRT HEHEITMPNQ 60
      MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSPYENEM IYKWFNFKE 120
      INEKNSWKLF QFDFTGVSNK TEIITTPVGD FMVMTIFFNV SRRFGYVAFQ NYVPSSVTM 180
      LSWVSFWIKT ESAPARTSLG ITSVLTMITL GTFSRKNFPR VSYITALDFY IAICFVFCFC 240

```

ALLEFAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE 300  
 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPDC EGSTWQQGRL 360  
 CIHVYRLDNY SRVVPVPTFF FPNVLYWLVC LNL

5

Seq ID NO: 617 DNA sequence  
 Nucleic Acid Accession #: NM\_004864.1  
 Coding sequence: 26..952

10 1 11 21 31 41 51  
 | | | | | |  
 CGGAACGAGG GCAACCTGCA CAGCCATGCC CGGGCAAGAA CTCAGGACGG TGAATGGCTC 60  
 TCAGATGCTC CTGGTGTGTC TGGTGCTCTC GTGGCTGCCG CATGGGGGCG CCCTGTCTCT 120  
 GGCCGAGGCG AGCCGCGCAA GTTCCCGGG ACCCTCAGAG TTGCACCTCCG AAGACTCCAG 180  
 15 ATTCCGAGAG TTGCGGAAAC GCTACGAGGA CCTGTAAACC AGGCTGCGGG CCAACCAGAG 240  
 CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCTGCA GTCCGGATAC TCACGCCAGA 300  
 AGTGCGGCTG GGATCCGGCG GCCACCTGCA CTGCGGTATC TCTCGGGCCG CCCTTCCCGC 360  
 GGGCTTCCC GAGGCTCCC GCCTTACCG GGCTCTGTTT CGGCTGTCCC CGACGGCGTC 420  
 AAGGTCGTGG GACGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC 480  
 20 GCCCGCGCTG CACCTGCGAC TGTGCGCGCC GCCGTGCGAG TCGGACCAAC TGCTGGCAGA 540  
 ATCTTCGTCC GCACGGCCCC AGCTGGAGTT GCACCTGCGG CCGCAAGCCG CCAGGGGGCG 600  
 CCGCAGAGCG CGTGCGGCGA ACGGGGACGA CTGTCCGCTC GGGCCCGGGC GTTGCTGCCG 660  
 TCTGCACACG GTCGCGCGT CGCTGGAAGA CTTGGGCTGG GCCGATTGGG TGCTGTGCCG 720  
 ACGGGAGGTG CAAGTGACCA TGTGCATCGG CGCGTGCCCG AGCCAGTTCC GGGCGGCAAA 780  
 25 CATGCACGCG CAGATCAAGA CGAGCCTGCA CGCCTGAAG CCGACACCG AGCCAGCGCC 840  
 CTGCTGCGTG CCGCGCAGT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT 900  
 GTCGCTCCAG ACCTATGATG ACTTGTAGC CAAAGACTGC CACTGCATAT GAGCAGTCTT 960  
 GGTCCTTCCA CTGTGCACCT GCGCGGGGGA GCGGACCTCA GTTGTCTTGC CCTGTGGAAT 1020  
 GGGCTCAAGG TTCTCTAGAC ACCCGATTCC TGCCCAAACA GCTGTATTTA TATAAGTCTG 1080  
 30 TTATTTATTA TTAATTTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA 1140  
 ACTGTGTATT TATTTAAAC TCTGGTGATA AAAATAAAGC TGTCTGAAC TTTAAAAAAA 1200  
 AAAA

Seq ID NO: 618 Protein sequence  
 Protein Accession #: NP\_004855.1

35

1 11 21 31 41 51  
 | | | | | |  
 MPGQELRTVN GSQMLLVLLV LSWLPHGGAL SLAEASRAS FPGSELHSED SRFRELKRY 60  
 40 EDLLRLRLAN QSWEDSNTDL VPAPAVRILT PEVRLGSGGH LHLRISRAAL PEGLPPEARL 120  
 HRLFRRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPFSQSDQLL AESSSARPL 180  
 ELHLRPQAAR GRRRARARNR DDCPLGPGRC CRLHTVRASL EDLWADWVL SPREVQVTMC 240  
 IGACPSQFRA ANMHAQIKTS LHRLKPDTEP APCCVPASYN PMVLIQKTD TGVSLQTYDDL 300  
 LAKDCHCI

45

Seq ID NO: 619 DNA sequence  
 Nucleic Acid Accession #: NM\_003979.2  
 Coding sequence: 254..1357

50 1 11 21 31 41 51  
 | | | | | |  
 ATAACAGCAT GAAGTGCCGT GGAAC TGAA TAGGCGTGTC CTCTCCCTCG ACCCTCCCCC 60  
 TCCTTGCTCC TCTGCTCACC CCTCGCTCGT TCCCTCCCTC CGGCGAGGGC CGCCTTTATA 120  
 ACAACTGCTC AGAGTGCGAG GCGGGGATAG CTGTCCAAGG TCTCCCCCAG CACTGAGGAG 180  
 55 CTGCGCTGCT GCCCTCTTGC GCGCGGGAAG CAGCACCAAG TTCACGGCCA ACGCCCTTGGC 240  
 ACTAGGGTCC AGAATGGCTA CAACAGTCCC TGATGGTTGC CGCAATGGCC TGAAATCCAA 300  
 GTACTACAGA CTTTGTGATA AGGCTGAAGC TTGGGGCATC GTCCCTAGAAA CGGTGGCCAC 360  
 AGCCGGGGTT GTGACCTCGG TGGCCTTCAT GCTCACTCTC CCGATCCTCG TGTGCAAGGT 420  
 60 GCAGGACTCC AACAGGCGAA AATAGCTGCC TACTCAGTTT CTCTTCTCTC TGGGTGTGTT 480  
 GGGCATCTTT GGCTCACCT TCGCCTTCAT CATCGGACTG GACGGGAGCA CAGGGGCCAC 540  
 ACGCTTCTTC CTCTTTGGGA TCCTCTTTTC CATCTGCTTC TCCTGCTTGC TGGCTCATGC 600  
 TGTCACTCTG ACCAAGCTCG TCCGGGGGAG GAAGCCCTTT TCCTGTGTTG TGATCTGGG 660  
 TCTGGCCGTG GGCTTCAGCG TAGTCCAGGA TGTATCGCT ATTGAATATA TTGTCCTGAC 720  
 CATGAATAGG ACCAAGCTCA ATGTCTTTTC TGAGCTTTCC GTCCTCTGTC GCAATGAAGA 780  
 65 CTTTGTCTTC CTGCTCACCT ACGTCTCTT CTGTATGGCG CTGACCTTCC TCATGTCTTC 840  
 CTTACCTTTC TGTGGTTCCT TCACGGGCTG GAAGAGACAT GGGGCCACA TCTACCTCAC 900  
 GATGCTCTTC TCATTGCCA TCTGGGTGGC CTGGATCACC CTGCTCATGC TTCTGACTT 960  
 TGACCGCAGG TGGGATGACA CCATCCTCAG CTCGCGCTTG GCTGCCAATG GCTGGGTGTT 1020  
 CCTGTGCTTC TATGTTAGTC CCGAGTTTTC GCTGCTCACA AAGCAACGAA ACCCATGGA 1080  
 70 TTATCTGTTT GAGGATGCTT TCTGTAAACC TCAACTCGTG AAGAAGAGCT ATGGTGTGGA 1140  
 GAACAGAGCC TACTCTCAAG AGGAAATCAC TCAAGTTTTC GAAGAGACAG GGGACACGCT 1200  
 CTATGCCCCC TATTCCACAC ATTTTCAGCT GCAGAACCCG CTCCCCAAA AGGAATTCTC 1260  
 CATCCCACGG GCCCAGCTT GGCAGAGCCC TTACAAGAC TATGAAGTAA AGAAAGAGGG 1320  
 CAGCTAACTC TGTCTTGAAG AGTGGGACAA ATGCAGCCGG GCGGCAGATC TAGCGGGAGC 1380  
 75 TCAAAAGGAT GTGGGCGAAA TCTTGAGTCT TCTGAGAAAA CTGTACAAGA CACTACGGGA 1440  
 ACAGTTTGCC TCCTTCCCG CTTCAACCAC AATCTTCCA TGCTGGGGCT GATGTGGGCT 1500  
 AGTAAGACTC CAGTCTCTAG AGGCGCTGTA GTATTTTTTT TTTTTGTCT CATCCTTTGG 1560  
 ATACTTCTTT TAAGTGGGAG TCTCAGGCAA CTCAAGTTTA GACCCTTACT CTTTTGTGTT 1620  
 80 GTTTTTTGAA ACAGGATCTT GCTCTGTAC CCAAGCTTGA GTGCACTGGT GCGATCACAG 1680  
 CCAGTGACG CCTCGACCC CTGTGCTCAA GCAATCTTCC CATCTCCATC TCCCAAAGTG 1740  
 CTGGGATGAC AGGCGTGAGC CACAGCTCCC AGCCTAGGCC CTTAATCTTG CTGTTATTTT 1800  
 CCATGGACTA AAGGTCTTGGT CATCTGAGCT CACGCTGGCT CACACAGCTC TAGGGGCGCT 1860  
 CTCTCTTAAC TCACAGTGGG TTTTGTGAGG CTCTGTGGCC CAGAGCAGAC CTGCATATCT 1920  
 GAGCAAAAAT AGCAAAAGCC TCTCTCAGCC CACTGGCCTG AATCTACACT GGAAGCCAAC 1980  
 TTGCTGGCAC CCCCCTCTCC CAACCTTCTT TGCTGGGTA GGAGAGGCTA AAGATCACCC 2040

TAAATTTACT CATCTCTCTA GTGCTGCCTC ACATTGGGCC TCAGCAGCTC CCCAGCACCA 2100  
 ATTCACAGGT CACCCCTCTC TTCTTGCACT GTCCCCAAAC TTGCTGTCAA TTCCGAGATC 2160  
 TAACTCTCCC CTAGCCTCTG CCAGGAATTC TTTAGACCT CACTAGCACA AGCCCGGTG 2220  
 CTCCTTGTC GAGAAATTTG TAGATCATTC TCACTTCAAA TTCCTGGGGC TGATACTTCT 2280  
 CTCATCTTGC ACCCAACCT CTGTAAATAG ATTTACCGCA TTTACGGCTG CATCTGTAA 2340  
 GTGGGCATGG TCTCTAATG GAGGAGTGT CATTGTATAA TAAGTTATTC ACCTGAGTAT 2400  
 GCAATAAAGA TGTGTGGCC ACTCTTTCAT GGTGGTGGCA GCAAAAAA AAAAAA

Seq ID NO: 620 Protein sequence

Protein Accession #: NP\_003970.1

1 11 21 31 41 51  
 | | | | |  
 MATTVPDGR NGLKSKYRL CDKAEAWGIV LETVATAGVV TSVAFMLTLP ILVCKVQDSN 60  
 RRKMLPTQFL FLLGLVGF LTFAFIIGLD GSTGPTRFLL FGILFSICFS CLLAHAVSLT 120  
 KLVRGRKPLS LLVILGLAVG FSLVQDVIAI EYIVLTMRNT NVNVFSELSA PRRNEDFVLL 180  
 LTYVLFLMAL TFLMSSFTFC GSFTGWRHGH AHYILTMLLS IAIWVAVITL LMLPDFDRRW 240  
 DDTLLSSALA ANGVWFLLAY VSPFWLLTK QRNPMDYPVE DAFCKPQLVK KSYGVENRAY 300  
 SQEITQFGE ETGDTLYAPY STHFQLQNP PQKEFSIPRA HAWPSPYKDY EVKKEGS

Seq ID NO: 621 DNA sequence

Nucleic Acid Accession #: NM\_002423.2

Coding sequence: 48..851

1 11 21 31 41 51  
 | | | | |  
 ACCAAATCAA CCATAGGTCC AAGAACAATT GTCTCTGGAC GGCAGCTATG CGACTCACCG 60  
 TGCTGTGTGC TGTGTGCTCG CTGCTGGCCA GCCTGGCCCT GCCGCTGCCT CAGGAGGCGG 120  
 GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT 180  
 ATGACTCAGA AAAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAT 240  
 TCTTTGGCCT ACCTATAACT GGAATGTTAA ACTCCGCGT CATAGAAATA ATGCAGAAGC 300  
 CCAGATGTGG AGTGCCAGAT GTTGCAAGAT ACTCACTATT TCCAAATAGC CCAAAATGGA 360  
 CTTCCAAAGT GGTCACTTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG 420  
 TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTTCA 480  
 GGAAAGTTGT ATGGGGAATC GCTGACATCA TGATTGGCTT TGCGCGAGGA GCTCATGGGG 540  
 ACTCTACCC ATTGTATGGG CCAGGAAACA CGCTGGCTCA TGCCTTTGCG CTGGGACAG 600  
 GTCTCGGAGG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG 660  
 GGATTAACCT CCTGTATGCT GCAACTCATG AACTTGGCCA TTCTTTGGGT ATGGGACATT 720  
 CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA 780  
 AACTTTCCCA GGATGATATT AAAGGCATTC AGAAACTATA TGGAAAGAGA AGTAATTTCA 840  
 GAAAGAAATA GAAACTTCAG GCAGAACATC CATTCACTCA TTCATTGGAT TGTATATCAT 900  
 TGTGACAAA TCAGAAATGA TAAGCACTGT TCCTCCACTC CATTTAGCAA TTATGTCCAC 960  
 CTTTTTATT GCAGTTGGTT TTTGAATGTC TTCTACTCCT TTTATGGTT AAACCTCCTT 1020  
 ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTTGTCA GTGCGGTAG ATGTCAATAA 1080  
 ATGTTACATA CACAAATAAA TAAATGTTT ATTCCATGGT AAATTTA

Seq ID NO: 622 Protein sequence

Protein Accession #: NP\_002414.1

1 11 21 31 41 51  
 | | | | |  
 MRLTVLCVAV LLPGLALPL PQEAGGMSSEL QWEQAQDYLK RFYLYDSETK NANSLEAKLK 60  
 EMQKFGLPI TGMINSRVIE IMQKPRGVDP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL 120  
 PHITVDRLVS KALNMWKEI PLHFRKVVWG TADIMIGFAR GAHGDSPYFD GPGNTLAHAF 180  
 APGTGLGGDA HFDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYNGND 240  
 PQNFKLSQDD IKGIQKLYGK RSNRKK

Seq ID NO: 623 DNA sequence

Nucleic Acid Accession #: NM\_031457.1

Coding sequence: 204..956

1 11 21 31 41 51  
 | | | | |  
 AAACAGGAAA TAAATACGAA TGAAACTGAG CTCTAAGCAG CATGTAACCT GGCCTGCATC 60  
 CAGGAAATAG AGGACTTCGG ATCCTTCTAA CCTACCACC CAACTGGCCC CAGTACATTC 120  
 ATTCTCTCAG GAAAAAATC AAGGTCCCCA CAGCAAGAA AAGGAATAGG ATCAAGAGAT 180  
 ACGTGGCTGC TGGCAGAGCA AGCATGAATT CGATGACTTC AGCAGTTCCG GTGGCCCAAT 240  
 CTGTGTTGGT GGTGGCACCC CACAATGGTT ATCCTGTGAC CCCAGGAATT ATGTCTCACG 300  
 TGCCCTGTGA TCCAAACAGC CAGCCGCAAG TCCACCTAGT TCCTGGGAAC CCACCTAGTT 360  
 TGGTGTGAAA TGTGAATGGG CAGCCTGTGC AGAAAGCTCT GAAAGAAGGC AAAACCTTGG 420  
 GGGCATCCCA GATCATCATT GGCTTGGCTC ACATCGGCCT CGGCTCCATC ATGGCGACGG 480  
 TTCTCGTAGG GGAATACCTG TCTATTTTCT TCTACGGAGG CTTTCCCTTC TGGGGAGGCT 540  
 TGTGGTTTAT CATTTACAGA TCTCTCTCCG TGGCAGCAGA AAATCAGCCA TATCTTTATT 600  
 GCCTGCTGTC TGGCAGTTTG GGCTTGAACA TCGTCAGTGC AATCTGCTCT GCAGTTGGAG 660  
 TCATACTCTT CATCACAGAT CTAAGTATTC CCCACCCATA TGCTTACCCC GACTATTATC 720  
 CTTACGCTCG GGTGTTGAAC CCTGGAATGG CGATTTCTGG CGTGTCTGCG GTCTTCTGCG 780  
 TCCTGGAGTT TGGCATCGCA TGCAGCATCT CCCACTTTGG CTGCCAGTTG GTCTGCTGTC 840  
 AATCAAGCAA TGTGAGTCTC ATCTATCCAA ACATCTATGC AGCAAAACCA GTGATCACCC 900  
 CAGAACCGGT GACCTCACCA CCAAGTTATT CCAAGTATGC CCAAGCAAA AAGTAAGGCT 960  
 ACAGATTCTG GAAGCATCTT TCACTGGGAC CAAAGAAGT CCTCCTCCTT TCTGGGCTT 1020  
 CCATAACCCA GGTGTTTCTT GTTCTGACAG CTGAGGAAAC GTCTCTCCCA CTGTTTGTAC 1080  
 TCTCACCTTC ATTCTTCAAT TCAGTCTAGG AAACCATGCT GTTCTCTTAT CAAGAAGAAG 1140  
 ACAGAGATTT TAAACAGATG TTAACCAAGA GGGACTCCCT AGGGCACATG CATCAGCACA 1200  
 TATGTGGGCA TCCAGCCTCT GGGCCTTGG CACACACACA TTCGTGTGCT CTGCTGCATG 1260

TGAGCTTGTG GGTTAGAGGA ACAAATATCT AGACATTCAA TCTTCACTCT TTCAATTGTG 1320  
CATTCAATTA ATAAATAGAT ACTGAGCATT CAAAAA AAAAAA

Seq ID NO: 624 Protein sequence  
Protein Accession #: NP\_113645.1

1 11 21 31 41 51  
MNSMTSAVPV ANSVLVVAPH NGYPVTPGIM SHVPLYPNPQ PQVHLVPGNP PSLVSNVNGQ 60  
PVQKALKEGK TLGAIQIIIG LAHIGLGSIM ATVLVGEYLS ISFYGGFFFW GGLWFIISGS 120  
LSVAENQPY SYCLLSGSLG LNIIVSAICSA VGVILFITDL SIPHPYAYPD YYPYAWGVNP 180  
GMAISGVLLV FCLLEFGIAC ASSHFGCQLV CQSSNVSVI YPNIYAANPV ITPEPVTSPF 240  
SYSSEIQANK

Seq ID NO: 625 DNA sequence  
Nucleic Acid Accession #: NM\_005221.3  
Coding sequence: 1..870

1 11 21 31 41 51  
ATGACAGGAG TGTTTGACAG AAGGGTCCCC AGCATCCGAT CCGGCGACTT CCAAGCTCCG 60  
TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACTTT GCCCGAGTCT 120  
TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCCACACGG CTACTGCTCT 180  
CCTACCTCGG CTCTCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGGCGTG 240  
AACGGCTCCG CCGGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC 300  
TACCACCAAT AGCGCGGCGC CTACAACCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360  
GAAGTGACCG AGCCCCAGGT GAGAATGGTG AATGGCAAAC CAAAGAAAGT TCGTAAACCC 420  
AGGACTATT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG 480  
TACCTCGCCT TGCCGGAACG CGCCGAGCTG GCCGCCTCGC TGGGATTGAC ACAAAACACAG 540  
GTGAAAATCT GGTTCAGAAA CAAAAGATCC AAGATCAAGA AGATCATGAA AAACCGGGGAG 600  
ATGCCCCCGG AGCACAGTCC CAGCTCCAGC GACCCAATGG CGTGTAACTC GCCGCACTCT 660  
CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCAC 720  
CCTCCGACCT CCAACAGTCC CCCAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC 780  
ACAAGTGCAG CCAGCTCAAT CAATTCCAC CTGCCGCCG CCGGCTCCTT ACAGCACCCG 840  
CTGGCGCTGG CTCCCGGAC ACTCTATTAG

Seq ID NO: 626 Protein sequence  
Protein Accession #: NP\_005212.1

1 11 21 31 41 51  
MTGVFDRRVP SIRSGDFQAP FQTSAAHHP SQESPTLPES SATDSYYSP TGGAPHGYCS 60  
PTSASYGKAL NPYQYQYHGV NGSAGSYPK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120  
EVTEPEVRMV NGKPKKVRKP RTIYSSFOLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ 180  
VKIWFQNKRS KIKKIMKNGE MPEHSPSSS DPMACNSPQS PAVWEPQSSS RSLSHHPHAH 240  
PPTSNOQSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLV

Seq ID NO: 627 DNA sequence  
Nucleic Acid Accession #: NM\_014420  
Coding sequence: 118..792

1 11 21 31 41 51  
GCACGAGAGA CGAGCTGCTG AGCTGCCAGC TTAGTGGAAG CTCTGCTCTG GGTGGAGAGC 60  
AGCCTCGCTT TGGTGACGCA CAGTGCTGGG ACCCTCCAGG AGCCCCGGA TTGAAGGATG 120  
GTGGCGGCGG TCCTGCTGGG GCTGAGCTGG CTCTGCTCTC CCTGGGAGC TCTGGTCTCTG 180  
GACTTCAACA ACATCAGGAG CTCTGCTGAC CTGCATGGGG CCGGAAGGG CTCACAGTGC 240  
CTGTCTGACA CGGACTGCAA TACCAGAAAG TTCTGCCTCC AGCCCCGCGA TGAGAAGCCG 300  
TTCTGTGCTA CATGTCGTGG GTTGGCGAGG AGGTGCCAGC GAGATGCCAT GTGCTGCCCT 360  
GGGACACTCT GTGTGAACGA TGTTTGTACT ACGATGGAAG ATGCAACCCC AATATTAGAA 420  
AGGCAGCTTG ATGAGCAAGA TGGCACACAT GCAGAAGGAA CAACTGGGCA CCCAGTCCAG 480  
GAAAACCAAC CAAAAGGAA GCCAAGTATT AAGAAATCAC AAGGCAGGAA GGGACAAGAG 540  
GGAGAAAGTT GTCTGAGAAC TTTTGACTGT GGCCCTGGAC TTTGCTGTGC TCGTCATTTT 600  
TGGACGAAAA TTTGTAAGCC AGTCCTTTTG GAGGGACAGG TCTGCTCCAG AAGAGGGCAT 660  
AAAGACACTG CTCAAGCTCC AGAAATCTTC CAGCGTTGCG ACTGTGGCCC TGGACTACTG 720  
TGTGGAAGCC AATTGACCAG CAATCGGCAG CATGCTCGAT TAAGAGTATG CCAAAAAATA 780  
GAAAAGCTAT AAATATTTCA AAATAAGAA GAATCCACAT TGCAAAAAA AAAAAAATA 840  
A

Seq ID NO: 628 Protein sequence  
Protein Accession #: NP\_055235

1 11 21 31 41 51  
MVAAVLLGLS WLCSPLGALV LDFNNIRSSA DLHGARKGSQ CLSDTDCNTR KFCLQPRDEK 60  
PFCATCRGLR RRCQRDAMCC PGTLCVNDVC TTMEDATPIL ERQLDEQDGT HAEGTTGHPV 120  
QENQPKRKPS IKKSQGRKGQ EGESCLRTFD CGPGLCCARH FWTKICKPVL LEGQVCSRRG 180  
HKDTAQAPEI FQRCDGPGFL LCRSQTLSNR QHARLRVCQK IEKL

Seq ID NO: 629 DNA sequence  
Nucleic Acid Accession #: NM\_002448.1  
Coding sequence: 241..1134

1 11 21 31 41 51

	CGCGGAGTGC	TCGCCGGAAAC	CTGCTCTGCG	CGGCGGCAGC	GACCGGAGGC	CAGGCCCAGC	60
	ACGCCGGAGC	TGGCCTGCTG	GGGAGGGGCG	GGAGGCGCGC	GCGGGAGGGT	CCGCCCGGCC	120
5	AGGCCCGGGG	CCCTCGCAGA	GGCCGGCCCG	GCTCCCAGCC	CGCCCCGAGC	CCATGCCCGG	180
	CGGCTGGCCA	GTGCTGCGGC	AGAAGGGGGG	GCCCGGCTCT	GCATGGCCCC	GGCTGCTGAC	240
	ATGACTTCTT	TGCCACTCGG	TGTCAAAGTG	GAGGACTCCG	CCTTCGGCAA	GCCGGCGGGG	300
	GGAGGCGCGG	GCCAGGCCCC	CAGCGCCGCC	GCGGCCACGG	CAGCCGCCAT	GGGCGCGGAC	360
	GAGGAGGGGG	CCAAGCCCAA	AGTGTCCCCT	TCGCTCCTGC	CCTTCAGCGT	GGAGGCGCTC	420
10	ATGGCCGACC	ACAGGAAGCC	GGGGGCCAAG	GAGAGCGCCC	TGGCGCCCTC	CGAGGGCGTG	480
	CAGGCGGCGG	GTGGCTCGGC	GCAGCCACTG	GGCGTCCC GC	CGGGTTCGCT	GGGAGCCCCG	540
	GACGCGCCCT	CTTCGCCGCG	GCCGCTCGGC	CATTCTCTCG	TGGGGGGACT	CCTCAAGCTG	600
	CCAGAAGATG	CGCTCGTCAA	AGCCGAGAGC	CCCGAGAAGC	CCGAGAGGAC	CCCGTGGATG	660
	CAGAGCCCCC	GCTTCTCCCC	GCCGCCGGCC	AGGCGGCTGA	GCCCCCAGC	CTGCACCCCT	720
	CGCAAACACA	AGACGAACCG	TAAGCCGCGG	ACGCCCTTCA	CCACCGCGCA	GCTGTGGCG	780
15	CTGGAGCGCA	AGTTCGCCCA	GAAGCAGTAC	CTGTCCATCG	CCGAGCGCGC	GGAGTTCTCC	840
	AGTCTCGTCA	GCCTCACTGA	GACGCAGGTG	AAGATATGGT	TCCAGAACCG	CCGCGCCAA	900
	CCAAAGAGAC	TACAAGAGCC	AGAGCTGGAG	AAGCTGAAGA	TGGCCGCCAA	GCCCATGCTG	960
	CCACCGGCTG	CCTTCGCGCC	CTCCTTCCCT	CTCGGCGGCC	CCGCAGCTGT	AGCGGCCGCG	1020
	GCGGGTGCCT	CGCTCTACGG	TGCCTCTGGC	CCCTTCCAGC	GCGCCGCGCT	GCCTGTGGCG	1080
20	CCCGTGGGAC	TCTACACGGC	CCATGTGGGC	TACAGCATGT	ACCACCTGAC	ATAGAGGGTC	1140
	CCAGGTCCCC	ACCTGTGGGC	CAGCCGATTC	CTCCAGCCCT	GGTGTGTATC	CCCCGACGTG	1200
	CTCCCTTGCT	CGGCACGCGC	AGCCGCTTTC	CCTTAAACCC	TCACACTGCT	CCAGTTTCAC	1260
	CTCTTTGCTC	CCTGAGTTCA	CTCTCCGAAG	TCTGATCCCT	GCCAAAAGT	GGCTGGAAGA	1320
25	CTCCCTTAGT	ACTCTTCTAG	CATTAGATC	TACACTCTCG	AGTTAAAGAT	GGGGAAACTG	1380
	AGGGCAGAGA	GGTTAAACAGA	TTTATCTAGG	GTCCCCAGCA	GAATTGACAG	TTGAACAGAG	1440
	CTAGAGGCCA	TGTCTCCTGC	ATAGCTTTTC	CCTGTCTGTA	CACCAGGCAA	GAAAAGCGCA	1500
	GAGAAATCGG	TGTCTGACGA	TTTTGGAAAT	GAGAACCAAT	TCAAAAAAAA	AAAAAAGGAA	1560
	AAAAAAGGAA	GAAAAGAGAA	AAAAAAGACT	AGCCAGCCAG	GAAGATGAAT	CCTAGCTTCT	1620
30	TCCATTGGAA	AATTAAAGAC	AAGTTCAACA	ACAAAACATT	TGCTCTGGGG	GGCAGGGAAA	1680
	ACACAGATGT	GTTGCAAAGG	TAGGTTGAAG	GGA			

Seq ID NO: 630 Protein sequence  
Protein Accession #: NP\_002439.1

35	1	11	21	31	41	51	
	MTSLPLGVKV	EDSAFGKPGK	GGAGQAPSAA	AATAAAMGAD	EEGAKPKVSP	SLLPFSVEAL	60
	MADHRKPGAK	ESALAPSEVG	QAAGGSAQPL	GVPPGSLGAP	DAPSSSPRLG	HFSVGGLLKL	120
40	PEDALVKAES	PEKPERTPWM	QSPRFSPPPA	RRLSPPACTL	RKHKTNRKPR	TPFTTAQLLA	180
	LERKFRQKQY	LSIAERAEFS	SSLSLTETQV	KIWFQNRRAK	AKRLQEAEL	KLKMAAKPML	240
	PPAAGFLSFP	LGGPAVAANA	AGASLYGASG	PFQRAALPVA	PVGLYTAHV	YSMYHLT	

Seq ID NO: 631 DNA sequence  
Nucleic Acid Accession #: NM\_002557.1  
Coding sequence: 13..2049

45	1	11	21	31	41	51	
	CAGACCATTG	AGATGTGGAA	GCTGTTGCTG	TGGGTTGGGC	TGGTTCTTGT	GCTGAAACAC	60
50	CACGATGGTG	CTGCCATATA	ACTCGTGTGT	TATTTACACCA	ACTGGGCACA	CAGTCGGCCA	120
	GGCCCTGCTC	CGATCTTGCC	CCATGACCTG	GACCCCTTTC	TCTGCACCCA	CCTGATATTT	180
	GCCTTTGCCT	CAATGAACAA	CAATCAGATT	GTTGCTAAGG	ATCTCCAGGA	TGAGAAAATT	240
	CTCTACCCAG	AGTTCAACAA	ACTAAAGGAG	AGGAACAGAG	AGCTGAAAC	ACTACTGTCC	300
55	ATCGGGGGGT	GGAACCTTGG	CACCTCAAGA	TTCACCACTA	TGTTGTCCAC	ATTTGCCAAC	360
	CGTGAAAAGT	TTATTGCTTC	AGTTATATCC	CTTCTGAGGA	CACATGACTT	TGATGGTCTT	420
	GACCTTTTCT	TCTTATATCC	TGGACTAAGA	GGCAGCCCCA	TGCATGACCG	GTGGACTTTT	480
	CTCTTCTTAA	TGGAAGAGCT	CCTGTTTGCC	TTCGGGAAGG	AGGCACTGCT	CACCATGCGC	540
	CCGAGGCTGC	TGCTGTCTGC	TGCTGTTTCT	GGGGTCCCAC	ACATCGTCCA	AACATCCTAT	600
60	GATGTGCGCT	TTCTAGGAAG	ACTCCTGGAT	TTTCATCAATG	TCTTGTCTTA	TGACTTACAT	660
	GGAGTTGGG	AAAGGTTTAC	AGGACATAAT	AGCCCCCTCT	TCTCTCTGCC	TGAAGACCCC	720
	AAATCTTCGG	CATATGCTAT	GAATTATTGG	AGAAAGCTTG	GGGCACCCCTC	AGAGAAGCTC	780
	ATCATGGGGA	TCCCCACCTA	TGGACGTACC	TTTCGCCTCC	TCAAAGCCCTC	TAAGAAATGGG	840
	TTGCAGGCCA	GAGCGATCGG	ACCAGCATCT	CCAGGGGAAGT	ACACCAAGCA	AGAAGGCTTC	900
65	TTGGCTTATT	TTGAGATTTG	TTCTTTTGTC	TGGGGAGCGA	AGAAGCACTG	GATTGATTAC	960
	CAGTATGTCC	CGTATGCCAA	CAAGGGGAAA	GAGTGGGTTG	GCTATGACAA	TGCCATCAGC	1020
	TTCAAGTTACA	AGGCATGGTT	TATAAGGCGA	GAGCATTTTG	GGGGGGCCAT	GGTGTGGACA	1080
	TTGGACATGG	ATAGCGTCAG	GGGCACGTTT	TGTGGCACTG	GCCCTTTCCC	CCTTGTCTAC	1140
70	GTATTGAATG	ATATCCTGGT	GCGGGCTGAG	TTCAAGTTCAA	CTTCTTTACC	ACAATTTTGG	1200
	CTGTCACTCTG	CTGTGAATTC	TTCAAGCACT	GACCCTGAAA	GGCTGGCTGT	GACCACGGCA	1260
	TGGACCACTG	ATAGTAAGAT	TTTGCCCCCA	GGAGGAGAGG	CTGGGGTTCAC	TGAGATCCAC	1320
	GGAAAGTGTG	AAAATATGAC	TATAACCCCT	AGAGGTACAA	CTGTGACCCC	TACAAAAGGAA	1380
	ACTGTATCCC	TTGGAAAGCA	CACGTAGCT	CTAGGAGAGA	AGACTGAGAT	CACTGGGGCA	1440
	ATGACCATGA	CTTCTGTGGG	TCATCAGTCC	ATGACCCCTG	GAGAGAAGGC	CCTGACCCCT	1500
75	GTGGGTCAATC	AATCTGTGAC	CACCTGGACAG	AAGACCCTGA	CCTCTGTGGG	TTATCAGTCT	1560
	GTGACCCCTG	GGGAAAAGAC	CCTGACCCCT	GTGGGTCAATC	AGTCTGTGAC	CCCTGTGAGT	1620
	CATCAGTCTG	TGAGCCCTGG	AGGAACGACT	ATGACCCCTG	TCCATTTTCA	GACTGAGACC	1680
	CTTAGACAGA	ATACAGTGGC	CCCTAGAAGG	AAGGCTGTGG	CCCGTGAAAA	GGTGACTGTC	1740
	CCCTCCAGAA	ACATATCAGT	CACCCCTGAA	GGGCAGACTA	TGCCTTTAAG	AGGGGAGAA	1800
80	TTGACTTCTG	AGGTGGGCGC	TCACCCGAGG	ATGGGTAAC	TGGGTCTTCA	GATGGAAGCT	1860
	GAAAACAGGA	TGATGCTGTC	CTCCAGCCCC	GTCATCCAGC	TCCCGGAACA	AACTCCTCTA	1920
	GCTTTTGACA	ACCGCTTTGT	TCCCATCTAT	GGAAACCAAT	CCTCTGTCAA	CTCAGTAACC	1980
	CCTCAACAAA	GTCCCTTTTTC	TCTAAAAAAA	GAATCCCAAG	AAAACTCTGC	TGTGGATGAA	2040
	GAAGCCTAAG	CCCCCTCTGT	GTCAGAAACC	AGGGAAACCC	CTTGTCTTTT	CTTCTAAGTG	2100
	ACATGTTGGA	AGCCCTTCTCA	TCCCGGGGCA	AAGCAGGCAT	CAAAACACGA	ATAGGCCAAT	2160

CTCTTTTCCA TTAAATAAAC TGTAAACACA AGAACCCA

Seq ID NO: 632 Protein sequence  
Protein Accession #: NP\_002548.1

5  
10  
15  
20

1	11	21	31	41	51	
MWKLWVGL	VLVLKHDGA	AHKLVCYFTN	WAHSRPGPAS	ILPHDLDPFL	CTHLIFAFAS	60
MNNQIVAKD	LQDEKILYPE	FNKLKERNRE	LKTLLSIGGW	NFGTSRFTTM	LSTFANREKF	120
IASVISLLRT	HDFDGLDLFF	LYPGLRGSPM	HDRWTFLLFI	EELLFAFRKE	ALLTMRPRL	180
LSAAVSGVPH	IVQTSYDVRF	LGRLDLFINV	LSYDLHGWE	RFTGHNSPLF	SLPEDPKSSA	240
YAMNYWRKLG	APSEKLIMGI	PTYGRTFRL	KASKNGLQAR	AIGPASPGKY	TKQEGFLAYF	300
EICSFVWGAK	KHWIDYQYVP	YANKGKEWVG	YDNAISFSYK	AWFIRREHFG	GAMVWTLDM	360
DVRGTFCTGT	PFPLVYVLND	ILVRAEFSST	SLPQFWLSSA	VNSSTDPER	LAVTTAWTTD	420
SKILPPGGEA	GVTEIHGKCE	NMTITPRGTT	VTPTKETVSL	GKHTVALGEK	TEITGAMTMT	480
SVGHQSMTPG	EKALTPVGHQ	SVTTGQKTLT	SVGYQSVTPG	EKTLTPVGHQ	SVTPVSHQSV	540
SPGGTTMTPV	HFQTETLRQN	TVAPRRKAVA	REKVTVPSPN	ISVTPEGQTM	PLRGENLTSE	600
VGTHPRMGNL	GLQMEAEARN	MLSSSPVIQL	PEQTPLAFDN	RFVPIYGNHS	SVNSVTPQTS	660
PLSLKKEIPE	NSAVDEEA					

Seq ID NO: 633 DNA sequence  
Nucleic Acid Accession #: NM\_003885.1  
Coding sequence: 98..1021

25  
30  
35  
40  
45

1	11	21	31	41	51	
AAACTCAGAA	TTTTCGCGGG	CTCGGTGAGC	GGTTTATCC	CTCCGGCCGG	CAGGCTGGGC	60
GCAGGGGGCG	AGCCCCCGCC	CGGCGCGCAG	CAGCACCATG	GGCACCGTGC	TGTCCCTGTC	120
TCCAGCTAC	CGGAAGGCCA	CGCTGTTTGA	GGATGGCGCG	GCCACCGTGG	GCCACTATAC	180
GGCCGTACAG	AACAGCAAGA	ACGCCAAGGA	CAAGAACCTG	AAGCGCCACT	CCATCATCTC	240
CGTGCTGCCT	TGGAAGAGAA	TCGTGGCCGT	GTCGGCCAAG	AAGAAGAACT	CCAAGAAGGT	300
GCAGCCTAAC	AGCAGCTACC	AGAACACAT	CACGCACCTC	AACAATGAGA	ACCTGAAGAA	360
GTCGCTGTCG	TGCGCCAACC	TGTCCACATT	CGCCAGCCCC	CCACCGGCCC	AGCCGCTGTC	420
ACCCCGGCC	AGCCAGCTCT	CGGTTCCCA	GACCGGGGCG	TCCTCCTCAG	TCAAGAAAGC	480
CCCTCACCT	GCCGTCACTC	CCGCAGGGAC	GCCCAACCGG	GTCATCGTCC	AGGCGTCCAC	540
CAGTGAGCTG	CTTCGCTGCC	TGGTGAGTT	TCTCTGCCGC	CGGTGCTACC	GCCTGAAGCA	600
CCTGTCCCCC	ACGGACCCCG	TGCTCTGGCT	GCGCAGCGTG	GACCGCTCGC	TGCTTCTGCA	660
GGGTGGCAG	GACCAGGGCT	TCATCACGCC	GGCCAACGTG	GTCTTCTCT	ACATGCTCTG	720
CAGGGATGTT	ATCTCCTCCG	AGGTGGGCTC	GGATCACGAG	CTCCAGGCCG	TCCTGCTGAC	780
ATGCTGTAC	CTCTCCTACT	CCTACATGGG	CAACGAGATC	TCCTACCCGC	TCAAGCCCTT	840
CCTGGTGGAG	AGCTGCAAGG	AGGCCTTTTG	GGACCGTTGC	CTCTCTGTCA	TCAACCTCAT	900
GAGCTCAAAG	ATGTGTCAGA	TAAATGCCGA	CCCACACTAC	TTCACACAGG	TCTTCTCCGA	960
CCTGAAGAAC	GAGAGCGGCC	AGGAGGACAA	GAAGCGGCTC	CTCCTAGGCC	TGGATCGGTG	1020
AGCACTGTAG	CCTGCGTCAT	GGCTCAAGGA	TTCAATGCAT	TTTAAAGAAT	TTATTATTAA	1080
ATCAGTTTTG	TGTACAG					

Seq ID NO: 634 Protein sequence  
Protein Accession #: NP\_003876.1

50  
55

1	11	21	31	41	51	
MGTVLSLSPS	YRKATLFEDG	AATVGHYTA	QNSKNAKDKN	LKRHSIISVL	PWKRIVAVSA	60
KKKNSKKVQP	NSSQNNITH	LNNENLKSL	SCANLSTFAQ	PPPAQPPAPP	ASQLSGSQTG	120
GSSSVKKAPH	PAVTSAGTPK	RVIVQASTSE	LLRCLGEFLC	RRCYRLKHL	PTDPVLNLS	180
VDRSLLQGW	QDQGFITPAN	VVFLYMLCRD	VISSEVSDH	ELQAVLLTCL	YLSYSYMGNE	240
ISYPLKPFIV	ESCKEAFWDR	CLSVINLMSS	KMLQINADPH	YFTQVFSDLK	NESQEDKKR	300
LLGLDR						



TABLE 79A:

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
	Seq ID No.:	Sequence identification number linking information in Table 79A to sequences in Table 80			
10	Pkey	ExAccn	UnigenelD	Unigene Title	Seq ID No.
15	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	Seq ID No. C1 & C217
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID No. C2 & C218
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C3 & C219
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C4 & C220
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. C5 & C221
20	443646	AI085198	Hs.164226	Thrombospondin 1	Seq ID No. C6 & C222
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	Seq ID No. C7 & C223
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	Seq ID No. C8 & C224
	444381	BE387335	Hs.283713	hypothetical protein BC014245	Seq ID No. C9 & C225
	421582	AI910275	Hs.350470	trefoil factor 1 (breast cancer, estroge	Seq ID No. C10 & C226
25	411789	AF245505	Hs.72157	Adican	Seq ID No. C11 & C227
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	Seq ID No. C12
	428698	AA852773	Hs.334838	KIAA1866 protein	Seq ID No. C13 & C228
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	Seq ID No. C14 & C229
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. C15 & C230
30	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	Seq ID No. C16 & C231
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	Seq ID No. C17 & C232
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	Seq ID No. C18 & C233
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	Seq ID No. C19 & C234
	432179	X75208	Hs.2913	EphB3	Seq ID No. C20 & C235
35	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	Seq ID No. C21 & C236
	409889	AW630041	Hs.56937	suppression of tumorigenicity 14 (colon	Seq ID No. C22 & C237
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C23 & C238
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C24 & C239
	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	Seq ID No. C25 & C240
40	434206	AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen i	Seq ID No. C26 & C241
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	Seq ID No. C27 & C242
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	Seq ID No. C28 & C243
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	Seq ID No. C29 & C244
	415214	AI445236	Hs.125124	EphB2	Seq ID No. C30 & C245
45	443247	BE614387	Hs.333893	c-Myc target JPO1	Seq ID No. C31 & C246
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	Seq ID No. C32 & C247
	410418	D31382	Hs.63325	transmembrane protease, serine 4	Seq ID No. C33 & C248
	446342	BE298665	Hs.14846	solute carrier family 7 (cationic amino	Seq ID No. C34 & C249
	411274	NM_002776	Hs.69423	kallikrein 10	Seq ID No. C35 & C250
50	104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	Seq ID No. C36 & C251
	422260	AA315993	Hs.105484	regenerating gene type IV	Seq ID No. C37 & C252
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C38 & C253
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	Seq ID No. C39 & C254
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	Seq ID No. C40 & C255
55	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	Seq ID No. C41 & C256
	422330	D30783	Hs.115263	epiregulin	Seq ID No. C42 & C257
	408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. C43 & C258
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	Seq ID No. C44 & C259
	437852	BE001836	Hs.256897	putative GPCR	Seq ID No. C45 & C260
60	408243	Y00787	Hs.624	interleukin 8	Seq ID No. C46 & C261
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. C47 & C262
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (lg),	Seq ID No. C48 & C263
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. C49 & C264
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	Seq ID No. C50 & C265
65	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	Seq ID No. C51 & C266
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. C52 & C267
	442006	AW975183	Hs.372210	ESTs, Weakly similar to S72482 hypotheti	Seq ID No. C53 & C268
	413048	M93221	Hs.75182	mannose receptor, C type 1	Seq ID No. C54 & C269
	443324	R44013	Hs.164225	ESTs	Seq ID No. C55 & C270
70	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C56 & C271
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C57 & C272
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	Seq ID No. C58 & C273
	442652	AI005163	Hs.201378	Homo sapiens cDNA FLJ40427 fis	Seq ID No. C59 & C274
	450726	AW204600	Hs.355462	HUMPSPBA Human pulmonary surfactant-asso	Seq ID No. C60 & C275
75	416965	N26223	Hs.160436	MDAC1	Seq ID No. C61 & C276
	442275	AW449467	Hs.54795	Homo sapiens secretoglobulin, family 3A, m	Seq ID No. C62 & C277
	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C63 & C278
	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C64 & C279
	453142	AA033648	Hs.7473	Homo sapiens gap junction protein, alpha	Seq ID No. C65 & C280
80	421659	NM_014459	Hs.106511	protocadherin 17	Seq ID No. C66 & C281
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	Seq ID No. C67 & C282
	421563	NM_006433	Hs.105806	granulysin	Seq ID No. C68 & C283
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	Seq ID No. C69 & C284
	414991	C17898		Homo sapiens up-regulated by BCG-CWS (LO	Seq ID No. C70 & C285
	419833	AA251131	Hs.220697	Homo sapiens tryptophanyl-tRNA synthetas	Seq ID No. C71 & C286
	424943	AU077260	Hs.153924	death-associated protein kinase 1	Seq ID No. C72 & C287

	430890	X54232	Hs.2699	glypican 1	Seq ID No. C73 & C288
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No. C74 & C289
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	Seq ID No. C75 & C290
	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No. C76 & C291
5	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	Seq ID No. C77 & C292
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	Seq ID No. C78 & C293
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	Seq ID No. C79 & C294
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C80 & C295
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C81 & C296
10	431846	BE019924	Hs.271580	uroplakin 1B	Seq ID No. C82 & C297
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	Seq ID No. C83 & C298
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	Seq ID No. C84 & C299
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	Seq ID No. C85 & C300
15	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. C86 & C301
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. C87 & C302
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	Seq ID No. C88 & C303
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	Seq ID No. C89 & C304
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	Seq ID No. C90 & C305
	418462	BE001596	Hs.85266	integrin, beta 4	Seq ID No. C91 & C306
20	439606	W79123	Hs.58561	G protein-coupled receptor 87	Seq ID No. C92 & C307
	407720	AB037776	Hs.38002	immunoglobulin superfamily, member 9	Seq ID No. C93 & C308
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	Seq ID No. C94 & C309
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	Seq ID No. C95 & C310
25	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C96 & C311
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C97 & C312
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C98 & C313
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C99 & C314
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C100 & C315
30	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C101 & C316
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C102 & C317
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C103 & C318
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C104 & C319
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C105 & C320
35	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	Seq ID No. C106 & C321
	440659	AF134160	Hs.7327	claudin 1	Seq ID No. C107 & C322
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C108 & C323
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C109 & C324
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C110 & C325
40	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	Seq ID No. C111 & C326
	414774	X02419	Hs.77274	plasminogen activator, urokinase	Seq ID No. C112 & C327
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	Seq ID No. C113 & C328
	453857	AL080235	Hs.35861	Ras-induced senescence 1 (RIS1)	Seq ID No. C114 & C329
	449101	AA205847	Hs.23016	G protein-coupled receptor	Seq ID No. C115 & C330
45	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	Seq ID No. C116 & C331
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	Seq ID No. C117 & C332
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	Seq ID No. C118 & C333
	408482	NM_000676	Hs.45743	adenosine A2b receptor	Seq ID No. C119 & C334
	426761	AI015709	Hs.172089	PORIMIN Pro-oncogene receptor inducing me	Seq ID No. C120 & C335
50	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	Seq ID No. C121 & C336
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	Seq ID No. C122 & C337
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	Seq ID No. C123 & C338
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	Seq ID No. C124 & C339
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	Seq ID No. C125 & C340
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	Seq ID No. C126 & C341
	428513	BE220806	Hs.184697	plexin C1	Seq ID No. C127 & C342
	430280	AA361258	Hs.237868	interleukin 7 receptor	Seq ID No. C128 & C343
	428486	AW583497	Hs.184604	pancreatic polypeptide	Seq ID No. C129 & C344
	457489	AI693815	Hs.127179	cryptic gene	Seq ID No. C130 & C345
	432874	W94322	Hs.279651	melanoma inhibitory activity	Seq ID No. C131 & C346
60	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C132 & C347
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C133 & C348
	404682			ortholog of mouse polydomain protein	Seq ID No. C134 & C349
	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	Seq ID No. C135 & C350
65	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C136 & C351
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C137 & C352
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C138 & C353
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	Seq ID No. C139 & C354
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	Seq ID No. C140 & C355
70	432596	AJ224741	Hs.278461	matrilin 3	Seq ID No. C141 & C356
	444006	BE395085	Hs.334762	type I transmembrane protein Fn14	Seq ID No. C142 & C357
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	Seq ID No. C143 & C358
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C144 & C359
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C145 & C360
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	Seq ID No. C146 & C361
75	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	Seq ID No. C147 & C362
	422109	S73265	Hs.1473	gastrin-releasing peptide	Seq ID No. C148 & C363
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	Seq ID No. C149 & C364
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	Seq ID No. C150 & C365
80	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	Seq ID No. C151 & C366
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	Seq ID No. C152 & C367
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	Seq ID No. C153 & C368
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	Seq ID No. C154 & C369
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	Seq ID No. C155 & C370

5	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	Seq ID No. C156 & C371
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	Seq ID No. C157 & C372
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	Seq ID No. C158 & C373
	413095	AA494359	Hs.30715	potassium voltage-gated channel, Isk-rel	Seq ID No. C159 & C374
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	Seq ID No. C160 & C375
	436729	BE621807	Hs.351316	transmembrane 4 superfamily member 1	Seq ID No. C161 & C376
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	Seq ID No. C162 & C377
	451820	AW058357	Hs.199248	ESTs	Seq ID No. C163 & C378
10	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	Seq ID No. C164 & C379
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	Seq ID No. C165 & C380
	421340	F07783	Hs.1369	decay accelerating factor for complement	Seq ID No. C166 & C381
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C167 & C382
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C168 & C383
15	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	Seq ID No. C169 & C384
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	Seq ID No. C170 & C385
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	Seq ID No. C171 & C386
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	Seq ID No. C172 & C387
	439659	AW970780	Hs.59483	leucine-rich repeat-containing G protein	Seq ID No. C173 & C388
20	411825	AK000334	Hs.352415	solute carrier family 39 (zinc transport	Seq ID No. C174 & C389
	412314	AA825247	Hs.356084	G protein-coupled receptor 27 (GPR27) (S	Seq ID No. C175 & C390
	429150	AF120103	Hs.197366	smoothened (Drosophila) homolog	Seq ID No. C176 & C391
	419073	AW372170	Hs.183918	transmembrane receptor Unc5H2 mRNA	Seq ID No. C177 & C392
	411828	AW161449	Hs.72290	wingless-type MMTV integration site fami	Seq ID No. C178 & C393
25	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C179 & C394
	421779	AI879159	Hs.108219	wingless-type MMTV integration site fami	Seq ID No. C180 & C395
	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	Seq ID No. C181 & C396
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2 (str	Seq ID No. C182 & C397
	436972	AA284679	Hs.25640	claudin 3	Seq ID No. C183 & C398
30	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No. C184 & C399
	416370	N90470	Hs.203697	CD38 antigen (p45)	Seq ID No. C185 & C400
	437052	AA861697	Hs.120591	ESTs	Seq ID No. C186 & C401
	421481	AW391972	Hs.104696	KIAA1324 protein	Seq ID No. C187 & C402
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	Seq ID No. C188 & C403
35	426174	AA547959	Hs.115838	Homo sapiens similar to Echinoidin (LOC1	Seq ID No. C189 & C404
	410037	AB020725	Hs.58009	KIAA0918 protein	Seq ID No. C190 & C405
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	Seq ID No. C191 & C406
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	Seq ID No. C192 & C407
	418576	AW968159	Hs.302740	Epithelial calcium channel 2, CaT-like A	Seq ID No. C193 & C408
40	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C194 & C409
	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	Seq ID No. C195 & C410
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C196 & C411
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C197 & C412
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C198 & C413
45	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C199 & C414
	430144	AI732722	Hs.98927	ERGL protein; ERGIC-53-like protein	Seq ID No. C200 & C415
	408833	AW612232	Hs.254835	ESTs	Seq ID No. C201 & C416
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	Seq ID No. C202 & C417
50	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C203 & C418
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C204 & C419
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	Seq ID No. C205 & C420
	425976	C75094	Hs.334514	NG22 protein	Seq ID No. C206 & C421
	432800	BE391046	Hs.278962	AIM-1 protein	Seq ID No. C207 & C422
55	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	Seq ID No. C208 & C423
	424339	BE257148	Hs.145416	endoglycan	Seq ID No. C209 & C424
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	Seq ID No. C210 & C425
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	Seq ID No. C211 & C426
	434293	NM_004445	Hs.3796	EphB6	Seq ID No. C212 & C427
	427715	BE245274	Hs.180428	KIAA1181 protein	Seq ID No. C213 & C428
60	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	Seq ID No. C214 & C429
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	Seq ID No. C215 & C430
	422424	AI186431	Hs.296638	prostate differentiation factor	Seq ID No. C216 & C431
	432378	AI493046	Hs.146133	ESTs	Seq ID No. C432 & C433
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C434 & C435

## 65 TABLE 79B

Pkey: Unique Eos probeset identifier number  
CAT number: Gene cluster number  
Accession: Genbank accession numbers

## 70

Pkey CAT Number Accession  
414991 1785136\_1 D78831 C17898 D78863

## 75 TABLE 79C

Pkey: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
Nt\_position: Indicates nucleotide positions of predicted exons.

## 80

Pkey Ref Strand Nt\_position

5	404682	9797231	Minus	40977-41150
	404287	2326514	Plus	53134-53281
	404287	2326514	Plus	53134-53281
	404287	2326514	Plus	53134-53281

Table 80:

Seq ID NO: C1 DNA Sequence  
Nucleic Acid Accession #: NM\_005814  
Coding sequence: 345..1304

	1	11	21	31	41	51	
5	CTACCCCTTT	GTGAGCAGTC	TAGGACTTTG	TACACCTGTT	AAGTAGGGAG	AAGGCAGGGG	60
10	AGGTGGCTGG	TTTAAGGGGA	ACTTGAGGGA	AGTAGGGAAG	ACTCCTCTTG	GGACCTTTGG	120
	AGTAGGTGAC	ACATGAGCCC	AGCCCCAGCT	CACCTGCCAA	TCCAGCTGAG	GAGCTCACCT	180
	GCCAAATCCAG	CTGAGGCTGG	GCAGAGGTGG	GTGAGAAGAG	GGAAAATTGC	AGGGACCTCC	240
	AGTTGGGCCA	GGCCAGAAGC	TGCTGTAGCT	TTAACCAGAC	AGCTCAGACC	TGTCGGAGG	300
15	CTGCCAGTGA	CAGGTTAGGT	TTAGGGCAGA	GAAGAAGCAA	GACCATGGTG	GGGAAGATGT	360
	GGCCTGTGTT	GTGGACACTC	TGTGCAGTCA	GGGTGACCGT	CGATGCCATC	TCTGTGGAAA	420
	CTCCGCAGGA	CGTTCCTCGG	GCTTCGCAGG	GAAAGAGTGT	CACGCTGCCC	TGCACCTACC	480
	ACACTTCAC	CTCCAGTCGA	GAGGGACTTA	TTCAATGGGA	TAAGCTCCTC	CTCACTCATA	540
	CGGAAAGGGT	GGTCATCTGG	CCGTTTTCAA	ACAAAACTA	CATCCATGGT	GAGCTTTATA	600
20	AGAATCGCGT	CAGCATATCC	AACAATGCTG	AGCAGTCCGA	TGCTCCTATC	ACCATTGATC	660
	AGCTGACCAT	GGCTGACAAC	GGCACCTACG	AGTGTCTGTT	CTCGCTGATG	TCAGACCTGG	720
	AGGGCAACAC	CAAGTCACGT	GTCCGCCCTGT	TGGTCCCTCG	GCCACCTCCT	AAACCGAAT	780
	GCGGCATCGA	GGGAGAGACC	ATAATTGGGA	ACAACATCCA	GCTGACCTGC	CAATCAAAGG	840
	AGGGCTCACC	AACCCCTCAG	TACAGCTGGA	AGAGGTACAA	CATCCTGAAT	CAGGAGCAGC	900
25	CCCTGGCCCA	GCCAGCCTCA	GGTCAGCCTG	TCTCCCTGAA	GAATATCTCC	ACAGACACAT	960
	CGGGTTACTA	CATCTGTACT	TCCAGCAATG	AGGAGGGGAC	GCAGTTCTGC	AACATCACGG	1020
	TGGCCGTGAG	ATCTCCCTCC	ATGAACGTGG	CCCTGTATGT	GGGCATCGCG	GTGGGCGTGG	1080
	TTGAGCCCT	CATTATCATT	GGCATCATCA	TCTACTGCTG	CTGCTGCCGA	GGGAAGGACG	1140
	ACAACACTGA	AGACAAGGAG	GATGCAAGGC	CGAACCAGGA	AGCCTATGAG	GAGCCACCAG	1200
30	AGCAGCTAAG	AGAAGTTTCC	AGAGAGAGGG	AGGAGGAGGA	TGACTACAGG	CAGAAGAGAG	1260
	AGAGGAGCAG	TGGGCGTGAA	TCCCGGAGCC	ACCTCGACCA	GTGACAGGCC	AGCAGCAGAG	1320
	GGCGGCGGAG	GAAGGGTTAG	GGGTTCATTG	TCCCGCTTCC	TGGCCTCCCT	TCTCCTTTCT	1380
	AAGCCCTGTT	CTCCTGTCCC	TCCATCCAG	ACATTGATGG	GGACATTTCT	TCCCCAGTGT	1440
	CAGCTGTGGG	GAACATGGCT	GGCCTGGTAA	GGGGGTCCCT	GTGCTGATCC	TGCTGACCTC	1500
35	ACTGTCTCTG	GAAGTAACCC	CTCCTGGCTG	TGACACCTGG	TGCGGGCCCTG	GCCCTCACTC	1560
	AAGACCAGGC	TGCAGCCTCC	ACTTCCCTCG	TAGTTGGCAG	GAGCTCCTGG	AAGCACAGCG	1620
	CTGAGCATGG	GGCGCTCCCA	CTCAGAACTC	TCCAGGGAGG	CGATGCCAGC	CTTGGGGGGT	1680
	GGGGGCTGTC	CTGCTCACCT	GTGTGCCAG	CACCTGGAGG	GGCACCAGGT	GGAGGGTTTG	1740
	CACCTCCAC	ATCTTTCTTG	AATGAATGAA	AGAATAAGTG	AGTATGCTTG	GGCCCTGCAT	1800
40	TGGCTTGCCC	TCCAGCTCCC	ACTCCCTTTC	CAACCTCACT	TCCCGTAGCT	GCCAGTATGT	1860
	TCCAAACCT	CCTGGGAAGG	CCACCTCCCA	CTCCTGTGTC	ACAGGCCCTG	GGGAGCTTTT	1920
	GCCCACACAC	TTTCCATCTC	TGCCCTGTCAA	TATCGTACCT	GTCCCTCCAG	GCCCATCTCA	1980
	AATACACAAG	ATTTCTCTAA	CCCTATCCTA	ATTGTCCACA	TACGTGGAAA	CAATCCTGTT	2040
	ACTCTGTCCC	ACGTCACATC	ATGGGCCACA	AGGCACAGTC	TTCTGAGCGA	GTGCTCTCAC	2100
45	TGTATTAGAG	CGCCAGCTCC	TTGGGGCAGG	GCCTGGGCCT	CATGGCTTGT	GCTTTCCCTG	2160
	AAGCCCTAGT	AGCTGGCGCC	CATCCTAGTG	GGCACTTAAG	CTTAATTGGG	GAAACTGCTT	2220
	TGATTTGGTT	TGCCTTCCCT	TCTCTGGTCT	CCTTGAGATG	ATCGTAGACA	CAGGATGAT	2280
	TCCCAACCAA	ACCCACGTAT	TCATTCACTG	AGTTAAACAC	GAATTGATTT	AAAGTGAACA	2340
	CACACAAGGG	AGCTTGCTTG	CAGATGGTCT	GAGTTCTTGT	GTCCTGGTAA	TTCCTCTCCA	2400
50	GGCCAGAATA	ATTGGCATGT	CTCCTCAACC	CACATGGGGT	TCCTGGTTGT	TCCTGCATCC	2460
	CGATACTTCA	GCCCTGGGCC	TGCCAGCCCC	ATTTGGGCTC	TGGTTTTCTG	GTGGGGCTGT	2520
	CCTGTGCCCC	TCCACAGCCC	TCCTTCTGTT	TGTCGAGCAT	TTCTTCTACT	CTTGAGAGCT	2580
	CAGGCAGCGT	TAGGTCCTAT	TAGGTCCTAT	GGACCACTGG	CTGGTCTCAC	CCAACCTGCAG	2640
	TTTACTATTG	CTATCTTTTC	TGGATGATCA	GAAAAATAAT	TCCATAAATC	TATTGTCTAC	2700
55	TTGCGATTTC	TTAAAAATG	TATATTTTAA	TATATATTGT	TAAATCCTTT	GCTTCATTCC	2760
	AAATGCTTTC	AGTAATAATA	AAATTGTGGG	TGG			2793

Seq ID NO: C2 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..3150

	1	11	21	31	41	51	
60	ATGGGGAGCC	GGACGCCAGA	GTCCCTCTCT	CACGCCGTGC	AGCTGCGCTG	GGGCCCCCGG	60
65	CGCCGACCCC	CGCTSSGTCC	GCTGCTGTTG	CTGCTSSGTC	CGCCGCCACC	CAGGGTCGGG	120
	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGGAGTTTAA	CGGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
	CCCAAGGCTA	ATACCAGCCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCTC	300
	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTG	ACAGCAAAGG	CTCTCGGCTC	360
70	CTGGAGTCTC	CACTGTCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCTTGCAG	420
	TGGTTCGGGG	CAACAGTTTC	AGCCCATGGC	TCCTCCATCT	TGGCATGCGC	TCCACTGTAC	480
	AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATAACTTCA	CCCGAATTC	GGAGTATGCA	CCCTGCCGCT	CAGATTTCAG	CTGGGCAGCA	600
	GGACAGGGTT	ACTGCCAAGG	AGGCTTCAGT	GCCGAGTTCA	CCAAGACTGG	CCGTGTGGTT	660
75	TTAGGTGGAC	CAGGAAGCTA	TTTCTGGCAA	GGCCAGATCC	TGTCCTGCCAC	TCAGGAGCAG	720
	ATTGCAGAAT	CTTATTTACCC	CGAGTACCTG	ATCAACCTGG	TTCAAGGGCA	GCTGCAGACT	780
	CGCCAGGCCA	GTTCCATCTA	TGATGACAGC	TACCTAGGAT	ACTCTGTGGC	TGTTGGTGAA	840
	TTCACTGGTG	ATGACACAGA	AGACTTTGTT	GCTGGTGTGC	CCAAAGGGAA	CCTCACTTAC	900
	GGCTATGTCA	CCATCTTTAA	TGGCTCAGAC	ATTTCGATCCC	TCTACAACCT	CTCAGGGGAA	960
80	CAGATGGCC	CTACTTTTGG	CTATGCAGTG	GCCGCCACAG	ACGTCAATGG	GGACGGGCTG	1020
	GATGACTTGC	TGGTGGGGCT	ACCCCTGCTC	ATGGATCGGA	CCCTTGACGG	GCGGCCCTCAG	1080
	GAGGTGGGCA	GGGTCTACGT	CTACCTGCAG	CACCCAGCCG	GCATAGAGCC	CACGCCACCC	1140
	CTTACCTTCA	CTGGCCATGA	TGAGTTTGGC	CGATTTGGCA	GCTCCTTGAC	CCCCCTGGGG	1200
	GACCTGGACC	AGGATGGCTA	CAATGATGTG	GCCATCGGGG	CTCCCTTTGG	TGGGGAGACC	1260
	CAGCAGGGAG	TAGTGTTTGT	ATTTCTCTGG	GGCCAGGAG	GGCTGGGCTC	TAAGCCTTCC	1320

5	CAGGTTCTGC	AGCCCCGTGT	GGCAGCCAGC	CACACCCCAG	ACTTCTTTGG	CTCTGCCCTT	1380
	CGAGGAGGCC	GAGACCTGGA	TGGCAATGGA	TATCCTGATC	TGATTGTGGG	GTCCCTTGGT	1440
	GTGGACAAGG	CTGTGGTATA	CAGGGGCCGC	CCCATCGTGT	CCGCTAGTGC	CTCCCTCACC	1500
	ATCTTCCCCG	CCATGTTCAA	CCCAGAGGAG	CGGAGCTGCA	GCTTAGAGGG	GAACCCCTGT	1560
	GCCTGCATCA	ACCTTAGCTT	CTGCCTCAAT	GCTTCTGGAA	AACACGTTGC	TGACTCCATT	1620
	GGTTTCACAG	TGGAACCTCA	GCTGGACTGG	CAGAAGCAGA	AGGGAGGGGT	ACGGCGGGCA	1680
	CTGTTCCCTG	CCTCCAGGCA	GGCAACCCTG	ACCCAGACCC	TGCTCATCCA	GAATGGGGCT	1740
	CGAGAGGATT	GCAGAGAGAT	GAAGATCTAC	CTCAGGAACG	AGTCAGAAAT	TCGAGACAAA	1800
10	CTCTCGCCGA	TTACATCGC	TCTCAACTTC	TCCTTGGACC	CCCCAGCCCC	AGTGACAGC	1860
	CACGGCTCA	GGCCAGCCCT	ACATTATCAG	AGCAAGAGCC	GGATAGAGGA	CAAGGCTCAG	1920
	ATCTTGCTGG	ACTGTGGAGA	AGACAACATC	TGTGTGCTTG	ACCTGCAGCT	GGAAGTGTTC	1980
	GGGGAGCAGA	ACCATGTGTA	CCTGGGTGAC	AAGAATGCCC	TGAACCTCAC	TTTCCATGCC	2040
	CAGAATGTGG	GTGAGGGTGG	CGCCTATGAG	GCTGAGCTTC	GGGTCAACCG	CCCTCCAGAG	2100
	GCTGAGTACT	CAGGACTCGT	CAGACACCCA	GGGAACCTCT	CCAGCCTGAG	CTGTGACTAC	2160
15	TTTGCCGTGA	ACAGAGCCG	CCTGCTGGTG	TGTGACCTGG	GCAACCCCAT	GAAGGCAGGA	2220
	GCCAGTCTGT	GGGGTGGCCT	TCGGTTTACA	GTCCCTCATC	TCCGGGACAC	TAAGAAAACC	2280
	ATCCAGTTTG	ACTTCCAGAT	CCTCAGCAAG	AATCTCAACA	ACTCGCAAAG	CGACGTGGTT	2340
	TCCTTTCCGG	TCCTCCGTGA	GGCTCAGGCC	CAGGTCACCC	TGAACGGTGT	CTCCAAGCCT	2400
	GAGGCAGTGC	TATTCACAGT	AAGCGACTGG	CATCCCCGAG	ACCAGCCTCA	GAAGGAGGAG	2460
20	GACCTGGGAC	CTGCTGTCCA	CCATGTCTAT	GAGCTCATCA	ACCAAGGCC	CAGCTCCATT	2520
	AGCCAGGGTG	TGCTGGAACT	CAGCTGTCCC	CAGGCTCTGG	AAGGTCAGCA	GCTCCTATAT	2580
	GTGACCAGAG	TTACGGGACT	CAACTGCACC	ACCAATCACC	CCATTAACCC	AAAGGGCCTG	2640
	GAGTTGGATC	CCGAGGGTTC	CCTGCACCAC	CAGCAAAAAC	GGGAAGCTCC	AAGCCGCAGC	2700
25	CTGCTTCCT	CGGGACCTCA	GATCCTGAAA	TGCCCCGAGG	CTGAGTGTTC	CAGGCTGCCG	2760
	TGTGAGCTCG	GGCCCCTGCA	CCAACAAGAG	AGCCAAAGTC	TGCAGTTGCA	TTTCCGAGTC	2820
	TGGGCCAAGA	TTTCTTGCA	GCGGGAGCAC	CAGCCATTTA	GCCTGCAGTG	TGAGGCTGTG	2880
	TACAAAGCCC	TGAAGATGCC	CTACCGAATC	CTGCCTCGGC	AGCTGCCCCA	AAAAGAGCGT	2940
	CAGGTGGCCA	CAGCTGTGCA	ATGGACCAAG	GCAGAAGGCA	GCTATGGCGT	CCCACCTGTG	3000
30	ATCATCATCC	TAGCCATCCT	GTTTGGCCTC	CTGCTCCTAG	GTCTACTCAT	CTACATCCTC	3060
	TACAAGCTTG	GATTCTTCAA	ACGCTCCCTC	CCATATGGCA	CGCCATGGA	AAAAGCTCAG	3120
	CTCAAGCCTC	CAGCCACCTC	TGATGCCTGA				3150

Seq ID NO: C3 DNA Sequence

Nucleic Acid Accession #: NM\_002421.2

Coding sequence: 1..1410

35	1	11	21	31	41	51	
40	ATGCACAGCT	TTCTTCCACT	GCTGCTGCTG	CTGTTCTGGG	GTGTGGTGTC	ACACAGCTTC	60
	CCAGCGACTC	TAGAAACACA	AGAGCAAGAT	GTGGACTTAG	TCCAGAAATA	CCTGGAAAAA	120
	TACTACAAAC	TGAAGAAATG	TGGGAGGCAA	GTTGAAAAGC	GGAGAAATAG	TGGCCCAAGT	180
	GTTGAAAAAT	TGAAGCAAAT	GCAGGAATTC	TTTGGGCTGA	AAGTGACTGG	GAAACCAGAT	240
	GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCTGATGT	GGCTCAGTTT	300
45	GTCTCTCACT	AGGGGAACCC	TCGCTGGGAG	CAAACACATC	TGACCTACAG	GATTGAAAAA	360
	TACACGCCAG	ATTTGCCAAG	AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	CTTCCAATC	420
	TGGAGTAATG	TCACACCTCT	GACATTCAAC	AAGGTCTCTG	AGGGTCAAGC	AGACATCATG	480
	ATATCTTTTG	TCAGGGGAGA	TCATCGGGAC	AACCTCTCCT	TTGATGGACC	TGGAGGAAAT	540
	CTTGCTCATG	CTTTTCAACC	AGGCCCAGGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600
50	GAAAGGTGGA	CCAACAATTT	CAGAGAGTAC	AACTTACATC	GTGTTGCGGC	TCATGAACTC	660
	GGCCATTCTC	TTGGACTCTC	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
	ACCTTCAGTG	GTGATGTTCA	GCTAGCTCAG	GATGACATTG	ATGGCATCCA	AGCCATATAT	780
	GGACGTTCCC	AAATCCCTGT	CCAGCCCATC	GGCCCAACAA	CCCCAAAAGC	ATGTGACAGT	840
	AAGCTAACCT	TTGATGCTAT	AACTACGATT	CGGGGAGAAG	TGATGTTCTT	TAAAGACAGA	900
55	TTCTACATGC	GCACAAATCC	CTTCTACCCG	GAAGTTGAGC	TCAATTTTCA	TTCTGTTTTT	960
	TGGCCACAAC	TGCCAAATGG	GCTTGAAGCT	GCTTACGAAT	TTGCCGACAG	AGATGAAGTC	1020
	CGGTTTTTCA	AAGGGAATAA	GTACTGGGCT	GTTCAGGGAC	AGAATGTGCT	ACACGGATAC	1080
	CCCAAGGACA	TCTACAGCTC	CTTTGGCTTC	CCTAGAACTG	TGAAGCATAT	CGATGCTGCT	1140
	CTTTCTGAGG	TGAAGGTGAT	AAAAACCTAC	TTCTTTGTGG	CTAACAAATA	CTGGAGGTAT	1200
60	GATGAATATA	AACGATCTAT	GGATCCAGGT	TATCCCAAAA	TGATAGCACA	TGACTTTCCT	1260
	GGAAATGGCC	ACAAAGTTGA	TGCAGTTTTC	ATGAAAGATG	GATTTTCTTA	TTTCTTTCAT	1320
	GGAACAAGAC	AATACAAATT	TGATCCTAAA	ACGAAGAGAA	TTTTGACTCT	CCAGAAAGCT	1380
	AATAGCTGGT	TCAACTGCAG	GAAAAATTAG				1410

Seq ID NO: C4 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1410

65	1	11	21	31	41	51	
70	ATGCACAGCT	TTCTTCCACT	GCTGCTGCTG	CTGTTCTGGG	GTGTGGTGTC	ACACAGCTTC	60
	CCAGCGACTC	TAGAAACACA	AGAGCAAGAT	GTGGACTTAG	TCCAGAAATA	CCTGGAAAAA	120
	TACTACAAAC	TGAAGAAATG	TGGGAGGCAA	GTTGAAAAGC	GGAGAAATAG	TGGCCCAAGT	180
	GTTGAAAAAT	TGAAGCAAAT	GCAGGAATTC	TTTGGGCTGA	AAGTGACTGG	GAAACCAGAT	240
75	GCTGAAACCC	TGAAGGTGAT	GAAGCAGCCC	AGATGTGGAG	TGCCTGATGT	GGCTCAGTTT	300
	GTCCTCACTG	AGGGGAACCC	TCGCTGGGAG	CAAACACATC	TGACCTACAG	GATTGAAAAA	360
	TACACGCCAG	ATTTGCCAAG	AGCAGATGTG	GACCATGCCA	TTGAGAAAGC	CTTCCAATC	420
	TGGAGTAATG	TCACACCTCT	GACATTCAAC	AAGGTCTCTG	AGGGTCAAGC	AGACATCATG	480
	ATATCTTTTG	TCAGGGGAGA	TCATCGGGAC	AACCTCTCCT	TTGATGGACC	TGGAGGAAAT	540
80	CTTGCTCATG	CTTTTCAACC	AGGCCCAGGT	ATTGGAGGGG	ATGCTCATTT	TGATGAAGAT	600
	GAAAGGTGGA	CCAACAATTT	CAGAGAGTAC	AACTTACATC	GTGTTGCGGC	TCATGCCCTC	660
	GGCCATTCTC	TTGACTCTCT	CCATTCTACT	GATATCGGGG	CTTTGATGTA	CCCTAGCTAC	720
	ACCTTCAGTG	TGAGATGTTCA	GCTAGCTCAG	GATGACATTG	ATGGCATCCA	AGCCATATAT	780
	GGACGTTCCC	AAATCCCTGT	CCAGCCCATC	GGCCCAACAA	CCCCAAAAGC	ATGTGACAGT	840
	AAGCTAACCT	TTGATGCTAT	AACTACGATT	CGGGGAGAAG	TGATGTTCTT	TAAAGACAGA	900

5  
 10  
 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCAT TTCTGTTTTTC 960  
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020  
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080  
 CCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140  
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTG CTAACAAATA CTGGAGGTAT 1200  
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCCT 1260  
 GGAATTGGCC ACAAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTTCTA TTTCTTTTCAT 1320  
 GGAACAAGAC AATACAAATG TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380  
 AATAGCTGGT TCAACTGCAG GAAAAATTAG 1410

Seq ID NO: C5 DNA Sequence  
 Nucleic Acid Accession #: NM\_014331.2  
 Coding sequence: 1..1506

15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 1  
 |  
 ATGGTCAGAA AGCCTGTTGT GTCCACCATC TCCAAAGGAG GTTACCTGCA GGGAAATGTT 60  
 AACGGGAGGC TGCCCTCCCT GGGCAACAAG GAGCCACCTG GGCAGGAGAA AGTGCAGCTG 120  
 AAGAGGAAAG TCACCTTACT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTGGAGCA 180  
 GGAATCTTCA TCTCTCTTAA GGGCGTGCTC CAGAACACGG GCAGCGTGGG CATGTCCTCTG 240  
 ACCATCTGGA CGGTGTGTGG GGTCTGTGCA CTATTGGAG CTTTGTCTTA TGCTGAATTG 300  
 GGAACAACFA TAAAGAAATC TGGAGGTCAT TACACATATA TTTTGGAGT CTTTGGTCCA 360  
 TTACCAGCTT TTGTACGAGT CTGGGTGGAA CTCCTCATAA TACGCCCTGC AGCTACTGCT 420  
 GTGATATCCC TGGCATTTGG ACGCTACATT CTGGAACCAT TTTTATTTC ATGTGAAATC 480  
 CCTGAACCTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTGAT GGTCTCTAAAT 540  
 AGCATGAGTG TCAGCTGGAG CGCCCGGATC CAGATTTTCT TAACCTTTTG CAAGCTCACA 600  
 GCAATTTCTGA TAATTATAGT CCCTGGAGTT ATGCAGCTAA TTAAGGTCA AACGCAGAAC 660  
 TTTAAAGACG CGTTTTTCAG AAGAGATTCA AGTATTACGC GGTGCGCACT GGCTTTTTAT 720  
 TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTTACTGA AGAAGTAGAA 780  
 AACCCTGAAA AAACCATTC CTTTGCAATA TGTATATCCA TGGCCATTGT CACCATTGGC 840  
 TATGTGCTGA CAATGTGGC CTACTTTACG ACCATTAATG CTGAGGAGCT GCTGCTTTCA 900  
 AATGCAGTGG CAGTGACCTT TTCTGAGCGG CTACTGGGAA ATTTCTCAT AGCAGTTCCG 960  
 ATCTTTGTTG CCTCTCCTCG CTTTGGCTCC ATGAACGGTG GTGTGTTTGC TGTCTCCAGG 1020  
 TTATCTATG TTGCGTCTCG AGAGGGTCAC CTCCAGAAA TCCTCTCCAT GATTCTATGC 1080  
 CGCAAGCACA CTCCTCTACC AGCTGTTATT GTTTTGCACC CTTTGACAAT GATAATGCTC 1140  
 TTCTCTGGAG ACCTCGACAG TCTTTTGAAT TTCCCTCAGT TTGCCAGGTG GCTTTTTTAT 1200  
 GGGCTGGCAG TTGCTGGGCT GATTTATCTT CGATACAAAT GCCCAGATAT GCATCGTCTC 1260  
 TTCAAGGTGC CACTGTTTAT CCCAGCTTTC TTTTCTTCA CATGCCTCTT CATGGTTGCC 1320  
 CTTTCCCTCT ATTCGGACCC ATTTAGTACA GGGATTGGCT TCGTCATCAC TCTGACTGGA 1380  
 GTCCCTGCGT ATTATCTCTT TATTATATGG GACAAGAAAC CCAGGTGGTT TAGAATAATG 1440  
 TCAGAGAAAA TAACCAGAAC ATTACAAATA ATACTGGAAG TTGTACCAGA AGAAGATAAG 1500  
 TTTATGAATA ATGGACTTGA GATCTTGGCA ATCTGCCCAA GGGGAGACAC AAAATAGGGA 1560  
 TTTTACTTTC ATTTCTGTA AGTCTAGAGA ATTACAACCT TGGTGATAAA CAAAAGGAGT 1620  
 CAGTTATTTT TATTCATATA TTTTAGCATA TTCGAACATA TTTCTAAGAA ATTTAGTTAT 1680  
 AACTCTATGT AGTTATAGAA AGTGAATATG CAGTTATTCT ATGAGTCGCA CAATTCTTGA 1740  
 GTCTCTGATA CCTACCTATT GGGGTTAGGA GAAAGACTA GACAATTACT ATGTGGTCAT 1800  
 TCTCTACAC ATATGTTTAC ACGCAAGA ACCTTCAAT TGAAGACTGA GATTTTCTG 1860  
 TATATATGGG TTTTGTAAAG ATGGTTTTAC AACTACAGA TGTCTATCT GTGAAAAGTG 1920  
 TTTTCAATTG TGAATAAAG CATACTCAT GATTATGGCA AAGAGGAGAG AAAGAAATTT 1980  
 ATTTTACATT GACATTGCA TGTCTCCCT TAGATACCAA TTTAGATAAC AAACACTCAT 2040  
 GCTTTAATGG ATTATACCCA GAGCCTTTG AACAAAGGTC AGTGGGGATT GTTGAATACA 2100  
 TTAAGAAGA GTTTCTAGGG GCTACTGTTT ATGAGACACA TCCAGGAGTT ATGTTTAAAGT 2160  
 AAAAATCCTT GAGAATTAT TATGTCAGAT GTTTTTTCAT TCATTATCAG GAAGTTTATG 2220  
 TTAATCTGTA TTTTCTTTT TCACTCAGT TTGATCAGGA AAGTGATATA CACATCTTAG 2280  
 AGCAAGAGTT AGTTTGGTAT TAAATCCTCA TTAGAACAAC CACCTGTTTC ACTAATAACT 2340  
 TACCCCTGAT GAGTCTATCT AAACATATGC ATTTTAAAGCC TTCAAATTAC ATTATCAACA 2400  
 TGAGAGAAAT AACCAACAAA GAAGATGTTT AAAATAATAG TCCCATATCT GTAATCATAT 2460  
 CTACATGCAA TGTAGTAAT TCTGAAGTTT FTTAAATTTA TGGCTATTTT TACACGATGA 2520  
 TGAATTTTGA CAGTTTGTGC ATTTCTTTA TACATTTTAT ATTCTTCTGT TAAATATCT 2580  
 CTTCAGATGA AACTGTCCAG ATTAATTAGG AAAAGGCATA TATTAACATA AAAATTGCAA 2640  
 AAGAAATGTC GCTGTAAATA AGATTTACAA CTGATGTTTC TAGAAAATTT CCACCTCTAT 2700  
 ATCTAGGCTT TGTGAGTAAT TTCCACACCT TAATTATCAT TCAACTTGCA AAAGAGACAA 2760  
 CTGATAAGAA GAAAATTGAA ATGAGAATCT GTGGATAAGT GTTGTGTTC AGAAGATGTT 2820  
 GTTTTGCCAG TATTAGAAAA TACTGTGAGC CGGGCATGGT GGCTTACATC TGTAAATCCA 2880  
 GCACCTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTGCG GAGTTCTAGA CCAGCCTGAC 2940  
 CAACATGGAG AAACCCCATC TCTACTAAAA ATACAAAATT AGCTGGGCAT GGTGGCACAT 3000  
 GCTGGTAATC TCACTATTG AGGAGGCTGA GGCAGGAGAA TTGCTTGAA CCGGGAGGCG 3060  
 GAGGTTGCAG TGAGCCAAGA TTGCACCACT GTACTCCAGC CTGGGTGACA AAGTCAGACT 3120  
 CCATCTCCAA AAAAAAATA AAAA 3144

Seq ID NO: C6 DNA Sequence  
 Nucleic Acid Accession #: NM\_003246.1  
 Coding sequence: 112..3624

75  
 80  
 1  
 |  
 GGACGCACAG GCATTCCCGG CGCCCTCCCA GCCCTCGCCG CCCTCGCCAC CGCTCCCGGC 60  
 CGCCGCGCTC CGGTACACAC AGGATCCCTG CTGGGCACCA ACAGCTCCAC CATGGGGCTG 120  
 GCCTGGGGAC TAGGCGTCTT GTTCTGATG CATGTGTGTG GCACCAACCG CATTCCAGAG 180  
 TCTGGCGGAG ACAACAGCTG GTTTGACATC TTTGAACTCA CCGGGGCGCG CCGCAAGGGG 240  
 TCTGGGCGCC GACTGTGTAA GGGCCCCGAC CCTTCCAGCC CAGCTTTCCG CATCGAGGAT 300  
 GCCAACCTGA TCCCCCTGT GCCTGATGAC AAGTTCCAAG ACCTGGTGGG TGCTGTGCGG 360  
 GCAGAAAAGG GTTTCCTCCT TCTGGCATCC CTGAGGCAGA TGAAGAAGAC CCGGGGCACG 420

5	CTGCTGGCCC	TGGAGCGGAA	AGACCACTCT	GGCCAGGTCT	TCAGCGTGGT	GTCCAATGGC	480
	AAGGCGGGCA	CCCTGGACCT	CAGCCTGACC	GTCCAAGGAA	AGCAGCACGT	GGTGTCTGTG	540
	GAAGAAGCTC	TCCTGGCAAC	CGGCCAGTGG	AAGAGCATCA	CCCTGTTTGT	GCAGGAAGAC	600
	AGGGCCCAAG	TGTACATCGA	CTGTGAAAAG	ATGGAGAATG	CTGAGTTGGA	CGTCCCCATC	660
	CAAAGCGTCT	TCACCAAGGA	CCTGGCCAGC	ATCGCCAGAC	TCCGCATCGC	AAAGGGGGGC	720
	GTCAATGACA	ATTTCAGGGG	GGTGCTGCAG	AATGTGAGGT	TTGTCTTTGG	AACCACACCA	780
	GAAGACATCC	TCAGGAACAA	AGGCTGCTCC	AGCTCTACCA	GTGTCTCTCT	CACCCCTTGAC	840
	AACAACGTGG	TGAATGGTTC	CAGCCCTGCC	ATCCGCACTA	ACTACATTGG	CCACAAGACA	900
10	AAGGACTTGC	AAGCCATCTG	CGGCATCTCC	TGTGATGAGC	TGTCCAGCAT	GGTCTCTGAA	960
	CTCAGGGGCC	TGGCACCAT	TGTGACCACG	CTGCAGGACA	GCATCCGCAA	AGTGACTGAA	1020
	GAGAACAAAG	AGTTGGCCAA	TGAGCTGAGG	CGGCCCTCCC	TATGCTATCA	CAACGGAGTT	1080
	CAGTACAGAA	ATAACGAGGA	ATGGACTGTT	GATAGCTGCA	CTGAGTGTCA	CTGTCAAGAC	1140
	TCAGTTACCA	TCGTCAAAAA	GGTGTCTGTC	CCCATCATGC	CCTGCTCCAA	TGCCACAGTT	1200
15	CCTGATGGAG	AATGCTGTCC	TCGCTGTTGG	CCCAGCGACT	CTGCGGACGA	TGGCTGGTCT	1260
	CCATGGTCCG	AGTGGACCTC	CTGTTCTACG	AGCTGTGGCA	ATGGAATTCA	GCAGCGCGGC	1320
	CGCTCTGCG	ATAGCCTCAA	CAACCGATGT	GAGGGCTCCT	CGGTCCAGAC	ACGGACCTGC	1380
	CACATTTCAG	AGTGTGACAA	AAAGTTTAAA	CAGGATGGTG	GCTGGAGCCA	CTGGTCCCCG	1440
	TGCTCATCTT	GTCTGTGTAC	ATGTGTGAT	GGTGTGATCA	CAAGGATCCG	GCTCTGCAAC	1500
20	TCTCCCAGCC	CCCAGATGAA	TGGGAAACCC	TGTGAAGGCG	AAGCGCGGGA	GACCAAAGCC	1560
	TGCAAGAAAG	ACGCCCTGCC	CATCAATGGA	GGCTGGGGTC	CTTGGTCAAC	ATGGGACATC	1620
	TGTTCTGTCA	CCTGTGGAGG	AGGGGTACAG	AAACGTAGTC	GCTCTGCAAA	CAACCCCGCA	1680
	CCCCAGTTTG	GAGGCAGGGA	CTGCGTTGGT	GATGTAACAG	AAAACCAAGT	CTGCAACAAG	1740
	CAGGACTGTC	CAATTGATGG	ATGCCCTGCT	AATCCCTGCT	TTGCCGGCGT	GAAGTGTACT	1800
25	AGCTACCCCTG	ATGGCAGCTG	GAAATGTGGT	GCTTGTCCCC	CTGTTTACAG	TGGAAATGGC	1860
	ATCCAGTGCA	CAGATGTTGA	TGAGTGCAAA	GAAGTGCCCTG	ATGCCCTGCT	CAACCAACAAT	1920
	GGAGAGCAC	GGTGTGAGAA	CACGGAACCC	GGCTACAAC	GCCTGCCCTG	CCCCCAACGC	1980
	TTCAACGGCT	CACAGCCCTT	CGGCCAGGGT	GTGCAACATG	CCACGGCCAA	CAAAACAGGTG	2040
	TGCAAGCCCC	GTAACCCCTG	CACGGATGGG	ACCCAGCACT	GCAACAAGAA	CGCCAAGTGC	2100
30	AACCTACTGG	GCCACTGTG	CGACCCATG	TACCGCTGCG	AGTGCAAGCC	TGGCTACGCT	2160
	GGCAATGGCA	TCATCTGCGG	GGAGGACACA	GACCTGGATG	GCTGGCCCAA	TGAGAACCTG	2220
	TGTTGCGTGG	CCAATGCGAC	TTACCACTGC	AAAAAGGATA	ATTGCCCCAA	CCTTCCCAAC	2280
	TCAGGGCAGG	AAGACTATGA	CAAGGATGGA	ATTGGTGATG	CCTGTGATGA	TGACGATGAC	2340
	AATGATAAAA	TTCAGATGTA	CAGGGACAAC	TGTCCATTCC	ATTACAACCC	AGCTCAGTAT	2400
35	GACTATGACA	GAGATGATGT	GGGAGACCGC	TGTGACAACT	GTCCCTACAA	CCACAACCCA	2460
	GATCAGGCAG	ACACAGACAA	CAATGGGGAA	GGAGACGCCT	GTGCTGCAGA	CATTGATGGA	2520
	GACGGTATCC	TCAATGAACG	GGACAACCTG	CAGTACGTCT	ACAATGTGGA	CCAGAGAGAC	2580
	ACTGATATGG	ATGGGGTTGG	AGATCAGTGT	GACAATTGCC	CCTTGGAACA	CAATCCGGAT	2640
	CAGCTGGACT	CTGACTCAGA	CCGCATTGGA	GATACCTGTG	ACAACATCA	GGATATTGAT	2700
40	GAAGATGGCC	ACCAGAACAA	TCTGGACAAC	TGTCCCTATG	TGCCCAATGC	CAACCAAGCT	2760
	GACCATGACA	AAGATGGCAA	GGGAGATGCC	TGTGACCACG	ATGATGACAA	CGATGGCATT	2820
	CCTGATGACA	AGGACAACCT	CAGACTCGTG	CCCAATCCCG	ACCAGAAGGA	CTCTGACGGC	2880
	GATGGTTCGAG	GTGATGGCTG	CAAAGATGAT	TTTGACCATG	ACAGTGTGCC	AGACATCGAT	2940
	GACATCTGTC	CTGAGAAATG	TGACATCAGT	GAGACCGATT	TCCGCCGATT	CCAGATGATT	3000
45	CCCTCTGGAC	CCAAAGGGAC	ATCCCAAAAT	GACCCTAACT	GGGTTGTACG	CCATCAGGGT	3060
	AAAGAACTCG	TCCAGACTGT	CAACTGTGAT	CCTGGACTCG	CTGTAGGTTA	TGATGAGTTT	3120
	AATGCTGTGG	ACTTTCAGTG	CACCTTCTTC	ATCAACACCG	AAAGGGACGA	TGACTATGCT	3180
	GGATTTGTCT	TTGGCTACCA	GTCCAGCAGC	CGCTTTTATG	TTGTGATGTG	GAAGCAAGTC	3240
	ACCCAGTCTC	ACTGGGACAC	CAACCCACAG	AGGGCTCAGG	GATACTCGGG	CCTTTCTGTG	3300
50	AAAGTTGTAA	ACTCCACACC	AGGGCCTGGC	GAGCACCTGC	GGAAACGCCCT	GTGGCACACA	3360
	GGAAACACCC	CTGGCCAGGT	GCGCACCTCG	TGGCATGACC	CTCGTCACAT	AGGCTGGAAA	3420
	GATTTTACCG	CCTACAGATG	GCGTCTCAGC	CACAGGCCAA	AGACGGGTTT	CATTAGAGTG	3480
	GTGATGTATG	AAGGGAAGAA	AATCATGGCT	GACTCAGGAC	CCATCTATGA	TAAAACCTAT	3540
	GCTGGTGGTA	GACTTAGGTT	GTTTGTCTTC	TCTCAAGAAA	TGGTGTCTTC	CTCTGACCTG	3600
55	AAATACGAAT	GTAGAGATCC	CTAATCATCA	AATTTGTGAT	TGAAAGACTG	ATCATAAACC	3660
	AATGCTGGTA	TTGCACCTTC	TGGAACATATG	GGCTTGAGAA	AACCCCAAGT	ATCACTTCTC	3720
	CTTGGCTTCC	TTCTTTTCTG	TGCTTGCATC	AGTGTGGACT	CCTAGAACGT	GCGACCTGCC	3780
	TCAAGAAAAT	GCAAGTTTTC	AAAACAGACT	CATCAGCATT	CAGCCCTCAA	TGAATAAGAC	3840
	ATCTTCCAAG	CATATAAACA	ATTGCTTTGG	TTTCTTTTGG	AAAAAGCATC	TACTTGCTTC	3900
60	AGTTGGGAAG	GTGCCCATTC	CACTCTGCCT	TTGTACAGAA	GCAGGGTGCT	ATTGTGAGGC	3960
	CATCTCT						3967

Seq ID NO: C7 DNA Sequence  
Nucleic Acid Accession #: NM\_002192  
Coding sequence: 86..1366

65	1	11	21	31	41	51	
	TCCACACACA	CAAAAAACCT	GCGCGTGAGG	GGGGAGGAAA	AGCAGGGCCT	TTAAAAAGGC	60
70	AATCACAACA	ACTTTTGTCTG	CCAGGATGCC	CTTGCTTTGG	CTGAGAGGAT	TTCTGTTGGC	120
	AAGTTGTCTGG	ATTATAGTGA	GGAGTTCCCC	CACCCACAGGA	TCCGAGGGGC	ACAGCGCGGC	180
	CCCCGACTGTG	CCGTCTCTGTG	CGCTGGCCGC	CCTCCCAAAG	GATGTACCCA	ACTCTCAGCC	240
	AGAGATGGTG	GAGGCCGTCA	AGAAGCACAT	TTTAAACATG	CTGCACTTGA	AGAAGAGACC	300
	CGATGTCAAC	CAGCCGGTAC	CCAAGGCGGC	GCTTCTGAAC	GCGATCAGAA	AGCTTCATGT	360
75	GGGCAAGTC	GGGAGAAACG	GGTATGTGGA	GATAGAGGAT	GACATTGGAA	GGAGGGCAGA	420
	AATGAATGAA	CTTATGAGAG	AGACCTCGGA	GATCATCACG	TTTGCCGAGT	CAGGAACAGC	480
	CAGGAAGACG	CTGCACCTTC	AGATTTCCAA	GGAAGGCAGT	AGCTGTCTAG	TGGTGGAGCG	540
	TGCAGAAGTC	TGGCTCTTCC	TAAAAGTCCC	CAAGGCCAAC	AGGACCAGGA	CCAAAGTCAC	600
	CATCCGCCCTC	TTCCAGCAGC	AGAAGCACCC	GCAGGGCAGC	TGGACACAG	GGGAAGAGGC	660
80	CGAGGAAGTG	GGCTTAAAGG	GGGAGAGGAG	TGAACTGTTG	CTCTCTGAAA	AAGTAGTAGA	720
	CGCTCGGAAG	AGCACCTGGC	ATGTCTTCCC	TGTCTCCAGC	AGCATCCAGC	GGTTGCTGGA	780
	CCAGGGCAAG	AGCTCCCTGG	ACGTTCCGAT	TGCCTGTGAG	CAGTGCCAGG	AGAGTGGCGC	840
	CAGCTTGGTT	CTCTCTGGCA	AGAAGAAGAA	GAAAGAAGAG	GAGGGGGAAG	GGAAAAAGAA	900
	GGGCGGAGGT	GAAGGTGGGG	CAGGAGCAGA	TGAGGAAAAG	GAGCAGTCGC	ACAGACCTTT	960
	CCTCATGCTG	CAGGCCCGGC	AGTCTGAAGA	CCACCTCAT	CGCCGGCGCT	GGCGGGCTTT	1020



5	GGAGTGTGAT	GGCAAGGTCA	ACATCTGCTG	TAAGAAACAG	TTCTTTGTCA	GTTTCAAGGA	1080
	CATCGGCTGG	AATGACTGGA	TCATTGCTCC	CTCTGGCTAT	CATGCCAACT	ACTGCGAGGG	1140
	TGAGTGCCCG	AGCCATATAG	CAGGCACGTC	CGGGTCCTCA	CTGTCTCTCC	ACTCAACAGT	1200
	CATCAACCAC	TACCGCATGC	GGGGCCATAG	CCCCTTTGCC	AACCTCAAAT	CGTGCTGTGT	1260
	GCCCAACCAAG	CTGAGACCCA	TGTCCATGTT	GTACTATGAT	GATGGTCAAA	ACATCATCAA	1320
	AAAGGACATT	CAGAACATGA	TCTGGAGGGA	GTGTGGGTGC	TCATAGAGTT	GCCCAGCCCA	1380
	GGGGGAAAGG	GAGCAAGAGT	TGTCCAGAGA	AGACAGTGCC	AAATGAAGA	AATTTTTAAG	1440
	GTTTCTGAGT	TAACCAGAAA	AATAGAAATT	AAAAACAAAA	CAAAAACAAA	AAAAAACAA	1500
10	AAAAAACAA	AAGTAAATTA	AAAACAAACC	TGATGAAACA	GATGAAACAG	ATGAAGGAAG	1560
	ATGTGGAAAT	CTTAGCCTGC	CTTAGCCAGG	GCTCAGAGAT	GAAGCAGTGA	AGAGACAGAT	1620
	TGGGAGGGAA	AGGGAGAATG	GTGTACCTTT	TATTTCTTCT	GAAATCACAC	TGATGACATC	1680
	AGTTGTTTAA	ACGGGGTATT	GTCTTTTCCC	CCCTTGAGGT	TCCCTTGTTA	GCTTGAATCA	1740
	ACCAATCTGA	TCTGCAGTAG	TGTGGACTAG	AACAACCCAA	ATAGCATCTA	GAAAGCCATG	1800
15	AGTTTGAAG	GGCCCATCAC	AGGCACCTTC	CTAGCCTAAT			1840

Seq ID NO: C8 DNA Sequence  
Nucleic Acid Accession #: NM\_000095.1  
Coding sequence: 26..2299

20	1	11	21	31	41	51	
	CAGCACCCAG	CTCCCCGCCA	CCGCCATGGT	CCCCGACACC	GCCTGCGTTC	TTCTGCTCAC	60
25	CCTGGCTGCC	CTCGGCGCGT	CCGGACAGGG	CCAGAGCCCG	TTGGGCTCAG	ACCTGGGCCC	120
	GCAGATGCTT	CGGGAAGTGC	AGGAAACCAA	CGCGGCGCTG	CAGGACGTGC	GGGACTGGGT	180
	GCGGCAGCAG	GTGAGGAGGA	TCACGTTCCCT	GAAAAACACG	GTGATGGAGT	GTGACGGGTG	240
	CGGGATGCAG	CAGTTCAGTAC	GCACCGGCCT	ACCAGCGGTG	CGGCCCTGTC	TCCACTGCGC	300
	GCCCGGCTTC	TGCTTCCCCG	GCCTGGCCTG	CATCCAGACG	GAGAGCGGCG	GCCGCTGCGG	360
30	CCCCTGCCCC	GCGGGCTTCA	CGGGCAACGG	CTCGCACTGC	ACCGACGTCA	ACGAGTGCAA	420
	CGCCCCCCCC	TGCTTCCCCC	GAGTCCGCTG	TATCAACACC	AGCCCCGGGT	TCCGCTGCGA	480
	GGCTTGCCCC	CCGGGGTACA	GCGGCCCCAC	CCACCAGGGC	GTGGGGCTGG	CTTTCGCCAA	540
	GGCCAAACAAG	CAGGTTTGCA	CGGACATCAA	CGAGTGTGAG	ACCGGGCAAC	ATAACTGCGT	600
	CCCCAACTCC	GTGTGCATCA	ACACCCGGGG	CTCCTTCCAG	TGCGGCCCGT	GCCAGCCCGG	660
35	CTTCTGGGGC	GACCAAGCGT	CCGGCTGCCA	GCGCGGCGCA	CAGCGCTTCT	GCCCCGACGG	720
	CTCGCCGAGC	GAGTGCCACG	AGCATGCAGA	CTGCTCCTTA	GAGCGCGATG	GCTCGCGGTC	780
	GTGCGTGTGT	CGGTTGGCTT	GGGCCGCAAA	CGGGATCCTC	TGTGGTCCGG	ACACTGACCT	840
	AGACGGCTTC	CCGGACGAGA	AGCTGCGCTG	CCCGGAGCCG	CAGTGCCGTA	AGGACAACCT	900
	CGTGACTGTG	CCCAACTCAG	GGCAGGAGGA	TGTGGACCCG	GATGGCATCG	GAGACGCGCT	960
40	CGATCCGGAT	CCCGACGGGG	ACGGGGTCCC	CAATGAAAAG	GACAACTGCC	CGCTGGTGCG	1020
	GAACCCAGAC	CAGCGCAACA	CGGACGAGGA	CAAGTGGGGC	GATGCGTGCG	ACAACCTGCC	1080
	GTCCCAAGA	AACGACGACC	AAAAGGACAC	AGACCAGGAC	GGCCGGGGCG	ATGCGTGCGA	1140
	CGACGACATC	GACGGCGACC	GGATCCGCAA	CCAGGCCGAC	AACTGCCCTA	GGGTACCCAA	1200
	CTCAGACCA	AAGGACAGTG	ATGGCGATGG	TATAGGGGAT	GCCTGTGACA	ACTGTCCCCA	1260
45	GAAGAGCAAC	CCGGATCAGG	CGGATGTGGA	CCACGACTTT	GTGGGAGATG	CTTGTGACAG	1320
	CGATCAAGAC	CAGGATGGAG	ACGGACATCA	GGACTCTCGG	GACAACTGTC	CCACGGTGCC	1380
	TAACAGTGCC	CAGGAGGACT	CAGACCACGA	TGGCCAGGGT	GATGCCCTGC	ACGACGACGA	1440
	CGACAATGAC	GGAGTCCCTG	ACAGTCGGGA	CAACTGCCGC	CTGGTGCCTA	ACCCCGGCCA	1500
	GGAGGACGCG	GACAGGGACG	GCGTGGGCGA	CGTGTGCCAG	GACGACTTTG	ATGCAGACAA	1560
50	GGTGGTAGAC	AAGATCGACG	TGTGTCCGGA	GAACGCTGAA	GTCAACGCTCA	CCGACTTCAG	1620
	GGCCTTCCAG	ACAGTCTGTG	TGGACCCGGA	GGGTGACGCG	CAGATTGACC	CCAACCTGGT	1680
	GGTGCTCAAC	CAGGGAAGGG	AGATCGTGCA	GACAATGAAC	AGCGACCCAG	GCCTGGCTGT	1740
	GGGTTACACT	GCCTTCAATG	GCGTGGACTT	CGAGGGCACG	TTCCATGTGA	ACACGGTCC	1800
	GGATGACGAC	TATGCGGGCT	TCATCTTTGG	CTACCAGGAC	AGCTCCAGCT	TCTACGTGGT	1860
55	CATGTGGAAG	CAGATGGAGC	AAACGTATTG	GCAGGCGAAC	CCCTTCCGTC	CTGTGGCCGA	1920
	GCCTGGCATC	CAACTCAAGG	CTGTGAAGTC	TTCCACAGGC	CCCGGGGAAC	AGCTGCGGAA	1980
	CGCTCTGTGG	CATACAGGAG	ACACAGAGTC	CCAGGTGCGG	CTGCTGTGGA	AGGACCCGCG	2040
	AAACGTGGGT	TGGAAGGACA	AGAAGTCTTA	TCGTTGGTTC	CTGCAGCACC	GGCCCCAAGT	2100
	GGGCTACATC	AGGGTGGCAT	TCTATGAGGG	CCCTGAGCTG	GTGGCCGACA	GCAACGTGGT	2160
60	CTTGGACACA	ACCATTGCGG	GTGGCGCCCT	GGGGGTCTTC	TGCTTCTCCC	AGGAGAACAT	2220
	CATCTGGGCC	ACCCTGCGTT	ACCGCTGCAA	TGACACCATC	CCAGAGGACT	ATGAGACCCA	2280
	TCAGCTGCGG	CAAGCCTAGG	GACCAGGGTG	AGGACCCGCC	GGATGACAGC	CACCCCTCACC	2340
	GCGGCTGGAT	GGGGGCTCTG	CACCCAGCCC	AAGGGGTGGC	CGTCTGAGG	GGGAAGTGAG	2400
	AAGGGCTCAG	AGAGGACAAA	ATAAAGTGTG	TGTGCAAGG			2439

Seq ID NO: C9 DNA Sequence  
Nucleic Acid Accession #: XM\_057014  
Coding sequence: 143..874

70	1	11	21	31	41	51	
	GGGAGGGAGA	GAGGCGCGCG	GGTGAAGGCG	GCATTGATGC	AGCCTGCGGC	GGCCTCGGAG	60
75	CGCGGCGGAG	CCAGACGCTG	ACCACGTTCC	TCTCCTCGGT	CTCCTCGGCC	TCCAGCTCCG	120
	CGCTGCCCCG	CAGCCGGGAG	CCATGCGACC	CCAGGGCCCC	GCCGCTCCCC	CGCAGCGGCT	180
	CCCGCGGCTC	CTGCTGCTCC	TGCTGCTGCA	GCTGCCGCGC	CCGTGAGGCG	CCTCTGAGAT	240
	CCCCAAGGGG	AAGCAAAGG	CGCAGTCCCG	GCAGAGGGAG	GTGGTGGACC	TGTATAATGG	300
	AATGTGCTTA	CAAGGGCCAG	CAGGAGTGCC	TGGTCGAGAC	GGGAGCCCTG	GGGCCAATGG	360
80	CATTCCGGGT	ACACCTGGGA	TCCCAGTTCG	GGATGGATTG	AAAGGAGAAA	AGGGGGAATG	420
	TCTGAGGGAA	AGCTTTGAGG	AGTCTCTGAC	ACCCAACTAC	AAGCAGTGTT	CATGGAGTTC	480
	ATTGAATTAT	GGCATAGATC	TTGGGAAAT	TGCGGAGTGT	ACATTTACAA	AGATGCGTTC	540
	AAATAGTGCT	CTAAGAGTTT	TGTTCACTGG	CTCACTTCGG	CTAAAATGCA	GAAATGCATG	600
	CTGTACGCGT	TGTTATTTCA	CATTCAATGG	AGCTGAATGT	TCAGGACCTC	TTCCCATTTG	660
	AGCTATATAT	TATTTGGACC	AAGGAAGCCC	TGAAATGAAT	TCAACAATTA	ATATTCATCG	720

5 CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780  
 CTGGGTGGC ACTTGTTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840  
 TTCTCGCATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900  
 TTTTCTTAT ATGCTTGGGA ATGGTTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960  
 CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020  
 TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAGTG GTTTCATAT TTTTCTTAGT 1080  
 TGGTTAGAAT ACTTTCTTCA TAGTCACATT CTCTCAACCT ATAATTTGGA ATATTGTTGT 1140  
 GGTCCTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAA ATATAAAAGC TACCAATCTT 1200  
 10 TGTACAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260  
 CAACCTTAAA AAAAAAAAAA AAAA 1284

Seq ID NO: C10 DNA Sequence  
 Nucleic Acid Accession #: NM\_003225  
 Coding sequence: 41..295

15 1 11 21 31 41 51  
 | | | | |  
 20 ATCCCTGACT CGGGGTCGCC TTTGGAGCAG AGAGGAGGCA ATGGCCACCA TGGAGAACAA 60  
 GGTGATCTGC GCCCTGGTCC TGGTGTCAT GCTGGCCCTC GGCACCCTGG CCGAGGCCCA 120  
 GACAGAGACG TGTACAGTGG CCCCCGTGA AAGACAGAAT TGTGGTTTTC CTGGTGTAC 180  
 GCCTCCCGG TGTGCAATA AGGGCTGCTG TTTGACGAC ACCGTTTCGT GGGTCCCTG 240  
 GTGCTTCTAT CCTAATACCA TCGACGTCCC TCCAGAAGAG GAGTGTGAAT TTTAGACACT 300  
 TCTGCAGGGA TCTGCTGCA TCTGACGGG GTGCCGTCCC CAGCAGGTTG ATTAGTCCCA 360  
 25 GAGCTCGGCT GCCACCTCCA CCGGACACCT CAGACACGCT TCTGCAGCTG TGCCTCGGCT 420  
 CACAACACAG ATTGACTGCT CTGACTTTGA CTACTCAAAA TTGGCCTAAA AATTAAGA 480  
 GATCGATATT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 540

Seq ID NO: C11 DNA Sequence  
 Nucleic Acid Accession #: NM\_015419.1  
 Coding sequence: 1..8487

30 1 11 21 31 41 51  
 | | | | |  
 35 ATGCCAAGC GCGCGCACTG GGGGGCCCTC TCCGTGGTGC TGATCCTGCT TTGGGGCCAT 60  
 CCGCGAGTGG CGCTGGCTCG CCGGCATCCT TGTGCCTGCT ACGTCCCCAG CGAGGTCCAC 120  
 TGCACGTTCC GATCCCTGGC TCCGTGCCCC GCTGGCATTG CTAGACACGT GGAAGAATC 180  
 AATTGGGGT TTAATAGCAT ACAGGCCCTG TCAGAAACCT CATTTGCAGG ACTGACCAAG 240  
 TTGGAGTAC TTAATGATCA CGGCAATGAG ATCCCAAGCA TCCCGATGG AGCTTTAAGA 300  
 40 GACCTCAGCT CTCTTCAGT TTTCAAGTTC AGCTACAACA AGCTGAGAGT GATCACAGGA 360  
 CAGACCTCC AGGCTCTCTC TAACTTAATG AGGCTGCACA TTGACCACAA CAAGATCGAG 420  
 TTTATCCACC CTCAAGCTTT CAACGGCTTA ACGTCTCTGA GGCTACTCCA TTTGGAAGGA 480  
 AATCTCCTCC ACCAGCTGCA CCCCAGCACC TTCTCCACGT TCACATTTT GGATTATTT 540  
 AGACTCTCCA CCTAAGGCA CCTCTACTTA GCAGAGAACA TGGTTAGAAC TCTTCTGCC 600  
 45 AGCATGCTTC GGAACATGCC GCTTCTGGAG AATCTTTACT TGCAGGGAAG TCCGTGGACC 660  
 TCGAGTTGTG AGATGAGATG GTTTTGGAA TGGGATGCAA AATCCAGAGG AATTCTGAAG 720  
 TGTAAAAAGG ACAAAGCTTA TGAAGGCGGT CAGTTGTGTG CAATGTGCTT CAGTCCAAAG 780  
 AAGTTGTACA AACATGAGAT ACACAAGCTG AAGGACATGA CTTGTCTGAA GCCTTCAATA 840  
 GAGTCCCCCTC TGAGACAGAA CAGGAGCAGG AGTATTGAGG AGGAGCAAGA ACAGGAAGAG 900  
 50 GATGGTGGCA GCCAGCTCAT CCTGGAGAAA TTCCAACCTGC CCCAGTGGAG CATCTCTTG 960  
 AATATGACCG ACCAGCCCGG GAACATGGTG AACTTGGTCT GTGACATCAA GAAACCAATG 1020  
 GATGTGTACA AGATTCACTT GAACCAACCG GATCCTCCAG ATATTGACAT AAATGCAACA 1080  
 GTTGCTTGG ACTTTGAGTG TCCAATGACC CGAGAAAACCT ATGAAAAGCT ATGGAAATTG 1140  
 ATAGCATACT ACAGTGAAGT TCCCGTGAAG CTACACAGAG AGCTCATGCT CAGCAAGAC 1200  
 55 CCCAGAGTCA GCTACCACTA CAGGCAGGAT GCTGATGAGG AAGCTCTTTA CTACACAGT 1260  
 GTGAGAGCCC AGATTCTTGC AGAACCAAG TGGGTCTATG AGCCATCCAT AGATATCCAG 1320  
 CTGAACCGAC GTCAGAGTAC GGCCAAGAAG GTGCTACTTT CTTACTACAC CCAGTATTCT 1380  
 CAAACAATAT CCACCAAGA TACAAGGCAG GCTCGGGGCA GAAGCTGGGT AATGATTGAG 1440  
 CCTAGTGGAG CTGTGCAAG AGATCAGACT GTCTTGGAAG GGGGTCCATG CCAAGTTGAGC 1500  
 60 TGCAACGTGA AAGCTTCTGA GAGTCCATCT ATCTTCTGGG TGCTTCCAGA TGGCTCCATC 1560  
 CTGAAAGCGC CCATGGATGA CCCAGACAGC AAGTTCTCCA TTCTCAGCAG TGGCTGGCTG 1620  
 AGGATCAAGT CCAATGGAGCC ATCTGACTCA GGCTTGATACC AGTGCAATGC TCAAGTGAGG 1680  
 GATGAAATGG ACCGCATGGT ATATAGGGTA CTTGTGCACT CTCCCTCCAC TCAGCCAGCC 1740  
 GAGAAAGACA CAGTGACAAT TGGCAAGAAC CCAGGGGAGT CGGTGACATT GCCTTGCAAT 1800  
 65 GCTTTAGCAA TACCCGAAGC CCACCTTAGC TGGATTCTTC CAAACAGAAG GATAATTAAT 1860  
 GATTGGCTA ACACATCACA TGTATACATG TTGCCAAATG GAACCTCTTC CATCCCAAAG 1920  
 GTCCAAGTCA GTGATAGTGG TTACTACAGA TGTGTGGCTG TCAACCAGCA AGGGGCAGAC 1980  
 CATTTTACGG TGGGAATCAC AGTGACCAAG AAAGGGTCTG GCTTGCCATC CAAAGAGGC 2040  
 AGACGCCGCA GTGCAAAAGC TCTTTCCAGA GTCAGAGAAG ACATCGTGA GATGAAGGG 2100  
 70 GGCTCGGCA TGGGAGATGA AGAGAACACT TCAAGGAGAC TTCTGCATCC AAAGGACCAA 2160  
 GAGGTGTTCC TCAAAACAAA GGATGATGCC ATCAATGGAG ACAAGAAAGC CAAGAAAGGG 2220  
 AGAAGAAAGC TGAAACTCTG GAAGCATTCG GAAAAAGAAC CAGAGACCAA TGTGTCAGAA 2280  
 GGTGCGAGAG TGTTTGAATC TAGACGAAGG ATAAACATGG CAAACAAACA GATTAATCCG 2340  
 GAGCGCTGGG CTGATATTTT AGCCAAAGTC CGTGGGAAAA ATCTCCCTAA GGGCACAGAA 2400  
 75 GTACCCCGCT TGATTAAGAC CACAAGTCC CTATCCTTGA GCCTAGAAGT CACACCACCT 2460  
 TTTCTGCTG TTTCTCCCCC CTCAGCATCT CCTGTGCAGA CAGTAACCAAG TGCTGAAGAA 2520  
 TCCTCAGCAG ATGTACCTCT ACTTGGTGAA GAAGAGCAGC TTTTGGGTAC CATTTCTCTCA 2580  
 GCCAGCATGG GGCTAGAACA CAACCACAAT GGAGTTATTC TTGTTGAACC TGAAGTAACA 2640  
 AGCACACCTC TGGAGGAAGT TGTGATGAC CTTTCTGAGA AGACTGAGGA GATAACTTCC 2700  
 80 ACTGAAGGAG ACCTGAAGGG GACAGCAGCC CTTACACTTA TATCTGAGCC TTATGAACCA 2760  
 TCTCTACTC TGCACACATT AGACACAGTC TATGAAAAGC CCACCCATGA AGAGACGGCA 2820  
 ACAGAGGGTT GGTCTGCAGC AGATGTTGGA TCGTCACCAG AGCCACATC CAGTGAGTAT 2880  
 GAGCCTCAT TGGATGCTGT CTCCTTGGCT GAGTCTGAGC CCAATGCAATA CTTTGACCCA 2940  
 GATTGAGAGA CTAAGTCACA ACCAGATGAG GATAAGATGA AAGAAGACAC CTTTGACAC 3000  
 CTTACTCCAA CCCCCACCAT CTGGGTTAAT GACTCCAGTA CATCACAGTT ATTTGAGGAT 3060

	TCTACTATAG	GGGAACCAGG	TGTCCCAGGC	CAATCACATC	TACAAGGACT	GACAGACAAC	3120
	ATCCACCTTG	TGAAAAGTAG	TCTAAGCACT	CAAGACACCT	TACTGATTAA	AAAGGGTATG	3180
	AAAGAGATGT	CTCAGACACT	ACAGGGAGGA	AATATGCTAG	AGGGAGACCC	CACACACTCC	3240
5	AGAAGTTCTG	AGAGTGAGGG	CCAAGAGAGC	AAATCCATCA	CTTTGCTCTGA	CTCCACACTG	3300
	GGTATAATGA	GCAGTATGTC	TCCAGTTAAG	AAGCCTGCGG	AAACCACAGT	TGGTACCCCTC	3360
	CTAGACAAAG	ACACCACAAC	AGTAACAACA	ACACCAAGGC	AAAAAGTTGC	TCCGTCTATCC	3420
	ACCATGAGCA	CTCACCTTTC	TCGAAGGAGA	CCCAACGGGA	GAAGGAGATT	ACGCCCCAAC	3480
	AAATTCCGCC	ACCGGCACAA	GCAAACCCCA	CCCACAACCT	TTGCCCCATC	AGAGACTTTT	3540
10	TCCTACTCAAC	CAACTCAAGC	ACCTGACATT	AAGATTTCAA	GTCAAGTGGA	GAGTTCTCTG	3600
	GTTCCTACAG	CTTGGGTGGA	TAACACAGTT	AATACCCCA	AACAGTTGGA	AATGGAGAAG	3660
	AATGCAGAAC	CCACATCCAA	GGGAACACCA	CGGAGAAAAC	ACGGGAAGAG	GCCAAACAAA	3720
	CATCGATATA	CCCTTCTTAC	AGTGAGCTCA	AGAGCGTCCG	GATCCAAGCC	CAGCCCTTCT	3780
	CCAGAAAATA	AACATAGAAA	CATTGTTACT	CCCAGTTCAG	AAACTATACT	TTTGCCCTAGA	3840
	ACTGTTTCTC	TGAAAACCTGA	GGGCCCTTAT	GATTCCTTAG	ATTACATGAC	AACCACCAGA	3900
15	AAAATATATT	CATCTTACCC	TAAAGTCCAA	GAGACACTTC	CAGTCACATA	TAAACCCACA	3960
	TCAGATGGAA	AAGAAATTGA	GGATGATGTT	GCCACAAATG	TTGACAAAAC	TAAAAGTGAC	4020
	ATTTTGTGCA	CTGGTGAATC	AAATTAATAA	GCCATACCAA	CTTCTCGCTC	CTTGGTCTCC	4080
	ACTATGGGAG	AAATTAAGTA	AGAATCCTCT	CCTGTAGGCT	TTCCAGGAAC	TCCAACCTGG	4140
20	AATCCCTCAA	GGACGGCCCA	GCCTGGGAGG	CTACAGACAG	ACATACCTGT	TACCACTTCT	4200
	GGGGAAAATC	TTACAGACCC	TCCCTTCTTT	AAAGAGCTTG	AGGATGTGGA	TTTCACTTCC	4260
	GAGTTTTTGT	CCCTTTTGAC	AGTCTCCACA	CCATTTTACC	AGGAAGAAGC	TGGTTCTTCC	4320
	ACAACTCTCT	CAAGCATAAA	AGTGGAGGTG	GCTTCAAGTC	AGGCAGAAAC	CACCACCCCT	4380
	GATCAAGATC	ATCTTGAAAC	CAGTGTGGCT	ATTCTCCTTT	CTGAAACTAG	ACCACAGAAT	4440
25	CACACCCCTA	CTGCTGCCCC	GATGAAGGAG	CCAGCATCCT	CGTCCCCATC	CACAAATCTC	4500
	ATGTCTTTGG	GACAAAACAC	CACCACTAAG	CCAGCATCTC	CCAGTCCAAG	AATATCTCAA	4560
	GCATCTAGAG	ATTCCAAGGA	AAATGTTTTT	TTGAATTATG	TGGGGAATCC	AGAAACAGAA	4620
	GCAACCCAGG	TCAACAATGA	AGGAACACAG	CATATGTCAG	GGCCAAATGA	ATTATCAACA	4680
	CCCTCTTCCG	ACCGGGATGC	ATTTAACTTG	TCTACAAAGC	TGGAAATTGGA	AAAGCAAGTA	4740
30	TTTGGTAGTA	GGAGTCTACC	ACGTGGGCCA	GATAGCCAAAC	GCCAGGATGG	AAGAGTTCAT	4800
	GCTTCTCATC	AACTAACACG	AGTCCCTGCC	AAACCCATCC	TACCAACAGC	AACAGTGAGG	4860
	CTACCTGAAA	TGTCACACA	AAGCGCTTCC	AGATACCTTG	TAACCTTCCA	GTCACTCTGT	4920
	CAGTGGACCA	ACAAACCCGA	AATAACTACA	TATCCTTCTG	GGGCTTTGCC	AGAGAACAAA	4980
	CAGTTTACAA	CTCCAAGATT	ATCAAGTACA	ACAATTCCTC	TCCCATTTGCA	CATGTCCAAA	5040
35	CCCAGCATTC	CTAGTAAGTT	TACTGACCGA	AGAACTGACC	AAATCAATGG	TTACTCCAAA	5100
	GTGTTTGGAA	ATAACAACAT	CCCTGAGGCA	AGAAACCCAG	TTGGAAAGCC	TCCCACTCCA	5160
	AGAATTCCTC	ATTATTCCAA	TGGAAGACTC	CCTTTCTTTA	CCAACAAGAC	TCTTTCTTTT	5220
	CCACAGTTGG	GAGTCACCCG	GAGACCCACG	ATACCCACTT	CTCCTGCCCC	AGTAATGAGA	5280
	GAGAGAAAAG	TTATTTCCAG	TTCTTACAAC	AGGATACATT	CCCATAGCAC	CTTCCATCTG	5340
40	GACTTTGGCC	CTCCGGCAC	TCCGTTGTTG	CACACTCCGC	AGACCACGGG	ATCACCTTCA	5400
	ACTAACTTAC	AGAATATCCC	TATGGTCTCT	TCCACCCAGA	GTTCTATCTC	CTTTATAACA	5460
	TCTTCTGTCC	AGTCTCTAGG	AAGCTTCCAC	CAGAGCAGCT	CAAAAGTTCT	TGCAGGAGGA	5520
	CCTCCTGCAT	CCAAATCTG	GTCTCTTGGG	GAAAAGCCCC	AAATCCTCAC	CAAGTCCCA	5580
	CAGACTGTGT	CCGTCAACGC	TGAGACAGAC	ACTGTGTTCC	CCTGTGAGGC	AACAGGAAAA	5640
45	CCAAAGCCCT	TGCTTACTTG	GACAAAGGTT	TCCACAGGAG	CTCTTATGAC	TCCGAATACC	5700
	AGGATACAAC	GGTTTGAGGT	TCTCAAGAAC	GGTACCTTAG	TGATACGGAA	GGTTCAAGTA	5760
	CAAGATCGAG	GCCAGTATAT	GTGCACCCGC	AGCAACCTGC	ACGGCCTGGA	CAGGATGGTG	5820
	GTCTTGCTTT	CGGTCAACGT	GCAGCAACCT	CAAACTCTAG	CCTCCCACTA	CCAGGACGTC	5880
	ACTGTCTACC	TGGGAGACAC	CATTGCAATG	GAGTGTCTGG	CCAAAGGGAC	CCCAGCCCCC	5940
50	CAAAATTTCT	GGATCTTCCC	TGACAGGAGG	GTGTGGCAAA	CTGTGTCCCC	CGTGGAGAGC	6000
	CGCATCACCC	TGCACAAAA	CCGGACCCCT	TCCAATCAAG	AGGCGTCTTT	CTCAGACAGA	6060
	GGCGTCTATA	AGTGCCTGGC	CAGCAATGCA	GCCGGGGCGG	ACAGCCTGGC	CATCCGCTCG	6120
	CACGTGGCGG	CAGTGCCCCC	CGTTATCCAC	CAGGAGAAGC	TGGAGAACAT	CTCGCTGCCC	6180
	CCGGGGCTCA	GCATTCACAT	TCACTGCACT	GCCAAGGCTG	CGCCCTGCC	CAGCGTGGC	6240
55	TGGGTGCTCG	GGGACGGTAC	CCAGATCCGC	CCCTCGCAGT	TCTTCCACGG	GAACCTTGTT	6300
	GTTTTCCCCA	CCGGGACGCT	CTACATCCGC	AACCTCGCGC	CCAAGGACAG	CGGGCGCTAT	6360
	GAGTGCCTGG	CCGCCAACCT	GGTAGGCTCC	GCGCGCAGGA	CGGTGCAGCT	GAACGTGCAG	6420
	CGTGACGACG	CCAACGCGCG	CATCAGCGGC	ACCTCCCCGC	GGAGGACGGA	CGTCAGGTAC	6480
	GGAGGAACCC	TCAAGCTGGA	CTGCAGCGCC	TGGGGGAGCC	CCTGGCCGCG	CATCCTCTGG	6540
60	AGGCTGCCGT	CCAAGAGGAT	GATCGACGCG	CTCTTCAGTT	TTGATAGCAG	AATCAAGGTG	6600
	TTTGCCAATG	GGACCTGGT	GGTGAATCA	GTGACGGACA	AAGATGCCGG	AGATTACCTG	6660
	TGCGTAGCTC	GAAATAAGGT	TGGTGATGAC	TACGTGGTGC	TCAAAGTGGA	TGTGGTGATG	6720
	AAACCGGCCA	AGATTGAACA	CAAGGAGGAG	AACGACCAAC	AAGTCTTCTA	CGGGGGTGAC	6780
	CTGAAAGTGG	ACTGTGTGGC	CACCGGGCTT	CCCAATCCCG	AGATCTCCTG	GAGCCTCCCA	6840
65	GACGGGAGTC	TGGTGAATC	CTTCATGCAG	TCCGATGACA	GCGGTGGACG	CACCAAGCGC	6900
	TATGTGCTCT	TCAACAAATG	GACACTCTAC	TTTAAACGAAG	TGGGGATGAG	GGAGGAAGGA	6960
	GACTACACCT	GCTTTGCTGA	AAATCAGGTC	GGGAAGGACG	AGATGAGAGT	CAGAGTCAAG	7020
	GTGGTGACAG	CGCCCGCCAC	CATCCGGAAC	AAGACTTACT	TGGCGGTTC	GGTGCCCTAT	7080
	GGAGACGTGG	TCACTGTAGC	CTGTGAGGCC	AAAGGAGAAC	CCATGCCCAA	GGTGACTTGG	7140
70	TTGTCCCCAA	CCAACAAGGT	GATCCCCACC	TCTCTGAGA	AGTATCAGAT	ATACCAAGAT	7200
	GGCACTCTCC	TTATTGAGAA	AGCCCCAGCG	TCTGACAGCG	GCAACTACAC	CTGCCCTGGT	7260
	AGGAACAGCG	CGGGAGAGGA	TAGGAAGACG	GTGTGGATTCT	ACGTCAACGT	CCAGCCACCC	7320
	AAGATCAACG	GTAACCCCAA	CCCCATCACC	ACCGTGCGGG	AGATAGCAGC	CGGGGGCAGT	7380
	CGGAAACTGA	TTGACTGCAA	AGCTGAAGGC	ATCCCCACCC	CGAGGGTGTT	ATGGGCTTTT	7440
75	CCCGAGGGTG	TGGTTCTGCC	AGCTCCATAC	TATGGAAACC	GGATCACTGT	CCATGGCAAC	7500
	GGTTCCCTCG	ACATCAGGAG	TTTGAGGAAG	AGCGACTCCG	TCCAGCTGGT	ATGCATGGCA	7560
	CGCAACGAGG	GAGGGGAGGC	GAGGTTGATC	GTGCAGCTCA	CTGTCTGGGA	GCCCCATGGG	7620
	AAACCCATCT	TCCACGACCC	GATCAGCGAG	AAGATCACGG	CCATGGCGGG	CCACACCATC	7680
	AGCCTCAACT	GCTCTGCCGC	GGGGACCCCG	ACACCCAGCC	TGGTGTGGGT	CCTTCCCAAT	7740
	GGCACCAGATC	TGCAGAGTGC	ACAGCAGCTG	CAGCGCTTCT	ACCACAAGGC	TGACGGCATG	7800
80	CTACACATTA	GCGGTCTCTC	CTCGGTGGAC	GCTGGGGCCT	ACCGCTGCGT	GGCCCGCAAT	7860
	GCCGCTGGCC	ACACGGAGAG	GCTGGTCTCC	CTGAAGGTGG	GACTGAAGCC	AGAAGCAAA	7920
	AAGCAGTATC	ATAACCTGGT	CAGCATCATC	AATGGTGAGA	CCCTGAAGCT	CCCTGCACCC	7980
	CCTCCCGGGG	CTGGGCGAGG	ACGTTTCTCC	TGGACGCTCC	CCAATGGCAT	GCATCTGGAG	8040
	GGCCCCAAA	CCCTGGGACG	CGTTTCTCTT	CTGGACAAATG	GCACCTCAC	GGTTCGTGAG	8100

	GCCTCGGTGT	TTGACAGGGG	TACCTATGTA	TGCAGGATGG	AGACGGAGTA	CGGCCCTTCG	8160
	GTCACCAAGCA	TCCCCGTGAT	TGTGATCGCC	TATCCTCCCC	GGATCACCAG	CGAGCCCACC	8220
	CCGGTCATCT	ACACCCGGCC	CGGGAACACC	GTGAACTGA	ACTGCATGGC	TATGGGGATT	8280
5	CCCAAAGCTG	ACATCAGCTG	GGAGTTACCG	GATAAGTCGC	ATCTGAAGGC	AGGGGTTCCAG	8340
	GCTCGTCTGT	ATGGAACACG	ATTTCTTCAC	CCCCAGGGAT	CAC TGACCAT	CCAGCATGCC	8400
	ACACAGAGAG	ATGCCGGCTT	CTACAAGTGC	ATGGCAAAAA	ACATTCTCGG	CAGTGACTCC	8460
	AAAACAACCT	ACATCCACGT	CTTCTGAAAT	GTGGATTCCA	GAATGATTGC	TTAGGAACTG	8520
	ACAACAAGC	GGGTTTGTGA	AGGGAAGCCA	GGTTGGGGAA	TAGGAGCTCT	TAAATAATGT	8580
10	GTACACAGTGC	ATGGTGGCCT	CTGGTGGGTT	TCAAGTTGAG	GTTGATCTTG	ATCTACAATT	8640
	GTTGGGAAAA	GGAAGCAATG	CAGACACGAG	AAGGAGGGCT	CAGCCTTGCT	GAGACACTTT	8700
	CTTTTGTGTT	TACATCATGC	CAGGGGCTTC	ATT CAGGGTG	TCTGTGCTCT	GACTGCAATT	8760
	TTTCTTCTTT	TGCAAAATGCC	ACTCGACTGC	CTTCATAAGC	GTCCATAGGA	TATCTGAGGA	8820
	ACATTTCATCA	AAAATAAGCC	ATAGACATGA	ACAACACCTC	ACTACCCCAT	TGAAGACGCA	8880
15	TCACCTAGTT	AACCTGCTGC	AGTTTTTACA	TGATAGACTT	TGTTCCAGAT	TGACAAGTCA	8940
	TCITTCAGTT	ATTTCCTCTG	TCACCTCAAA	ACTCCAGCTT	GCCCAATAAG	GATTTAGAAC	9000
	CAGAGTGACT	GATATATATA	TATATATTTT	AATTCAGAGT	TACATACATA	CAGCTACCAT	9060
	TTTATATGAA	AAAAGAAAAA	CATTCTCTCC	TGGAACCTCAC	TTTTTATATA	ATGTTTTATA	9120
	TATATATTTT	TTCTTTTCAA	ATCAGACGAT	GAGACTAGAA	GGAGAAATAC	TTTCTGTCTT	9180
20	ATTAAAAATTA	ATAAAATTAT	GGTCTTTACA	AGACTTGGAT	ACATTACAGC	AGACATGGAA	9240
	ATATAATTTT	AAAAAATTTT	TCTCCAACCT	CCTTCAAATT	CAGTCACCAC	TGTTATATTA	9300
	CCTTCTCCAG	GAACCTTCCA	GTGGGAAGG	CTGCGATATT	AGATTTCCTT	TGTACCAAG	9360
	TTTTTGTGTA	AAGCTGTGCT	CAGAGGAGGT	GAGAGGAGAG	GAAGGAGAAA	ACTGCATCAT	9420
	AACTTTACAG	AATTGAATCT	AGAGTCTTCC	CCGAAAAGCC	CAGAAACTTC	TCTGCAGTAT	9480
25	CTGGCTTGTC	CATCTGTGCT	AAGGTGGCTG	CTTCTTCCCC	AGCCATGAGT	CAGTTTGTGC	9540
	CCATGAATAA	TACACGACCT	GTTATTTCCA	TGACTGCTTT	ACTGTATTTT	TAAGGTCAAT	9600
	ATACTGTACA	TTTGATAATA	AAATAATATT	CTCCCAAAAA	AAAAA		9645

30 Seq ID NO: C12 DNA Sequence  
Nucleic Acid Accession #: AK001903  
Coding sequence: none

	1	11	21	31	41	51	
35	TATCATGCAT	GTGGGAAGGT	GGGTGTGGTG	AGAAAAGTTT	TAAGGCAAGA	GTAGATGGCC	60
	ATGTTTCACT	TTACAAAATT	TCTTGGAAAA	CTGGCAGTAT	TTTGAAGTGC	ATCTTCTTTG	120
	GTACCCGAAC	CTGCAGAAAC	AGTGTGAGAA	ATTAAGTCCT	GGTTCAGTGC	CGAGTAGCAA	180
	AGATGGTCAA	GGCCATGGAA	AAAGCAGAAA	TTTACCAAGA	AAGCTGATAC	CCATGTATAG	240
40	TTCCCACTCA	TCTCAAAATC	ATCTGCTATC	TTTTTAAGCT	AAGTCCTAGA	CATATCGGGG	300
	ATAACATGGG	GTTTGATTAG	TGACCACAGT	TATCAGAAAG	AGAGAAATGT	AATTCCTATG	360
	TTTATTTGAA	ACTTATTCCA	TATTTTAATT	GGATATTGAG	TGATTGGGTT	ATCAAAACAC	420
	CACAAACTTT	AATTTTGTAT	AATTATATG	GCTTTGAAAT	AGAAGTATAA	GTTGCTACCA	480
	TTTTTTGATA	ACATTGAAAG	ATAGTATTTT	ACCATCTTTA	ATCATCTTGG	AAAATACAAG	540
45	TCCTGTGAAC	AACCACCTCT	TCACCTAGCA	GCATGAGGCC	AAAAGTAAAG	GCTTTAAATT	600
	ATAACATATG	GGATTTCTAG	TAGTATGTTT	TTTTCTTGAA	ACTCAGTGCC	TCTATCTAAC	660
	CTTACTATCT	CCTCACTCTT	TCTCTAAGAC	TAAACTCTAG	GCTCTTAAAA	ATCTGCCCAC	720
	ACCAATCTTA	GAAGCTCTGA	AAAGAATTTG	TCTTTAAATA	TCTTTTAAATA	GTAACATGTA	780
	TTTTATGAGC	CAAAATTGACA	TTTTTCGACTA	TTTTTTCCAA	AAAAGTCAGG	TGAATTTTCAG	840
50	CACACTGAGT	TGGGAATTTT	TTATCCCAGA	AGACCAACCA	ATTTTCATATT	TATTTAAGAT	900
	TGATTCCTAA	CTCCGTTTTC	AAGGAGAAATC	CCTGCAGTCT	CCTTAAAGGT	AGAACAAATA	960
	CTTTCTATTT	TTTTTTTTCAC	CATTGTGGGA	TGGGACTTTA	AGAGGTGACT	CTAAAAAAAC	1020
	AGAGAACAAA	TATGTCTCAG	TTGTATTAAAG	CACGAGCCCA	TATTATCATA	TTCACTTAAA	1080
	AAAATGATTT	CCTGTGCACC	TTTTGGCAAC	TTCTCTTTTC	AATGTAGGGA	AAAACCTTAGT	1140
55	CACCTCGAAA	ACCACAAAAA	TAAATAAAAC	TTGTAGATGT	GGGCAGAAAG	TTTGGGGGTG	1200
	GACATTGTAT	GTGTTTAAAT	TAAACCCCTGT	ATCACTGAGA	AGCTGTTGTA	TGGGTCAGAG	1260
	AAAATGAATG	CTTAGAAGCT	GTTTCACATCT	TCAAGAGCAG	AAGCAAAACCA	CATGTCTCAG	1320
	CTATATTATT	ATTTATTTT	TATGCATAAA	GTGAATCATT	TCTTCTGTAT	TAATTTCCAA	1380
	AGGGTTTATC	CCTCTATTTA	AATGCTTTGA	AAAACAGTGC	ATTGACAATG	GTTTGATATT	1440
60	TTTCTTTAAA	AGAAAAATAT	AATTATGAAA	GCCAAAGATA	TCTGAAGCCT	GTTTTATTTT	1500
	AAAACTTTTT	ATGTTCTGTG	GTTGATGTTG	TTTGTGTTGT	TGTTTCTATT	TTGTTGGTTT	1560
	TTTACTTTGT	TTTTTGTTTT	GTTTTGTTTT	GTTTTGCATA	CTACATGCAG	TTCTTTAACC	1620
	AATGTCTGTT	TGGCTAATGT	AATTAAAGTT	GTTAATTTAT	ATGAGTGCAT	TTCAACTATG	1680
	TCAATGGTTT	CTTAATATTT	ATTGTGTAGA	AGTACTGGTA	ATTTTTTTAT	TTACAATATG	1740
65	TTTAAAGAGA	TAACAGTTTG	ATATGTTTTT	ATGTGTTTAT	AGCAGAAAGT	ATTTATTTCT	1800
	ATGGCATTCC	AGCGGATATT	TTGGTGTGTT	CGAGGCATGC	AGTCAATATT	TTGTACAGTT	1860
	AGTGGACAGT	ATTCAGCAAC	GCCTGATAGC	TTCTTTGGCC	TTATGTTAAA	TAAAAAGACC	1920
	TGTTTGGGAT	GT					1932

70 Seq ID NO: C13 Protein Sequence  
Nucleic Acid Accession #: Bos sequence  
Coding sequence: 1..5001

	1	11	21	31	41	51	
75	ATGCCAGGCA	CAAAACTAAC	CCGAACAGGC	GCCCCAGCAG	ACTACAGAGT	GATATTGAAG	60
	ACCTCTCAAG	AGGACGAATT	GGATGTACCT	GACGACATCA	GCGTCCGGGT	TATGTCACTC	120
	CAGTCTGTGC	TTGTGTCCCTG	GGTGGATCCT	GTTCTGGAAA	AACAGAAGAA	AGTTGTTGCA	180
80	TCAAGACAGT	ACACCGTGCG	CTATCGAGAG	AAGGGGAAT	TGGCCAGGTG	GGATTATAAG	240
	CAGATCGCTA	ACAGGCGTGT	GCTGATTGAG	AACCTGATTC	CAGACACTGT	GTATGAAATT	300
	GCAGTCCGTA	TTTCACAGGG	TGAAAGAGAT	GGCAAAATGA	GTACGTCACT	CTTCCAAAGA	360
	ACACCAAGAT	TGCCCCCTAC	CACAGCTCCT	GAAAACCTGA	ACGTCIGGCC	AGTCAATGGC	420
	AAACCTACAG	TTGTCTGTGC	ATCTTGGGAT	GCGCTACCA	AGACTGAGGG	GAAAGTGAAA	480
	GTCTGTCTGC	TGGACACAGG	ACTGTTTTCA	GTTTCCTCCT	TCCAACCATC	TGCCAAATCA	540

	TTTCAGAATA	CATTCTTTCA	TACGCCCCGG	CTCTCAAACC	ATTGAGGCA	AAGTCCCTCA	600
	CCTATCCTGG	AGACACTACT	TCTGCCTTGG	TGGATGGTCT	GCAGCCTGGG	GAACGCTATC	660
	TTTTCAAAT	CCGGGCCACA	AACAGGAGAG	GCCTGGGACC	TCACTCCAAA	GCCTTCATTG	720
5	TCGCTATGCC	AACAAGAAATG	CAGCTGTACC	CAGAAGGATT	TCAGTTGTCT	AGCTTACCTG	780
	ATCGATATCC	AAACCAACA	AGTTAATAAA	GATCCACAAC	TGGAAGGGAG	TGTTTTTGGG	840
	CCATGTTTTT	TTTTCTACTT	CCTCACATTT	ATGCTGGATA	TTGGCGGCTT	TTCTTTCATT	900
	ATGTGCTATG	AAGACCCANN	TGTTTCTTCT	TTGACAGGCA	ATTCTTTAAA	ATCTGTGCA	960
	GCCAGTAAGG	CGGATGTTC	GCAGAACACG	GAGGACAATG	GGAAACCCGA	AAAACCTGAG	1020
10	CCTTCCTCAC	CTTCTCCAG	AGCTCCAGCT	TCCTCCCAAC	ACCCCTCTGT	GCCTGCTTCT	1080
	CCCCAAGGGA	GAAATGCCAA	GGACCTTCTT	CTTGACTTGA	AGAACAAAAT	ATTGGCTAAT	1140
	GGTGGGGCGC	CCCGAAAACC	CCAGCTTCGC	GCCAAGAAGG	CAGAGGAGCT	GGATCTTCAG	1200
	TCGACAGAAA	TCACTGGGGA	GGAGGAGCTG	GGTTCCCGGG	AGGACTCGCC	CATGTACCCC	1260
	TCAGACACCC	AAGACCAGAA	ACGGACCTTG	AGGCCGCCAA	GTAGACACGG	CCACTCGGTG	1320
15	GTGTCTCCCG	GCAGGACTGC	AGTGAGGGCC	CGGATGCCAG	CGCTGCCCCG	AAGGGAAGGC	1380
	GTAGATAAGC	CTGGCTTTTC	CCTGGCCACG	CAGCCCCGCC	CAGGGGCGCC	CCCTCGGCT	1440
	TCGGCCTCTC	CTGCCACACA	CGCGTCCACC	CAGGGCACCT	CTCATCGTCC	TTCCCTGCCT	1500
	GCCAGCTTGA	ATGACAACGA	CTTGGTGGAC	TCAGACGAAG	ATGAGCGCGC	TGTGGGCTCC	1560
	CTCCACCCCA	AGGGCGCCTT	CGCCACAGCC	CGGCCAGCCC	TGTCCCCCAG	CCGCCAGTCC	1620
20	CCGTCCAGCG	TTCTCCGCGA	CAGAAGCTCT	GTGCACCCCG	CGCAGAAAGC	AGCCTCGCCG	1680
	CGCGGAGGGA	CCCCCATTC	AGGGGCGCGA	GAGGAAGATT	CCAGTGCCTC	AGCCCCACCC	1740
	TCAGACCTTT	CTCCACCCCA	TGGGGATCA	TCTCGGCTGC	TGCCACCCCA	GCCACACCTG	1800
	AGCTCTCCAC	TTTCCAAGGG	CGGAAGGAT	GGTGAGGACG	CCCCAGCCAC	CAACTCCAAT	1860
	GCGCCATCAC	GGTCCACCAT	GTCTCTCTCC	GTCTCTTCTC	ATCTCTCGTC	CAGGACGCG	1920
25	GTCTCTGAGG	GAGCGGAGGC	TTCTGATGGT	GAAAGCCACG	GTGACGCGCA	TAGGGAAGAC	1980
	GGCGGAAGGC	AGGCGGAGGC	CAGGCGCCAG	ACGCTGCGGG	CCGCGCTGCG	CTCTGGACAC	2040
	TTCCATTGCG	TCAGACACAA	ACCCTTTGCT	GCCAACGGGA	GGTCTCCAAG	CAGGTTTCAG	2100
	ATTGGGCGGG	GACCTCGGCT	GCAGCCCTCC	AGCTCCCCAC	AGTCGACTGT	GCCTCCCCGA	2160
	GCCCAACCCCA	GGGTTCCCTC	TCACTCTGAT	TCCCACCCCTA	AGCTTAGCTC	AGGTATCCAT	2220
30	GGAGACGAGG	AGGATCGAGG	GCCGCTTCTC	GCCACCGTTG	TCAATGACCA	CGTGCCTTCC	2280
	TCCTCCAGGC	AGCCCATCTC	CCGGGGCTGG	GAGGACTTAA	GGAGAAGCCC	GCAGAGAGGG	2340
	GCCAGCCTGC	ATCGGAAGGA	ACCCATCCCA	GAGAACCCCA	AATCCACAGG	GGCAGATACA	2400
	CATCTCTAGG	CAGAGTACCT	CTCCCTGGCC	TCCAAGGCTC	AGGATGTTC	ACAGAGCACA	2460
	GACGCGGACA	CGGAGGGTCA	TTCTCCCAAA	GCACAGCCAG	GGTCCACAGA	CCGCCACGCG	2520
35	TCCCTCTGCT	GTCTCTCCGC	AGCACGGTCA	CAGCAGCATC	CCAGTGTTC	CAGAAGGATG	2580
	ACACCCGGCC	GGGCCCCAGA	ACAGCAGCCC	CCTCCTCCCG	TCGCCACGTC	CCAGCACCAC	2640
	CCGGGACCCC	AGAGCAGAGA	CGCGGGTCGG	TCACTTCCCC	AGCCACAGGCT	CTCACTGACC	2700
	CAGGCGGGCG	GGCCCGCCCC	CACGTCCGAG	GGCCGCTCCC	ACTCCTCCTC	GGACCCCTAC	2760
	ACGGCGAGCT	CCAGAGGGAT	GCTCCCCACG	GCCCTCCAGA	ACCAGGACGA	GGATGCCCAG	2820
40	GGCAGCTACG	ACGACGACAG	CACAGAAGTC	GAGGCCCAGG	ATGTGCGGGC	CCCCGCGCAC	2880
	GCCCGCGCGC	CCRAAGGAGC	AGCTGCGTCC	CTTCCCAAGC	ACCAGCAGGT	GGAGTCTCCC	2940
	ACAGGCGCAG	GGGCAAGTGG	CGACCCAGG	TCCAGCGCG	GACATGCGGC	CTCCCCCGCC	3000
	AGGCCAGGCC	AGCCCGGCGG	CCCCAGTCC	CGCGCCCGGG	TCCCCAGCAG	GGCAGCGCGG	3060
	GGGAAGTCCG	AGCCTCCTTC	CAAGCGGCCC	CTGTCTTCCA	AGTCCCAGCA	GTGCGTCTCA	3120
45	GCCGAGGACG	AGGAGGAGGA	GGACGCGGGG	TTTTTTAAAG	GCGGGAAGA	AGACCTTCTG	3180
	TCTTCTCTGT	TGCCAAAGTG	GCCCTCTTCC	TCCACTCCCA	GGGCGCGCAA	AGACGCGCAT	3240
	GGGAGCCTCG	CCAAGGAAGA	GAGGGAGCCT	GCCATCGCGC	TTGCCCTCG	CGGAGGGAGC	3300
	CTGGCTCCTG	TGAAGCGACC	TCTCCCCCA	CCTCCAGGCA	GCTCCCCCAG	GGCCTCCCCC	3360
	GTCCCTTCCC	GACCGCGGCC	TGCGCAGCGT	GCCACCGTGA	GCCCCGTCGC	GGGCACCCAC	3420
50	CCCTGGCGCG	GGTACACCAC	GCGCGCCCGV	CCTGGCCACT	TCTCCACCAC	CCCGATGCTG	3480
	TCCTTGCGCG	AGAGGATGAT	GCATGCCAGA	TTCCGTAAAC	CTCTCTCCCG	ACAGCCTGCC	3540
	AGACCTCTT	ACAGACAAGG	TTATAATGGC	AGACCAAATG	TAGAAGGGAA	AGTCTTCTCT	3600
	GGTAGTAATG	GAAACCCGAA	TGGACAGAGA	ATTATCAATG	GCCCTCAAGG	AACAAAGTGG	3660
	GTTTGTGAGC	TTGATCTGGG	GTTAGTATTG	AATGCAGAAG	GAAGGTACCT	CCAAGATTCA	3720
55	CATGGAATC	CTCTTCGGAT	TAAACTAGGA	GGAGATGGTC	GAACCATGT	AGATCTGGAA	3780
	GGGACCCCGG	TGTTGAGTCC	TGACGGCCTC	CCACTCTTTG	GGCAGGGGCG	ACATGGGCAC	3840
	CCTCTGGCCA	ATGCCCAAAG	TAAGCCAATT	TTGAGTCTTG	GAGGAAAGCC	GCTGGTGGGC	3900
	TTGGAGGTCA	TCAAAAAAAC	CACCCATCCC	CCTACCACCTA	CCATGCAGCC	CACCACTACT	3960
	ACGACGCCCA	TGCCTACAC	TACAACCCCG	AGGCCACCA	CTGCCACCA	CATGCAGCCC	4020
60	ACCACTACTA	CGACGCCCTT	GCCTACCCT	ACACCGAGGC	CCACCACTGC	CACCACCCGC	4080
	CGCACGACCA	CCAGGCGTCC	AACAACCACA	GTCCGAACCA	CTACGCGGAC	AACCACCACC	4140
	ACCACCCCCA	AACCCACCAC	TCCCATCCCC	ACCTGTCCCC	CTGGGACCTT	GGAACGGCAC	4200
	GACGATGATG	GCAACCTGAT	AATGAGCTCC	AATGGGATCC	CAGAGTGCTA	CGCTGAAGAA	4260
	GATGAGTTCT	CAGGCTTGGG	GACTGCACCT	GCAGTACCTA	CGGAAGAGGC	CTACGTTATA	4320
65	TATGATGAAG	ATTATGAATT	TGAGACGTCA	AGGCCACCAA	CCACCACTGA	GCCTTCGACC	4380
	ACTGCTACCA	CACCGAGGGT	GATCCAGAG	GAAGGCGCCA	TCAGTTCTCT	TCCTGAAGAA	4440
	GAATTTGATC	TGGCTTGAAG	GAAACGATTT	GTTGCTCCTT	ACGTGACGTA	CCTAAATAAA	4500
	GACCCATCAG	CCCCGTGCTC	TCTGACTGAT	GCATGTGATC	ACTTCCAAGT	GGACAGCCTG	4560
	GATGAAATCA	TCCCCAATGA	CCTGAAGAAG	AGTGATCTGC	CTCCCCAGCA	TGCTCCCCGC	4620
70	AACATCACCG	TGGTGGCCGT	GGGAGGTTGC	CATCATTG	TCAATGTGGA	TTGGGACAAA	4680
	GCCACCCCGG	GAGATTTGGT	CACAGGTTAT	TTGGTTTACA	GTGCATCCTA	TGAAGATTTC	4740
	ATCAGGAACA	AGTTTTCCAC	TCAAGCTTCA	TCAGTAACCT	ACTTGCCCAT	TGAGAACCTA	4800
	AAGCCCAACA	CGAGGTATTA	TTTTAAAGTG	CAAGCACAAA	ATCCTCATGG	CTACGGACCT	4860
	ATCAGCCCTT	CGGTCTCAT	TGTCACCGAA	TCAGATAATC	CTCTGCTTGT	TGTGAGGCCC	4920
75	CCAGGCGGTG	AGCTATCTGG	ATCCCATTCG	CTTTCAAACA	TGATCCACAG	TACACGGACT	4980
	GCCATGGACG	GCAATATGTG	AAGCGCACGT	GGTATCGAAA	GTTGCTGGGA	GTTGTTCTTT	5040
	GTAATTCACT	GAGGTATAAA	ATCTACCTCA	GTGACAACTT	GAAAGATACA	TTCTACAGCA	5100
	TTGGAGACAG	CTGGGGAAGA	GGTGAAGACC	ATTGCCAATT	TGTGGATTCA	CACCTTGATG	5160
	GAAGAACACG	GCCTCAGTCC	TATGTAGAAG	CCCTCCCTAC	TATTCAAGGC	TACTATCGCC	5220
80	AGTATCGTCA	GGAGCTGTTC	AGGTTTGGGA	ACATCGGCTT	CGGAACCCCT	TACTACTATG	5280
	TGGGCTGGTA	CGAGTGTGGG	GTCTCCATCC	CTGGAAAGTG	GTAATCACAG	GACCGTCAATG	5340
	CTGCAAGCTT	GCCCTTGCCA	GCCCCACCAA	CTAGTTCGCA	CTAGGGGCTG	TGAGCAAGA	5400
	CAGCCAGACT	GCTCAGCCCC	GCTGCCCTAG	GTGCCAGGAA	GGTCACAGAT	GGCACTGGC	5460
	CATTCTGGTC	ATCTCAGTCT	GGAACCTCAGT	CCCCTTCTT	GGCCTGGACA	ATGAACAGGA	5520
	TTCAGTTTTG	CTGTTAACTT	TGCTTCTCTA	CTTTTTTTTG	TTTGTGTTGA	ATAGCACATC	5580

CCAGAGACAT CAGAAACCAG CAACTGATTC AGTGTGATTT CCCAGACTTT TTAGGCATGA 5640  
 AATTCCGACA CTTCAGTATT TCCAGGAATA GCATATGCAC GCTGTTCTTG CTTCATGGAA 5700  
 TGCTACATGC TTTCTGTTTT TCTCATTTTG GATTTCCTCA AAACCTAAGT AATTTAAGCT 5760  
 TCAGGTCCCT TTGTATGCAG TAGAAAGGAA TTATTAAAAA CACCACCAAA GAAAAATAAT 5820  
 ATATCCCTACT TGAATTTTAC TCTATGGACT TACCCACTGC TAGAATAAAT GTATCAAAATC 5880  
 TTATTGTGTA ATTCTCAATT TTGATATATA TATGTATATA TGCATATACA TATCCACACT 5940  
 TGTCTGCAAG AATATTGATT AAAATTGCTA AATTTGTACT TGTTTACCAC AAAAATAAAT 6000  
 AAAAAA 6007

Seq ID NO: C14 DNA Sequence  
 Nucleic Acid Accession #: NM\_003014  
 Coding sequence: 238..1278

1 11 21 31 41 51  
 | | | | |  
 GCGCGGTTTC GCGCCCGAAG GCTGAGAGCT GCGCGTGTCT GTGCCCTGTG TGCCAGACGG 60  
 CGGAGCTCCG CGGCCCGGACC CCGCGGCCCC GCTTTGCTGC CGACTGGAGT TTGGGGGAAG 120  
 AAACCTCCTT CGGCCCCAGA AGATTTCTTC CTCGGCGAAG GGACAGCGAA AGATGAGGGT 180  
 GGCAGGAAGA GAAGGCGCTT TCTGTCTGCC GGGGTGCGAG CGCGAGAGGG CAGTGCCATG 240  
 TTCTCTCCCA TCCTAGTGGC GCTGTGCTGT TGGCTGCACC TGGCGCTGGG CGTGCAGCGC 300  
 TGCCCTGTGC AGGCGGTGCG CATCCCTATG TGCCGGCACA TGCCCTGGAA CATCACGCGG 360  
 ATGCCCAACC ACCTGCACCA CAGCACGCGA GAGAAGCCCA TCCTGGCCAT CGAGCAGTAC 420  
 GAGGAGCTGG TGGACGTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTTCTG TGCCATGTAC 480  
 GCGCCCATTT GCACCTTGGG GTTCCTGCAC GACCCTATCA AGCCGTGCAA GTCGGTGTGC 540  
 CAACGCGCGC GCGACGACTG CGAGCCCTTC ATGAAGATGT ACAACACAG CTGCCCCGAA 600  
 AGCTGGCCTT GCGACGAGCT GCCTGTCTAT GACCGTGGCG TGTGCATTTT GCCTGAAGCC 660  
 ATCGTCACGG ACCTCCCGGA GGATGTAAAG TGGATAGACA TCACACCAGA CATGATGGTA 720  
 CAGGAAGAGC CTCTTGATGT TGACTGTAAG CGCCTAAGCC CCGATCGGTG CAAGTGTAAG 780  
 AAGGTGAAGC CAACTTTGGC AACGTATCTC AGCAAAACT ACAGCTATGT TATTCATGCC 840  
 AAAATAAAGC CTGTGCAGAG GAGTGGCTGC AATGAGGTCA CAACGGTGGT GGATGTAAAG 900  
 GAGATCTTCA AGTCCCTCAT ACCATCCCT CGAACTCAAG TCCCGCTCAT TACAAATTCT 960  
 TCTTGCCAGT GTCCACACAT CCTGCCCAT CAAGATGTTT TCATCATGTG TTACGAGTGG 1020  
 CGTTCAAGGA TGATGCTTCT TGAATAATGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080  
 AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAAG 1140  
 AAGAAAACAG CCGGGCGCAC CAGTCGTAGT AATCCCCCA AACCAAGGG AAAGCCTCCT 1200  
 GCTCCCAAC CAGCCAGTCC CAAGAAGAAC ATTAATACTA GGAGTGCCCA GAAGAGAACA 1260  
 AAGCCGAAAG GAGTGTGAGC TAACTAGTTT CCAAAGCGGA GACTTCCGAC TTCCTTACAG 1320  
 GATGAGGCTG GGCATGTCCT GGGACAGCCT ATGTAAGGCC ATGTGCCCTT TGCCCTAACA 1380  
 ACTCACTGCA GTGCTCTTCA TAGACACATC TTGCAGCAAT TTTCTTAAGG CTATGCTTCA 1440  
 GTTTTCTTTT GTAAGCCATC ACAAGCCATA GTGGTAGGTT TGCCCTTTGG TACGAAGGT 1500  
 GAGTTAAAGC TGGTGGAAAA GGCTTATTGC ATTGCATTCA GAGTAACCTG TGTGCATACT 1560  
 CTAGAAGAGT AGGGAATAAT ATGCTTGTGA CAATTGACC TAATATGTGC ATTGTAAAT 1620  
 AAATGCCATA TTTCAACAA AACACGTAAT TTTTTCAG TATGTTTTAT TACCTTTTGA 1680  
 TATCTGTGTG TGCAATGTGA GTGATGTTTT AAAATGTGAT GAAAAATATA TGTTTTTAAG 1740  
 AAGGAACAGT AGTGGAAATGA ATGTTAAAG ATCTTTATGT GTTTATGGTC TGCAGAAGGA 1800  
 TTTTGTGAT GAAAGGGGAT TTTTGAAGAA ATTAGAGAAG TAGCATATGG AAAATTATAA 1860  
 TGTGTTTTTT TACCAATGAC TTCAGTTTCT GTTTTAGCT AGAAACTTAA AAACAAAAAT 1920  
 AATAATAAAG AAAAAATAAT AAAAAGGAGA GGCAGACAAT GTCTGGATTG CTGTTTTTTG 1980  
 GTTACCTGAT TTCCATGATC ATGATGCTTC TTGTCACAC CCTCTTAAGC AGCACCAGAA 2040  
 ACAGTGAGTT TGTCTGTACC ATTAGGAGTT AGGTACTAAT TAGTTGGCTA ATGCTCAAGT 2100  
 ATTTTATACC CACAAGAGAG GTATGTCACT CATCTTACT CCCAGGACAT CCACCTGAG 2160  
 AATAATTGGA CAAGCTTAAA AATGGCCTTC ATGTGAGTGC CAAATTTTGT TTTTCTTCAT 2220  
 TTAAATATTT TCTTTGCCCTA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG 2280  
 AAAGTTGAGT TCCACCTCTG AAATGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA 2340  
 AAAAAGAAGT ATTTTGACG ATTTTATCAA CAAATTTTAT AATTGTGGAC AATTGGAGGC 2400  
 ATTTATTTTA AAAACAATT TTATTGGCCT TTTGCTAACA CAGTAAGCAT GTATTTTATA 2460  
 AGGCATTCAA TAAATGCACA ACGCCCAAG GAAATAAAT CCTATCTAAT CCTACTCTCC 2520  
 ACTACACAGA GGTAAATCACT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580  
 GCACTTATAA AATGATTTGA CAAATAAAA CTAGGAACCT GTATACATGT GTTTTATAAC 2640  
 TGCCTCCTT TGCTTGGCC TTTATTGAGA TAAGTTTTC TGTCAGAAA GCAGAAACCA 2700  
 TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760  
 TATTGATAC TTAGTGGTT TCTTCACTGA CAATACGAA TAAACATCTC ACCGGAATTC 2820

Seq ID NO: C15 DNA Sequence  
 Nucleic Acid Accession #: NM\_005940  
 Coding sequence: 23..1489

1 11 21 31 41 51  
 | | | | |  
 AAGCCAGCA GCGCCGGGGC GGTGCTCTCC GCGCGCTGG CTCGCGAGCG CGGCCGCGCG 60  
 CGCCCTCCTG CCCCCGATGC TGCTGCTGCT GCTCCAGCG CCGCCGCTGC TGGCCCGGGC 120  
 TCTGCCGCGG GACGTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180  
 AGCCCTGCCC AGTAGCCCGG CACCTGCCCT TGCCACGCAG GAAGCCCCC GGCCTGCCAG 240  
 CAGCCTCAGG CTCCCCCGCT GTGGCGTGGC CGACCATCT GATGGGTGA GTGCCCGCAA 300  
 CCGACAGAAG AGGTTCTGTC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG 360  
 GATCCTTCGG TTCCCATGCG AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420  
 CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCAG AGGGCGGTGC 480  
 TGACATCATG ATCGACTTCG CCAGGTACTG GCATGGGGAC GACCTGCCCT TTGATGGGCC 540  
 TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600  
 CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCAGGGC ACAGACCTGC TGCAGGTGGC 660  
 AGCCCATGAA TTTGGCCACG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCTGAT 720  
 GTCCGCTTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGCGGT 780  
 TCACACCTTA TATGGCCAGC CTGGGCCAC TGTCACCTCC AGGACCCCG CCCTGGGCC 840  
 CCAGGTCTGG ATAGACACCA ATGAGATTGC ACCGCTGGAG CCAGACGCCC GCGCAGATGC 900

CTGTGAGGCC TCCTTTGACG CGGTCTCCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC 960  
 GGGCTTTGTG TGGGCGCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTTGGCCTC 1020  
 TCGCCACTGG CAGGGACTGC CCAGCCCTGT GGACGCTGCC TTCGAGGATG CCCAGGGCCA 1080  
 CATTTGTGTC TTCCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCTCTGG 1140  
 CCCCACACCC CTCACCGAGC TGGGCTTGGT GAGGTTCCCG GTCCATGCTG CCTTGGTCTG 1200  
 GGGTCCCAGG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCACCCC 1260  
 CAGCACCCGG CGTGTAGACA GTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC 1320  
 CTCTGAGATC GACGCTGCCT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGGCGGGCCG 1380  
 CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCCGTCTCGT 1440  
 GGGTCTTGAC TTCTTTGGCT GTGCCGAGCC TGCCAAACACT TTCTCTGAC CATGGCTTGG 1500  
 ATGCCCTCAG GGGTGTCTGAC CCCTGCCAGG CCACGAATAT CAGGCTAGAG ACCCATGGCC 1560  
 ATCTTTGTGG CTGTGGGCAC CAGGCATGGG ACTGAGCCCA TGTCTCTGTC AGGGGGATGG 1620  
 GGTGGGGTAC AACCACCATG ACAACTGCCG GGAGGGCCAC GCAGGTCGTG GTCACCTGCC 1680  
 AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGGCAGTCTT 1740  
 GGGACCCGCT ATGCAGGTCC TGGCAAACCT GGTGCGCCCTG TCTCATCCCT GTCCTCAGG 1800  
 GTAGCACCAT GCGAGGACTG GGGGAACTGG AGTGTCTTGT CTGTATCCCT GTTGTGAGGT 1860  
 TCCTTCCAGG GGTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCCTT CAGCCCTGGC 1920  
 TGAGCAACTG GGTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCCTGC 1980  
 ATCTGTCTGC CTCTGTGCTG ACAATCCTGG AAATCTGTTT TCCAGAATCC AGGCCAAAAA 2040  
 GTTCACAGTC AAATGGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100  
 CAACATACCT CAATCCTGTC CCAGGCCGGA TCCTCCTGAA GCCCTTTTCG CAGCACTGCT 2160  
 ATCTTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220  
 TTTTAAACT GAGGATTGTC ATTAACACA GTTGTTTTCT 2260

Seq ID NO: C16 DNA Sequence  
 Nucleic Acid Accession #: NM\_024022  
 Coding sequence: 202..1563

1 11 21 31 41 51  
 | | | | |  
 ACCGGGCACC GGCAGGCTCG GGTACTTTTC TTCTTAATTA GGTTCATGCC GTGTGAGCCA 60  
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGGGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180  
 AGAGGTCTCG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTGGG CCTTGTATGAT TTGAAAATAA GTCCCTGTGC ACCAGATGCA 300  
 GATGCTGTTG CTGCACAGAT CTTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTGACTGTC 420  
 TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAGA CCATGTGCTC CGATGACTGG 600  
 AAGGGTCACT ACGCAAATGT TGCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTCA 660  
 GATAACCTCA GAGTGAGCTC GCTGGAGGGC CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTG GCCACGTGTT TACCTTGCAG TGCACAGCCT GTGGTCTAG AAGGGGTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCA AGTGGCCCTG GCAGGCCAGC 900  
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGTCTGTGTA TCACGCCCTT GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTGTGAC CTCCTCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGTGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080  
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCTGGCCA 1140  
 CTCAGTTTCA ATGAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACTTCCCC 1200  
 GATGGAAGA TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGG TGACGCTTCC 1260  
 CCTGTCTTGA ACCACGCGTC CGTCCCTTTG ATTTCCAACA AGATCTGCAA CCACAGGGAC 1320  
 GTGTACGGTG GCATCATCTC CCCCTCCATG CTCTGCGCGG GCTACCTGAC GGGTGGCGTG 1380  
 GACAGCTGCC AGGGGGACAG CGGGGGGCC CTGCTGTGTC AAGAGAGGAG GCTGTGGAAG 1440  
 TTAGTGGGAG CGACAGCTT TGGCATCGGC TGCGCAGAGG TGAACAAGCC TGGGGTGTAC 1500  
 ACCGTGTGTA CCTCTTCTT GGACTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAAACC 1560  
 TGAAGAGGAA GGGGACAAGT AGCCACCTGA GTTCTGAGG TGAAGAAGAC AGCCCGATCC 1620  
 TCCCTTGAG TCCGTGTAG GAACCTGCAC ACGAGCAGAC ACCCTTGGAG CTCTGAGTTC 1680  
 CGGCACCACT AGCAGGCCCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA 1740  
 GCTGCTTTT GTTTTTTGT TTTTGTAGGT GGAGTCTGCG TCTGTGCCC AGGCTGGAGT 1800  
 GCAGTGGCGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAAGC GATTCTCTTG 1860  
 CCTCAGCTTC CCCAGTAGCT GGGACCACAG GTGCCCGCCA CCACACCAA CTAATTTTGT 1920  
 TATTTTGTAG AGAGACAGGG TTTCAACATG TTGGCCAGGC TGCTCTCAA CCCCTGACCT 1980  
 CAAATGATGT GCCTGCTTCA GCCTCCACA GTGCTGGGAT TACAGGCATG GGCCACCACG 2040  
 CCTAGCCTCA CGTCTCTTTC TGATCTTAC TAAGAACAAA AGAAGCAGCA ACTTGCAAGG 2100  
 GCGGCTTTTC CCATGGTTC ATCTGGTTT CTCTCCAGGG GTCTTGCAA ATTCTGACG 2160  
 AGATAAGCAG TTAGTGAC TCACGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA 2220  
 CCAGCCCAGA AGTGCAGAAC TGCAGTCACT GCACGTTTTC ATCTCTAGGG ACCAGAACA 2280  
 AACCACCCCT TTCTACTTCC AAGACTTATT TTCACATGTG GGGAGGTTAA TCTAGGAATG 2340  
 ACTCGTTTAA GGCCTATTTC CATGATTCT TTGTAGCATT TGGTGTGTA CGTATTATTG 2400  
 TCCTTTGATT CCAATAATA TGTTCCTTC CCTCAAAAAA AAAAAAAA AAAAAAAA 2460  
 AAAAA 2465

Seq ID NO: C17 DNA Sequence  
 Nucleic Acid Accession #: NM\_003220  
 Coding sequence: 63..1376

1 11 21 31 41 51  
 | | | | |  
 GAATTCGGGC TCTCTGGGTG AGAGACCGAG AGGGGCATAT CCGTTCACGC CGATCCATGA 60  
 AAATGCTTTG GAAATTGACG GATAATATCA AGTACGAGGA CTGCGAGGAC CGTCACGACG 120  
 GCACAGCAA CGGACCGGCA CGGTGCCCC AGCTGGGCAC TGTAGGTCAA TCTCCCTAC 180  
 CGAGCGCCCC GCCGTGTGCC CACACCCCA ATGCCGACTT CCAGCCCCA TACTTCCCC 240  
 CACCTACCA GCCTATCTAC CCCCAGTCGC AAGATCCTTA CTCCACGTC AACGACCCCT 300

ACAGCCTGAA CCCCCTGCAC GCCCAGCCGC AGCCGCAGCA CCCAGGCTGG CCCGGCCAGA 360  
 GGCAGAGCCA GGAGTCTGGG CTCCTGCACA CGCACCGGGG GCTGCCTCAC CAGCTGTCCG 420  
 GCCTGGATCC TCGCAGGGAC TACAGGCGGC ACGAGGACCT CTTGCACGGC CCACACGCGC 480  
 TCAGCTCAGG ACTCGGAGAC CTCTCGATCC ACTCCTTACC TCACGCCATC GAGGAGGTCC 540  
 CGCATGTAGA AGACCCGGGT ATTAACATCC CAGATCAAAC TGTAATTAAAG AAAGGCCCCG 600  
 TGTCCCTGTC CAAGTCCAAAC AGCAATGCCG TCTCCGCCAT CCCTATTAAC AAGGACAACC 660  
 TCTTCGCGCG CGTGGTGAAC CCCAACGAAG TCTTCTGTTC AGTTCCGGGT CGCCTCTCGC 720  
 TCCTCAGCTC CACCTCGAAG TACAAGGTCA CGGTGGCGGA AGTGACAGCG CGGCTCTCAC 780  
 CACCCGAGTG TCTCAACGCG TCGCTGCTGG GCGGAGTGCT CCGGAGGGCG AAGTCTAAAA 840  
 ATGGAGGAAG ATCTTTAAGA GAAAAACTGG ACAAATAGG ATTAATCTG CCGTCAGGGA 900  
 GACGTAAAGC TGCCACGTT ACCCTGCTCA CATCACTAGT AGAGGGAGAA GCTGTCCACC 960  
 TAGCCAGGGA CTTTGGGTAC GTGTGCGAAA CCGAATTTCC TGCCAAAGCA GTAGCTGAAT 1020  
 TTCTCAACCG ACAACATTCC GATCCCAATG AGCAAGTGAC AAGAAAAAAC ATGCTCCTGG 1080  
 CTACAAAAAC GATATGCAAA GAGTTCACCG ACCTGCTGGC TCAGGACCGA TCTCCCTGG 1140  
 GGAACCTCAG GCCCAACCCC ATCCTGGAGC CCGGCATCCA GAGCTGCTTG ACCCACTTCA 1200  
 AACCTATCTC CACAGGCTTC GGCAGCCCG CGGTGTGTGC CGCGGTACG GCCCTGCAGA 1260  
 ACTATCTCAC CGAGGCCCTC AAGGCCATGG ACAAATGTA CCTCAGCAAC AACCCCAACA 1320  
 GCCACACGGA CAACACGCC AAAAGCAGTG ACAAAGAGGA GAAGCACAGA AAGTGAGGCT 1380  
 CTCCTCCCGC CCGCCCTCTC CCACGCTCA CCAGCCCCC CGCGGCCAC CCTCCGGCGG 1440  
 GTGACAGCTC CGGGATCAGC AACCTTCTCT GCTGCTGCTA CTGCTGCTGC TGCTGCCGCC 1500  
 GCGGCCGCGC CGCTGCCCTT TGGGTCCCC CGAGTCTCCG GGAATGCCCT CTCGACTGTC 1560  
 AGTGGGGCAG CCTCTCCGAC TCTGCACCCG CCTCGACCTC CCCACCCGCT CCCACACCCC 1620  
 TGTGCCCCCG GAATTC 1636

Seq ID NO: C18 DNA Sequence  
 Nucleic Acid Accession #: NM\_002988  
 Coding sequence: 71..340

1 11 21 31 41 51  
 | | | | | |  
 CCGGCACGAG AGGAGTTGTG AGTTTCCAAG CCCAGCTCA CTCTGACCAC TTCTCTGCCT 60  
 GCCCAGCATC ATGAAGGGCC TTGCAGCTGC CCTCCTGTCT CTCGTCTGCA CCATGGCCCT 120  
 CTGCTCCTGT GCACAAGTTG GTACCAACAA AGAGCTCTGC TGCTCTGTCT ATACCTCCTG 180  
 GCAGATTCCA CAAAAGTTCA TAGTTGACTA TTCTGAAACC AGCCCCAGT GCCCAGAGC 240  
 AGGTGTCATC CTCTTAACCA AGAGAGGCCG GCAGATCTGT GCTGACCCCA ATAAGAAGTG 300  
 GGTCCAGAAA TACATCAGCG ACCTGAAGCT GAATGCCTGA GGGGCTGGA AGCTCGGAGG 360  
 GTCCTAGTAA CTTGGTGGGC CCAGGAGGGA ACAGGAGCCT GAGCCAGGGC AATGGCCCTG 420  
 CCACCTGGA GGCACCTCT TCTAAGAGTC CCATCTGCTA TGCCAGCCA CATTAATAA 480  
 CTTTAATCTT AGTTTATGCA TCATATTTCA TTTTGAAATT GATTTCTATT GTTGAGCTGC 540  
 ATTATGAAAT TAGTATTTTC TCTGACATCT CATGACATTG TCTTTATCAT CCTTTCCCT 600  
 TTCCCTTCAA CTCTCTGTAC ATTCAATGCA TGGATCAATC AGTGTGATTA GCTTTCTCAG 660  
 CAGACATTGT GCCATATGTA TCAAATGACA AATCTTTATT GAATGGTTT GCTCAGCACC 720  
 ACCTTTTAAAT ATATTGGCAG TACTTATTAT ATAAAGGTA AACCAGCATT CTCACTGTGA 780  
 AAAAAAAAAA AAAAAAAAAA AAA 803

Seq ID NO: C19 DNA Sequence  
 Nucleic Acid Accession #: NM\_004063  
 Coding sequence: 121..2619

1 11 21 31 41 51  
 | | | | | |  
 AGGGAGTGTT CCCGGGGGAG ATACTCCAGT CGTAGCAAGA GTCTCGACCA CTGAATGGAA 60  
 GAAAAGGACT TTTAACCACC ATTTGTGAC TTACAGAAAG GAATTTGAAT AAAGAAAAC 120  
 ATGATACTTC AGGCCATCT TCACTCCCTG TGTCTTCTTA TGCTTTATTT GGCAACTGGA 180  
 TATGGCCAAG CCGGGGAAGTT TAGTGGACCC CTGAAACCCA TGACATTTTC TATTTATGAA 240  
 GGGCAAGAAG CGAGTCAAAAT TATATTCCAG TTTAAGGCCA ATCTCCTGCT TGTGACTTTT 300  
 GAACATAACT GGGAGACAGA CAACATATTT GTGATAGAAC GGGAGGGACT TCTGTATTAC 360  
 AACAGAGCCT TGACAGGGGA AACAGATCT ACTCACAATC TCCAGGTTGC AGCCCTGGAC 420  
 GCTAATGGAA TTATAGTGA GGTCCAGTC CCTATCACC TAAGAAGTGA GGACATCAAC 480  
 GACAAATGAC CCACGTTTCT CCAGTCAAAG TACGAAGGCT CAGTAAGGCA GAACCTCTCGC 540  
 CCAGGAAAGC CCTCTTGTA TGTCAATGCC ACAGACCTGG ATGATCCGGC CACTCCCAAT 600  
 GGCAGCTTTT ATTACCAGAT TGTCTCCAG CTTCCCATGA TCAACAATGT CATGTACTTT 660  
 CAGATCAACA ACAAACCGG AGCCATCTCT CTTACCCGAG AGGGATCTCA GGAATTGAAT 720  
 CCTGCTAAGA ATCCTTCTTA TAATCTGGTG ATCTCAGTGA AGGACATGGG AGGCCAGAGT 780  
 GAGAATTCCT TCAGTGATAC CACATCTGTG GATATCATAG TGACAGAGAA TATTTGGAAA 840  
 GCACCAAAAC CTGTGGAGAT GGTGGAAGC TCAACTGATC CTCACCCCAT CAAATCACT 900  
 CAGGTGCGGT GGAATGATCC CGGTGCACAA TATTCCTTAG TTGACAAAGA GAAGCTGCCA 960  
 AGATTCCCAT TTTCAATTGA CCAGGAAGGA GATATTTACG TGACTCAGCC CTTGGACCGA 1020  
 GAAGAAAAGG ATGCATATGT TTTTATGCA GTTGCAAGG ATGAGTACGG AAAACCACTT 1080  
 TCATATCCGC TGGAAATTCA TGTAAAAGTT AAAGATATTA ATGATAATCC ACCTACATGT 1140  
 CCGTCACCAG TAACCGTATT TGAGGTCCAG GAGAATGAAC GACTGGGTAA CAGTATCGGG 1200  
 ACCCTTACTG ACATGTGACG GGATGAAGAA AATACTGCCA ACAGTTTCT AAACACAGG 1260  
 ATTGTGGAGC AAACCTCCAA ACTTCCCATG GATGGACTCT TCCTAATCCA AACCTATGCT 1320  
 GGAATGTTAC AGTTAGCTTA ACAGTCCCTT AAGAAGCAAG ATACTCTCA GTACAACCTA 1380  
 ACGATAGAGG TGTCTGACAA AGATTTCAG ACCCTTTGTT TTGTGCAAAAT CAACGTTATT 1440  
 GATATCAATG ATCAGATCCC CATCTTTGAA AAATCAGATT ATGAAAACCT GACTCTTGCT 1500  
 GAAGACACAA ACATTGGGTC CACCATCTTA ACCATCCAGG CCAGTGATGC TGATGAGCCA 1560  
 TTTACTGGGA GTTCTAAAT TCTGTATCAT ATCATAAAGG GAGACAGTGA GGGACGCTG 1620  
 GGGGTTGACA CAGATCCCCA TACCAACACC GGATATGTCA TAATTAAAAA GCCTCTTGAT 1680  
 TTTGAAACAG CAGCTGTTTC CAACATTGTG TTCAAAGCAG AAAATCCTGA GCCTCTAGTG 1740  
 TTTGGTGTGA AGTACAATTC AAGTCTTTT GCCAAGTTC CGCTTATTGT GACAGATGTG 1800  
 AATGAAGCAC CTCAATTTTC CCAACAGTGA TTCCAAGCGA AAGTCAGTGA GGATGTAGCT 1860  
 ATAGGCACTA AAGTGGGCAA TGTGACTGCC AAGGATCCAG AAGTCTGGA CATAGCTTAT 1920  
 TCACTGAGGG GAGACACAAG AGGTTGGCTT AAAATTGACC ACGTGACTGG TGAGATCTTT 1980



5	AGTGTGGCTC	CATTGGACAG	AGAAGCCGGA	AGTCCATATC	GGGTACAAGT	GGTGGCCACA	2040
	GAAGTAGGGG	GGTCTTCCCT	GAGCTCTGTG	TCAGAGTTCC	ACCTGATCCT	TATGGATGTG	2100
	AATGACAACC	CTCCAGGCT	AGCCAAGGAC	TACACGGGCT	TGTTCTTCTG	CCATCCCCCTC	2160
	AGTGCACTTG	GAAGTCTCAT	TTTCGAGGCT	ACTGATGATG	ATCAGCACTT	ATTTCCGGGGT	2220
	CCCCATTTTA	CATTTTCCCT	CGGCAGTGGG	AGCTTACAAA	ACGACTGGGA	AGTTTCCAAA	2280
	ATCAATGGTA	CTCATGCCCG	ACTGCTCTAC	AGGCACACAG	AGTTTGAGGA	GAGGGAGTAT	2340
	GTGCTCTTGA	TCCGCATCAA	TGATGGGGGT	CGGCCACCCT	TGGAAGGCAT	TGTTTCTTTA	2400
10	CCAGTTACAT	TCTGCAGTTG	TGTGGAAGGA	AGTTGTTTCC	GGCCAGCAGG	TCACCAGACT	2460
	GGGATACCCA	CTGTGGGCAT	GGCAGTTGGT	ATACTGCTGA	CCACCCCTCT	GGTGATTGGT	2520
	ATAATTTTAG	CAGTTGTGTT	TATCCGCATA	AAGAAGGATA	AAGGCAAAAG	TAATGTTGAA	2580
	AGTGCTCAAG	CATCTGAAGT	CAAACCTCTG	AGAAGCTGAA	TTTGAAAAGG	AATGTTTGAA	2640
	TTTATATAGC	AAGTGTCTAT	TCAGCAACAA	CCATCTCATC	CTATTACTTT	TCATCTAACG	2700
	TGCATTATAA	TTTTTTAAAC	AGATATTCCC	TCTTGCTCCT	TAATATTTCG	TAAATATTTT	2760
15	TTTTTTGAGG	TGGAGTCTTG	CTCTGTGCGC	CAGGCTGGAG	TACAGTGGTG	TGATCCCAGC	2820
	TCAGTGAAC	CTCCGCTCTC	TGGGTTTACA	TGATTCTCCT	GCCTCAGCTT	CCTAAGTAGC	2880
	TGGGTTTACA	GGCACCCACC	ACCATGCCCA	GCTAATTTTT	GTATTTTAA	TAGAGACGGG	2940
	GTTCGCCCAT	TTGGCCAGGC	TGGTCTTGAA	CTCCTGACGT	CAAGTGATCT	GCCTGCCTTG	3000
	GTCTCCCAAT	ACAGGCATGA	ACCACCTGCAC	CCACCTACTT	AGATATTTCA	TGTGCTATAG	3060
20	ACATTAGAGA	GATTTTTCAT	TTTTCCATGA	CATTTTTCCT	CTCTGCAAT	GCCTTAGCTA	3120
	CTTGTTGTTT	TCCTTTTGG	GGCAAGACAG	ACTCATTA	TATTTCTGAC	ATTTTCTCTT	3180
	TATCAAGGAG	ATATATCATG	GTGTCTCAT	AGAACTGCCT	GGATTCCATT	TATGTTTTTT	3240
	CTGATTCCAT	CTGTGTCTCC	CTTCATCCTT	GACTCCTTTG	GTATTTCACT	GAATTTCAAA	3300
	CATTTGTCAG	AGAAGAAAAA	CGTGAGGACT	CAGGAAAAAT	AAATAAATAA	AAGAACAGCC	3360
25	TTTTCCCTTA	GTATTAAACG	AAATGTTTCT	GTGTCAATTA	CCATCTTTAA	TCAATGTGAC	3420
	ATGTTGCTCT	TTGGCTGAAA	TTCTTCAACT	TGGAATGAC	ACAGACCCAC	AGAAGGTGTT	3480
	CAAACACAAC	CTACTCTGCA	AACCTTGGTA	AAGGAACCAG	TCAGCTGGCC	AGATTTCTCT	3540
	ACTACCTGCC	ATGCATACAT	GCTGCGCATG	TTTTCTTCAT	TCGTATGTTA	GTAAAGTTTT	3600
	GGTTATTATA	TATTTAACAT	GTGGAAGAAA	ACAAGACATG	AAAAGAGTGG	TGACAAATCA	3660
30	AGAATAAACA	CTGGTTGTAG	TCAGTTTGT	TTGTTAA			3697

Seq ID NO: C20 DNA Sequence  
Nucleic Acid Accession #: NM\_004443  
Coding sequence: 28..3024

35	1	11	21	31	41	51	
	GGCTCGGCTC	CTAGAGCTGC	CACGGCCATG	GCCAGAGCCC	GCCCGCCGCC	GCCGCCGCTG	60
40	CCGCCGCCGG	GGCTTCTGCC	GCTGCTCCCT	CCGCTGCTGC	TGCTGCCGCT	GCTGCTGCTG	120
	CCGCCGGGCT	CGCCGGCGCT	GGAGAGAGCC	CTCATGGACA	CAAAATGGGT	AACATCTGAG	180
	TTGGCGTGGA	CATCTCATCC	AGAAAGTGGG	TGGGAAGAGG	TGAGTGGCTA	CGATGAGGCC	240
	ATGAATCCCA	TCCGCACATA	CCAGGTGTGT	AATGTGCGCG	AGTCAAGCCA	GAACAACCTG	300
	CTTCGCACGG	GGTTTCTCTG	GCGGCGGGAT	GTGCAGCGGG	TCTACGTGGA	GCTCAAGTTC	360
45	ACTGTGCGTG	ACTGCAACAG	CATCCCCAAC	ATCCCCGGCT	CCTGCAAGGA	GACCTTCAAC	420
	CTCTTCTACT	ACGAGGCTGA	CAGCGATGTG	GCCTCAGCCT	CCTCCCCCTT	CTGGATGGAG	480
	AACCCCTACG	TGAAGTGA	CACCATTGCA	CCCGATGAGA	GCTTCTCGCG	GCTGGATGCC	540
	GGCCGTGTCA	ACACCAAGGT	GCGCAGCTTT	GGGCCACTTT	CCAAGGCTGG	CTTCTACCTG	600
	GCCTTCCAGG	ACCAGGGCGC	CTGCATGTG	CTCATCTCCG	TGCGCGCCTT	CTACAAGAAG	660
50	TGTGCAATCA	CCACCGCAGG	CTTCGCACTC	TTCCCCGAGA	CCCTCACTGG	GGCGGAGCCC	720
	ACCTCGCTGG	TCATTGCTCC	TGGCACCTGC	ATCCCTAACG	CCGTGGAGGT	GTGGTGCCCA	780
	CTCAAGCTCT	ACTGCAACGG	CGATGGGGAG	TGGATGGTGC	CTGTGGGTGC	CTGCACCTGT	840
	GCCACCGGCC	ATGAGCCAGC	TGCCAAGGAG	TCCCAAGTGC	GCCCCGTGTC	CCCTGGGAGC	900
	TACAAGGCGA	AGCAGGCTGA	GGGGCCCTGC	CTCCCATGTC	CCCCCAACAG	CCGTACCACC	960
55	TTCCCGAGCG	CCAGCATCTG	CACCTGCCAC	AATAACTTCT	ACCGTGACAG	CTCGGACTCT	1020
	GCGGACAGTG	CCTGTACCAC	CGTGCCATCT	CCACCCGAG	GTGTGATCTC	CAATGTGAAT	1080
	GAAACCTCAC	TGATCTTCGA	GTGGAGTGA	CCCCGGGACC	TGGGTGGCCG	GGATGACCTC	1140
	CTGTACAAAT	TCATCTGCAA	GAAGTGCCAT	GGGGCTGGAG	GGGCCTCAGC	CTGCTCACGC	1200
	TGTGATGACA	ACGTGGAGTT	TGTGCTCGG	CAGCTGGGCC	TGACGGAGCG	CCGGTCCAC	1260
60	ATCAGCCATC	TGCTGGCCCA	CACGCGCTAC	ACCTTTGAGG	TGCAGGCGGT	CAACGGTGTG	1320
	TCGGGCAAGA	GCCTCTGCTC	GCCTCGTTAT	GCGGCGGTGA	ATATCACCAC	AAACCAAGGT	1380
	GCCCCGTCTG	AAGTGCCAC	ACTACGCTG	CACAGCAGCT	CAGGCAGCAG	CCTCACCCCTA	1440
	TCTTGGGCAC	CCCCAGAGCG	GCCCAACGGA	GTCTCTCTGG	ACTACGAGAT	GAAGTACTTT	1500
	GAGAAGAGCG	AGGCATCTGC	CTCCACAGTG	ACCAGCCAGA	TGAATCCGT	GCAGCTGGAC	1560
65	GGGCTTCGGC	CTGACGCCCC	CTATGTGGTC	CAGGTCCGTC	CCCGCACAGT	AGCTGGCTAT	1620
	GGGCAGTACA	GCCGCCCTGC	CGAGTTTGTG	ACCACAAGTG	AGAGAGGCTC	TGGGGCCGAG	1680
	CAGCTCCAGG	AGCAGCTTGC	CCTCATCGTG	GGTCCGCTA	CAGCTGGGCT	TGTCTTCTGT	1740
	GTGGCTGTG	TGTCATCTGC	TATCGTCTGC	CTCAGGAAGC	AGCGACACGG	CTCTGATTCG	1800
	GAGTACACGG	AGAAGCTGCA	GCAGTACATT	GCTCCTGGAA	TGAAGGTTTA	TATTGACCTT	1860
70	TTTACCTACG	AGGACCTTAA	TGAGGCTGTT	CGGGAGTTTG	CCAAGGAGAT	CGACGTGTCC	1920
	TGCGTCAAGA	TCGAGGAGGT	GATCGGAGCT	GGGGAATTTG	GGGAAGTGTG	CCGTGGTCTG	1980
	CTGAAACAGC	CTGGCCGCGG	AGAGGTGTTT	GTGGCCATCA	AGACGCTGAA	GGTGGGCTAC	2040
	ACCGAGAGGC	AGCGGCGGGA	CTTCTTAAGC	GAGGCCTCCA	TCATGGGTCA	GTTTGATCAC	2100
	CCCAATATAA	TCCGGCTCGA	GGGCGTGGTC	ACCAAAAGTC	GGCCAGTTAT	GATCCTCACT	2160
75	GAGTTCTATG	AAAACCTGCG	CCTGACTTCC	TTCTCCGGC	TCAACGATGG	GCAGTTCACG	2220
	GTCTATCCAGC	TGGTGGGCAT	GTTGCGGGGC	ATTGCTGCCG	GCATGAAGTA	CCTGTCCGAG	2280
	ATGAACTATG	TGCACCGCGA	CCTGGCTGCT	CGCAACATCC	TTGTCAACAG	CAACCTGGTC	2340
	TGCAAAAGTCT	CAGACTTTGG	CCTCTCCGCG	TTCTTGAGG	ATGACCCCTC	CGATCCTACC	2400
	TACACCAAGT	CCCTGGGCGG	GAAGATCCCC	ATCCGCTGGA	CTGCCCCAGA	GGCCATAGCC	2460
80	TATCGGAAGT	TCACTTCTGC	TAGTGATGTC	TGGAGCTACG	GAATTGTCT	GTGGGAGGTC	2520
	ATGAGCTATG	GAGAGCGACC	CTACTGGGAC	ATGAGCAACC	AGGATGTCT	CAATGCCGTG	2580
	GAGCAGGATT	ACCGGCTGCC	ACCACCATG	GACTGTCCCA	CAGCAGTGA	CCAGCTCATG	2640
	CTGGACTGCT	GGGTGCGGGG	CCGGAACCTC	AGGCCCAAT	TCTCCAGAT	TGTCAATACC	2700
	CTGACACAGC	TCATCCGCAA	TGCTGCCAGC	CTCAAGGTCA	TTGCCAGCGC	TCAGTCTGGC	2760
	ATGTCACAGC	CCCTCCTGGA	CCGCACGGTC	CCAGATTACA	CAACCTTCAC	GACAGTTGGT	2820

5 GATTGGCTGG ATGCCATCAA GATGGGGCGG TACAAGGAGA GCTTCGTCAG TCGGGGGTTT 2880  
 GCATCTTTTG ACCTGGTGGC CCAGATGACG GCAGAAGACC TGCTCCGTAT TGGGGTCACC 2940  
 CTGGCCGGCC ACCAGAAGAA GATCCTGAGC AGTATCCAGG ACATGCGGCT GCAGATGAAC 3000  
 CAGACGCTGC CTGTGCAGGT CTGACACCGG CTCCACCGGG GACCTTGAGG ACCGTGCAGG 3060  
 GATGCCAAGC AGCCGGCTGG ACTTTCGGAC TCTTGGACTT TTGGATGCCT GGCCCTAGGC 3120  
 TGTGGCCAG AAGCTGGAAG TTTGGGAAAG GCCCAAGCTG GGACTTCTCC AGGCTGTGT 3180  
 TCCCTCCCCA GGAAGTGCAG CCCAAACCTC TTCATATTGA AGATGGATTA GGAGAGGGGG 3240  
 TGATGACCCC TCCCCAAGCC CCTCAGGGCC CAGACCTTCC TGCTCTCCAG CAGGGGATCC 3300  
 CCACAACCTC ACACCTGTCT GTTCTTCAGT GCTGGAGGTC CTGGCAGGGT CAGGCTGGGG 3360  
 10 TAAGCCGGGG TTCCACAGGG CCCAGCCCTG GCAGGGGTCT GGCCCCCAG GTAGGCGGAG 3420  
 AGCAGTCCCT CCCTCAGGAA CTGGAGGAGG GGACTCCAGG AATGGGGAAA TGTGACACCA 3480  
 CCATCTGAA GCCAGCTTGC ACCTCCAGTT TGCACAGGGA TTTGTCTTGG GGGCTGAGGG 3540  
 CCCTGTCCCC ACCCCCGCCC TTGGTGTCTG CATAAAAGGG CAGGCAGGGG CAGGCTGAGG 3600  
 15 AGTTGCCCTT TGCCCCCAG AGACTGACTC TCAGAGCCAG AGATGGGATG TGTGAGTGTG 3660  
 TGTGTGTGTG TGTGCGCGCG CGCGCGCGTG TGTGTGTGCA CGCACTGGCC TGCACAGAGA 3720  
 GCATGGGTGA GCGTGTAAA GCTTGGCCCT GTGCCCTACA ATGGGGCCAG CTGGGCCGAC 3780  
 AGCAGAATAA AGGCAATAAG ATGAA 3805

20 Seq ID NO: C21 DNA Sequence  
 Nucleic Acid Accession #: NM\_001804  
 Coding sequence: 82..879

25 1 11 21 31 41 51  
 AGGTGAGCGG TTGCTCGTCG TCGGGGCGGC CGGCAGCGGC GGCTCCAGGG CCCAGCATGC 60  
 GCGGGGGACC CCGCGGCCAC CATGTATGTG GGCTATGTGC TGGACAAGGA TTCGCCCCGTG 120  
 TACCCCGGGC CAGCCAGGCG AGCCAGCCTC GGCTTGGGCG CGGCAAACTA CGGCCCCCGG 180  
 30 GCGCGCGCCC CGCGCGCCCC GCAGTACCCC GACTTCTCCA GCTACTCTCA CGTGGAGCCG 240  
 GCGCCCGCGC CCCCAGCGCG CTGGGGGGCG CCCTTCCCTG CGCCCAAGGA CGACTGGGCC 300  
 GCGGCTACG GCGCGGGCCC CGCGGCCCTT GCGCCAGCC CAGCTTCGCT GGCAATTCGGG 360  
 CCCCCTCCAG ACTTTAGCCC GGTGCGCGCG CCCCCTGGGC CCGGCCCGGG CCTCTGGCG 420  
 CAGCCCTCG GGGGCCCGGG CACACCGTCC TCGCCCGGAG CGCAGAGGCC GACGCCCTAC 480  
 35 GAGTGGATGC GCGCGAGCGT GGCGGCCGGA GGCGGCGGTG GCAGCGGTAA GACTCGGACC 540  
 AAGGCAAGT ACCGCGTGGT CTACACCGAC CACCAACGCC TGGAGCTGGA GAAGGAGTTT 600  
 CATTACAGCC GTTACATCAC AATCCGGCGG AAATCAGAGC TGGCTGCCAA TCTGGGGCTC 660  
 ACTGAACGCG AGGTGAAGAT CTGGTTCCAA AACCGGCGGG CAAAGGAGCG CAAAGTGAAC 720  
 AAGAAGAAAC AGCAGCAGCA ACAGCCCCCA CAGCCGCGGA TGGCCACAGA CATCACGGCC 780  
 40 ACCCAGCCG GGCATCCCT GGGGGGCGCT GTTCCAGCA ACACAGCCT CCTGGCCACC 840  
 TCCTCTCAA TGCTGTGAA AGAGGAGTTT CTGCCATAGC CCCATGCCCA GCCTGTGCGC 900  
 CGGGGGACCT GGGGACTCGG GTGCTGGGAG TGTGCTCCT GTGGGCCCAG GAGGTCTGGT 960  
 CGAGTCTCA GCGCTGACCT TCTGGACAT GGTGGACAGT CACCTATCCA CCCTCTGCAT 1020  
 CCCTTGGCC CATTGTGTGC AGTAAGCCTG TTGGATAAAG ACCTTCCAGC TCCTGTGTTC 1080  
 45 TAGACCTCTG GGGGATAAGG GAGTCCAGGG TGGATGATCT CAATCTCCCG TGGGCACTTC 1140  
 AAGCCCCAAA TGGTTGGGG AGGGGCTTAG ACAAGGCTCC AGGCCCCACC TCCTCTCCA 1200  
 TACGTTTCA GGTGAGCTG GAGGCCTGTG TGGGGACCAC ACTGATCCTG GAGAAAAGGG 1260  
 ATGGAGCTGA AAAAGATGGA ATGCTTGCA AGCATGACCT GAGGAGGGAG GAACGTGGTC 1320  
 AACTCACACC TGCTCTTCT GCAGCCTCAC CTCTACCTGC CCCCATCATA AGGGCACTGA 1380  
 50 GCGCTTCCCA GGCTGGATAC TAAGACAAAA GCCCATAGCA CTGGGCTCTG ATGGCTGTCT 1440  
 CACTGGTTA CAGATCACA GCGCTCATGA TCATTCTCAG TGAGGGCTCT GGATTGAGAG 1500  
 GGAGGCCCTG GGAGGAGAGA AGGGGCGAGA GTCTTCCCTA CCAAGTTTCT ACACCCCGGC 1560  
 CAGGCTGCC ATCAGGGCCC AGGGAGCCCC CAGAGGACTT TATTGCGACC AAGCAGAGCT 1620  
 55 CACAGCTGGA CAGGTGTTGT ATATAGAGTG GAATCTCTTG GATGCAGCTT CAAGAATAAA 1680  
 TTTTCTTCT CTTTTCAAA 1699

Seq ID NO: C22 DNA Sequence  
 Nucleic Acid Accession #: NM\_021978  
 Coding sequence: 36..2603

60 1 11 21 31 41 51  
 GACGCTGTG AGACCCGCGA GCGGCCTCGG GGACCATGGG GAGCGATCGG GCCCGCAAGG 60  
 GCGGAGGGGG CCCGAAGGAC TTCGGCGCGG GACTCAAGTA CAACTCCGG CACGAGAAAG 120  
 65 TGAATGGCTT GGAGGAAGGC GTGGAGTTCC TGCCAGTCAA CAACGTCAAG AAGGTGGAAA 180  
 AGCATGGCCC GGGGCGCTGG GTGGTGTCTG CAGCCGTGCT GATCGGCCCT CTCTTGGTCT 240  
 TGCTGGGGAT CGGCTTCTG GTGTGGCATT TGCAGTACCG GGACGTGCGT GTCCAGAAGG 300  
 TCTTCAATGG CTACATGAGG ATCACAATG AGAATTTTGT GGATGCCTAC GAGAACTCCA 360  
 ACTCCACTGA GTTTGTAAGC CTGGCCAGCA AGGTGAAGGA CGCGCTGAAG CTGCTGTACA 420  
 70 GCGGAGTCCC ATTCTGGGC CCCTACCACA AGGAGTCGGC TGTGACGGCC TTCAGCGAGG 480  
 GCAGCGTCAT CGCTTACTAC TGGTCTGAGT TCAGCATCCC GCAGCACCTG GTGGAGGAGG 540  
 CCGAGCGCGT CATGGCCGAG GAGCGCGTAG TCATGCTGCC CCGCGGGGCG GCTCCCTGA 600  
 AGTCCTTTGT GTTCACTCA GTGGTGGCTT TCCCAACGGA CTCRAAACA GTACAGAGGA 660  
 CCCAGGACAA CAGCTGCAGC TTTGGCCTGC ACGCCCGCGG TGTGGAGCTG ATGCGCTTCA 720  
 75 CCACGCGCGG CTTCCTGAC AGCCCTTACC CCGCTCATGC CCGCTCCAG TGGGCCCTGC 780  
 GGGGGACGCG CAGCTCAGTG CTGAGCCTCA CCTTCCGCG CTTTGACCTT GCGTCTCGC 840  
 ACGAGCGCGG CAGCGACCTG GTGACGTTGT ACAACACCT GAGCCCCATG GAGCCCCACG 900  
 CCTGTGTGCA GTTGTGTGGC ACCTACCTC CCTCTACAA CTGACCTTC CACTCCTCCC 960  
 AGAACGTCTT GCTCATACA CTGATAACCA AACTGAGCG GCGGCATCCC GGCTTTGAGG 1020  
 80 CCACCTTCTT CAGCTGCTT AGGATGAGCA GCTGTGGAG CCGCTTACGT AAAGCCCAGG 1080  
 GGACATTCAA CAGCCCTAC TACCCAGGCC ACTACCCACC CAACATTGAC TGACATGGA 1140  
 ACATTGAGGT GCCCAACAAC CAGCATGTGA AGGTGCGCTT CAAATCTTCT TACCTGCTGG 1200  
 AGCCCCGCGT GCGTGGGGC ACCTGCCCA AGGACTACGT GGAGATCAAT GGGGAGAAAT 1260  
 ACTGCGGAGA GAGGTCCCAG TTCGTCTGTA CCAGCAACAG CAACAAGATC ACAGTTCGCT 1320  
 TCCACTCAGA TCAGTCTTAC ACCGACACCG GCTTCTTAGC TGAATACCTC TCCTACGACT 1380

5	CCAGTGACCC	ATGCCCCGGG	CAGTTCACGT	GCCGCACGGG	GCGGTGTATC	CGGAAGGAGC	1440
	TGCGCTGTGA	TGGCTGGGGC	GACTGCACCG	ACCACAGCGA	TGAGCTCAAC	TGCAGTTGCG	1500
	ACGCCGGCCA	CCAGTTCACG	TGCAAGAAC	AGTTCTGCAA	GCCCCCTCTC	TGGGTCTGCG	1560
	ACAGTGTGAA	CGACTGCGGA	GACAACAGCG	ACGAGCAGGG	GTGCAGTTGT	CCGGCCCAGA	1620
	CCTTCAGGTG	TTCCAATGGG	AAGTGCCTCT	CGAAAAGCCA	GCAGTGCAAT	GGGAAGGACG	1680
	ACTGTGGGGA	CGGGTCCGAC	GAGGCTCCTC	GCCCCAAGGT	GAACGTCGTC	ACTTGTACCA	1740
	AACACACCTA	CCGCTGCCTC	AATGGGCTCT	GCTTGAGCAA	GGGCAACCCT	GAGTGTGACG	1800
	GGAAAGGAGG	CTGTAGCGAC	GGCTCAGATG	AGAAGGACTG	CGACTGTGGG	CTGCGGTCTAT	1860
10	TCACGAGACA	GGCTCGTGTT	GTTGGGGGCA	CGGATGCGGA	TGAGGGCGAG	TGGCCCTGCG	1920
	AGGTAAACCT	GCATGCTCTG	GGCCAGGGCC	ACATCTGCGG	TGCTTCCCTC	ATCTCTCCCA	1980
	ACTGGCTGGT	CTCTGCCGCA	CACTGCTACA	TCGATGACAG	AGGATTCAGG	TACTCAGACC	2040
	CCACGCAGTG	GACGGCCTTC	CTGGGCTTGC	ACGACCAGAG	CCAGCGCAGC	GCCCCCTGGG	2100
	TGCAGGAGCG	CAGGCTCAAG	CGCATCATCT	CCCACCCCTT	CTTCAATGAC	TTCACCTTCG	2160
15	ACTATGACAT	CGCGCTGCTG	GAGCTGGAGA	AACCGGCAGA	GTACAGCTCC	ATGGTGC CGG	2220
	CCATCTGCCT	GCCGAGCGCC	TCCCATGTCT	TCCCTGCCCG	CAAGGCCATC	TGGGTCAACG	2280
	CTGTGGGACA	CACCCAGTAT	GGAGGCACCT	GCGCGCTGAT	CCTGCAAAAG	GGTGAGATCC	2340
	GGGTATCAAA	CCAGACCACC	TGCGAGAAC	TCTTGCCGCA	GCAGATCACG	CCGCGCATGA	2400
	TGTGCGTGGG	CTTCTCAGC	GGCGGCGTGG	ACTCTTGCCA	GGGTGATTCC	GGGGGACCCC	2460
20	TGTCAGGCT	GAGGCGGAT	GGGCGGATCT	TCCAGGCCGG	TGTGGTGAGC	TGGGGAGACG	2520
	GCTGCGCTCA	GAGGAACAAG	CCAGGCGTGT	ACACAGGCT	CCCTCTGTTT	CGGGACTGGA	2580
	TCAAAGAGAA	CACTGGGGTA	TAGGGGCCGG	GGCCACCCAA	ATGTGTACAC	CTGCGGGGCC	2640
	ACCCATCGTC	CACCCAGTGG	TGCACGCTTG	CAGGCTGGAG	ACTGGACCGC	TGACTGCACC	2700
	AGCGCCCCCA	GAACATACAC	TGTGAACCTA	ATCTCCAGGG	CTCCAAATCT	GCCTAGAAAA	2760
25	CCTCTCGCTT	CCTCAGCCTC	CAAAAGTGGG	CTGGGAGGTA	GAAGGGGAGG	ACACTGGTGG	2820
	TTCTACTGAC	CCAACCTGGG	GCAAGGTTT	GAAGACACAG	CCTCCCCCGC	CAGCCCCAAG	2880
	CTGGGCGGAG	GCGCGTTTGT	GTATATCTGC	CTCCCCCTGT	TGTAAGGAGC	AGCGGGAACG	2940
	GAGCTTCGGA	GCTCTCTCAG	TGAAGTGGT	GGGGCTGCCG	GATCTGGGCT	GTGGGGCCCT	3000
	TGGGCCACGC	TCTTAGAGAA	GCCAGGCTC	GGAGGACCC	GGAAACACAG	CGGGTCTGAG	3060
30	ACTGAAAATG	TTTACCAGC	TCCCAGGTGA	CTTCAGTGTG	TGTATTGTGT	AAATGAGTAA	3120
	AACATTTTAT	TTCTTTTATA	AAAAAATA				3149

Seq ID NO: C23 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2268

35	1	11	21	31	41	51	
	ATGCCCCCTT	TCCTGTGCT	GGAAGCCGTC	TGTGTTTTCC	TGTTTTCCAG	AGTGCCCCCA	60
40	TCTCTCCCTC	TCCAGGAAGT	CCATGTAAGC	AAAGAAACCA	TCGGGAAGAT	TTGAGCTGCC	120
	AGCAAAATGA	TGTGGTGCTC	GGCTGCAGTG	GACATCATGT	TTCTGTGAGA	TGGGTCTAAC	180
	AGCGTCGGGA	AAGGGAGCTT	TGAAAGGTCC	AAGCACTTTG	CCATCACAGT	CTGTGACGGT	240
	CTGGACATCA	GCCCCGAGAG	GGTCAGAGTG	GGAGCATTCC	AGTTCACTTC	CACCTCTCAT	300
	CTGGAATTCC	CCTTGGATTG	ATTTTCAACC	CAACAGGAAG	TGAAGGCAAG	AATCAAGAGG	360
45	ATGGTTTTCA	AAGGAGGGCG	CACGGAGACG	GAACCTTGCTC	TGAAATACCT	TCTGCACAGA	420
	GGGTGCGCTG	GAGGCGGATG	TGCTTCTGTG	CCCCAGATCC	TCATCATCGT	CACCTGATGG	480
	AAGTCCCAGG	GGGATGTGGC	ACTGCCATCC	AAGCAGCTGA	AGGAAAGGGG	TGTCACTGTG	540
	TTTGCTGTGG	GGGTCAAGTT	TCCAGGTTGG	GAGGAGCTGC	ATGCACCTGG	CAGCGAGCCT	600
	AGAGGGCAGC	ACGTGCTGTT	GGCTGAGCAG	GTGGAGGATG	CCACCAACGG	CCTCTTCAGC	660
50	ACCTCAGCA	GCTCGGCCAT	CTGCTCCAGC	GCCACGCCAG	ACTGCAGGGT	CGAGGCTCAC	720
	CCCTGTGAGC	ACAGGACGCT	GGAGATGGTC	CGGAGATTTC	CTGGCAATGC	CCCATGCTGG	780
	AGAGGATCGC	GGCGGACCCT	TGCGGTGCTG	GCTGCACACT	TGCTTCTCTA	CAGCTGGAAG	840
	AGAGTGTTC	TAACCCACCC	TGCCACCTGC	TACAGGACCA	CCTGCCCAGG	CCCTCTGTAC	900
	TCGCGAGCCT	GCCCAATGAG	AGGCACATGT	GTTCCAGAA	GACTGGACGG	CTACCACTGC	960
55	CTCTGCCCGC	TGGCCTTTGG	AGGGGAGGCT	AACGTGCCCC	TGAAGCTGAG	CCTGGAATGC	1020
	AGGGTCGACC	TCTCTCTCCT	GCTGGACAGC	TCTGCGGGCA	CCACTCTGGA	CGGCTTCTCT	1080
	CGGGCCAAAG	TCTTCTGTGA	GCGGTTTGTG	CGGGCCGTGC	TGAGCGAGGA	CTCTCGGGCC	1140
	CGAGTGGGGT	TGGCCACATA	CAGCAGGGAG	CTGCTGGTGG	CGGTGCTCTG	GGGGGAGTAC	1200
	CAGGATGTGC	CTGACCTTGT	CTGGAGCCTC	GATGGCATTG	CCTTCCGTGG	TGGCCCCACC	1260
60	CTGACGGGCA	GTGCTTGGCG	GCAGGCGGCA	GAGCGTGGCT	TCGGGAGCGC	CACCAAGACA	1320
	GGCCAGGACC	GGCCACGTA	AGTGGTGGTT	TTGCTCACTG	AGTCACACTC	CGAGGATGAG	1380
	GTTGCGGGCC	CAGCGCGTCA	CGCAAGGGCG	CGAGAGCTGC	TCTGCTGGG	TGTAGGCAGT	1440
	GAGGCGGTGC	GGGCAGAGCT	GGAGGAGATC	ACAGGCAGCC	CAAAGCATGT	GATGGTCTAC	1500
	TCGGATCCTC	AGGATCTGTT	CAACCAATC	CCTGAGCTGC	AGGGGAAGCT	GTGCAGCCCG	1560
65	CAGCGGCCAG	GGTGCCGAG	ACAAGCCCTG	GACCTCGTCT	TCATGTTGGA	CACCTCTGCC	1620
	TCAGTAGGGC	CCGAGAATTT	TGCTCAGATG	CAGAGCTTTG	TGAGAAGCTG	TGCCCTCCAG	1680
	TTTGAGGTGA	ACCTGACGCT	GACACAGGTC	GGCTTGGTGG	TGTATGGCAG	CCAGGTGCAG	1740
	ACTGCCTTCG	GGCTGGACAC	CAAAACCCACC	CGGGCTGCGA	TGCTGCGGGC	CATTAGCCAG	1800
	GCCCCCTACC	TAGGTGGGGT	GGGCTCAGCC	GGCACCAGCC	TGCTGCACAT	CTATGACAAA	1860
70	GTGATGACCG	TCCAGAGGGG	TGCCCGGCTT	GGTGTCCCA	AAAGCTGGGT	GGTGTCTACA	1920
	GGCGGGAGAG	GCGCAGAGGA	TGCAGCCGTT	CCTGCCCAGA	AGCTGAGGAA	CAATGGCATC	1980
	TCTGTCTTGG	TGCTGGGCGT	GGGGCTGTGC	CTAAGTGAGG	GTCTGCGGAG	GCTTGCAGGT	2040
	CCCCGGGATT	CCCTGATCCA	CGTGGCAGCT	TACGCCGACC	TGCGGTACCA	CCAGGACGTG	2100
	CTCATTGAGT	GGCTGTGTGG	AGAAGCCAAG	CGGCCAGTCA	ACCTCTGCAA	ACCCAGCCCG	2160
75	TGCATGAATG	AGGGCAGCTG	CGTCTGCAG	AATGGGAGCT	ACCGCTGCAA	GTGTGCGGAT	2220
	GGCTGGGAGG	GCCCCCACTG	CGAGAACCGA	TTCTTGAGAC	GCCCCCTGA		2268

Seq ID NO: C24 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..2424

80	1	11	21	31	41	51	
	ATGCCCCCTT	TCCTGTGCT	GGAGGCCGTC	TGTGTTTTCC	TGTTTTCCAG	AGTGCCCCCA	60
	TCTCTCCCTC	TCCAGGAAGT	CCATGTAAGC	AAAGAAACCA	TCGGGAAGAT	TTGAGCTGCC	120

5	AGCAAAATGA	TGTGGTGTCT	GGCTGCAGTG	GACATCATGT	TTCTGTAGA	TGGGTCTAAC	180
	AGCGTCGGGA	AAGGGAGCTT	TGAAAGSTCC	AAGCACTTTG	CCATCACAGT	CTGTGACGGT	240
	CTGGACATCA	GCCCCGAGAG	GGTCAGAGTG	GGAGCATTTCC	AGTTTCAGTTC	CACCTCCTCAT	300
	CTGGAATTCC	CCTTGGATTCC	ATTTTCAACC	CAACAGGAAG	TGAAGGCAAG	AATCAAGAGG	360
	ATGGTTTTC	AAGGAGGGCG	CACGGAGACG	GAACCTGTCT	TGAAATACCT	TCTGCACAGA	420
	GGGTTGCCTG	GAGGCAGAAA	TGCTTCTGTG	CCCAGATCC	TCATCATCGT	CACTGATGGG	480
	AAGTCCAGG	GGGATGTGGC	ACTGCCATCC	AAGCAGCTGA	AGGAAAGGGG	TGTCACGTGTG	540
	TTTGCTGTGG	GGGTACAGTT	TCCCAGGTGG	GAGGAGCTGC	ATGCACTGGC	CAGCGAGCCT	600
10	AGAGGGCAGC	ACGTGCTGTT	GGCTGAGCAG	GTGGAGGATG	CCACCAACGG	CCTCTTCAGC	660
	ACCTCAGCA	GCTCGGCCAT	CTGCTCCAGC	GCCACGCCAG	ACTGCAGGGT	CGAGGCTCAC	720
	CCCTGTGAGC	ACAGGACGCT	GGAGATGGTC	CGGGAGTTCC	CTGGCAATGC	CCCATGCTGG	780
	AGAGGATCGC	GGCGGACCCCT	TGCGGTGCTG	GCTGCACACT	GTCCCTTCTA	CAGCTGGGAG	840
	AGAGTGTTC	TAACCCACCC	TGCCACCTGC	TACAGGACCA	CCTGCCCAGG	CCCCTGTGAC	900
15	TCGCAGCCCT	GCCAGAATGG	AGGCACATGT	GTTCCAGAAG	GACTGGACGG	CTACCAGTGC	960
	CTCTGCCCGC	TGGCCCTTTGG	AGGGGAGGGCT	AACTGTGCCC	TGAAGCTGAG	CCTGGAATGC	1020
	AGGGTCGACC	TCTCTTTCCT	GCTGGACAGC	TCTGCGGGCA	CCACTCTGGA	CGGCTTCCTG	1080
	CGGGCCAAAG	TCTTCGTGAA	GCGGTTTGTG	CGGGCCGTGC	TGAGCGAGGA	CTCTCGGGCC	1140
	CGAGTGGGTG	TGGCCATGTA	CAGCAGGGAG	CTGCTGGTGG	CGGTGCCTGT	GGGGGAGTAC	1200
20	CAGGATGTGC	CTGACCTGGT	CTGGAGCCTC	GATGGCATTG	CCTTCCGTGG	TGGCCCCACC	1260
	CTGACGGGCA	GTGCTTTGCG	GCAAGCGGCA	GAGCGTGGCT	TGCGGAGCGC	CACCAGGACA	1320
	GGCCAGGACC	GGCCACGTAG	AGTGGTGGTT	TTGCTCACTG	AGTCACACTC	CGAGGATGAG	1380
	GTTGCGGGCC	CAGCGCCTCA	CGCAAGGGCG	CGAGAGCTGC	TCCTGCTGGG	TGTAGGCAGT	1440
	GAGGCCGTGC	GGGCAGAGCT	GGAGGAGATC	ACAGGCAGCC	CAAAGCATGT	GATGGTCTAC	1500
25	TCGGATCCTC	AGGATCTGTT	CAACCAAATC	CCTGAGCTGC	AGGGGAAAGT	GTGCAGCCGG	1560
	CAGCGGCCAG	GGTGCCGGAC	ACAAGCCCTG	GACCTCGTCT	TCATGTTGGA	CACCTCTGCC	1620
	TCAGTAGGGC	CCGAGAAATT	TGCTCAGATG	CAGAGCTTTG	TGAGAAGCTG	TGCCCTCCAG	1680
	TTTGAGGTGA	ACCCTGACGT	GACACAGGTC	GGCCTGGTGG	TGTATGGCAG	CCAGGTGCAG	1740
	ACTGCTTCG	GGGTGGACAC	CAAAACCCACC	CGGGCTGCGA	TGCTGCGGGC	CATTAGCCAG	1800
30	GCCCCCTACC	TAGGTGGGGT	GGGCTCAGCC	GGCACCCGCC	TGCTGCACAT	CTATGACAAA	1860
	GTGATGACCG	TCCAGAGGGG	TGCCCGGCCT	GGTGTCCCCA	AAGCTGTGGT	GGTGCTCACA	1920
	GGCGGGAGAG	GCGCAGAGGA	TGCAGCCGTT	CCTGCCCAGA	AGCTGAGGAA	CAATGGCATC	1980
	TCTGTCTTGG	TCGTGGGCGT	GGGGCCTGTC	CTAAGTGAGG	GTCTGCGGAG	GCTTGCAAGT	2040
	CCCCGGGATT	CCCTGATCCA	CGTGGCAGCT	TACGCCGACC	TGCGGTACCA	CCAGGACGTG	2100
35	CTCATTGAGT	CCCTGTGTGG	AGAAAGCCAAG	CAGCCAGTCA	ACCTCTGCAA	ACCCAGCCCG	2160
	TGCATGAATG	AGGGCAGCTG	CGTCTGCAG	AATGGGAGCT	ACCGCTGCAA	GTGTGCGGAT	2220
	GGCTGGGAGG	GCCCCCACTG	CGAGAACCCT	GAGTGGAGCT	CTTGCTCTGT	ATGTGTGAGC	2280
	CAGGGATGGA	TTCTTGAGAC	GCCCCTGAGG	CACATGGCTC	CCGTGCAGGA	GGGCAGCAGC	2340
40	CGTACCCCTC	CCAGCAACTA	CAGAGAAGGC	CTGGGCACCT	AAATGGTGCC	TACCTTCTGG	2400
	AATGTCTGTG	CCCCAGGTCC	TTAG				2424

Seq ID NO: C25 DNA Sequence

Nucleic Acid Accession #: XM\_097386.3

Coding sequence: 142..795

45	1	11	21	31	41	51	
	CTCGCAGAAC	CACCTGGACT	CTGTCCGTGT	CTGTCCCCCG	GCCTCCAGGG	CTCCTCTCCC	60
	GGGACCCCGG	TCCCACGCCT	GGGCCCCGCG	CCGGGGGAAG	CGCCTGCTGC	CTATCTCTGT	120
50	CTACCTCAGG	TCTGACTTTT	GATGCCAAAA	TCTGAGCCCC	TGGGGTGCCT	CTCCCCCGCC	180
	TCCCGTGAC	CAGGGTCTGC	AGCAGCCACT	GGGGCCTGGC	TGCTGTCTGC	ATCTGGCGCG	240
	CCTGGACCCC	TGGGGCCCCC	GTGCACCTGC	CCACCTCGGA	GCCTGGGGAG	GGGCCGTGCA	300
	GGGTGCGAGG	CTGGGTCTGT	TCCCTCGGGC	TGCGTGTGTG	TGTGCGGAAT	CCTGCGTGTG	360
	GTGTCTGTGG	GCGATCCGGC	CTCCCGCGCG	TGGGTGGACC	TGGATTCTAA	CTCAGAGGAC	420
55	TTGAGCCTGC	TGTTAACTCC	GATGATTGTA	GGGACAGGCG	GGGTGGGTGG	GGGGTGGGCG	480
	CGAGGCTGGG	TCCCGGCCCA	GGAGAAGGAA	GTCTGTAAG	GCAGTGGCCA	TGCTGGCCGT	540
	GGAATGGGA	GGCGGTTGCA	GAGGTTCTAT	GGGGCCCCGT	CCTGGATACT	CGGCAGGAAG	600
	CCGTGTCTGC	AGAGGCTCCT	CCCTGCCTCA	GGTGGCCCCG	TTCAACCCCA	GCCGTGCCCA	660
	TCTCCTGCCA	CCGCTCTGTC	GTGGGGGTTT	AAATTGCGTG	TGGCTTTCTG	GGGTGCAGCT	720
60	CAGCACCCCC	CCTTATGAGC	ACTGGGAGGG	GGTGGGGCAG	TCCCTCAGC	CACGAGGACC	780
	CTGGATGGGT	TCTAGTTTCA	TTGGGACCGT	GGGGCCTGGC	TGCGTACTGA	GTGGGTGCCC	840
	CACAGTCAAG	GCCAAACGGG	GCTCCCCCTG	CTCTGAGATG	TTGGGAGAAA	GGCGGCTTCT	900
	GGAACCTTCC	GTGGGACCCG	TAAGTGGCTG	TCCAGAAAGG	CGGGAGGGTG	GGCACGGGGC	960
	ACGGGGGGGA	GCTGGGGTGG	TTGTTAAGGG	TCACGCATCT	GTACAGTTGA	ATTTCTTTTC	1020
65	TCTTATCATG	TTTTACCCAC	CTTGTCCCTT	TTTTCCCCAA	TTGTGCTTTT	GCATTTTTTT	1080
	CCTTGGCAAA	TGTAACCTCA	GCCTTTCATT	CATGACGTGT	GAAATTTTCA	TTTCTCTGGA	1140
	GTTTGTGAGA	CGCGTGGGGA	ACCACGCTG	AAACTCAGGT	AATAGGAGGA	AAAAAAAAAA	1200
	AACTTAAAAA	AATTTTAAAA	AAACATAAAA	CTACTCTCTA	CCTCTGGCTG	GGCCAGCCTT	1260
	GTCTCGCCCT	GGCGCGGCA	GGGTGGCCTG	TAACAATTTT	AGTTTTTCGA	GAACATTGAG	1320
70	GTATTAAAAA	GAAAAA					1337

Seq ID NO: C26 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 95..2128

75	1	11	21	31	41	51	
	GGGGTAGTTT	GTAGGGACGC	AGCTCTCCAC	GTGCGCGACT	GCGAGGCTGG	ACGCTACGGG	60
	CTCCTGGAAA	GGAGAGACAC	CAGCATTTGC	CACATGCTG	TCATCCACTG	ACTTTACATT	120
80	TGCTTCTTGG	GAGCTTGTGG	TCCGCGTTGA	CCATCCCAAT	GAAGAGCAGC	AGAAAGACGT	180
	CACACTGAGA	GTATCTGGAG	ACCTTCATGT	TGGAGGAGTG	ATGCTCAAGT	TAGTAGAACA	240
	GATCAATATA	TCCCAAGACT	GGTCAGACTT	TGCTCTTTGG	TGGGAACAGA	AGCATTGCTG	300
	GCTTCTGAAA	ACCCCTGAGA	CCCTGGACAA	ATATGGGGTC	CAGGCAGATG	CAAGCTTCTT	360
	CTTCAACCC	CAGCATAAAA	TGCTGCGCCT	TCGTCTGCCG	AATTTGAAGA	TGGTGAGGTT	420
	GCGAGTCAGC	TTCTCAGCTG	TGGTTTTTAA	AGCTGTCACT	GATATCTGCA	AAATCCTGAA	480

5	TATTAGAAGA	TCAGAAGAGC	TTTCTTGTT	AAAGCCGTCT	GGTGACTATT	TTAAGAAGAA	540
	GAAGAAAAAA	GACAAAAATA	ATAAGGAACC	CATAATTGAA	GATATTTCTAA	ACCTGGAGAG	600
	TTCTCCAACA	GCTTCAGGTT	CATCAGTAAG	TCTTGGTTTA	TACAGTAAAA	CCATGACCCC	660
	TATATATGAC	CCCATCAATG	GAACACCAGC	ATCATCCACC	ATGACTTGGT	TCACTGACAG	720
	CCCTTTGACG	GAACAAAAC	GCAGCATCCT	CGCATTACAG	CAACCCCCC	AGTCCCCAGA	780
	AGCACTTGCG	GATATGTACC	AGCCTCGGTC	TCTGGTTGAT	AAAGCCAAGC	TCAATGCAGG	840
	TTGGCTAGAC	TCCTCAGGCT	CCCTTATGGA	ACAAGGCATC	CAAGAGGATG	AGCAGCTGCT	900
	CTTACGATTT	AAATATTATT	CTTCTTCGA	CTTGAATCCT	AAATATGATG	CTGTCCGAAT	960
10	AAACCAACTC	TATGAGCAAG	CCAGGTGGGC	CATTCTCTTA	GAAGAAATTG	ATTGCACAGA	1020
	GGAAGAAATG	TTGATCTTTG	CAGCTCTACA	GTACCACATT	AGCAAACTGT	CGTTGTCTGC	1080
	TGAAACACAG	GATTTTGCAG	GCGAGTCCGA	GGTTGATGAA	ATAGAAGCGG	CGCTTCTTAA	1140
	TTTGGAAGTA	ACCCTAGAAG	GTGGAAAAAG	GGACAGCCTT	TTGGAGGACA	TTACTGATAT	1200
	CCCTAAACTT	GCAGATAATC	TCAAATTATT	TAGGCCCAAG	AAGTTACTAC	CAAAAGCTTT	1260
15	CAAACAATAT	TGGTTTATCT	TTAAAGACAC	ATCCATAGCA	TACTTTAAAA	ATAAGGAACT	1320
	TGAACAAGGA	GAACCACTAG	AAAAACTAAA	TCTTAGAGGC	TGCGAAGTTG	TGCCCGATGT	1380
	AAATGTAGCA	GGAAGGAAAT	TTGGAATCAA	GTTACTAATC	CCTGTGCGCG	ATGGTATGAA	1440
	TGAAATGTAT	TTGAGATGTG	ACCATGAGAA	TCAATACGCC	CAATGGATGG	CTGCCTGCAT	1500
	GTTGGCATCG	AAGGGCAAAA	CCATGGCAGA	CAGCTCCTAC	CAGCCAGAGG	TCCTCAACAT	1560
20	CCTTTCATTT	CTGAGGATGA	AAAACAGGAA	CTCTGCATCT	CAGGTGGCTT	CCAGTCTCGA	1620
	AAACATGGAT	ATGAACCCAG	AATGTTTTGT	GTCAACACGG	TGTGCAAAAA	GACACAAATC	1680
	CAACACAGCTG	GCCGCCCGGA	TCCTGGAGGC	GCACCAGAAC	TGGGCCCAGA	TGCCCTTGTT	1740
	CGAAGCCAAG	CTGCGGTTCA	TCCAGGCGTG	GCAGTCACTG	CCTGAGTTTG	GCCTCACCTA	1800
	CTACCTTGTC	AGATTTAAAG	GAAGCAAAAA	AGATGACATT	CTGGGAGTTT	CATATAACAG	1860
25	GTTGATTAAA	ATTGATGCGAG	CCACCGGGAT	TCCAGTGACA	ACATGGAGAT	TCACAAATAT	1920
	CAACACAGTGG	AATGTAATAT	GGGAAACCCG	GCAGGTGGTC	ATCGAGTTTG	ACCAAAACGT	1980
	CTTTACTGCT	TTACCTGCC	TGAGTGACAG	TTGCAAGATT	GTGCACGAGT	ACATTGGCGG	2040
	CTACATTTTC	TTGTCCACCC	GCTCCAAGGA	CCAGAATGAA	ACACTCGATG	AGGACTTGTT	2100
	CCACAAATTTG	ACCGGCGGCT	AGGATTGAAA	CAAGCACCGG	TGCTCGGCTC	ACACCAACAA	2160
30	GGCAAGCCAA	AGCGCGCCCT	CCCCAGAGGG	ATCCCTAACG	TGCCCAGCAT	GTAGATTCTG	2220
	GACTAACAGA	CAACATACAT	TCACCGCTGG	TCACCCAGAT	CCTCATTCAA	ACCCACTGCT	2280
	GGCACATCCC	TTTCTTACT	TTGCCCTGTG	CTACCAGCCA	CGGAAGGAGC	CTCTCTTGTT	2340
	TTTTCTATAA	AATGGGTAGG	CAGGAGAAAA	GCAGGTGCC	TAAGATTGCT	CTAAGGCCCA	2400
	GCATGTGGTT	ACAGTTCTCT	GACTTGCAGA	ACCTGCCAGG	TGTATGGCTA	CAAGTTATCC	2460
35	TCGTGCTGAT	CTGTCTCATT	ACTAAGTCAA	TGGAGAAGAC	AGAAAGGTAA	AAATCACGTG	2520
	TAGCAAGAAC	AACCTTTATT	TCACAACTC	AGGTATGAAA	CGAAACGCCT	GTCTTTCATG	2580
	GAAGTCTTTT	TAGCTCCTGT	CTTTTCAAAA	TGGCAGAGGG	AGTTCTTACA	CACACTTTTT	2640
	CCCTGGAGGC	CAAGGCTTAG	GGGTAGAAA	GGGAGGGGTG	GGGCTACCAG	GTAGCAGTTG	2700
	ACAACCCAAG	GTGAGAGGAG	TGGCCCTCAG	TGTCATCTGT	CCACAGTGAT	ACCTGCCAAG	2760
40	ATGACCACTG	ACCCACATCT	GGTCTTAGTC	ATTGGTCTCC	TCAGATTTCT	GGGGCCACCT	2820
	GCAAGCCCCA	TTCCATTCTC	ACAGATCTCT	CAGCCACCTG	TAAGTCCTTT	GTGAAGATGT	2880
	GGGTGACACA	GGGGGACAGG	AAAACCCATT	TCTCAACCCA	GATCCATGTC	TCCACTGCTT	2940
	CTACTCTGGG	TTGGGATTCA	GGAAGACAGG	CACAGTCCTC	TCTGTTTATA	GAAACACCTG	3000
	CCAGTGTCAA	GGATTCCAGT	CAGGTGTCTA	TCCCAACTGG	TCAGGGAGAG	AAGGGCAGAC	3060
45	CCATTCTCAA	AGACCACCAT	GTCCAAAGGT	TGACAGCTCC	CCACTGGCTG	CCCCCAGG	3120
	GGCTTTAGGC	TGGTCTGGGT	CATGGGGAAG	CGTCCCTCTT	ATCGCTGGTC	TGTGTTCTCC	3180
	TGGATTGGGT	ATCTATGTTG	GTACGACTCC	TGGCCTTTTA	TCTAAAGGAC	TTTGGCTTTT	3240
	GTAATACACA	AGCCAATAAT	AGACTTTTTT	CTCCCCCTCT	GTTTTTTGCT	GTGTCTCTC	3300
	TGCCTTGAGA	CTGCCCTGAG	ACAGTGCTTG	CCTTGAGAGA	GTGAGCCAAT	TAACAGCTGC	3360
50	CTGAATTGTC	ATTTTCCATT	TTGGTTTGT	AGAGGTGGGA	GGGGTGGGTT	TTGAGAAGGT	3420
	CAAAAGCAAT	ACCAGAAGTA	AAGGGAAATA	TCAGACAATA	TTTTATTATT	TTTTCATAGA	3480
	TGTTCTGCCA	CACAAAGAAC	TTGGGGTGTA	AGGATAAGGC	AAAAGCTCCA	ATCCCATTTT	3540
	TCAGTTCTTC	TAGGATGCAC	CCCTCAGGGA	GCCTGGCCAG	AGTTCAGAGG	CCCGTGAGCG	3600
	TCAGCTGTTG	CTTTATTTTC	CATCAAAGCC	CTCTGAGAAG	TGAGACCTCA	GCAATTCCGG	3660
55	GAGCCACATA	GAGACAGACT	TGGCAAGGGA	CCCCCTGGTT	CTGAGCCAGT	AGCTGCCATC	3720
	TGGAAATTC	TCCTTTAGCC	TCCTCTAGA	GGTGAATGTG	AATGAAGCCT	CCAGGCACC	3780
	CGCTGAATTT	CTGAGGCTTT	GCTTAAAGCT	CAGAAGTGGT	TTAGGCATTT	GGAAAATCTG	3840
	GTTACATCA	TAAAGAACTT	GATTTGAAAT	GTTTTCTATA	GAAACAAGTG	CTAAGTGATC	3900
	CGTATTATAC	TTGAGTTTGG	TCATTTCTCA	GTCTATTTC	TCAGTTCTAT	TATTTTAGAA	3960
60	CCTAGTCAGT	TCCTTAAGAT	TATACTGGT	CCTACATTAA	AATAATGCTT	CTCGATGTCA	4020
	GATTTTACCT	GTTTGTCTGT	GAGAACATCT	CTGCCTAATT	TACCAAGGCC	AGACCTTCAG	4080
	TTCAACATGC	TTCTTAGCT	TTTCATAGTT	GTCTGACATT	TCCATGAAAA	CAAAAGGAACC	4140
	AACTTTGTTT	TAAACAAACT	TTGTTTGGTT	ACAGTTTTC	GGGGAGCGTT	TCTTCCATGA	4200
	CACACAGCAA	CATCCCCAAG	AAATAACAA	GTGTGACAAA	AAAAAATAAA	AACAAACCTA	4260
65	AATGCTACTG	TTCCAAAGAG	CAACTTGATG	GTTTTTTTTA	ATACTGAGTG	CAAAAGGTCA	4320
	CCCAAATTC	TATGATGAAA	TTTAAATTA	ATGGGCACCT	TTCAACATCA	TTTGCTTCCT	4380
	TATCTACAGT	TGATTTCAGAA	ATCTGCATTT	TTTATTCTTT	TATATGACTT	TTAAGTAAAA	4440
	GATTTATATG	GATTTGAAAA	AAAAAATAAA	A			4471

Seq ID NO: C27 Protein Sequence  
Protein Accession #: NP\_005161.1

75	1	11	21	31	41	51	
	MDGGTLPRSA	PPAPPVPGVC	AARRRPASPE	LLRCSRRRRP	ATAETGGGAA	AVARRNERER	60
	NRVKLVNLGF	QALRQVPHFG	GASKKLSKVE	TLRSAYEYIR	ALQRLLAHEH	AVRNALAGGL	120
	RPQAVRPSAP	RGPPTTFPVA	ASPSRASSSP	GRGGSSEPGS	PRSAYSDDSD	GCEGALSPAE	180
	RELLDFSSWL	GGY					193

Seq ID NO: C28 DNA Sequence  
Nucleic Acid Accession #: NM\_017763  
Coding sequence: 169..2520

80	1	11	21	31	41	51

	AAAAA	AACTTTAGAG	AAAGGAAGGG	CCAAACTAC	GACTTGGCTT	TCTGAAACGG	60
	AAGCATAAAT	GTTCTTTTCC	TCCATTGTGC	TGGATCTGAG	AACTTGCATT	TGGTATTAGC	120
	TAGTGAAGC	AGTATGTATG	GTTGAAGTGC	ATTGCTGCAG	CTGGTAGCAT	GAGTGGTGGC	180
5	CACCAGCTGC	AGCTGGCTGC	CCTCTGGCCC	TGGCTGCTGA	TGGCTACCCCT	GCAGGCAGGC	240
	TTTGGACGCA	CAGGACTGGT	ACTGGCAGCA	GCGGTGGAGT	CTGAAAGATC	AGCAGAACAG	300
	AAAGCTGTTA	TCAGAGTGAT	CCCCTTGAAA	ATGGACCCCA	CAGGAAAACT	GAATCTCACT	360
	TGGGAAGGTG	TGTTTGCTGG	TGTTGCTGAA	ATAACTCCAG	CAGAAGGAAA	ATTAATGCAG	420
	TCCCACCCAC	TGTACCTGTG	CAATGCCAGT	GATGACGACA	ATCTGGAGCC	TGGATTCACT	480
10	AGCATCGTCA	AGCTGGAGAG	TCCTCGACGG	GCCCCCGGCC	CCTGCCTGTC	ACTGGCTAGC	540
	AAGGCTCGGA	TGGCGGGTGA	GCGAGGAGCC	AGTGCTGTCC	TCTTTGACAT	CACCTGAGGAT	600
	CGAGCTGCTG	CTGAGCAGCT	GCAGCAGCCG	CTGGGGCTGA	CCTGGCCAGT	GGTGTGATC	660
	TGGGGTAATG	ACGCTGAGAA	GCTGATGGAG	TTTGTGTACA	AGAACCAAAA	GGCCCATGTG	720
	AGGATTGAGC	TGAAGGAGCC	CCCCGCCCTGG	CCAGATTATG	ATGTGTGGAT	CCTAATGACA	780
15	GTGGTGGGCA	CCATCTTTGT	GATCATCTCTG	GCTTCGGTGC	TGCGCATCCG	GTGCCGCCCC	840
	CGCCACAGCA	GGCCGGATCC	GCTTCAGCAG	AGAACAGCCT	GGGCCATCAG	CCAGCTGGCC	900
	ACCAGGAGGT	ACCAGGCCAG	CTGCAGGCAG	GCCCCGGGTG	AGTGGCCAGA	CTCAGGGAGC	960
	AGCTGCAGCT	CAGCCCCGTG	GTGTGCCATC	TGCTGGAGG	AGTTCTCTGA	GGGGCAGGAG	1020
	CTACGGGTCA	TTTCTGCTCT	CCATGAGTTC	CATCGTAACT	GTGTGGACCC	CTGGTTACAT	1080
20	CAGCATCGGA	CTTGCCCCCT	CTGCGTGTTC	AACATCACAG	AGGGAGATTTC	ATTTTCCAG	1140
	TCCCTGGGAC	CCTCTCGATC	TTACCAAGAA	CCAGGTCGAA	GACTCCACCT	CATTGCGCAG	1200
	CATCCCGGCC	ATGCCCACTA	CCACCTCCCT	GCTGCCTACC	TGTTGGGCC	TTCCCGGAGT	1260
	GCAGTGGCTC	GGCCCCCAGC	ACCTGGTCCC	TTCTTGCCAT	CCCAGGAGCC	AGGCATGGGC	1320
	CCTCGGCATC	ACCGCTTCCC	CAGAGCTGCA	CATCCCCGGG	CTCCAGGAGA	GCAGCAGCGC	1380
25	CTGGCAGGAG	CCCAGCACCC	CTATGCACAA	GGCTGGGGAA	TGAGCCACCT	CCAATCCACC	1440
	TCACAGCACCC	CTGCTGCTTG	CCCAGTGCCC	CTACGCCGGG	CCAGGCCCCC	TGACAGCAGT	1500
	GGATCTGGAG	AAAGCTATTG	CACAGAACGC	AGTGGGTACC	TGGCAGATGG	GCCAGCCAGT	1560
	GACTCCAGCT	CAGGGCCCTG	TCATGGCTCT	TCCAGTGACT	CTGTGGTCAA	CTGCACGGAC	1620
	ATCAGCCTAC	AGGGGGTCCA	TGGCAGCAGT	TCTACTTTCT	GCAGCTCCCT	AAGCAGTGAC	1680
30	TTTGACCCCC	TAGTGTACTG	CAGCCCTAAA	GGGGATCCCC	AGCGAGTGA	CATGCAGCCT	1740
	AGTGTGACCT	CTCGGCCCTG	TTCTTTGGAC	TCGGTGGTGC	CCACAGGGGA	AACCCAGGTT	1800
	TCCAGCCATG	TCCACTACCA	CCGCCACCGG	CACCACCCT	ACAAAAAGCG	GTTCCAGTGG	1860
	CATGGCAGGA	AGCCTGGCCC	AGAAACCGGA	GTCCCCCAGT	CCAGGCCCTC	TATTCTCGG	1920
	ACACAGCCCC	AGCCAGAGCC	ACCTTCTCCT	GATCAGCAAG	TCACCGGATC	CAACTCAGCA	1980
35	GGCCCTTCGG	GGCGGCTCTC	TAACCCACAG	TGCCCCAGGG	CCCTCCCTGA	GCCAGCCCCCT	2040
	GGCCAGTTG	ACGCGCTCAG	CATCTGCCCC	AGTACCAGCA	GTCTGTTCAA	CTTGCAAAAA	2100
	TCCAGCCTCT	CTGCCCGACA	CCCACAGAGG	AAAAGGCGGG	GGGGTCCCTC	CGAGCCCCACC	2160
	CCTGGCTCTC	GGCCCCAGGA	TGCAACTGTG	CACCCAGCTT	GCCAGATTTC	TCCCCATTAC	2220
	ACCCCCAGTG	TGGCATATCC	TTGGTCCCCA	GAGGCACACC	CCTTGATCTG	TGGACCTCCA	2280
40	GGCCTGGACA	AGAGGCTGCT	ACCAGAAACC	CCAGGCCCTC	GTTACTCAA	TTACAGCCA	2340
	GTGTGGTTGT	GCCTGACTCT	TCGCCAGCCC	CTGGAACCC	ATCCACCTGG	GGAGGGGCTC	2400
	TCTGAATGGA	GTTCTGACAC	CGCAGAGGGC	AGGCCATGCC	CTTATCCGCA	CTGCCAGGTG	2460
	CTGTGCGCCC	AGCCTGGCTC	AGAGGAGGAA	CTCGAGGAGC	TGTGTGAACA	GGCTGTGTGA	2520
	GATGTTTCAGG	CCTAGCTCCA	ACCAAGAGTG	TGCTCCAGAT	GTGTTTGGGC	CCTACCTGGC	2580
45	ACAGAGTCCT	GCTCCTGGGA	AAGGAAAGGA	CCACAGCAAA	CACCATTCTT	TTTGCCGTAC	2640
	TTCTTAGAAG	CACCTGGAAG	GGACTGGTGA	TGGTGGAGGG	TGAGAGGGTG	CCGTTTCCCTG	2700
	CTCCAGCTCC	AGACCTTGTC	TGCAGAAAC	ATCTGCAGTG	CAGCAATCC	ATGTCCAGCC	2760
	AGGCAACCCAG	CTGCTGCCCT	TGGCGTGTGT	GGGCTGGATC	CCTTGAAGGC	TGAGTTTTTG	2820
	AGGGCAGAAA	CTAGCTATG	GGTAGCCAGG	TGTTACAAAG	GTGCTGCTCC	TTCTCCAACC	2880
50	CCTACTTGGT	TTCCCTCACC	CCAAGCCTCA	TGTTTATACC	AGCCAGTGGG	TTGAGCAGAA	2940
	CGCATGACAC	CTTATCACCT	CCCTCCTTGG	GTGAGCTCTG	AACACCAAGT	TTGGCCCCCTC	3000
	CACAGTAAGG	CTGCTACATC	AGGGGCAACC	CTGGCTCTAT	CATTTTCTCT	TTTTGCCAAA	3060
	AGGACACAGTA	GCATAGGTGA	GCCTTGAGCA	CTAAAAGGAG	GGGTCCCTGA	AGCTTTCCCA	3120
	CTATAGTGTG	GAGTTTCTGT	CCTGAGGTGG	GTACAGCAGC	CTTGGTTCTT	CTGGGGGTTG	3180
55	AGAATAAGAA	TAGTGGGGAG	GGAAAACTC	CTCCTTGAAG	ATTCTCTGTC	TCAGAGTCCC	3240
	AGAGAGGTAG	AAAGGAGGAA	TTTCTGCTGG	ACTTTATCTG	GGCAGAGGAA	GGATGGAATG	3300
	AAAGGTAGAAA	AGGCAGAAAT	ACAGCTGAGC	GGGGACAACA	AAGAGTTCTT	CTCTGGGAAA	3360
	AGTTTTGTCT	TAGAGCAAGG	ATGGAAAATG	GGGACAACAA	AGGAAAAGCA	AAGTGTGACC	3420
	CTTGGGTTTG	CACAGCCCAG	AGGCCAGCT	CCCCAGTATA	AGCCATACAG	GCCAGGGACC	3480
60	CACAGGAGAG	TGGATTAGAG	CACAAGTCTG	GCCTCACTGA	GTGGACAAGA	GCTGATGGGC	3540
	CTCATCAGGG	TGACATTAC	CCCAGGGCAG	CCTGACCACT	CTTGGCCCCCT	CAGGCATTAT	3600
	CCCATTTGGA	ATGTGAATGT	GGTGGCAAG	TGGGCAGAGG	ACCCACCTGT	GGAACCTTTT	3660
	TCCTCAGTT	AGTGGGGAGA	CTAGCACCTA	GGTACCCACA	TGGGTATTTA	TATCTGAACC	3720
	AGACAGACGC	TTGAATCAGG	CACATGTGTA	AGAAATATAT	TTATTGTGCTA	ATATATTTAT	3780
65	CCACAAAAA	AAAAA	AA				3802

Seq ID NO: C29 Protein Sequence  
Protein Accession #: NP\_004280.2

70	1	11	21	31	41	51	
	MNSSAHYHVN	FSQAISQDVN	LHEAILLCPN	NTFRRDPTAR	TSQSQEPFLQ	LNSHTTNPEQ	60
	TLFPTNLTF	LSPVDNHRN	LTSQDLYDL	DINIFDEINL	MSLATEDNFD	PIDVSQFLDE	120
	PDSDSLGLD	SSHNNTSVIK	SNSSHVCDE	GAIGYCTDHE	SSSHHDLGA	VGGYYPEPSK	180
75	LCHLDQSDSD	PHGDLTFQHV	FNHNTYHLQP	TAPESTSEPF	PWPGKSQKIR	SRYLEDTDRN	240
	LSRDEQRAKA	LHPIFVSDEI	VGMPVDSFNS	MLSRYLYTDL	QVSLIRDIRR	RGKNKVAAGN	300
	CRKKRLDII	NLEDDVCNLQ	AKKETLKREQ	AQCNKAINIM	KQKLHDLYHD	IFSRLRDDQ	360
	RPVNPNIHAL	QCTHDGSLI	VPKELVASGH	KKETQKGRK			400

80 Seq ID NO: C30 DNA Sequence  
Nucleic Acid Accession #: NM\_004442  
Coding sequence: 19..2982

1 11 21 31 41 51

	GCCCCGGGAA	GCGCAGCCAT	GGCTCTGCGG	AGGCTGGGGG	CCGCGCTGCT	GCTGCTGCCG	60
	CTGCTCGCCG	CCGTGGAAGA	AACGCTAATG	GACTCCACTA	CAGCGACTGC	TGAGCTGGGG	120
5	TGGATGGTGC	ATCCTCCATC	AGGGTGGGAA	GAGGTGAGTG	GCTACGATGA	GAACATGAAC	180
	ACGATCCGCA	CGTACCAGGT	GTGCAACGTG	TTTGAGTCAA	GCCAGAACAA	CTGGCTACGG	240
	ACCAAGTTTA	TCCGGCGCCG	TGGCGCCAC	CGCATCCACG	TGGAGATGAA	GTTTTCGGTG	300
	CGTGACTGCA	GCAGCATCCC	CAGCGTGCCT	GGCTCCTGCA	AGGAGACCTT	CAACCTCTAT	360
	TACTATGAGG	CTGACTTTGA	CTCGGCCACC	AAGACCTTCC	CCAACCTGGAT	GGAGAATCCA	420
10	TGGGTGAAGG	TGGATACCAT	TGCAGCCGAC	GAGAGCTTCT	CCCAGGTGGA	CCTGGGTGGC	480
	CGCGTCATGA	AAATCAACAC	CGAGGTGCGG	AGCTTCGGAC	CTGTGTCCCG	CAGCGGCTTC	540
	TACCTGGCCT	TCCAGGACTA	TGGCGGCTGC	ATGTCCCTCA	TCGCCGTGCG	TGTCTTCTAC	600
	CGCAAGTGCC	CCCGCATCAT	CCAGAATGGC	GCCATCTTCC	AGGAAACCTT	GTCGGGGGCT	660
	GAGAGCACAT	CGCTGGTGGC	TGCCCGGGGC	AGCTGCATCG	CCAATGCGGA	AGAGGTGGAT	720
15	GTACCCATCA	AGCTCTACTG	TAACGGGGAC	GGCGAGTGGC	TGGTGCCCAT	CGGGCGCTGC	780
	ATGTGCAAG	CAGGCTTCGA	GGCCGTGAG	AATGGCACCG	TCTGCCGAGG	TTGTCCATCT	840
	GGGACTTTCA	AGGCCAACCA	AGGGGATGAG	GCCTGTACCC	ACTGTCCCAT	CAACAGCCGG	900
	ACCACTCTCT	AAGGGGCCAC	CAACTGTGTC	TGCCGCAATG	GCTACTACAG	AGCAGACCTG	960
	GACCCCTTGG	ACATGCCCTG	CACAACCATC	CCCTCCGCGC	CCCAGGCTGT	GATTTCCAGT	1020
20	GTCAATGAGA	CCTCCCTCAT	GCTGGAGTGG	ACCCCTCCCG	GCGACTCCCG	AGGCCGAGAG	1080
	GACCTCGTCT	ACAACATCAT	CTGCAAGAGC	TGTGGCTCGG	GCCGGGGTGC	CTGCACCCGC	1140
	TGCGGGGACA	ATGTACAGTA	CGCACCAAGC	CAGTAGGCC	TGACCGAGCC	ACGCAATTAC	1200
	ATCAGTGACC	TGCTGGCCCA	CACCCAGTAC	ACCTTCGAGA	TCCAGGCTGT	GAACGGCGTT	1260
	ACTGACAGCA	GCCCCCTTCT	GCCTCAGTTC	GCCTCTGTGA	ACATCACCAC	CAACCAAGGA	1320
25	GCTCCATCGG	CAGTGTCCAT	CATGCATCAG	GTGAGCCGCA	CCGTGGACAG	CATTACCCTG	1380
	TCGTGGTCCC	AGCCAGACCA	GCCCAATGGC	GTGATCCTGG	ACTATGAGCT	GCAGTACTAT	1440
	GAGAAGGAGC	TCAGTGAGTA	CAACGCCACA	GCCATAAAAA	GCCCCACCAA	CACGGTCACC	1500
	GTGAGGGGCC	TCAAAGCCGG	CGCCATCTAT	GTCTTCAGG	TGCGGGCAGC	CACCGTGGCA	1560
	GGGTACGGGG	GCTACAGCGG	CAAGATGTAC	TTCCAGACCA	TGACAGAAGC	CGAGTACCAG	1620
30	ACAAGCATCC	AGGAGAAGTT	GCCACTCATC	ATCGGCTCCT	CGGCCGTGG	CCTGGTCTTC	1680
	CTCATTGCTG	TGGTTGTCTAT	CGCCATCGTG	TGTAACAGAA	GACGGGGGTT	TGAGCGTGCT	1740
	GACTCGGAGT	ACACGGACAA	GCTGCAACAC	TACACCAAGT	GCCACATGAC	CCCAGGCAATG	1800
	AAGATCTACA	TCGATCCTTT	CACCTACGAG	GACCCCAACG	AGGCAGTGCG	GGAGTTTGCC	1860
	AAGGAAATTG	ACATCTCCTG	TGTCAAATTT	GAGCAGGTGA	TCCGAGCAGG	GGAGTTTGGC	1920
35	GAGGTCTGCA	TGCGCCACCT	GAAGCTGCCA	GGCAAGAGAG	AGATCTTTGT	GGCCATCAAG	1980
	ACGCTCAAGT	CGGGCTACAC	GGAGAAGCAG	CGCCGGGACT	TCTTGAGCGA	AGCCTCCATC	2040
	ATGGGCAGGT	TCGACCATCC	CAACGTATC	CACCTGGAGG	GTGTCGTGAC	CAAGAGCACA	2100
	CCTGTGATGA	TCTATCCCGA	GTTTATGGAG	AATGGCTCCC	TGGACTCCTT	TCTCCGGCAA	2160
	AACGATGGGC	AGTTTACAGT	CATCCAGCTG	GTGGGCATGC	TTCCGGGCAT	CGCAGCTGGC	2220
40	ATGAAGTACC	TGGCAGACAT	GAACATATGT	CACCGTGACC	TGGCTGCCCG	CAACATCCTC	2280
	GTCAACAGCA	CACTGGTCTG	CAAGGTGTGC	GACTTTGGGC	TCTCACGCTT	TCTAGAGGAC	2340
	GATACCTCAG	ACCCCACTTA	CACCAAGTGC	CTGGGCGGAA	AGATCCCCAT	CCGCTGGACA	2400
	GCCCCGAAG	CCATCCAGTA	CCGGAAGTTT	ACCTCGGCCA	GTGATGTGTG	GAGCTACGGC	2460
	ATTGTCTATG	GGGAGGTGAT	GTCTATGGG	GAGCGGGCCT	ACTGGGACAT	GACCAACCAG	2520
45	GATGTAATCA	ATGCCATTTGA	GCAGGACTAT	CGGCTGCCAC	CGCCCATGGA	CTGCCCGAGC	2580
	GCCCTGCACC	AACTCATGCT	GGACTGTTGG	CAGAAGGACC	GCAACCACCG	GCCCAAGTTC	2640
	GGCCAAATTG	TCAACAGGCT	AGACAAGATG	ATCCGCAATC	CCAACAGCCT	CAAAGCCATG	2700
	GCGCCCCCTCT	CCTCTGGCAT	CAACCTGCCG	CTGCTGGACC	GCAGATCCCC	CGACTACACC	2760
	AGCTTTAACA	AGGAAGGCTG	TGACTGTTCT	TGCGGGGGAT	AAAAAAGGGC	TGGGAGATT	2820
50	TTGCGCAATG	CCGGCTTACC	CTCCTTTGAC	GTCTGTCTCT	AGATGATGAT	GGAGGACATT	2880
	CTCCGGGTTG	GGCTCACTTT	GGCTGGCCAC	CAGAAAAAAA	TCCTGAACAG	TATCCAGGTG	2940
	ATGCGGGGCG	AGATGAACCA	GATTCACTCT	GTGGAGGTTT	GACATTCACC	TGCCCTCGGT	3000
	CACCTCTTCC	TCCAAGCCCC	GCCCCCTCTG	CCCCACGTGC	CGGCCCTCCT	GGTGCTCTAT	3060
	CCACTGCAGG	GCCAGCCACT	CGCCAGGAGG	CCACGGGCCA	CGGGAAGAAC	CAACGGGTGC	3120
55	CAGCCACGAG	ACGTACACCA	GAAAAACATG	AACTCAAACG	ACGGAAAAAA	AAAGGGAATG	3180
	GGAAAAAAGA	AAACAGATCC	TGGGAGGGGG	CGGGAAATAC	AAGGAATATT	TTTTAAAGAG	3240
	GATTCTCAT	AGGAAGGCTG	TGACTGTTCT	TGCGGGGGAT	AAAAAAGGGC	TGGGAGATT	3300
	CATGCGATGT	GTCCAATCGG	AGACAAAAGC	AGTTTCTCTC	CAACTCCCTC	TGGGAAGGTG	3360
	ACCTGGCCAG	AGCCAAGAAA	CACTTTCAGA	AAAACAATG	TGAAGGGGAG	AGACAGGGGC	3420
60	CGCCCTTGGC	TCTGTCTCCT	GCTGCTCCTC	TAGGCCTCAC	TCAACAACCA	AGCGCCTGGA	3480
	GGACGGGACA	GATGGACAGA	CAGCCACCCT	GAGAACCCCT	CTGGGAAAT	CTATTCTCTG	3540
	CACCACTGGG	CAACAGAGAG	AATTTTCTG	TCTTTGGAGA	GTATTTTAGA	AACTCCAATG	3600
	AAAGACACTG	TTTCTCCTGT	TGGCTACAG	GGCTGAAAGG	GGCTTTTGTC	CTCCTGGGTC	3660
	AGGAGAACG	CGGGGACCCC	AGAAAGGTCA	GCCTTCCTGA	GGATGGGCAA	CCCCAGGTCT	3720
65	GCAGCTCCAG	GTACATATCA	CGCGCACAGC	CTGGCAGCCT	GGCCCTCTCT	GTGCCCACTC	3780
	CCGCCAGCCC	CTGCTCCGAG	GACTGATACT	GCAGTGACTG	CCGTGAGCTC	CGACTGCCGC	3840
	TGAGAAGGGT	TGATCCTGCA	TCTGGGTTTG	TTTACAGCAA	TTCTTGGAAT	CGGGGGTATT	3900
	TTGGTACAG	GGTGGTTTGT	GTTTAGGGGG	TTTGTGTTGT	GGGTGTTTGT	TTGTTTTTTG	3960
	GTTTTTTTTA	ATGACAAATG	AGTGACACTT	TGACATTTC	TACCTTTTGA	GGACTTGATC	4020
70	CTTCTCCAGG	AAGAAGGTGC	TTTCTGCTTA	CTGACTTAGG	CAATACACCA	AGGGCGANAT	4080
	TTTATATGCA	CATTCTCTGA	TTTTTTTATA	CGGTTTTCAT	TGACACTCTT	CCCTCCTCCC	4140
	ACCTGCCACC	AGGCTCACCC	AAAGCCCACT	GCCATGGGGC	CATCTGGGCC	ATTTCAGAGC	4200
	TGGAGTGAGA	TTTGGGTGTG	GAGGGGGAGG	CGCCAAGGTG	GAGGAGCTTC	CCACTCCAGG	4260
	ACTGTTGATG	AAAGGGACAG	ATTGAGGAGG	AAGTGGGCTC	TGAGGCTGCA	GGGCTGGAAG	4320
75	TCCTTGCCCA	CTTCCCACTC	TCCTGCCCA	ATCTATCTAG	TACTTCCAG	GCAAAATAGG	4380
	CCCTTTGAGG	CTCCTGAGTG	CCCTCAGATG	GTCAAAACCC	AGTTTTCCTT	CTGGGAGCCT	4440
	AAACCAGGCT	GCATCGGAGG	CCAGGACCCG	GATCATTAC	TGTGATACCC	TGCCCTCCAG	4500
	AGGGTGGCCT	CAGAGACAG	GGCAAGCATG	CCTCTTCCCT	TCCCTGGAGA	GAAAGTGTGT	4560
	GATTTCTCTC	CCACTCTCTT	CCCCCACC	GACCTTGTCT	GGGCTAAAG	GTCTTGGCCA	4620
80	TGGGACGCG	CTCAGTCTAG	GGATCTGGCC	ACAGACTCCC	TCCTGTGAAC	CAACACAGAC	4680
	ACCCAAGCAG	AGCAATCAGT	TAGTGAATTG	GAATTCCTCA	AGTCTTTGCT	ATTGTGAATA	4740
	GTGCTGCAAT	AAACATACGT	GTGCAATGTG	CTTTATAGTA	GAATGATCTA	TAATCCTCTG	4800
	GGTATGTACC	CAGTAATGGG	ATTGCTGGGT	CAAAATGGTT	TTCTGGTTCT	AGATCCTTGA	4860
	GGAATTGCCA	CATGTCTTT	CACAATGGTT	GAACATAATT	ACACTCTCTAC	CAACAGTGTA	4920
	AAAGTCTTCC	TGTTTCTCCA	CATCTCTCCC	AGCATCTGTT	GTTTCTCTGAC	TTTTTAATGA	4980

TTGCCATTCT AACTGGTGTG AGATGGTATC TCATTGTGGG TTTGATTGTC ATTTCTCTAA 5040  
 TGACCAAGTGA AGATGAGCTT TTTTTCATAT GTTTGTGTGGC CACATGTTTG TGTGTTCTTT 5100  
 TGAGAAAGTGT CTGTTTCATAA CCTTCACCAA TTTTGTATGA GGTGTGTTGT TCTTTCTTG 5160  
 TAAACTTAAT GAAATAAAGC ATGAAGACAA GATTAGAAGA AAAAGAATGA AAAGGAACAA 5220  
 ACAAAGCGTC CAAGAAATAT GGGACTATGT GACAAGAACA AACTTACGTT TGACTGGTGT 5280  
 GCTGAAAATG ACAGGGAGAA TGAAACCAAG TTGGAACAA CTCTTCAGGA TATTATCCAG 5340  
 GAGAACTTCT CCAACCTAGC AAGACAGACC AACGTTCAAA TTCAGGAAAT ACAGAGAAAC 5400  
 CCCAAAGATA TTTCTCGAGA AGAGCAACCC GAAGACACAT AATTGTGAGA TTCACCAAGG 5460  
 TTGAAATGAA GGAATAAATG CTAAGGGCAG CCAGAGAGAA AGGTCAGGTT ACTCACAAC 5520  
 GGAAGCCCAT CAGACTAACA GCAGATCTCT CTGCAGAAAC CCTACAACCT AGAAGAGAGT 5580  
 GGGGACCAAT ATTCAACATT CACAAAGAAA AGAATTTTCA ATCCAGAAAT TCATATCCAG 5640  
 CCAAACCTAAG CTTCATAAGC AAAGGAGAAA TAAATCCTT TACAGACAAG CAAATCCTGG 5700  
 GAGATTTTGT CACCACCAGG CCTGCCCTTAC AAGACATCCT GAAGGAAGCA CTAAATATGG 5760  
 AAAAGAAAAA CTGGTGCCAG CCACTGCAAA AAATACCAAA TTGTAGAGAC CATTGACACT 5820  
 ATGAAGAAAC CGTGTCAACT AATGGGCAAA ATAACCAGCT AGTATCATAA TGACAGGATC 5880  
 AGATTACAC ATACACATAT TAACCTTATA TCTAAATGGG CTAAATCCCC CAATTAAAG 5940  
 ACGCAGACTG GCATAATTGGT TAAAGAGTCA AGACTCATTG GTGTGCCGTA TTCAGGAGAC 6000  
 CCATCTCACG TGCAAAGACA CACATAGGCT CAGAGTAAAA GGGATACAGG GGAATTC 6057

Seq ID NO: C31 DNA Sequence  
 Nucleic Acid Accession #: NM\_031942.1  
 Coding sequence: 145..1260

1 11 21 31 41 51  
 CCCGAGCCCC GCCCTCCCGG GCCCGGGTCG GCGCGCCCGC CTGCCCAGCC GCGCTGCTGC 60  
 TGCTCTCTCT GCTGTGGGAC CGCTGACCGC GCGGCTGCTC CGCTCTCCCC GCTCCAAGCG 120  
 CCGATCTGGG CACCCGCCAC CAGCATGGAC GCTCGCCGCG TGCCCGAGAA AGATCTCAGA 180  
 GTAAAGAGA ACTTAAAGAA ATTACAGATAT GTGAAGTTGA TTTCCATGGA AACCTCGTCA 240  
 TCCTCTGATG ACAGTTGTGA CAGCTTTGCT TCTGATAATT TTGCAAAAC GAGGCTGCAG 300  
 TCAGTTCCGG AAGGCTGTAG GACCCGAGC CAGTGCAGGC ACTCTGGACC TCTCAGGGTG 360  
 CGCATGAAGT TTCCAGCGCG GAGTACCAGG GGAGCAACCA ACAAAAAGC AGAGTCCCGC 420  
 CAGCCCTCAG AGAATTCTGT GACTGATTCC AACTCCGATT CAGAAGATGA AAGTGAATG 480  
 AATTTTTTGG AGAAAAGGGC TTTAAATATA AAGCAAAACA AAGCAATGCT TGCAAAACTC 540  
 ATGTCTGAAT TAGAAAGCTT CCTGGCTCG TCCGTTGGAA GACATCCCCC CCGAGGCTCC 600  
 GACTCACAAT CAAGGAGACC GCGAAGGCGT ACATTCGCCG GTGTTGCTTC CAGGAGAAAC 660  
 CCTGAACGGA GAGCTCGTCC TCTTACCAGG TCAAGGTCCC GGATCCTCGG GTCCCTTGAC 720  
 GCTCTACCCA TGGAGGAGGA GGAGGAAGAG GATAAGTACA TGTGTTGAG AAAGAGGAAG 780  
 ACCGTGGATG GCTACATGAA TGAAGATGAC CTGCCAGAA GCCGTGCTC CAGATCATCC 840  
 GTGACCCCTC CGCATATAAT TCGCCAGTG GAAGAAATTA CAGAGGAGGA GTTGAGAAC 900  
 GTCTGCAGCA ATTCTCGAGA GAAGATATAT AACCGTTCAC TGGGCTCTAC TTGTCTCAA 960  
 TGCCGTGAGA AGACTATTGA TACCAAAACA AACTGCAGAA ACCCAGACTG CTGGGCGGTT 1020  
 CGAGGCCAGT TCTGTGGGCC CTGCCCTCGA AACCGTTATG GTGAAGAGGT CAGGGATGCT 1080  
 CTGCTGGATC CGAAGTGGCA TTGCCCGCCT TGTGAGAGAA TCTGCACTG CAGTTTCTGC 1140  
 CGGCAGCGAG ATGGACGGTG TGGACTGGG GTCCTTGTGT ATTTAGCCAA ATATCATGGC 1200  
 TTTGGGAATG TGCATGCCTA CTTGAAAAGC CTGAAACAGG AATTTGAAAT GCAAGCATAA 1260  
 TATCTGGAAA ATTTGCTGCC TGCCCTTCTAC TTCTCAAATC TTTCTTGTA AAGTTTCCAA 1320  
 TTTTTCAT GAAACCTGAG TTAATAATCT TGATGATCAG CCGTGTTCAT AAGAAACTCC 1380  
 AATCAAGTTA ATCTTAGCAG ACATGTGTTT CTGGAGCATC ACAGAAGGTA TATTGCTAGT 1440  
 TACACTTGC CTFCTGCAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCCC 1500  
 TCTATTTCCA ATGCTCTCTT CCAACCGCTT AGTTTCTGAA TTTCTTTTAA ATTACAGTTT 1560  
 TATGAAAGCA TATTTTATTT ACTTGGTGT GAAATAGCCC TCATAAAACC TAAGCACTTG 1620  
 GAAACACAAT AATAGTATTA ACTAACTAGA TCTATTGAAT TTCAGAGAAG AGCCTTCTAA 1680  
 CTGTGTTACA CAAAACGAG TATGATTAG CACTCATACT AGTTGAAATT TTTAATAGAA 1740  
 TCAAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800  
 CTCTCAATCC CATGTATTGC GCTTATGTTA CAAGTTGTGT TCACAGTTGA GACTTAATTT 1860  
 CTCCTAATTT CTCTGCCCCG AAGGGTAAAG GGTGCGTCCA GCTTACACGA TCATAATTCA 1920  
 AAGGTTGGTG GGCATGTAA TACTTAATTA AAATAATGAT GGAAGAGCTA TCTGGAGATT 1980  
 ATGAGTAAGC TGATTTGAAT TTTCAGTATA AAACCTTAGT ATAATTGTAG TTTGCAAGT 2040  
 TTATTTCAAT TCACATGTAA GGTATTGCAA ATAAATCTT GGAACAATTT GTATGGAAC 2100  
 TTGATATTAA AAACATAGCT GTGGTTCTTT GCAGTTTCTT GTAAATTTAT AAACAGGCA 2160  
 CAAGGTTCAA GTTTAGATTT TAAGCACTTT TATAACATG ATAAGTGCCT TTTGGAGAT 2220  
 GTAACTTTTA GCAGTTTGTG AACCTGACAT CTCGCGCAGT CTAGTTTCTG GGCAGGTTTC 2280  
 CTGTGTCAAT ATCTCCCTC CTCTTTGCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT 2340  
 AAGTGTGTGT ATGTCCAATT TACTTGACAT TGTAAACCAT TGCTGTGCCA TTCATGTTT 2400  
 GATGCATAAT TGGACCTTGA ATCGATAAGT GTAATACAG CTTTGTATCT GTAATGCTTT 2460  
 TATACAAAAG TTTATTTTAA TAATAAATG TTTGTTCTAA AAAAAA 2510

Seq ID NO: C32 DNA Sequence  
 Nucleic Acid Accession #: NM\_012445.1  
 Coding sequence: 276..1271

1 11 21 31 41 51  
 GCACGAGGGA AGAGGGTGAT CCGACCCGGG GAAGGTCGCT GGGCAGGGCG AGTTGGGAAA 60  
 GCGGCAGCCC CCGCGGCCCC CGCAGCCCTT TCTCTCTCT TCTCCCAGT CCTATCTGCC 120  
 TCTCGCTGGA GGCAGGCGCG TGCAGCATCG AAGACAGGAG GAACTGGAGC CTCAATGGCC 180  
 GGCCCGGGGC GCGCGCTCG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG GGACCCGACC 240  
 GCTGCGGGCC GCGCTCCGCG TGCTCCTGCC GGGTGATGGA AAACCCAGC CCGGCCGCCG 300  
 CCCTGGGCAA GGCCTCTGCG GCTCTCTTCC TGGCCACTCT CGGCGCGGCC GGCAGCCTC 360  
 TTGGGGGAGA GTCCATCTGT TCCGCCAGAG CCCCGGCCAA ATACAGCATC ACCTTACAGG 420  
 GCAAGTGGAG CCAAGCGGCC TTCCCAAGC AGTACCCCTT GTTCCGCCCC CCGCGCAGT 480  
 GGTCTTCGCT GCTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACAGT 540  
 ACGTCAGTAA CGGGCTGCGC GACTTTGCGG AGCGCGGCGA GGCCTGGGCG CTGATGAAGG 600



5  
10  
15  
20

```

AGATCGAGGC GCGGGGGGAG GCGCTGCAGA GCGTGCACGC GGTGTTTTCG GCGCCCGCCG 660
TCCCCAGCGG CACCGGGCAG ACCTCGGCGG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG 720
TCTCGTTTGT GTGCGGCATC GTGCCAGGCC CCGACTGGTT CGTGGGCGTG GACAGCCTGG 780
ACCTGTGCGA CCGGGACCGT TGGCGGGAAC AGGCGGCGCT GGACCTGTAC CCTACGACG 840
CGGGACGGGA CAGCGGCTTC ACCTTCTCCT CCCCCAATT CGCCACCATC CCGCAGGACA 900
CGGTGACCGA GATAACGTCC TCCTCTCCCA GCCACCCGGC CAACTCCTTC TACTACCCGC 960
GGCTGAAGGC CCTGCCTCCC ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA 1020
GGGCCTTCAT CCCTCCCGCC CCAGTCTCTG CCAGCAGGGA CAATGAGATT GTAGACAGCG 1080
CCTCAGTTCC AGAAACGCCG CTGGACTGCG AGGTCTCCCT GTGGTCGTCC TGGGGACTGT 1140
GCGGAGGCCA CTGTGGGAGG CTCGGGACCA AGAGCAGGAC TCGCTACGTC CCGGTCCAGC 1200
CCGCCAACAA CCGGAGCCCC TGCCCCGAGC TCGAAGAAGA GGCTGAGTGC GTCCTGATA 1260
ACTGCGTCTA AGACCAGAGC CCGCAGCCCC CTGGGGCCCC CGGAGCCATG GGGTGTGCGG 1320
GGCTCCTGTG CAGGCTCATG CTGCAGGCGG CCGAGGCACA GGGGGTTTCG CGCTGCTCCT 1380
GACCGCGGTG AGGCCGCGCC GACCATCTCT GCACTGAAGG GCCCTCTGGT GCGCGGCACG 1440
GGCATTGGGA AACAGCCTCC TCCTTTCCCA ACCTTGCTTC TTAGGGGCCC CCGTGTCCCG 1500
TCTGCTCTCA GCCCTCCTCT CCTGCAGGAT AAAGTCATCC CCAAGGCTCC AGCTACTCTA 1560
AATTATGGTC TCCTTATAAG TTATTGCTGC TCCAGGAGAT TGTCTTCAT CGTCCAGGGG 1620
CCTGGCTCCC ACCTGGTTGC AGATACCTCA GACCTGGTGC TCTAGGCTGT GCTGAGCCCC 1680
CTCTCCCGAG GCGCATCCCA AGCGGGGGCC ACTTGAGAAG TGAATAAATG GGGCGGTTTC 1740
GGAAGCGTCA GTGTTTCCAT GTTATGGATC TCTCTGCGTT TGAATAAAGA CTATCTCTGT 1800
TGCTCAC 1807

```

Seq ID NO: C33 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1314

25  
30  
35  
40  
45  
50

```

1 11 21 31 41 51
| | | | |
ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA 120
CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCAGTGGCAG TCCGCCCTCT CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
GGGAACCTGG TCTCTGCTTG TTTGACAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGAGAGATTG CCAGAGCCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACTCAAGT 540
GGGCCCTGTC TCTCAGGCTC CTGGTCTCC CTGCACTGTC TTGCTGTGG GAAAGAGCTG 600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATCTTGGGCC TTGGCAGGTC 660
AGCATCCAGT ACACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
CTCAGCGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
TTCAACCCCA TGTAACCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
ACTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATACTGC TGCAAGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAAGCAT 1080
GCGTACCAGG GGAAGTACAC CGAGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGCTGGA AGGCTGAGCT GTAA 1314

```

Seq ID NO: C34 DNA Sequence

Nucleic Acid Accession #: NM\_003045.1

Coding sequence: 148..2037

55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
CGATCCTGCC GGAGCCCCGC CGCCGCCGGC TTGGATTCTG AAACCTTCCT TGTATCCCTC 60
CTGAGACATC TTTGCTGCAA GATCGAGGCT GTCTCTGGT GAGAAGGTGG TGAGGCTTCC 120
CGTCATATTC CAGCTCTGAA CAGCAACATG GGGTGCAAAG TCTGTCTCAA CATTGGGCAG 180
CAGATGCTGC GCGGGAAGGT GGTGGACTGT AGCCGGGAGG AGACGCGGCT GTCTCGCTGC 240
CTGAACACTT TTGATCTGGT GGCCTCGGG GTGGGCAGCA CACTGGGTGC TGGTGTCTAC 300
GTCTGGCTG GAGCTGTGGC CCGTGAGAA GCAGGCCCTG CCATTGTCTA CTCTTCCCTG 360
ATCGCTGCGC TGGCCTCAGT GCTGGCTGGC CTGTGCTATG GCGAGTTTGG TGCTCGGGTC 420
CCCAAGAGCG GCTCAGCTTA CCTCTACAGC TATGTACCCG TTGGAGAGCT CTGGGCCCTT 480
ATCACCGGCT GGAACCTAAT CCTCTCTAC ATCATCGGTA CTTCAAGCGT AGCGAGGGCC 540
TGGAGCGCCA CCTTCGACGA GCTGATAGGC AGACCCATCG GGGAGTTCTC ACGGACACAC 600
ATGACTCTGA ACGCCCCCGG CGTGCTGGCT GAAAACCCCG ACATATTGCG AGTGATCATA 660
ATTCTCATCT TGACAGGACT TTTAACTCTT GGTGTGAAAG AGTCGGCCAT GGTCAACAAA 720
ATATTCACTT GTATTAACTG CCTGGTCTGT GGTTCATAA TGGTGTGAGG ATTTGTGAAA 780
GGATCGGTGA AATCTGGCA GCTCACGGAG GAGGATTTTG GGAACATAC AGCCCGTCTC 840
TGTTTGAACA ATGACACAAA AGAAGGGAAG CCCGGTGTG GTGGATTCTA GCCCTTCGGG 900
TTCTCTGGTG TCTGTGCGG GGCAGCGACT TGCTTCTATG CCTTCGTGGG CTTTGACTGC 960
ATCGCCACCA CAGGTGAAGA GTGAAGAAG CCACAGAAGG CCATCCCCGT GGGGATCGTG 1020
GCGTCCCTCT TGATCTGCTT CATCGCTTAC TTTGGGTGT GCGCTGCCCT CACGCTCATG 1080
ATGCCCTACT TCTGCCTGGA CAATAACAGC CCCCTGCCCG ACGCCTTTAA GCACGTGGGC 1140
TGGGAAGGTG CCAAGTACGC AGTGGCCGTG GGCTCCCTCT GCGCTCTTTC CGCCAGTCTT 1200
CTAGGTTCCA TGTTTCCCAT GCCTCGGGTT ATCTATGCCA TGGCTGAGGA TGGACTGCTA 1260
TTTAAATTCT TAGCCAACGT CAATGATAGG ACCAAAACAC CAATAATCGC CACTTAGGCC 1320
TCGGGTGCCG TTGTGTCTGT GATGGCCTTC CTCTTTGACC TGAAGGACTT GGTGGACCTC 1380
ATGTCCATTG GCACTCTCTT GGCTTACTCG TTGGTGGCTG CCTGTGTGTT GGTCTTACCG 1440
TACCAGCCAG AGCAGCCTAA CCTGGTATAC CAGATGGCCA GTACTTCCGA CGAGTTAGAT 1500
CCAGCAGACC AAAATGAATT GGCAAGCACC AATGATTCCC AGCTGGGGTT TTTACCAGAG 1560
GCAGAGATGT TCTCTTTGAA AACCATACTC TCACCCAAAA ACATGGAGCC TTCCAAAATC 1620

```

TCTGGGCTAA TTGTGAACAT TTCAACCAGC CTTATAGCTG TTCTCATCAT CACCTTCTGC 1680  
 ATTGTGACCG TGCTTGGAAG GGAGGGCTCTC ACCAAGGGGG CGCTGTGGGC AGTCTTTCTG 1740  
 CTCGCAGGGT CTGCCCTCCT CTGTGCCGTG GTACAGGGCG TCATCTGGAG GCAGCCCGAG 1800  
 AGCAAGACCA AGCTCTCATT TAAGGTTCCT TTCTGCCAG TGCTCCCAT CCTGAGCATC 1860  
 TCGTGAACG TCTATCTCAT GATGCAGCTG GACCAGGGCA CCTGGGTCCG GTTTGCTGTG 1920  
 TGGATGCTGA TAGGCTTCAT CATCTACTTT GGCTATGGCC TGTGGCACAG CGAGGAGGCG 1980  
 TCCTTGATG CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCAAGT CAAGTGACGC 2040  
 ACAGCCCCG CCCCCGGAGG TGGCAGCAGC CCGAGGGGAC GCCCCAGAG GACCGGAGG 2100  
 CACCCACCC TCCCCACCAG TGCAACAGAA ACCACCTGCG TCCACACCCT CACTGCA 2157

Seq ID NO: C35 DNA Sequence  
 Nucleic Acid Accession #: NM\_002776.1  
 Coding sequence: 82..912

1 11 21 31 41 51  
 | | | | | |  
 ACCAGCGGCA GACCACAGGC AGGGCAGAGG CACGTCTGGG TCCCTCCCT CCTTCCTATC 60  
 GGCGACTCCC AGATCTTGGC CATGAGAGCT CCGCACCTCC ACCTCTCCGC CGCCTCTGGC 120  
 GCGCGGGCTT TGGCGAAGCT GCTGCCGTG CTGATGGCG AACTCTGGGC CGCAGAGGCG 180  
 GCGCTGCTCC CCCAAACGA CACGCGCTTG GACCCCGAAG CCTATGGCGC CCCGTGCGCG 240  
 CGCGGCTCGC AGCCCTGGCA GGTCTGCTC TTCAACGGCC TCTCGTTCCA CTGCGCGGGT 300  
 GTCTGGTGG ACCAGAGTTG GGTGCTGACG GCGCGCACT GCGGAAACAA GCCACTGTGG 360  
 GCTCGAGTAG GGGATGATCA CCTGCTGCTT CTTACGGGCG AGCAGCTCCG CCGGACGACT 420  
 CGCTCTGTTG TCCATCCCAA GTACCAACAG GGCTCAGGCC CCATCCTGCC AAGGCGAAGC 480  
 GATGAGCAGC ATCTCATGTT GCTAAAGCTG GCCAGGCGCG TAGTGCGGGG GCCCGCGCTC 540  
 CGGCGCCTGC AGCTTCCCTA CCGCTGTGCT CAGCCCGGAG ACCAGTGCCA GGTGCTGGC 600  
 TGGGCGACCA CGGCCCGCGG GAGAGTGAAG TACAACAAGG GCCTGACCTG CTCCAGCATC 660  
 ACTATCTCTG GCCTTAAAGA GTGTGAGGTC TTCTACCCCT GCGTGGTCAC CAACAACATG 720  
 ATATGTGCTG GACTGGACCG GGGCCAGGAC CCTTGCCAGA GTGACTCTGG AGGCCCCCTG 780  
 GTCTGTGACG AGACCTCCA AGGCATCCTC TCGTGGGGTG TTTACCCCTG TGGCTCTGCC 840  
 CAGCATCCAG CTGTCTACAC CCAGATCTGC AAATACATGT CCTGGATCAA TAAAGTCATA 900  
 CGCTCCAACG GATCCAGATG CTACGCTCCA GCTGATCCAG ATGTTATGCT CCGTCTGATC 960  
 CAGATGCCCA GAGGCTCCAT CGTCCATCCT CTTCTCCCTC AGTCGGCTGA ACTCTCCCT 1020  
 TGTCTGCACT GTTCAAACCT CTGCCGCCCT CCACACCTCT AAACATCTCC CCTCTCACCT 1080  
 CATTCCCCCA CCTATCCCCA TTCTCTGCCT GTACTGAAGC TGAATGCGAG GAAGTGGTGG 1140  
 CAAAGGTTTA TTCCAGAGAA GCCAGGAAGC CGGTATCAC CCAAGCTCTG AGAGCAGTTA 1200  
 CTGGGGTCAC CCAACCTGAC TTCTCTGCC ACTCCCGCT GTGTGACTTT GGGCAAGCCA 1260  
 AGTGCCCTCT CTGAACCTCA GTTTCCTCAT CTGCAAAATG GGAACAATGA CGTGCCTACC 1320  
 TCTTAGACAT GTTGTGAGGA GACTATGATA TAACATGTGT ATGTAAATCT TCATGTGATT 1380  
 GTCATGTAAG GCTTAACACA GTGGGTGGTG AGTTCTGACT AAAGGTTACC TGTGTGCTG 1440  
 AAAAAAAAAA AAAA 1454

Seq ID NO: C36 DNA Sequence  
 Nucleic Acid Accession #: XM\_095088  
 Coding sequence: 1..4074

1 11 21 31 41 51  
 | | | | | |  
 ATGACCCGGG CCGCGACAGC CGAGCCGGGC CGCGTGTCTC CCGCTCGCC CGCGCGCAGC 60  
 ACGGCGGGCC TCGCGCGCGC CTTCTGCGAG AGCCTGCGCA CCTGTGTAGA CATCTGGAC 120  
 GACTGGCAGC GCGGCTGCGT GCACCTGCGA GAGATCCAGT CCTCTGCGG CGAAGCGCGG 180  
 GAGCTGCCAA GCGGGGTGCT GGAGGGCCTG AGCCAGCGGC GCGGGCCGCA GCCGGGAGCA 240  
 GCTGTACGCT CCCGCCGAGG CGGCGCAGTG CCGCGCGGGG CCGGAGCGGT TCCAGAGCGC 300  
 TGGCTGGGAA CGGAGACCCG GCGCGGACGC AGGTGCAGCG GCCTGCAGCG CCTTGGAGGC 360  
 GGATTCAGGG GATGCCCGGC GGACCCCTGT GCCCGAGGGG AACACCCGAG GCACACCATC 420  
 ACCAGCGGCG TGGACTGCGG CCTGCTGAAG CAGATGAAGG AGCTGGAGCA GGAGAAGGAG 480  
 GTGCTGTAC AGGGTTTGA GATGATGGCG CAGGGCCGCG ATTTGGTACCA GCAGCAGCTG 540  
 CAACAAGTGC AGGAGCGCCA GTGCGCCCTG GGCCAGAGCA GAGCCAGCGC CGACTTTGGG 600  
 GCCGTGGGGA GCCCTCGCCC ACTGGGACGG CTACTGCCCA AGGTACAGGA GGTGGCCCGG 660  
 TGGCTGGGGG AGCTGTGGC TGAGGCTGTG GCCGTGCGG CCTGCCCCAC ATCTCTCTCC 720  
 GGGCCCCCTT GCTCTGCCCT GACGTCCACC TCGTCCCGCG GCTGGCAGCA GCAGATCATC 780  
 CTCATGTGTA AGGAGCAGAA CCGACTCCTC ACCCAGGAGG TGACCGAGAA GAGTGAGCGC 840  
 ATCAGCAGC TGGAGCAGAA GTCGCGCTC ATTAAGCAGC TATTTGAGGC CCGCGCCCTG 900  
 AGCCAGCAGG ATGGGGGCTT GTCCCGGCTT GGCCCCACA TTGAGCCCTT GACTCGGTTT 960  
 CGGCTTCCGG TGCTGACATG GGTGGGGCT CTCTTGAGTC CGCATAGTCC GCAGCTACTA 1020  
 CTGCCGCTGT CAGCGGACAG TGGGGGACCC CTCACGAGT TACCAGATAC CTGGTTTCCA 1080  
 GCGGTGTGTC TTTGGGTCCC ATCTCCAGGG AAAAGAACTG CTCACGCCAG GCTGCACTTC 1140  
 CACCAAGGC CAGCAGAGGG CGCGTGGCAG CTCGGATGCG GCGCTGAGGC TGCGCCCGAG 1200  
 ACCTGCGGGA CGCTGCCCCA CTTTGTAGT CACAAAAACA CCTGTGAGCC TGACTCCCTC 1260  
 GGAGGGCCCT GTCCCCAGGA GGGGGATCGC AGCTGGAGCC ACCTGGGCGC AGCGTTTGAT 1320  
 GTGGCACCTG CAGTGGCCAA AGTGACCCC AACCGTGAGG ACGCTGCAGG GAGTGGGCAC 1380  
 GGAGACATCT GTCCCTCTG TCCCAAGGGA CTGTTGACAT TCAGAGACAT AGCTATAGAA 1440  
 TTCTCTCTGG CGGAGTGGCA ATGCTTGAT CATGCTCAGC AGAATTTATA TAGAGATGTG 1500  
 ATGTTAGAGA ACTACAGAAA CCTGTTCTCC CTGGGTATGA CTGTCTCTAA GCCAGACTTG 1560  
 ATCGCCTGTC TGGAGCAAAA TAAAGAGCCC CAGAATATAA AGAGAAATGA GATGGCAGCC 1620  
 AAACACCCAG TTACATGTTT TCATTTCAAC CAAGACCTTC AGCCAGAGCA GAGCATAAAA 1680  
 GATTCACTCC AAAAAGTAAT ACCAAGAACA TATGGAATAT GTGGACATGA GAATTTACAA 1740  
 TTAATAAAT GTTTGTAAGG AGTAGATGAG TGTGAGGTGC ACAGAGGAGG TTATAATGAC 1800  
 CTTAACCAAT GTTTGTCAA TACCCAAAC AAAATATTTC AGACTCATAA ATGTGTCAA 1860  
 GTCTTCAGTA AATTTTCAAA TTCCAATAGA CACAATGCAA GATATACTGG AAAGAAACAT 1920  
 TTGAAATGTA AAAAATATGG CAAATCATTT TGCAATGTTT CACACCTAAA TCAACATCAG 1980  
 ATAATTCATA CTAAGGAGAA GTCCTACAAA TGTGAAGAA GTGGCAATAT CTTTAACAC 2040  
 TCCTCAAGCG GTACTACACA TAAAGAAATT CTTACTGGAG AGAAACCCTA CAGATGTGAG 2100  
 GAATGTGGCA AAGCCTTTAG GTGGCCCTCA AACCTTACTA GACATAAGAG AATTCACT 2160

GGAGAGAAAC CCTACGCATG TGAAGATGT GGCCAAGCCT TTAGGCGCTC CTCAACACTT 2220  
 ACTAACCACA AGAGAATTCA TACTGGAGAG AGACCCTACA AATGTGAAGA ATGTGGCAAA 2280  
 GCCTTTAGCG TATCCTCAGC CCTCATTTAC CACAAGAGAA TTCATACTGG AGAGAAACCC 2340  
 5 TACACATGTG AAGAATGTGG CAAAGCCTTT AACTGCTCCT CGACTCTTAA GACACATAAG 2400  
 ATAATTCATA CTGGAGAGAA ACCCTACACA TGTGAAGAAT GTGGCAGAAC CTTTAACTGC 2460  
 TCCTCAACTG TAAAGGCACA TAAGAGAATT CATACTGGAG AGAAACCATA CAAATGTGAA 2520  
 GAATGTGACA AAGCTTTTAA GTGGCATTCA AGTCTTGCTA AACATAAGAT AATTACACACT 2580  
 GGAGAGAAAC CCTACAAATG CAGTGACAGC AAAGCCTTAG CCAAAATCAT AGAAGTGCAA 2640  
 10 AAGGTCTACT CTGGAGATGG GGAATAATGGA ATCCGTGTAC ATAAGAAAAA GGAGACACAG 2700  
 GGCTGGCTTG TGAGAAACAA GAACGAAAAT AGAACAGGGC TGTTCAGAT CCGGGCTGCC 2760  
 GTGAGACCTA ACAGGGACCC TTCATGGGGA CAGCAAGAAG GTTCACTGAC TGACCCAATT 2820  
 CAGAGGAAGG AGGAACCTGA CCTTCAAAAT CACTATGACC ATCAGAATGC CTTAGAAGAT 2880  
 CAAAGAAATA CTGGAGTGGG TGGACTGTTG ACATTACAGAG ATGTAGTCAT AGAATTCTCT 2940  
 15 CTGGAGGAGT GGCAATGCCT GGATCACGCT CAGCAGAAAT TATATAGAGA TGTGATGTTA 3000  
 GAGAACTACA GAAACCTGGT CTCCTGGGT ATTGCTGTCT CTAAGCCAGA CTTGATCACC 3060  
 TGTCTGGAGC AAAATAAAGA GCCTTGAAT ATAAAGAGAA ATGAGATGGT AACCAAACAC 3120  
 CCAGACCTTC CGCCAGAGCT AGGCATAAAA GATTCACTCC AAAAGTAAT ACCAAGAAGA 3180  
 TATGGAAAAA TGGGACATGA CAATTTACAA GTAAAAACAT GTAAAAGCAT GGGTGAGTGT 3240  
 20 GAGGTGCAAA AAGGAGGTTG TAATGAAGTT AACCAATGTT TGTCAACTAC CCAAAACAAA 3300  
 ATATTTTACA CTCATAAATG TGTCAAAGTC TTCGGCAAAT TTTCAAAATC CAATAGACAT 3360  
 AAGACAAGAC ATACTGGAAG GAAACATTTT AAATGTAAAA AATATGGCAA ATCATTTTGC 3420  
 ATGGTTTTCAC AACTACATCA ACATCAGATA ATTCATACTA GGGAGAATTG CTACCAATGT 3480  
 GAAGAAATGCG GCAAAACCTT CAACTGCTCT TCAACCTTTT CTAAACATAA AAGAATTCAT 3540  
 25 ACTGGAGAGA AACCTTACAG ATGTGAGGAA TGTGGCAAAG CTTTTACCTG GTCCTCAACC 3600  
 CTTACTAAAC ATAGGGAAT TCATACCTGGA GAAAAACCCT ACACATGTGA AGAATGTGGC 3660  
 CAAGCCTTTA GCGCTCTCTC AACACTTGCT AACCAACAAG GAATTCATAC TGGAGAGAAA 3720  
 CCATACACAT GTGAAGAATG TGGCAAAGCC TTAGCTTAT CCTCATCCCT CACTTACCAC 3780  
 AAGAGAATTC ATACTGGAGA GAAACCTTAC ACATGTGAAG AATGTGGCAA AGCCTTTAAC 3840  
 30 TGCTCCTCAA CCCTTAAGAA ACATAAGATA ATTCACTAGT GAGAGAAACC CTACAAATGT 3900  
 AAAGAATGTG GGAAGGCCCT TGCCCTTCTCC TCAACTCTTA ATACTCATAA GAGGATTCAT 3960  
 ACTGGAGAGG AACCTTACAA ATGTGAAGAA TGTGACAAAG CTTTAAAGTG GTCCTCAAGT 4020  
 CTTGCTAATC ATAAGAGTAT GCATACTGGA GAGAAACCCT ACAAATGTGA ATAA 4074

Seq ID NO: C37 DNA Sequence  
 Nucleic Acid Accession #: NM\_032044  
 Coding sequence: 182..658

1 11 21 31 41 51  
 40 AAGATATAAA AGCTCCAGAA ACGTTGACTG GGACCACTGG AGACACTGAA GAAGGCAGGG 60  
 GCCCTTAGAG TCTTGGTTGC CAAACAGATT TGCAGATCAA GGAGAACCCA GGAGTTTCAA 120  
 AGAAGCGCTA GTAAGGTCTC TGAGATCCTT GCACTAGCTA CATCCTCAGG GTAGGAGGAA 180  
 GATGGCTTCC AGAAGCATGC GGCTGCTCCT ATTGCTGAGC TGCCCTGGCA AAACAGGAGT 240  
 45 CCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCCTGGA TGGTTTTACC ACAAGTCCAA 300  
 TTGCTATGGT TACTTCAGGA AGCTGAGGAA CTGGTCTGAT GCCGAGCTCG AGTGTCACTC 360  
 TTACGGAAC GGAGCCACCC TGGCATCTAT CCTGAGTTTA AAGGAAGCCA GCACCATAGC 420  
 AGAGTACATA AGTGGCTATC AGAGAAGCCA GCCGATATGG ATTGGCCTGC ACGACCCACA 480  
 GAAGAGGAG CAGTGGCAGT GGATTGATGG GGCCATGTAT CTGTACAGAT CCTGGTCTGG 540  
 50 CAAGTCCATG GGTGGGAACA AGCACTGTGC TGAGATGAGC TCCAATAACA ACTTTTTAAC 600  
 TTGGAGCAGC AACGAATGCA ACAAGCGCCA ACACCTCCTG TGCAAGTACC GACCATAGAG 660  
 CAAGAATCAA GATTCTGCTA ACTCCTGCAC AGCCCCGTCC TCTTCTTTTC TGCTAGCCTG 720  
 GCTAAATCTG CTCATTATTT CAGAGGGGAA ACCTAGCAAA CTAAGAGTGA TAAGGGCCCT 780  
 ACTACACTGG CTTTTTTAGG CTTAGAGACA GAAACTTTAG CATTGGCCCA GTAGTGGCTT 840  
 55 CTAGCTCTAA ATGTTTGGCC CGCCATCCCT TTCCACAGTA TCCTTCTTCC CTCTCCCTCT 900  
 GTCTCTGGCT GTCTCGAGCA GTCTAGAAGA GTGCATCTCC AGCCTATGAA ACAGCTGGGT 960  
 CTTTGGCCAT AAGAAGTAAA GATTTGAAGA CAGAAGGAAG AAACCTCAGGA GTAAGCTTCT 1020  
 AGACCCCTTC AGCTTCTACA CCCTTCTGCC CTCTCTCCAT TGCCCTGCACC CCACCCACGC 1080  
 60 CACTCAACTC CTGCTTGTCT TTCTTTTGGC CATAGGAAGG TTTACAGTA GAATCCTTGC 1140  
 TAGGTTGATG TGGGCCATAC ATTCTTTTAA TAAACCATG TGTACATAAG AAAAAAAAAA 1200

Seq ID NO: C38 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 52..3042

1 11 21 31 41 51  
 65 GCTCACCAG GAAAAATATG CAATCGTCCC ATTGATATAC AGGCCACTAC AATGGATGGA 60  
 GTTAACCTCA GCACCGAGGT TGTCTACAAA AAAGGCCAGG ATTATAGGTT TGCTTGCTAC 120  
 70 GACCGGGGCA GAGCCTGCCG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180  
 CCCAACTCA CAGTCACCAT TGACACCAAT GTGAACAGCA CCATCTGTAA CTTGGAGGAT 240  
 AATGTACAGT CATGGAACCC TGGAGATACC CTGGTCAATG CCAGTACTGA TTAATCCATG 300  
 TACCAGGCAG AAGAGTTCCA GGTGCTTCCC TGCAGATCCT GCGCCCCCAA CCAGGTCAAA 360  
 GTGGCAGGGA AACCAATGTA CCTGCACATC GGGGAGGAGA TAGACGGCGT GGACATGCGG 420  
 75 GCGGAGGTTG GGCTTCTGAG CCGGAACATC ATAGTGATGG GGGAGATGGA GGACAAATGC 480  
 TACCCTTACA GAAACACAT CTGCAATTTT TTTGACTTCG ATACCTTTGG GGGCCACATC 540  
 AAGTTTGTCT TGGGATTTAA GGCAGCACAC TTGGAGGGCA CGGAGCTGAA GCATATGGGA 600  
 CAGCAGCTGG TGGTCACTA CCCGATTAC TCCACCTGG CCGGTGATGT AGACGAAAGG 660  
 GGAGGTTATG ACCCACCCAC ATACATCAGG GACCTCTCCA TCCATCATAC ATTCTCTCGC 720  
 80 TGCGTACAG TCCATGGCTC CAATGGCTTG TTGATCAAGG ACGTTGTGGG CTATAACTCT 780  
 TTGGGCCACT GCTTCTTAC GGAAGATGGG CCGGAGGAAC GCAACACTTT TGACCACCTG 840  
 CTTGGCCTCC TTGTCAAGTC TGGAACCTTC CTCCCTCGG ACCGTGACAG CAAGATGTGC 900  
 AAGATGATCA CAGGAGACTC CTACCCAGGG TACATCCCCA AGCCCCAGGA AGACTGCAAT 960  
 GCTGTGTCCA CCTTCTGGAT GGCCAAATCC AACACAACC TCATCAACTG TGCCGCTGCA 1020  
 GGATCTGAGG AAACCTGGATT TTGTTTTATT TTTACCACG TACCAACGGG CCCCTCGTGC 1080

	GGAATGTACT	CCCCAGGTTA	TTCAGAGCAC	ATTCCACTGG	GAAAATTCTA	TAACAACCGA	1140
	GCACATTCCA	ACTACCGGGC	TGGCATGATC	ATAGACAACG	GAGTCAAAAC	CACCGAGGCC	1200
	TCTGCCAAGG	ACAAGCGGCC	GTTCTCTCTA	ATCATCTCTG	CCAGATACAG	CCCTCACCAG	1260
5	GACGCCGACC	CGCTGAAGCC	CCGGGAGCCG	GCCATCATCA	GACACTTCAT	TGCCTACAAG	1320
	AACCGAGACC	ACGGGGCCTG	GCTGCGCGGC	GGGGATGTGT	GGCTGGACAG	CTGCCGTTTT	1380
	GCTGACAATG	GCATTGGCCT	GACCTTGGCC	AGTGGTGGAA	CCTTCCCCTA	TGACGACGGC	1440
	TCCAAGCAAG	AGATAAAGAA	CAGCTTGTTC	GTTGGCGAGA	GTGGCAACGT	GGGGACGGAA	1500
	ATGATGGACA	ATAGGATCTG	GGGCCCTGGC	GGCTTGGACC	ATAGCGGAAG	GACCCCTCCT	1560
10	ATAGGCGAGA	ATTTTCCAAT	TAGAGGAATT	CAGTTATATG	ATGGCCCCAT	CAACATCCAA	1620
	AACTGCACTT	TCCGAAGTTT	TGTGGCCCTG	GAGGGCCGGC	ACACCAGCGC	CCTGGCCTTC	1680
	CGCCTGAATA	ATGCCCTGGCA	GAGCTGCCCC	CATAACAACG	TGACCGGCAT	TGCCTTTGAG	1740
	GACGTTCCGA	TTACTTCCAG	AGTGTCTTTC	GGAGAGCCTG	GGCCCTGGTT	CAACCAGCTG	1800
	GACATGGATG	GGGATAAGAC	ATCTGTGTTC	CATGACGTCG	ACGGCTCCGT	GTCGAGTAC	1860
15	CCTGGCTCCT	ACCTCACGAA	GAATGACAAC	TGGCTGTGTC	GGCACCAGCA	CTGCATCAAT	1920
	GTTCCCGACT	GGAGAGGGGC	CATTTGCACT	GGGTGCTATG	CACAGATGTA	CATTCAAGCC	1980
	TACAAGACCA	GTAACTTCGC	AATGAAGATC	ATCAAGAATG	ACTTCCCCAG	CCACCTCTTT	2040
	TACCTGGAGG	GGGCGCTCAC	CAGGAGCACC	CATTACCAGC	AATACCAACC	GGTTGTCAAC	2100
	CTGCAGAAGG	GCTACACCAT	CCACTGGGAC	CAGACGGCCC	CCGCCGAATC	CGCCATCTGG	2160
20	CTCATCAACT	TCAACAAGGG	CGACTGGATC	CGAGTGGGGC	TCTGCTACCC	GCGAGGCACC	2220
	ACATTCTCCA	TCCTCTCGGA	TGTTCACAAT	CGCCTGTCTA	AGCAAAACGTC	CAAGACGGGC	2280
	GTCTTCTGTA	GGACCTTGCA	GATGGACAAA	GTGGAGCAGA	GCTACCTTGG	CAGGAGCCAC	2340
	TACTACTGGG	ACGAGGACTC	AGGGCTGTTG	TTCCTGAAGC	TGAAGCTCA	GAACGAGAGA	2400
	GAGAAGTTTG	CTTTCTGCTC	CATGAAAGGC	TGTGAGAGGA	TAAAGATTAA	AGCTCTGATT	2460
25	CCAAAGAACG	CAGGCGTCAG	TGACTGCACA	GCCACAGCTT	ACCCCAAGTT	CACCGAGAGG	2520
	GCTGTCGATG	ACGTGCCGAT	GCCCAAGAAG	CTCTTTGGTT	CTCAGCTGAA	AACAAAGGAC	2580
	CATTTCCTGG	AGGTGAAGAT	GGAGAGTTCC	AAGCAGCACT	TCTTCCACCT	CTGGAACGAC	2640
	TTCGCTTACA	TTGAAGTGGG	TGGGAAGAAG	TACCCAGATT	CGGAGGATGG	CATCCAGGTG	2700
	GTGGTGATTG	ACGGGAACCA	AGGGCGCGTG	GTGAGCCACA	CGAGCTTCAG	GAACCTCCATT	2760
30	CTGCAAGGCA	TACCATTGGC	GCTTTTCAAC	TATGTGGCGA	CCATCCCTGA	CAATTCCATA	2820
	GTGCTTATGG	CATCAAGGGG	AAGATACGTC	TCCAGAGGCC	CATGGACCAG	AGTGCTGGAA	2880
	AAGCTTGGGG	CAGACAGGGG	TCTCAAGTTG	AAAGAGCAAA	TGGCATTTCGT	TGGCTTCAAA	2940
	GGCAGCTTCC	GGCCCATCTG	GGTGACACTG	GACACTGAGG	ATCACAAAGC	CAAAATCTTC	3000
	CAAGTTGTGC	CCATCCCCTGT	GGTGAAGAAG	AAGAAGTTGT	GAGGACAGCT	GCCGCCCGGT	3060
35	GCCACCTCGT	GGTAGACTAT	GACGCTGACT	CTTGGCAGCA	GACCAGTGGG	GGATGGCTGG	3120
	GTCCCCCAGC	CCCTGCCAGC	AGCTGCCTGG	GAAGGCCGTG	TTTCAGCCCT	GATGGGCCAA	3180
	GGGAAGGCTA	TGAGAGACCC	TGGTGCTGCC	ACCTGCCCTT	ACTCAAGTGT	CTACCTGGAG	3240
	CCCTTGGGGC	CCCTTGGGAA	AATGCTGGAA	ACATTCACTT	TCCTGCGAGC	TCTTGGGTGC	3300
	TTCTCTCCTA	TCTGTGCCTC	TTCAGTGGGG	GTTTGGGGAC	CATATCAGGA	GACCTGGGTT	3360
40	GTGCTGACAG	CAAAGATCCA	CTTTGGCAGG	AGCCCTGACC	CAGCTAGGAG	GTAGTCTGGA	3420
	GGGCTGGTCA	TTACAGATCA	CCCATGGTCT	TCAGCAGACA	AGTGAGGGTG	GTAAATGTAG	3480
	GAGAAAGAGC	CTTGGCCTTA	AGGAAATCTT	TACTCCTGTA	AGCAAGAGCC	AACCTCACAG	3540
	GATTAGGAGC	TGGGATAGAA	CTGGCTATCC	TGGGGAAGA	GGCAAGCCCT	GCCCTTGGCC	3600
	GTGTCCACCT	TTCAGGAGAC	TTTGAGTGGC	AGGTTTGGAC	TTGGACTAGA	TGACTCTCAA	3660
45	AGGCCCTTTT	AGTTCTGAGA	TTCCAGAAAT	CTGCTGCATT	TCACATGGTA	CCTGGAACCC	3720
	AACAGTTTCA	GGATATCCAC	TGATATCCAT	GATGCTGGGT	GCCCCAGCGC	ACACGGGATG	3780
	GAGAGGTGAG	AACATAATGCC	TAGCTTGAGG	GGTCTGCAGT	CCAGTAGGGC	AGGCAGTCAG	3840
	GTCATGTGTC	ACTGCAATGC	CAGGTGGAGA	AATCACAGAG	AGGTAAATATG	GAGGCCAGTG	3900
	CCATTTCAGA	GGGAGGGCTC	AGGAAGGCTT	CTTGCTTACA	GGAATGAAGG	CTGGGGGCAT	3960
50	TTTGCTGGGG	GGAGATGAGG	CAGCCTCTGG	AATGGCTCAG	GGATTTCAGCC	CTCCCTGCCG	4020
	CTGCTGCTGC	AAGCTGTGTA	CTACGGGGTC	GCCCTTTGCT	CACGCTCTCT	TGGCCCACTC	4080
	ATGATGGAGA	AGTGTGGTCA	GAGGGGAGCA	ATGGGCTTTG	CTGCTTATGA	GCACAGAGGA	4140
	ATTCAGTCCC	CAGGCAGCCC	TGCCTCTGAC	TCCAAGAGGG	TGAAGTCCAC	AGAAGTGAGC	4200
	TCCTGCTCTA	GGGCTCTATT	TGCTCTTCAT	CCAGGGAATC	GAGCACAGGG	GGCCTCCAGG	4260
55	AGACCCTAGA	TGIGCTCTGTA	CTCCCTCGGC	CTGGGATTTC	AGAGCTGGAA	ATATAGAAAA	4320
	TATCTAGCCC	AAAGCCTTCA	TTTTAACAGA	TGGGGAAAGT	GAGCCCCCAA	GATGGGAAAG	4380
	AACCACACAG	CTAAGGGAGG	GCCTGGGGAG	CCCCACCCTA	GCCCTTGCTG	CCACACCACA	4440
	TTGCCCTCAA	AACCGGCCCC	AGAGTGCCCC	GGCACTCCTG	AGGTAGCTTC	TGGAAATGGG	4500
	GACAAGTCCC	CTCGAAGGAA	AGGAATGAC	TAGAGTAGAA	TGACAGCTAG	CAGATCTCTT	4560
60	CCCTCCTGCT	CCCAGCGCAC	ACAAACCCGC	CCTCCCTCTG	GTGTTGGCGG	TCCCTGTGGC	4620
	CTTCACTTTG	TTCATACCTT	GTCAGCCGAG	CCTGGGTGCA	CAGTAGCTGC	AACTCCCCAT	4680
	TGGTGCTACC	TGGCTCTCCT	GTCTCTGCAG	CTCTACAGGT	GAGGCCAGGC	AGAGGGAGTA	4740
	GGGCTCGCCA	TGTTTCTGGT	GAGCCAAATT	GGCTGATCTT	GGGTGTCTGA	ACAGCTATTG	4800
	GGTCCACCCC	AGTCCCTTTC	AGCTGCTGCT	TAATGCCCTG	CTCTCTCCCT	GGCCCACTTT	4860
65	ATAGAGAGCC	CAAAGAGCTC	CTGTAAGAGG	GAGAACTCTA	TCTGTGGTTT	ATAATCTTGC	4920
	ACGAGGCACC	AGAGTCTCCC	TGGGTCTTGT	GATGAACCTA	ATTTATCCCC	TTTCTGCCCC	4980
	CAACCACAAA	CTCTTCTCTT	CAAGAGGGGC	CTGCCTGGCT	CCCTCCACCC	AACTGCACCC	5040
	ATGAGACTCG	GTCGAAGAGT	CCATTCCCCA	GGTGGGAGCC	AACTGTACAG	GAGGTCTTTC	5100
	CCACCACAAA	TCTTTCACTG	GCTGGGAGGT	GACCATAGGG	CTCTGCTTTT	AAAGATATGG	5160
70	CTGCTTCAAA	GGCCAGAGTC	ACAGGAAGGA	CTTCTTCCAG	GGAGATTAGT	GGTGATGGAG	5220
	AGGAGAGTTA	AAATGACCTC	ATGTCCTTCT	TGTCCACGGT	TTTGTGAGT	TTTCACTCTT	5280
	CTAATGTCAAG	GGTCTCACAC	TGTGAACCA	TAGGATGTG	ATCACTTTCA	GGTGGCCAGG	5340
	AATGTGAAT	GTCTTGGGCT	CAGTTCACTT	AAAAAAGATA	TCTATTTGAA	AGTTCTCAGA	5400
	GTTGTACATA	TGTTTACACG	TACAGGATCT	GTACATAAAA	GTTTCTTTCC	TAAACCATTC	5460
75	ACCAAGAGCC	AATATCTAGG	CATTTTCTTG	GTAGCACAAA	TTTTCTTATT	GCTTAGAAAA	5520
	TGTCTCTCCT	TGTTATTTCT	GTTTGTAAAG	CTTAAGTGAG	TGAGGTCTTT	AAGGAAAGCA	5580
	ACGCTCTCTT	GAAAATGCTT	TCTTTTTTCT	GTTGCCGAAA	TAGCTGGTCC	TTTTTCGGGA	5640
	GTTAGATGTA	TAGAGTGTTC	GTATGTAAAC	ATTTCTTGTA	GGCATCACCA	TGAACAAAGA	5700
	TATATTTTCT	ATTTATTTAT	TATATGTGCA	CTTCAAGAAG	TCACTGTGAG	AGAAATAAAG	5760
80	AATTGTCTTA	AATGTCAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA		5808

Seq ID NO: C39 DNA Sequence  
Nucleic Acid Accession #: NM\_014373  
Coding sequence: 322.1338

	1	11	21	31	41	51	
	GTGGCCTCGA	GGTGGTGCCA	GGGCCGCCCC	CTGCAGTCCG	GAGACGAACG	CACGGACCGG	60
5	GCCTCCGGAG	GCAGGTTCCG	CTGGAAGGAA	CCGCTCTCGC	TTCTGCTTAC	ACTTGCCGCA	120
	ATGTCTCCGA	GCTTACTCAC	ATAGCATATT	GGTATATCAA	AATGAAATGC	AAGGAACCAA	180
	AAATAACATA	ATTGAAGGCA	GTAAGAGTGA	AATTAAATAG	GAAGATCATC	AGTCAAGGAA	240
	GACCCACTGG	AGAGGACAGA	AAATGAAGCA	GTGTTTTATC	ATGTGTATTT	CAGCAGGTCT	300
	TCTTGAATTT	TAACTAAAAA	TATGACTGCT	CTCTCTTCAG	AGAACTGCTC	TTTTCAGTAC	360
10	CAGTTACGTC	AAACAAACCA	GCCCTAGAC	GTTAACTATC	TGCTATTCTT	GATCATACTT	420
	GGGAAAAATAT	TATTAAATAT	CCTTACACTA	GGAATGAGAA	GAAAAAACAC	CTGTCAAAAT	480
	TTTATGGAAT	ATTTTTCGAT	TTCAC TAGCA	TTCGTGATC	TTTTACTTTT	GGTAAACATT	540
	TCCATTATAT	TGTATTTTCA	GGATTTTGTA	CTTTAAAGCA	TTAGGTTTCA	TAAATACCAC	600
	ATCTGCCTAT	TACTCAAAAT	TATTTCCCTT	ACTTATGGCT	TTTTGCATTA	TCCAGTTTTC	660
15	CTGCAGGCTT	GTATAGATTA	TGCGCTGAAT	TTCTCTAAAA	CAACCAAGCT	TTCATTTAAG	720
	TGTCAAAAAT	TATTTTATTT	CTTTACAGTA	ATTTTAAATTT	GGATTTTCA	CCTTGCTTAT	780
	GTTTTGGGAG	ACCCAGCCAT	CTACCAAAAG	CTGAAGGCAC	AGAATGCTTA	TTCTCGTCAC	840
	TGTCCTTTCT	ATGTCAGCAT	TCAGAGTTAC	TGGCTGTCAT	TTTTTCATGG	GATGATTTTA	900
	TTTGTAGCTT	TCATAACCTG	TTGGGAAGAA	GTTACTACTT	TGGTACAGGC	TATCAGGATA	960
20	ACTTCCTATA	TGAATGAAAC	TATCTTATAT	TTTCTTTTAT	CATCCCACTC	CAGTTATACT	1020
	GTGAGATCTA	AAAAAATATT	CTTATCCAAG	CTCATTTGCT	GTTTTCTCAG	TACCTGGTTA	1080
	CCATTGTGAC	TACTTCAGGT	AATCATTGTT	TTACTTAAAG	TTGAGATTCC	AGCATATATT	1140
	GAGATGAATA	TTCCCTGGTT	ATACTTTGTC	AATAGTTTTT	TCATTGCTAC	AGTGTATTGG	1200
	TTTAATTGTC	ACAAGCTTAA	TTTAAAGAAC	ATTGGATTAC	CTTTGGATCC	ATTTGTCAAC	1260
25	TGGAAGTGCT	GCTTCATTCC	ACTTACAATT	CCTAATCTTG	AGCAAATTGA	AAAGCCTATA	1320
	TCAATAATGA	TTTGTTAATA	TATTAATTA	AAAGTTACAG	CTGTCATAAG	ATCATAATTT	1380
	TATGAACAGA	AAGAATCAG	GACATATTAA	AAAAATAACT	GAATCAAAAC	AACCTTTGCC	1440
	CCCTGACTGA	TAGCATTTC	GAATGTGCT	TTTGAAGGTC	TATACCAGTT	ATTAATAGT	1500
	GTTTATTATT	AAAAACAAA	TAAATCCAAG	AAGTTTTTAT	AGTTATTTCAG	GGACACTATA	1560
30	TTACAAATAT	TACTTTGTTA	TTAACACAAA	AAGTGATAAG	AGTTAAACATT	TGGCTATACT	1620
	GATGTTTGTG	TTACTCAAAA	AAACTACTGG	ATGCAAACTG	TTATGTAAAT	CTGAGATTTT	1680
	ACTGACAACT	TTAGATATAT	AACCTAAACA	TTTTTATTAA	ATGTTCAAAT	GTAAGCAAGA	1740
	AAAAAAA						1749

Seq ID NO: C40 DNA Sequence  
Nucleic Acid Accession #: BC012089  
Coding sequence: 1..2571

	1	11	21	31	41	51	
40	ATGGCCCTCG	TACTCGGCTC	CCTGTTGCTG	CTGGGGCTGT	GCGGGAACTC	CTTTTCAGGA	60
	GGGCAGCCTT	CATCCACAGA	TGCTCCTAAG	GCTTGGAAAT	ATGAATTGCC	TGCAACAAAT	120
	TATGAGACCC	AAGACTCCCA	TAAAGCTGGA	CCCATTTGCA	TTCTCTTTGA	ACTAGTGCAAT	180
	ATCTTTCTCT	ATGTGGTACA	GCCGCGTGAT	TTCCCAAGAG	ATACTTTGAG	AAAATTTCTTA	240
45	CAGAAGGCAT	ATGAATCCAA	AATTGATTAT	GACAAGATTG	TCTACTATGA	AGCAGGGATT	300
	ATTCTATGCT	GTGTCTGGGG	GCTGCTGTTT	ATTATTCTGA	TGCCTCTGGT	GGGGTATTTC	360
	TTTTGTATGT	GTGTTGCTG	TAACAATGT	GGTGGAGAAA	TGCACCAGCG	ACAGAAGGAA	420
	AATGGGCCCT	TCTTGAGGAA	ATGCTTTGCA	ATCTCCCTGT	TGGTGATTGT	TATAATAATA	480
	AGCATTTGCA	TCTTCTATGG	TTTGTGGCA	AATCACCAGG	TAAGAACCAG	GATCAAAAGG	540
50	AGTCGGAAC	TGGCAGATAG	CAATTTCAAG	GACTTGGCAA	CTCTCTTGAA	TGAAACTCCA	600
	GAGCAAAATCA	AATATATATT	GGCCCAAGTAC	AACACTACCA	AGGACAAGCG	GTTCAAGAT	660
	CTGAACAGTA	TCAATTCAAGT	GCTAGGAGGC	GGAATTTCTG	ACCGACTGAG	ACCCAACATC	720
	ATCCCTGTTT	TTGATGAGAT	TAAAGTCCAT	GCAACAGCGA	TCAAGGAGAC	CAAAGAGGCG	780
	TTGGAGAACA	TGAACAGCAC	CTTGAAGAGC	TTGCACCAAC	AAAGTACACA	GCTTAGCAGC	840
55	AGTCTGACCA	CGGTGAAAAC	TAGCCTGCGG	TCATCTCTCA	ATGACCCTCT	GTGCTTGGTG	900
	CATCCATCAA	GTGAAACCTG	CAACAGCATC	AGATTGTCTC	TAAGCCAGCT	GAATAGCAAC	960
	CCTGAACCTGA	GGCAGCTTCC	ACCCGTGGAT	GCAGAACTTG	ACAAAGTTAA	TAAAGTTCTT	1020
	AGGACAGATT	TGGATGGCCT	GGTCCAACAG	GGCTATCAAT	CCCTTAATGA	TATACCTGAC	1080
	AGAGTACAAC	GCCAAACCC	GACTGTGCTA	GCAGGTATCA	AAAGGGTCTT	GAATTTCCATT	1140
60	GGTTTCAGATA	TCGACAATGT	AACCTAGCGT	CTTCTATTTC	AGGATATACT	CTCAGCATTC	1200
	TCTGTTTATG	TTAATAACAC	TGAAAGTTAC	ATCCACAGAA	ATTTACCTAC	ATTGGAAGAG	1260
	TATGATTTCAT	ACTGTTGGCT	GGGTGGCCTG	GTCTCTGCTG	CTCTGCTGAC	CCTCATCGTG	1320
	ATTTTITACT	ACCTGGGCTT	ACTGTGTGGC	GTGTGCGGCT	ATGACAGGCA	TGCCACCCCG	1380
	ACCACCCGAG	GCTGTGTCTC	CAACACCCGA	GGCGTCTTCC	TCATGGTTGG	AGTTGGATTA	1440
65	AGTTTCTCTT	TTTGCTGGAT	ATTGATGATC	ATTGTGGTTC	TTACCTTTGT	CTTTGGTGCA	1500
	AATGTGGAAT	AACCTGATCT	TGAACCTTAC	ACGAGCAAGG	AATTATTCCG	GGTTTTGGAT	1560
	ACACCTTACT	TACTAAATGA	AGACTGGGAA	TACTATCTCT	CTGGGAAGCT	ATTTAATAAA	1620
	TCAAAAATGA	AGCTCACTTT	TGAACAAGTT	TACAGTGACT	GCAAAAAAAA	TAGAGGCACT	1680
	TACGGCACTC	TTACCTTGCA	GAACAGCTTC	AATATCAGTG	AACATCTCAA	CATTAAATGAG	1740
70	CATACTGGAA	GCATAAGCAG	TGAATTGGAA	AGTCTGAAGG	TAAATCTTAA	TATCTTTCTG	1800
	TTGGGTGTCAG	CAGGAAGAAA	AAACCTTCAG	GATTTTGTCT	CTTGTGGAAT	AGACAGAAATG	1860
	AATTATGACA	GCTACTTGGC	TCAGACTGGT	AAATCCCCCG	CAGGAGTGAA	TCTTTTATCA	1920
	TTTGCAATATG	ACTTAGAAGC	AAAAGCAAAAC	AGTTTGGCCC	CAGGAAATTT	GAGGAACTCC	1980
	CTGAAAAGAG	ATGCACAAAC	TATTAACAAC	ATTCACCAGC	AACGAGTCTT	TCCTATAGAA	2040
75	CAATCACTGA	GCACTCTATA	CCAAAGCGTC	AAGATACTTC	AACGCACAGG	GAATGGATTG	2100
	TTGGAGAGAG	TAACTAGGAT	TCTAGCTTCT	CTGGATTTTG	CTCAGAACTT	CATCACAAC	2160
	AAACTTTCCT	CTGTTATTAT	TGAGGAAACT	AAGAAGTATG	GGAGAACAAAT	AATAGGATAT	2220
	TTTGAACATT	ATCTGCAGTG	GATCGAGTTC	TCTATCAGTG	AGAAAGTGGC	ATCGTGCAAA	2280
	CCTGTGGCCA	CCGCTCTAGA	TACTGCTGTT	GATGCTTTTC	TGTGTAGCTA	CATTATCGAC	2340
80	CCCTTGAATT	TGTTTTGGTT	TGGCATAGGA	AAAGCTACTG	TATTTTACT	TCCGGCTCTA	2400
	ATTTTGTGCG	TAAACTGGC	TAACTACTAT	CGTCGAATGG	ATTCGGAGGA	CGGTACGAT	2460
	GATGTTGAAA	CTATACCCAT	GAAAAATATG	GAAAAATGTA	ATAATGGTTA	TCATAAGAT	2520
	CATGTATATG	GTATTCACAA	TCCTGTTATG	ACAAGCCCAT	CACAACATTG	A	2571

Seq ID NO: C41 DNA Sequence

Nucleic Acid Accession #: NM\_033049  
Coding sequence: 28..1566

5	1	11	21	31	41	51	
	CCACGCGTCC	GAGCAAGAAC	AGCTAAAAATG	AAAGCCATCA	TTCATCTTAC	TCTTCTTGCT	60
	CTCCTTTCTG	TAAACACAGC	CACCAACCAA	GGCAACTCAG	CTGATGCTGT	AACAACCACA	120
	GAAACTGCCA	CTAGTGGTCC	TACAGTAGCT	GCAGCTGATA	CCACTGAAAC	TAATTTCCCT	180
10	GAAACTGCTA	GCACCACAGC	AAATACACCT	TCTTTCCCAA	CAGCTACTTC	ACCTGCTCCC	240
	CCCATAATTA	GTACACATAG	TTCTCCACA	ATTCTACAC	CTGCTCCCC	CATAATTAGT	300
	ACACATAGTT	CCTCCACAAT	TCCTATACCT	ACTGCTGCAG	ACAGTGAGTC	AACCACAAAT	360
	GTAAATTCAT	TAGCTACCTC	TGACATAATC	ACCGCTTCAT	CTCCAAATGA	TGGATTAAATC	420
	ACAAATGGTTC	CTTCTGAAAC	ACAAAGTAAC	AATGAAATGT	CCCCCACCAC	AGAAGACAAT	480
15	CAATCATCAG	GGCCTCCCAC	TGGCACCGCT	TTATTGGAGA	CCAGCACCTC	AAACAGCACA	540
	GGTCCCGACA	ATCCTTGCCA	AGATGATCCC	TGTGCAGATA	ATTCTGTATG	TGTTAAGCTG	600
	CATAATACAA	GTTTTTGCCT	GTGTTTAGAA	GGGTATTACT	ACAACTCTTC	TACATGTAAG	660
	AAAGGAAAGG	TATTCCTTGG	GAAGATTTCA	GTGACAGTAT	CAGAAACATT	TGACCCAGAA	720
	GAGAAACATT	CCATGGCCTA	TCAAGACTTG	CATAGTGAAA	TTACTAGCTT	GTTTAAAGAT	780
20	GTATTGGACA	CATCTGTTTA	TGGACAGACT	GTAATTCCTA	CTGTAAGCAC	ATCTCTGTCA	840
	CCAAGATCTG	AAATGCGTGC	TGATGACAAG	TTGTTAATG	TAAACAATAGT	AACAATTTTG	900
	GCAGAAACCA	CAAGTGACAA	TGAGAAGACT	GTGACTGAGA	AAATTAATAA	AGCAATTAGA	960
	AGTAGCTCAA	GCAACTTTCT	AAACTATGAT	TTGACCCCTC	GGTGTGATTA	TTATGGCTGT	1020
	AACAGACTGT	CGGATGACTG	CCTCAATGGT	TTAGCATGCG	ATTGCAAAATC	TGACCTGCAA	1080
25	AGGCCCTAAC	CCAGAGCCCC	TTTCTGCGTT	GCTTCCAGTC	TCAAGTGTCC	TGATGCTGTC	1140
	AACGCACAGC	ACAAGCAATG	CTTAATAAAG	AAGAGTGGTG	GGGCCCTTGA	GTGTGCGTGC	1200
	GTGCCCGGCT	ACCAGGAAGA	TGCTAATGGG	AACTGCCAAA	AGTGTGCATT	TGGGTACAGT	1260
	GGACTCGACT	GTAAGGACAA	ATTTCAAGTG	ATCCTCACTA	TTGTGGGCAC	CATCGCTGGC	1320
	ATTGTCACTT	TGAGCATGAT	AATTGCATTG	ATTGTACACG	CAAGATCAAA	TAAACAAACG	1380
30	AAGCATATTG	AAGAAGAGAA	CTTGATTGAC	GAAGACTTTC	AAAATCTAAA	ACTGCGGTGC	1440
	ACAGGCTTCA	CCAATCTTGG	AGCAGAAGGG	AGCGTCTTTC	CTAAGGTCAG	GATAACGGCC	1500
	TCCAGAGACA	GCCAGATGCA	AAATCCCTAT	TCAAGACACA	GCAGCATGCC	CCGCCCTGAC	1560
	TATTAGAATC	ATAAGAATGT	GGAACCCGCC	ATGGCCCCCA	ACCAATGTAC	AAGCTATTAT	1620
	TTAGAGTGTT	TAGAAAGACT	GATGGAGAAG	TGAGCACCAG	TAAAGATCTG	GCCTCCGGGG	1680
35	TTTTTCTTCC	ATCTGACATC	TGCCAGCCTC	TCTGAATGGA	AGTTGTGAAT	GTTTGCAACG	1740
	AATCCAGCTC	ACTTGTCTAA	TAAGAATCTA	TGACATTAAA	TGTAGTAGAT	GCTATTAGCG	1800
	CTTGTCAAGG	AGGTGGTTTT	CTTCAATCAG	TACAAAGTAC	TGAGACAATG	GTTAGGGTTG	1860
	TTTTCTTAAT	CTTTTCTCTG	GTAGGGCAAC	AAGAACCATT	TCCAATCTAG	AGGAAGCTC	1920
	CCCAGCATTG	CTTGCTCCTG	GGCAAACATT	GCTCTTGAGT	TAAGTGACCT	AATTCCTCTG	1980
40	GGAGACATAC	GCATCAACTG	TGGAGGTCCG	AGGGGATGAG	AAGGGATACC	CACCACCTTT	2040
	CAAGGCTCAC	AAGCTCACTC	TCTGACAAGT	CAGAATAGGG	ACACTGCTTC	TATCCCTCCA	2100
	ATGGAGAGAT	TCTGGCAACC	TTTGAACAGC	CCAGAGCTTG	CAACCTAGCC	TCACCCAAGA	2160
	AGACTGGAAA	GAGACATATC	TCTCAGCTTT	TTCAGGAGGC	GTGCCCTGGG	ATCCAGGAAC	2220
	TTTTTTGATG	TAATTTAGAAG	GCCTGGACTA	AAAATGTCCA	CTATGGGGTG	CACCTCTACG	2280
45	TTTTTGAAT	GCTAGGAGGG	AGAAGGGGCA	GAGAGTAAAA	AACATGACCT	GGTAGAAGGA	2340
	AGAGAGGCAA	AGGAAACTGG	GTGGGAGGGA	TCAATTAGAG	AGGAGGCACC	TGGGATCCAC	2400
	CTTCTTCTTT	AGGTCCCTTC	CTCCATCAGC	AAAGGAGCAC	TTCTCTAATC	ATGCCCTCCC	2460
	GAAAGCTGGC	TGGGAGAAGG	TTTAAAAACA	AAAAATCCAG	GAGTAAGAGC	CTTAGGTCAG	2520
	TTTGAAATTT	GAGACAAACT	GTCTGGCAAA	GGGTGCGAGA	GGGAGCTTGT	GCTCAGGAGT	2580
50	CCAGCCGTCC	AGCCTCGGGG	TGTAGGTTTC	TGAGGTGTGC	CATTGGGGCC	TCAGCCTTCT	2640
	CTGGTGACAG	AGGCTCAGCT	GTGGCCACCA	ACACACAACC	ACACACACAC	AACCACACAC	2700
	ACAAATGGGG	GCAACCACAT	CCAGTACAAG	CTTTTACAAA	TGTTATTAGT	GTCTCTTTTT	2760
	ATTTCTAATG	CCTTGTCTCT	TTAAAAGTTA	TTTTATTGTT	TATTATTATT	TGTTCTTGAC	2820
	TGTTAATTGT	GAATGGTAAT	GCAATAAAGT	GCCTTTGTTA	GATGGTGAAA	AAAAAAAAAA	2880
55	AAAAAAA						2887

Seq ID NO: C42 DNA Sequence  
Nucleic Acid Accession #: NM\_001432.1  
Coding sequence: 167..676

60	1	11	21	31	41	51	
	TCACTTGCCCT	GATATTTCCT	GTGTCAGAGG	GACACAGCCA	ACGTGGGGTC	CCTTCTAGGC	60
	TGACAGCCGC	TCTCCAGCCA	CTGCCCGGAG	CCCGTCTGCT	CCGCCCTGTC	CCGTGCACTC	120
65	TCCGCAGCCG	CCCTCCGCCA	AGCCCCAGCG	CCCGCTCCCA	TGCGCGATGA	CCGCGGGGAG	180
	GAGGATGGAG	ATGCTCTGTG	CCGGCAGGGT	CCCTGCGCTG	CTGCTCTGCC	TGGGTTTCCA	240
	TCTTCTACAG	GCACTCTCTA	GTACAAGTGT	GATTCATCA	TGTATCCCAG	GAGAGTCCAG	300
	TGATAACTGC	ACAGCTTTAG	TTCAGACAGA	AGACAATCCA	CGTGTGGCTC	AAGTGTCAAT	360
	AACAAAGTGT	AGCTCTGACA	TGAATGGCTA	TTGTTTGCAT	GGACAGTGCA	TCTATCTGGT	420
70	GGACATGAGT	CAAACTACT	GCAGGTGTGA	AGTGGGTTAT	ACTGGTGTCC	GATGTGAACA	480
	CTTCTTTTGA	ACCGTCCACC	AACCTTTAAG	CAAAGAGTAT	GTGGCTTTGA	CCGTGATTCT	540
	TATTATTTTG	TTTCTTATCA	CAGTCTGCGG	TTCCACATAT	TATTTCTGCA	GATGGTACAG	600
	AAATCGAAAA	AGTAAAGAAC	CAAGAAGGGA	ATATGAGAGA	GTTACCTCAG	GGGATCCAGA	660
	GTTCGCCCAA	GTCTGAATAT	GAGAGAGTTA	CCTCAGGGGA	TCCAGAGTTG	CCGCAAGTCT	720
75	GAATGGCGCG	ATCAAACTTA	TGGGCAGGGA	TAACAGTGTG	CTGGTTAAT	ATTAATATTC	780
	CATTTTATTA	ATAATATTTA	TGTTGGGTCA	AGTGTTAGGT	CAATAACACT	GTATTTTAAT	840
	GTACTTGAAA	AATGTTTTTA	TTTTTGTTTT	ATTTTTGACA	GACTATTGTC	TAATGTATAA	900
	TGTGCAGAAA	ATATTTAATA	TCAAAAGAAA	ATTGATATTT	TTATACAAGT	AATTTCCCTGA	960
	GCTAAATGCT	TCATTGAAAG	CTTCAAAGTT	TATATGCCTG	GTGCACAGTG	CTTAGAAGTA	1020
80	AGCAATTCCC	AGGTCAATAG	TCAAGAATTG	TTAGCAAAATG	ACAGATTCTT	GTAAGCCTAT	1080
	ATATATAGTC	AAGTCGATTT	AGTAAGTATG	TTTTTTATGT	TCTCTCAAATC	AGTGATAATT	1140
	GGTTTGACTG	TACCATGGTT	TGATATGTAG	TTGGCACCAT	GGTATCATAT	ATTAAACAAA	1200
	TAATGCAATT	AGAAATTTGGG	AGAAGCAAAT	ATAGGTCCTG	TGTTAAACAC	TACACATTTG	1260
	AAACAAGCTA	ACCTGGGGGA	GTCTATGGTC	TCTTCACTCA	GGTCTCAGCT	ATAATTCTGT	1320
	TATATGAGGG	GCAGTGGACA	GTTCCCTATG	CCAACCTCAG	ACTCCTACAG	GTACTAGTCA	1380

5	CTCATCTACC	AGATTCTGCC	TATGTAAAT	GAATTGAAAA	ACAATTTTCT	GTAATCTTTT	1440
	ATTTAAGTAG	TGGGCATTTC	ATAGCTTCAC	AATGTTCCCT	TTTTGTATAT	TACAACATTT	1500
	ATGTGAGGTA	ATTATTGCTC	AACAGACAAT	TAGAAAAAAG	TCCACACTTG	AAGCCTAAAT	1560
	TTGTGCTTTT	TAAGAAATAT	TTTAGACTAT	TTCTTTTAT	AGGGGCTTGG	CTGAATCTTA	1620
	ACATTAAATC	ACAGCCCAAA	ATTTGATGGA	CTAATTATTA	TTTTAAAAA	TATGAAGACA	1680
	ATAATCTTAC	ATGTTGTCTT	AAGATGGAAA	TACAGTTATT	TCATCTTTTA	TTCAAGGAAG	1740
	TTTTAACTTT	AATACAGCTC	AGTAAATGGC	TTCTTCTAGA	ATGTAAAGTT	ATGTATTTAA	1800
	AGTTGTATCT	TGACACAGGA	AATGGGAAAA	AACTTAAAAA	TTAATATGGT	GTATTTTTC	1860
10	AAATGAAAAA	TCTCAATTGA	AAGCTTTTAA	AATGTAGAAA	CTTAAACACA	CCTTCTCTGT	1920
	GAGGCTGAGA	TGAAAACTAG	GGCTCATTIT	CCTGACATTT	GTTTATTTTT	TGGAAGAGAC	1980
	AAAGATTTCT	TCTGCACTCT	GAGCCCATAG	GTCTCAGAGA	GTTAATAGGA	GTATTTTGGG	2040
	GCTATTGCAT	AAGGAGCCAC	TGCTGCCACC	ACTTTTGGAT	TTTATGGGAG	GCTCCTTCAT	2100
	CGAATGCTAA	ACCTTTGAGT	AGAGTCTCCC	TGGATCACAT	ACCAGGTCAG	GGAGGATCTG	2160
15	TTCTTCTCT	ACGTTTATCC	TGGCATGTGC	TAGGGTAAAC	GAAGGCATAA	TAAGCCATGG	2220
	CTGACCTCTG	GAGCACCAGG	TGCCAGGACT	TGCTTCCATG	TGTATCCATG	CATTATATAC	2280
	CCTGGTGCAA	TCACACGACT	GTCACTTAAA	GTCTTGGCCC	TGGCCCTTAC	TATTAGGAAA	2340
	ATAAACAGAC	AAAAACAAGT	AAATATATAT	GGTCTTATAC	ATATTGTATA	TATATTCTAA	2400
	TACAAACATG	TATGTATACA	TGACCTTAAT	GGATCATAGA	ATTGCGATCA	TTTGGTGCTC	2460
20	TGCTAACCAT	TTATATAAAA	CTTAAAAACA	AGAGAAAAAG	AAAAATCAAT	AGATCTAAAC	2520
	AGTTATTTCT	GTTCCTCTAT	TAATATAGCT	GAAGTCAAAA	TATGTAAAGAA	CACATTTTAA	2580
	ATACCTACT	TACAGTTGGC	CCTCTGTGGT	TAGTTCCACA	TCTGTGGATT	CAACCAACCA	2640
	AGGACGGAAA	ATGCTTAAAA	AATAATACAA	CAACAACAAA	AAATACATTA	TAACAACATAT	2700
	TTACTTTTTT	TTTTTTCTTT	TTGAGATGGA	GTCTCGCTCT	GTGCCCAGG	TTGGAGTGCA	2760
25	TGCGCACGAT	CTCGGCTCAC	TGCAACCTCA	CCTCCCGGGT	TCAAGAGATC	CTCCTGCCTC	2820
	AGCCCTCTGA	GCAGCTGGGA	CTACAGGCGC	ATGCCACCAT	GCCCAGCTAA	TTTTTGTATT	2880
	TTTAGTAGAG	GCGGGGTTTC	ACCATGTTGG	CCAGGATGGT	CTCAATCTCC	TAACCTTGAG	2940
	ATCCACCCCT	CACAGCCTCC	CAAAGTCTG	GGATTACAGG	CGTGAGCCAC	CGCAGGTAGC	3000
	ATTTTACATTA	GGTATTTACAA	GTAATGTAAA	GATGATTTAA	GTATACAGGA	GGATGTGAAT	3060
30	AGGTTATATG	CAAGCACTAT	GCCCTTTTAT	ATAAGTGACT	TGAACATCTG	TGCCCGATT	3120
	TAGTATGTGC	AGGGGGGCGA	CTGGGAATC	AGTCCCTGT	GGATACCAAG	GTACAACCTGT	3180
	ATTTATTAAC	GCTTACTAGA	TGTGAGGAGA	GTCTGAATAT	TTTCAGTGAT	CTTGGCTGTT	3240
	TCAAAAAAT	CTATTGACTT	TTCAATAAAT	CAGCTGCAAT	CCATTATTTT	CATTTACAAA	3300
	AGATTATTTG	TAAGCCTCTC	AATCTTGGTT	TTTCAGTTGA	TCTTAAGCAT	GTCAATTCAT	3360
35	AAAAACAAGT	CATTTTGTGA	TTTTTCATCT	TTAAGAATGC	TTAAAAAAGC	TAATCCCTAA	3420
	AATAGTTAGA	TCTTTGTAAA	TGCATATTAA	ATAATAAAGT	ATGACCCACA	TTACTTTTTTA	3480
	TGGGTGAAAA	TAAGACAAAA	ATAATAGTTT	TAGTGAGGAT	GGTGCTGAGT	AAACATAAAA	3540
	ACTGATTTGC	TCTCAGCTGA	TGTGCTCTGT	ACACAGTGGG	AAGATTTTAG	TTCAACTTAA	3600
	GTCTAACTCC	CCCATTTTAC	AGATTCTCA	CTATATATAT	TTCTAGAAGG	GGCTATGCAT	3660
40	ATTCATGTGA	TTGAGAACCA	AAGCAACCAC	AAATGCATAA	ATGCATAATT	TATGGTCTTC	3720
	AACCAAGGCC	ACATAATAAC	CCAGTTAACT	TACTCTTTAA	CCAGGAATAT	TAAGTTCTAT	3780
	AACATAGTACT	CAAGGTTTAA	CCTTAAAAAT	AAGATTTCCT	TAACTTAACT	CTTAAAAATTG	3840
	ATATTATATT	AAACATACAT	AATACAATGT	AACCTCACTG	TTCTCTGTAA	TATTTTGTGC	3900
	TCTAATCTCT	CTGCCGAAAG	TCAAAGTGAT	GGGAGAATTG	GTATACTGGT	ATGACTACGT	3960
45	CTTAAGTCAG	ATTTTATTTT	ATGAGTCTTT	GAGACTAAAT	TCAATCACC	CCAGGTATCA	4020
	AATCAACTTT	TATGCAGCAA	ATATATGATT	CTAGTGTCTG	ACTTTTGTGA	AATTCAAGTAA	4080
	TGCAGTTTTT	AAAAACCTGT	ATCTGACCCA	CTTTGTAAAT	TTTGCTCCAA	TATCCATTCT	4140
	GTAGACTTTT	GAAAAAAGAG	TTTTTAATTT	GATGCCCAAT	ATATTCTGAC	CGTTAAAAAA	4200
	TTCTTGTTC	TATGGGAGAA	GGGGGAGTAA	TGACTTGTAC	AAACAGTATT	TCTGGTGTAT	4260
50	ATTTTAAATGT	TTTTAAAAAG	AGTAATTTCA	TTTAAATATC	TGTTATTCAA	ATTTGATGAT	4320
	GTAAATGTGA	TTTTCATGTA	TTTTCTTTT	ATTTTGCAC	CTGTAAATGC	ACTTTTAAAG	4380
	TTTGAAGAGC	CATTTTGTGA	AACGGTTTTT	ATTAAAGATG	CTATGGAACA	TAAAGTTGTA	4440
	TTGCATGCAA	TTTAAAGTAA	CTTATTGAC	TATGAATATT	ATCGGATTAC	TGAATTGTAT	4500
	CAATTGTTTT	TGTTTCAATT	TCAGCTTTGA	TAATTGTGTA	CCTTAAGATA	TTGAAGGAGA	4560
55	AAATAGATAA	TTTACAAGAT	ATTATTAAAT	TTTATTATAT	TTCTTGGGA	ATTGAAAAAA	4620
	ATTGAATAAA	ATAAAAATGC	ATTGAACATC	TTGCATTCAA	AATCTTCACT	GAC	4673

Seq ID NO: C43 DNA Sequence  
Nucleic Acid Accession #: AF011468.1  
Coding sequence: 257..1468

60	1	11	21	31	41	51	
	GGAAGACTTG	GGTCTCTGGG	TCGCAGGTGG	GAGCCGACGG	GTGGGTAGAC	CGTGGGGGAT	60
65	ATCTCAGTGG	CGGACGAGGA	CGGCGGGGAC	AAGGGGCGGC	TGGTTCGAGT	GGCGGAGCGT	120
	CAAGTCCCCT	GTCCGTTCTT	CCGTCCCTGA	GTGTCTTGG	CGCTGCCTTG	TGCCCGCCCA	180
	GCGCCTTTC	ATCCGCTCCT	GGGCACCGAG	GCGCCCTGTA	GGATACTGCT	TGTTACTTAT	240
	TACAGCTAGA	GGCATCATGC	ACCGATCTAA	AGAAAACTGC	ATTTACAGGAC	CTGTTAAGGC	300
70	TACAGCTCCA	GTTCGAGGTT	CAAAACGTGT	TCTCGTGACT	CAGCAAATTC	CTGTGAGAA	360
	TCCATTACCT	GTAATAGTGG	GCCAGGCTCA	GCGGGTCTTG	TGTCCTTCAA	ATTCTTCCCA	420
	GCGCGTTCTT	TTGCAAGCAC	AAAAGCTTGT	CTCCAGTCAC	AAGCCGGTTC	AGAATCAGAA	480
	GCAGAAGCAA	TTGCAGGCAA	CCAGTGTACC	TCATCTGTCT	TCCAGGCCAC	TGAATAACAC	540
	CCAAAAAGAGC	AAGCAGCCCC	TGCCATCGGC	ACCTGAAAAT	AATCCTGAGG	AGGAACCTGC	600
75	ATCAAAACAG	AAAAATGAAG	AATCAAAAAA	GAGGCAGTGG	GCTTTGGAAG	ACTTTGAAAT	660
	TGGTCGCCCT	CTGGGTAAAG	GAAAGTTTGG	TAATGTTTAT	TTGGCAAGAG	AAAAGCAAAG	720
	CAAGTTTATT	CTGGCTCTTA	AAGTGTATT	TAAAGCTCAG	CTGGAGAAAG	CCGGAGTGGG	780
	GCATCAGCTC	AGAAGAGAA	TAGAAATACA	GTCCACCTT	CGGCATCCTA	ATATTCTTAG	840
	ACTGTATGGT	TATTTCCATG	ATGCTACCG	AGTCTACCTA	ATTCTGGAAT	ATGCACCAT	900
80	TGGAACAGTT	TATAGAGAAC	TTCAAGAACT	TTCAAGTTT	GATGAGCAGA	GAACTGCTAC	960
	TTATATAACA	GAATTGGCAA	ATGCCCTGTC	TTACTGTCAT	TCGAAGAGAG	TTATTCATAG	1020
	AGACATTAAG	CCAGAGAACT	TACTTCTTGG	ATCAGCTGGA	GAGCTTAAAA	TTGCAGATTT	1080
	TGGGTGGTCA	GTACATGCTC	CATCTTCCAG	GAGGACCACT	CTCTGTGGCA	CCCTGGACTA	1140
	CCTGCCCCCT	GAAATGATTG	AAGGTGCGAT	GCATGATGAG	AAGGTGGATC	TCTGGAGCCT	1200
	TGGAGTTCTT	TGCTATGAAT	TTTATGTTGG	GAAGCCTCCT	TTTGAGGCAA	ACACATACCA	1260

AGAGACCTAC AAAAGAATAT CACGGGTTGA ATTCACATTC CCTGACTTTG TAACAGAGGG 1320  
 AGCCAGGGGAC CTCATTTCAC GACTGTTGAA GCATAATCCC AGCCAGAGGC CAATGCTCAG 1380  
 AGAAGTACTT GAACACCCCT GGATCACAGC AAATTCATCA AAACCATCAA ATTGCCAAAA 1440  
 CAAAGAATCA GCTAGCAAAC AGTCTTAGGA ATCGTGCAGG GGGAGAAATC CTTGAGCCAG 1500  
 GGCTGCCATA TAACCTGACA GGAACATGCT ACTGAAGTTT ATTTTACCAT TGACTGCTGC 1560  
 CCTCAATCTA GAACGCTACA CAAGAAATAT TTGTTTTACT CAGCAGGTGT GCCTTAACCT 1620  
 CCTTATTCAG AAAGCTCCAC ATCAATAAAC ATGACACTCT GAAGTGAAAG TAGCCACGAG 1680  
 AATTGTGCTA CTTATACTGG TTCATAATCT GGAGGCAAGG TTCGACTGCA GCCGCCCCGT 1740  
 CAGCCTGTGC TAGGCATGGT GTCTTCACAG GAGGCAAATC CAGAGCCTGG CTGTGGGGAA 1800  
 AGTGACCACT CTGCCCCTGAC CCCGATCAGT TAAGGAGCTG TGCAATAAACC TTCTTAGTAC 1860  
 CTGAGTGAGT GTGTAACCTA TTGGGTTGGC GAAGCCTGGT AAAGCTGTTG GAATGAGTAT 1920  
 GTGATTCTTT TTAAGTATGA AAATAAAGAT ATATGTACAG ACTTGTATTT TTTCTCTGGT 1980  
 GGCAATTCCTT TAGGAATGCT GTGTGTCTGT CCGGCACCCC GGTAGGCCCTG ATTGGGTTTC 2040  
 TAGTCTCTCT TAACCACTTA TCTCCCATAT GAGAGTGTGA AAAATAGGAA CACGTGCTCT 2100  
 ACCTCCATTT AGGGATTGTC TTGGGATACA GAAGAGGCCA TGTGTCTCAG AGCTGTTAAG 2160  
 GGCCTTATTT TTTAAACAT TGGAGTCATA GCATGTGTGT AAACTTTAAA TATGCAATA 2220  
 AATAAGTATC TATGTCTAAA AAAAAAAAAA AAA 2253

Seq ID NO: C44 DNA Sequence  
 Nucleic Acid Accession #: NM\_013372  
 Coding sequence: 63..617

1 11 21 31 41 51  
 | | | | |  
 25 GCGGCCGCAC TCAGCGCCAC GCGTCGAAAG CGCAGGCCCC GAGGACCCGC CGCACTGACA 60  
 GTATGAGCCG CACAGCCTAC ACGGTGGGAG CCCTGCTTCT CCTCTTGGGG ACCCTGCTGC 120  
 CGGCTGCTGA AGGGAAAAAG AAAGGTGCCAT CCCCCTGCCA GACAAAGGCC 180  
 AGCACAATGA CTAGAGCAG ACTCAGTCGC CCCAGCAGCC TGGCTCCAGG AACCGGGGGC 240  
 GGGGCCAAGG GCGGGGCACG GCCATGCCCC GGGAGGAGGT GCTGGAGTCC AGCCAAGAGG 300  
 30 CCCTGCATGT GACGGAGCGC AAATACCTGA AGCGAGACTG GTGCAAAACC CAGCCGCTTA 360  
 AGCAGACCAT CCACGAGGAA GGCTGCAACA GTCGCACCAT CATCAACCCG TTCTGTACG 420  
 GCCAGTGCAA CTCTTTCTAC ATCCCAGGC ACATCCGGAA GGAGGAAGGT TCCTTTCAGT 480  
 CCTGCTCCTT CTGCAAGCCC AAGAAATTC AATCCATGAT GGTCACTCTC AACTGCCCTG 540  
 35 AACTACAGCC ACCTACCAAG AAGAAGAGAG TCACACGTGT GAAGCAGTGT CGTTGCATAT 600  
 CCATCGATTG GGATTAAGCC AAATCCAGGT GCACCCAGCA TGTCTTAGGA ATGCAGCCCC 660  
 AGGAAGTCCC AGACCTAAAA CAACCAGATT CTTACTTGGC TTAACCTTAG AGGCCAGAAG 720  
 AACCCCCAGC TGCTCTCTGG CAGGAGCCTG CTTGTGCGTA GTTCGTGTGC ATGAGTGTGG 780  
 ATGGGTGCCT GTGGGTGTTT TTAGACACCA GAGAAAACAC AGTCTCTGCT AGAGAGCACT 840  
 40 CCTATTTTGG TAAACATATC TGCTTTAATG GGGATGTACC AGAAAACCCAC CTCACCCCGG 900  
 CTACATCTTA AAGGGCGGGG GCGGTGTCTT GGTCTGACT TTGTGTTTTT GTGCGCTCCT 960  
 GGGGACAGGA ATCTCCTTTC GGAATGAATG TTCATGGAAG AGGCTCCTCT GAGGGCAAGA 1020  
 GACCTGTTTT AGTGCTGCAT TCGACATGGA AAAGTCTCTT TAACCTGTGC TTGCATCCTC 1080  
 CTTTCTCTCT CCTCTCACA ATCCATCTCT TCTTAAGTTG ATAGTACTA TGTCAGTCTA 1140  
 45 ATCTCTTGTT TGCCAGAGGT CCTAAATTA TCACTTAAC CATGATGCAA ATGTTTTTCA 1200  
 TTTTGTGAAG ACCCTCCAGA CTCTGGGAGA GGCTGGTGTG GGCAAGGACA AGCAGGATAG 1260  
 TGGAGTGAGA AAGGGAGGGT GGAGGGTGAG GCCAAATCAG GTCCAGCAAA AGTCAGTAGG 1320  
 GACATTGCAG AAGCTTGAAA GGCCAATACC AGAACACAGG CTGATGCTTC TGAGAAAGTC 1380  
 TTTTCTTAGT ATTTAACAGA ACCCAAGTGA ACAGAGGAGA AATGAGATTG CCAGAAAGTG 1440  
 50 ATTAACCTTG GCCGTGCAA TCTGCTCAA CCTAACCCA AACTGAAAC ATAAATACTG 1500  
 ACCACTCCTA TGTTCCGACC CAAGCAAGTT AGCTAAACCA AACCAACTCC TCTGCTTTGT 1560  
 CCTCAGGGT GAAAAGAGAG GTAGTTTAGA ACTCTCTGCA TAGGGGTGGG AATAATACAA 1620  
 AAACCKCAGA GGCTGAAATT CCTAATACCT TTCTTTATC GTGGTTATAG TCAGCTCATT 1680  
 TCCATTCCAC TATTTCCCAT AATGCTTCTG AGAGCCACTA ACTTGATTGA TAAAGATCCT 1740  
 55 GCCTCTGCTG AGTGTACCTG ACAGTAAGTC TAAAGATGAR AGAGTTTAGG GACTACTCTG 1800  
 TTTTAGCAAG ARATATKTGT GGGGTCTTTT TGTTTTAACT ATGTGTCAGG GATTGGGCTA 1860  
 RAGAGAAGAC AGGAAAGTA AGGAAATAAA GGGRATTGCC TCTGGCTAGA GAGTAAGTTA 1920  
 GGTGTTAATA CCTGGTAGAA ATGTAAGGGA TATGACCTCC CTTTCTTTAT GTGCTCACTG 1980  
 AGGATCTGAG GGGACCTGTG TAGGAGAGCA TAGCATCATG ATGTATTAGC TGTTCATCTG 2040  
 60 CTACTGGTTG GATGGACATA ACTATTGTAA CTATTGAGTA TTTACTGGTA GGCAGTGTCC 2100  
 TCTGATTAAA CTTGGCCCTAC TGGCAATGGC TACTTAGGAT TGATCTAAGG GCCAAAGTGC 2160  
 AGGGTGGGTG AACTTTATTTG TACTTTGGAT TTGGTTAACC TGTTTTCTTC AAGCTGAGG 2220  
 TTTTATATAC AAACCTCCTG AATACTCTTT TTGCCTTGTA TCTTCTCAGC CTCCTAGCCA 2280  
 AGTCCTATGT AATATGAAAA ACAAACTCTG CAGACTTGAG ATTCAGTTGC CGATCAAGGC 2340  
 65 TCTGGCATTC AGAGAACCCT TGCAACTCGA GAAGCTGTTT TTATTTCTGT TTTGTTTGA 2400  
 TCCAGTGCTC TCCCATCTAA CAACTAAACA GGAGCCATTT CAAGGCGGGA GATATTTTAA 2460  
 ACACCCAAAA TGTGGGTCTT GATTTTCAAA CTTTAAACT CACTACTGAT GATTCTCAGC 2520  
 CTAGGCGAAT TTGTCCAAAC ACATAGTGTG TGTGTTTGT ATACACTGTA TGACCCACC 2580  
 CCAAACTCTT GTATTGTCCA CATCTCCAA CAATAAAGCA CAGAGTGGAT TTAATTAAGC 2640  
 70 ACACAAATGC TAAGGCAGAA TTTTGAGGGT GGGAGAGAAG AAAAGGGAAA GAAGCTGAAA 2700  
 ATGTAAACC ACACAGGGA GGAATAATGA CATTGAGAAC CAGCAACAC TGAATTTCTC 2760  
 TTGTTGTTTT AACTCTGCCA CAAGAATGCA ATTTGCTTAA TGGAGATGAC TTAAGTTGGC 2820  
 AGCAGTAATC TTCTTTTAGG AGCTTGATAC ACAGTCTTGC ACATAAGTGC AGATTTGGCT 2880  
 CAAGTAAAGA GAATTTCTCT AACACTAAT TCACTGGGAT AATCAGCAGC GTAACCTACC 2940  
 75 TAAAGCATA TCACTAGCCA AAGAGGAAA TATCTGTCT TCTTACTGTG CCTATATTAA 3000  
 GACTAGTACA AATGTGGTGT GTCTTCCAAC TTTCAATTGA AATGCCATAT CTATACCATA 3060  
 TTTTATTGCA GTCACTGATG ATGTAATGAT ATATTTTTC ATATTATTAG TAGAATATTT 3120  
 TTAATGGCAAG ATATTTTGGG TCTTGATCAT ACCATTAAAT ATAATGCCAA ACACCAATA 3180  
 TGAATTTTAT GATGTACACT TTGTGCTTGG CATTAAAGA AAAAAACACA CATCTGGAA 3240  
 80 GTCGTGAAGT GTTTTTTTT TACTGTAGGT CTTCAAAGTT AAGAGTGTAA GTGAAAAATC 3300  
 TGGAGGAGAG GATAAATTTT ACTGTGTGGA ATGTGAATAG TTAATGAAA AGTTATGGTT 3360  
 ATTTAATGTA ATATTACTT CAAATCCTTT GGTCACTGTG ATTTCAAGCA TGTTTTCTTT 3420  
 TTCTCTTTTA TCTGAGTTGG GCAAGAAGA AGCTGACACA CCGTATGTTG 3480  
 TTAGAGTCTT TTATCTGGTC AGGGGAAACA AAATCTTGAC CCAGCTGAAC ATGTCTTCCT 3540  
 GAGTCAGTGC CTGAATCTTT ATTTTAAAA TTGAATGTTT CTTAAAGGTT AACATTCTA 3600



AAGCAATATT AAGAAAGACT TTAATGTGTT TTTTGAAGA CTTACGATGC ATGTATACAA 3660  
 ACGAATAGCA GATAATGATG ACTAGTTCAC ACATAAAGTC CTTTAAAGGA GAAATCTTAA 3720  
 AATGAAAAGT GGATAAACAG AACATTTATA AGTGATCAGT TAATGCCCTAA GAGTGAAAGT 3780  
 AGTTCTATTG ACATTCCCTCA AGATATTTAA TATCAACTGC ATTATGTATT ATGTCTGCTT 3840  
 AAATCATTTA AAAACGGCAA AGAATTATAT AGACTATGAG GTACCTTGCT GTGTAGGAGG 3900  
 ATGAAAGGGG AGTTGATAGT CTCATAAAAC TAATTTGGCT TCAAGTTTCA TGAATCTGTA 3960  
 ACTAGAATT T AATTTTCACC CCAATAATGT TCTATATAGC CTTTGCTAAA GAGCAACTAA 4020  
 TAAATTAAC CTATTCTTTC AAAAAAAA 4049

Seq ID NO: C45 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 200..2932

1 11 21 31 41 51  
 ATTGCTGATG GATCAGTGAG CCTGTGTTCA TGCCAGTGAG CTGCTGTGGC TCAGATACTG 60  
 ATACTTTCTT TCCAAACAGC ATAAGAAGTG ATTGAGCCAC AAGTATACTG AAGGAAGGGC 120  
 TCCCTCGAGT TCTGGTGTGA AGAGATAAAT CACCAGTCAC AGACTATGCA CCCGACTGCT 180  
 GCTGTTTCACT CCAGGGAATA TGAAAGTTGG AGTGCTGTGG CTCATTCTCT TCTTCACTT 240  
 CACTGACGGC CACGGTGGCT TCTTGGGGAA AAATGATGGC ATCAAACAA AAAAGAAGT 300  
 CATTGTGAAT AAGAAAAAAC ATCTAGGCCC AGTCGAAGAA TATCAGCTGC TGCTTCAGGT 360  
 GACCTATAGA GATTCCAAGG AGAAAAGAGA TTTGAGAAAT TTTCTGAAGC TCTTGAAGCC 420  
 TCCATTATTA TGGTCAATG GGCTAATTAG AATTATCAGA GCAAAGGCTA CCACAGACTG 480  
 CAACAGCCTG AATGGAGTCC TGCAGTGTAC CTGTGAAGAC AGCTACACCT GGTTCCTCC 540  
 CTCATGCCCT GATCCCCAGA ACTGCTACCT TCACACGGCT GGAGCACTCC CAAGCTGTGA 600  
 ATGTCACTCT AACAACTCA GCCAGAGTGT CAATTTCTGT GAGAGAACAA AGATTGGGG 660  
 CACTTTCAA ATTAATGAAA GGTTTACAAA TGACCTTTT AATTCACTCT CTGCTATATA 720  
 TCCAAATAT GCAAAATGGA TTGAAATCA ACTTAAAAA GCATATGAAA GAATTCAAGG 780  
 TTTTGAGTCG GTTCAGGTCA CCCAATTCG AAATGGAAGC ATCGTTGCTG GGTATGAAGT 840  
 TGTGGCTCC AGCAGTGCAT CTGAAGTCTG GTCAGCCATT GAACATGTTG CCGAGAAGGC 900  
 TAAGACAGCC CTTCAACAGC TGTTCCTATT AGAAGACGGC TCTTCAGAG TGTTCGGAAA 960  
 AGCCCAAGTG AATGACATTG TCTTTGGATT TGGGTCCAAG GATGATGAAT ATACCTGCTC 1020  
 CTGCAGCAGT GGCTACAGGG GAAACATCAC AGCCAAGTGT GAGTCCCTCT GGTGGCAGGT 1080  
 CATCAGGGAG ACTTGTGTGC TCTCTCTGCT TGAAGAACTG AACAAGAAAT TCAGTATGAT 1140  
 TGTAGCAAT GCCACTGAGG CAGCTGTGTC ATCCTTCGTG CAAAATCTTT CTGCTATCAT 1200  
 TCGGCAAAAC CCAATCAACCA CAGTGGGGAA TCTGGCTTCG GTGGTGTGCA TTTGAGCAA 1260  
 TATTTCACT CTGTCACTGG CCAGCCATT CAGGGTGTCC AATTCAACAA TGGAGGATGT 1320  
 CATCAGTATA GCTGACAATA TCCTTAATTC AGCCTCAGTA ACCAACTGGA CAGTCTTACT 1380  
 GCGGGAAGAA AAGTATGCCA GCTCAGGTT ACTAGAGACA TTAGAAAACA TCAGCACTCT 1440  
 GGTGCTCTCG ACAGCTCTTC CTCTGAATTT TTCTCGGAAA TTCATTGACT GGAAAGGGAT 1500  
 TCCAGTGAAC AAAAGCCAAC TCAAAAGGGG TTACAGCTAT CAGATTAAAA TGTGTCCCA 1560  
 AAATACATCT ATTCCCATCA GAGGCCGTGT GTTAATTGGG TCAGACCAAT TCCAGAGATC 1620  
 CCTTCAGAAA ACTAATTATCA GCATGGCCTC GTTGACTCTG GGAACATTCT TACCCGTTTC 1680  
 CAAAATGGA AATGCTCAGG TCAATGGACC TGTGATATCC ACGGTTATTC AAAACTATTC 1740  
 CATAAATGAA GTTTTCTCAT TTTTTCCAA GATAGAGTCA AACCTGAGCC AGCCTCATTT 1800  
 TGTGTTTTGG GATTTCAGTC ATTTGCAGTG GAACGATGCA GGCTGCCACC TAGTGAATGA 1860  
 AACTCAAGAC ATCGTGACGT GCCAATGTAC TCACCTGACC TCCTTCTCCA TATTGATGTC 1920  
 ACCTTTTGTG CCTCTACAA TCTTCCCGT TGTAAATGG ATCACTATG TGGGACTGGG 1980  
 TATCTCCATT GGAAGTCTCA TTTTATGCC TATCATCGAG GCTTTCTTTT GGAAGCAGAT 2040  
 TAAAAAAGC CAAACCTCTC ACACACGTCG TATTTGCATG GTGAACATAG CCCTGTCCCT 2100  
 CTTGATTGCT GATGCTGGT TTATTGTTGG TGCCACAGTG GACACCACGG TGAACCCCTC 2160  
 TGGAGTCTGC ACAGCTGCTG TGTCTTTTAC ACACCTCTTC TACCTCTCTT TGTCTCTG 2220  
 GATGCTCATG CTGTGGCTCC TGCTGGCTTA CCGGATCATC CTCGTGTTCC ATCAGATGGC 2280  
 CCAGCATTTG ATGATGGCTG TTGGATTTTG CCTGGGTTAT GGGTGCCCTC TCATTATATC 2340  
 TGTCAATACC ATTGCTGTCA CGCAACCTAG CAATACCTAC AAAAGGAAAG ATGTGTGTTG 2400  
 GCTTAACCTG TCCCAAGTGA GCAAACCACT CCTGGCTTTT GTTGTCCCTG CACTGGCTAT 2460  
 TGTGGCTGTG AACTTCGTTG TGGTGTGCT AGTCTCACA AAGCTCTGGA GGCCGACTGT 2520  
 TGGGGAAGAA CTGAGTCGGG ATGACAAGGC CACCATCATC CGCGTGGGGA AGAGCCTCCT 2580  
 CATCTGACC CTTCTGTAG GGCTCACCTG GGGCTTTGGA ATAGGAACAA TAGTGGACAG 2640  
 CCAGAACTCT GCTTGGCATG TTATTTTTCG TTTACTCAAT GCATTCCAGG GATTTTTTAT 2700  
 CTTATGCTTT GGAATACCT TGGACAGTAA GCTGCGACAA CTTCTGTCCA ACAAGTTGTC 2760  
 TGCCTTAAGT TCTTGAAGC AAACAGAAAA GCAAACTCA TCAGATTAT CTGCCAAACC 2820  
 CAAATCTCA AAGCCTTTCA ACCCACTGCA AAACAAAGGC CATATGCAT TTTCTCATAC 2880  
 TGGAGATTCC TCCGACAACA TCATGCTAAC TCAGTTTGTG TCAATGAAT AAGGCAAGGA 2940  
 ATCATAAAT CAAGAAAAA TTTCCAGAAC AACTTGACAT TTAGAGACAA ATGTCAATGA 3000  
 AGAAATTATG CTAGTATTC GATCGGGTT TCTGATTTAG GGGTCTGGGA ATAAACAAG 3060  
 AATGTCTCAG TGCTTCA 3078

Seq ID NO: C46 DNA Sequence  
 Nucleic Acid Accession #: NM\_000584.1  
 Coding sequence: 75..374

1 11 21 31 41 51  
 AGCAGAGCAC ACAAGCTTCT AGGACAAGAG CCAGGAAGAA ACCACCGGAA GGAACCATCT 60  
 CACTGTGTGT AAACATGACT TCCAAGCTGG CCGTGGCTCT CTTGGCAGCC TTCCTGATTT 120  
 CTGCAGCTCT GTGTGAAGGT GCAGTTTTCG CAAGGAGTGC TAAAGAAGTT AGATGTGAGT 180  
 GCATAAAGAC ATACTCCAAA CCTTCCACC CCAATTTTAT CAAAGAAGCT AGAGTGATTG 240  
 AGAGTGGACC ACACCTGCAC AACACAGAAA TTATTGTAAA GCTTCTGAT GGAAGAGAGC 300  
 TCTGTCTGGA CCCCAAGGAA AACTGGGTGC AGAGGGTGTG GGAGAAGTTT TTGAAGAGGG 360  
 CTGAGAAATC ATAAAAAAT TCATTCTCTG TGGTATCCAA GAATCAGTGA AGATGCCAGT 420  
 GAAACTTCAA GCAATCTTAC TTCACACTT CATGTATTGT GTGGGTCTGT TGTAGGGTTG 480  
 CCAGATGCAA TACAAGATTC CTGGTTAAAT TTGAATTTCA GTAAACAATG AATAGTTTTT 540  
 CATGTACCA TGAATATACC AGAACATACT TATATGTAAA GTATTATTTA TTTGAATCTA 600

CAAAAACAA CAAATAATTT TTAATATATA GGATTTTCCT AGATATTGCA CGGGAGAATA 660  
 TACAAATAGC AAAATTGAGC CAAGGGCCAA GAGAATATCC GAACTTTAAT TTCAGGAATT 720  
 GAATGGGTTT GCTAGAATGT GATATTTGAA GCATCACATA AAAATGATGG GACATAAAT 780  
 TTTGCCATAA AGTCAAATTT AGCTGGAAAT CCTGGATTTT TTTCTGTAA ATCTGGCAAC 840  
 CCTAGCTGCG TAGCCAGGAT CCACAAGTCC TTGTTCCT GTGCCTTGCT TTCTCCTTTA 900  
 TTTCTAAGTG GAAAAAGTAT TAGCCACCAT CTACCTCAC AGTGATGTTG TGAGGACATG 960  
 TGGAGCACT TTAAGTTTTT TCATCATAAAC ATAAATTATT TTCAAGTGA ACTTATTAAAC 1020  
 CTATTATTA TTTATGTATT TATTTAAGCA TCAATATTT GTGCAAGAAT TTGAAAAAT 1080  
 AGAAGATGAA TCATTGATTG AATAGTTATA AAGATGTTAT AGTAAATTTA TTTTATTTTA 1140  
 GATATTAAT GATGTTTTAT TAGATAAAT TCAATCAGGG TTTTATGATT AAACAAAGAA 1200  
 ACAATTGGGT ACCCAGTTAA ATTTTCATTT CAGATAAACA ACAAATAATT TTTTAGTATA 1260  
 AGTACATTAT TGTTTATCTG AAAGTTTTAA TTGAACATAA AATCCTAGTT TGATACTCCC 1320  
 AGTCTTGTC TGGCCAGCTG TGTGGGTAGT GCTGTGTTGA ATTACGGAAT AATGAGTTAG 1380  
 AACTATTAA ACAGCCAAAA CTCCACAGTC AATATTAGTA ATTTCTTGCT GGTGAAACT 1440  
 TGTTTATTAT GTACAAATAG ATTCTTATAA TATTATTAA ATGACTGCAT TTTTAAATAC 1500  
 AAGGCTTTAT ATTTTAACT TTAAGATGTT TTTATGTGCT CTCCAATTT TTTTACTGT 1560  
 TTCTGATTGT ATGGAATAT AAAAGTAAAT ATGAACATT TAAATATATA TTTGTGTGCA 1620  
 AAGTAAAAA AAAAAAAA 1639

Seq ID NO: C47 DNA Sequence  
 Nucleic Acid Accession #: NM\_005603.1  
 Coding sequence: 1..3756

1 11 21 31 41 51  
 | | | | |  
 ATGAGTACAG AAAGAGACTG AGAAACGACA TTTGACGAGG ATTCTCAGCC TAATGACGAA 60  
 GTGGTTCCTT ACAGTGTATG TGAAACAGAA GATGAACCTG ATGACCAGGG GTCTGCTGTT 120  
 GAACCAGAAC AAAACCGAGT CAACAGGGAA GCAGAGGAGA ACCGGGAGCC ATTCAGAAAA 180  
 GAATGTACAT GGCAAGTCAA AGCAAACGAT CGCAAGTACC ACGAACCAACC TCACCTTTATG 240  
 AACACAAAAA TCTTGTGTAT TAAGGAGAGT AAATATGCGA ATAATGCAAT TAAACATAC 300  
 AAGTACAACG CATTTACCTT TATACCAATG AATCTGTTTG AGCAGTTTAA GAGAGCAGCC 360  
 AATTATATAT TCCTGGCTCT TCTTATCTTA CAGGCAGTTC CTCAAATCTC TACCCTGGCT 420  
 TGGTACACCA CACTAGTGCC CCTGCTTGCT GTGCTGGGCG TCACCTGCAAT CAAAGACCTG 480  
 GTGGACGATG TGGCTCGCCA TAAATGGAT AAGGAAATCA ACAATAGGAC GTGTGAAGTC 540  
 ATTAAGGATG GCAGGTTCAA AGTTGCTAAG TGGAAAGAAA TTCAAGTTGG AGACGTCATT 600  
 CGTCTGAAAA AAAATGATTT TGTTCAGCT GACATTCTCC TGCTGTCTAG CTCTGAGCCT 660  
 AACAGCCTCT GCTATGTGGA AACAGCAGAA CTGGACGGAG AAACCAATTT AAAATTTAAG 720  
 ATGTCACTTG AAATCACAGA CCAGTACCTC CAAAGAGAAG ATACATTGGC TACATTTGAT 780  
 GGTTTTATTG AATGTGAAGA ACCCAATAAC CGACTAGATA AGTTTACAGG AACACTATTT 840  
 TGGAGAAACA CAAGTTTTCC TTTGGATGCT GATAAAATTT TGTACGTTGG CTGTGTAATT 900  
 AGGAACACCG ATTTCTGCCA CGGCTTAGTC ATTTTTCGAG GTGCTGACAC TAAATAATG 960  
 AAGAATAGTG GGAACACCAG ATTTAAAAGA ACTAAAATTG ATTACTTGAT GAACCTACATG 1020  
 GTTTACACGA TCTTTGTTTG TCTTATCTCT CTTTCTGCTG GTCTTGCCAT CGGCCATGCT 1080  
 TATTGGGAAG CACAGGTGGG CAATTCTCT TGGTACCTCT ATGATGAGGA AGACGATACA 1140  
 CCCTCTACCC GTGGATTCTT CATTTCTGCG GGCTATATCA TTGTTCTCAA CACCATGGTA 1200  
 CCCATCTCTC TCTATGTGAG CGTGGAAGTG ATTCGTCTTG GACAGAGTCA CTTCTATCAAC 1260  
 TGGGACCTGC AAATGTACTA TGCTGAGAAG GACACACCCG CAAAAGCTAG AACCAACACA 1320  
 CTCAATGAAC AGCTCGGGCA GATCCATTAT ATCTTCTCTG ATAAGACGGG GACACTCACA 1380  
 CAAAATATCA TGACCTTTAA AAAGTGCTGT ATCAACGGCG AGATATATGG GGACCATCGG 1440  
 GATGCTCTC AACACAACA CAACAAAATA GAGCAAGTTG ATTTTAGCTG GAATACATAT 1500  
 GCTGATGGGA AGCTTGCATT TTATGACCAC TATCTTATTG AGCAAAATCCA GTCAGGGAAA 1560  
 GAGCCAGAAG TACGACGATT CTTCTTCTTG CTCGCAGTTT GCCACACAGT CATGGTGGAT 1620  
 AGGACTGATG GTCAGCTCAA CTACCAAGCA GCCTCTCCCG ATGAAGGTGC CCTGGTAAAC 1680  
 GCTGCCAGGA ACTTTGGCTT TGCCTTCTCT GCCAGGACCC AGAACACCAT CACCATCAGT 1740  
 GAACCTGGCA CTGAAGGAGC TTACAATGTT CTTGCCATT TGGACTTCAA CAGTGACCGG 1800  
 AAGCGAATGT CTATCATTGT AAGAACCCCA GAAGGCAATA TCAAGCTTTA CTGTAAAGGT 1860  
 GCTGACACTG TTATTATGTA ACGGTTACAT CGAATGAATC CTACTAAGCA AGAAACACAG 1920  
 GATGCCCTGG ATATCTTTGC AAATGAAACT CTTAGAACCC TATGCTTTTG CTACAAGGAA 1980  
 ATTGAAGAAA AAGAATTTAC AGAATGGAAT AAAAAGTTTA TGGCTGCCAG TGTGGCCTCC 2040  
 ACCAACCGGG ACGAAGCTCT GGATAAAGTA TATGAGGAGA TTGAAAAAGA CTTAATTCTC 2100  
 CTGGGAGCTA CAGCTATTGA AGACAAGCTA CAGGATGGAG TTCCAGAAAC CATTTCAAAA 2160  
 CTTGCAAAAG CTGACATTAA GATCTGGGTG CTTACTGGAG ACAAAGGA AACTGCTGAA 2220  
 AATATAGGAT TTGCTGTGTA ACTTCTGACT GAAGACACCA CCATCTGCTA TGGGGAGGAT 2280  
 ATTAATTTCT TCTTCTATGC AAGGATGGAA AACCAGAGGA ATAGAGGTGG CGTCTACGCA 2340  
 AAGTTTGAC CTCTGTGCA GGAATCTTTT TTTCCACCCG GTGGAACCG TGCCCTAATC 2400  
 ATCACTGGTT CTGTGTTGAA TGAATTTCTT CTCGAGAAAA AGACCAAGAG AAATAAGATT 2460  
 CTGAAGCTGA AGTTCCCAAG AACAGAAGAA GAAAGACGGA TGCGGACCCA AAGTAAAGG 2520  
 AGGCTAGAAG CTAAGAAAAG GCAGCGGCAG AAAAAGCTTG TGGACCTGGC CTGCGAGTGC 2580  
 AGCGCAGTCA TCTGCTGCCG CGTCACCCCC AAGCAGAAAG CCATGGTGGT GGACCTGGTG 2640  
 AAGAGGTACA AGAAGCCAT CACGCTGGCC ATCGGAGATG GGGCCAATGA CGTGAACATG 2700  
 ATCAAACTG CCCACATTGG CGTTGGAATA AGTGACAAG AAGGAATGCA AGCTGTCTATG 2760  
 TCGAGTGACT ATTCCTTTGC TCAGTTCCGA TATCTGCAGA GGCTACTGCT GGTGCTATGC 2820  
 CGATGGTCTT ACATAAGGAT GTGCAAGTTC CTACGATACT TCTTTTACAA AAACCTTGCC 2880  
 TTTACTTTGG TTCATTCTG GTACTCTTTC TTCAATGGCT ACTCTGCGCA GACTGCATAC 2940  
 GAGGATTTGT TCATCACCTT CTACACCTG CTGTACACCA GCCTGCCCGT GCTCCTCATG 3000  
 GGGCTGCTCG ACCAGGATGT GAGTGACAAA CTGAGCCTCC GATTCCTTGG GTTATACATA 3060  
 GTGGGACAAA GAGACTTACT ATTCAACTAT AAGAGATTCT TTGTAAGCTT GTTGCTATGG 3120  
 GTCCTAACAT CGATGATCCT CTTCTTCATA CCTCTTGGAG CTTATCTGCA AACCGTAGGG 3180  
 CAGGATGGAG AGGCACCTTC CGACTACCA TCTTTTCCCG TCACCATGCT CTCTGCTCTT 3240  
 GTAATAACAG TCAATTTCCA GATTGGCTTG GATACTTCTT ATTGGACTTT TGTGAATGCT 3300  
 TTTTCAATT TTGGAAGCAT TGCACCTTAT TTTGGCATCA TGTTTGACTT TCATAGTGCT 3360  
 GGAATACATG TTCTCTTTCC ATCTGCATTT CAATTTACAG GCACAGCTTC AAACGCTCTG 3420  
 AGACAGCCAT ACATTTGGTT AACTATCATC CTGACTGTTG CTGTGTGCTT ACTACCCGTC 3480

GTTGCCATTC GATTCTGTG AATGACCATC TGGCCATCAG AAAGTGATAA GATCCAGAAG 3540  
 CATCGCAAGC GGTGGAAGGC GGAGGAGCAG TGGCAGCGAC GGCAGCAGGT GTTCCGCCGG 3600  
 GGCGTGTCAA CGCGGCGCTC GGCTACGCC TTCTCGCACC AGCGGGGCTA CGCGGACCTC 3660  
 ATCTCCTCCG GCGCAGCAT CGCAAGAAG CGCTCGCCG TTGATGCCAT CGTGGCGGAT 3720  
 GGCACGCGG AGTACAGCG CACCGGGGAC AGCTGA 3756

Seq ID NO: C48 DNA Sequence  
 Nucleic Acid Accession #: XM\_044533  
 Coding sequence: 238..2751

1 11 21 31 41 51  
 GCTCTGCCCA AGCCGAGGCT GCGGGGCGGG CGCCGGCGGG AGGACTGCGG TGCCCCGCGG 60  
 AGGGGCTGAG TTTGCCAGGG CCCACTTGAC CCTGTTTCCC ACCTCCCGCC CCCAGGTCC 120  
 GGAGGCGGGG GCGCCCGGGG CGACTCGGGG GCGGACCGCG GGGCGGAGCT GCGGCCGCTG 180  
 AGTCCGGCCG AGCCACTGA GCCGAGCCG CGGGACACCG TCGCTCTGCT TCTCCGAATG 240  
 CTGCGCACCG CGATGGCCCT GAGGAGCTGG CTCGCCGCCC CATGGGGCGC GCTGCCGCT 300  
 CGGCCACCGC TGCTGTGCT CTGTGCTGCT CTGCTCTGCT TGCGGCGGCC GCCTCCGACC 360  
 TGGGCGCTCA GCCCCGCGAT CAGCCTGCCT CTGGGCTCTG AAGAGCGGCC ATTCCTCAGA 420  
 TTCTGAAGCTG AACACATCTC CAACTACACA GCCCTTCTGC TGAGCAGGGA TGGCAGGACC 480  
 CTGTAGTGG GTGCTCGAGA GGCCCTCTTT GCACCTAGTA GCAACCTCAG CTTCCTGCCA 540  
 GGCGGGGAGT ACCAGGAGCT GCTTTGGGGT GCAGACGCG AGAAGAAACA GCAGTGCAGC 600  
 TTCAAGGGCA AGGACCCACA GCGCGACTGT CAAAACCTACA TCAAGATCCT CTGCGCGCTC 660  
 AGCGGCGAGT ACCTGTTCAC CTGTGGCACA GCAGCCTTCA GCCCATGTG TACCTACATC 720  
 AACATGGAGA ACTTCACCCT GCGAAGGGAC GAGAAGGGGA ATGTCTCTCT GGAAGATGGC 780  
 AAGGGCCGTT GTCCCTTCGA CCGAATTTT AAGTCCACTG CCTTGGTGGT TGATGGCGAG 840  
 CTCTACACTG GAACAGTCAG CAGCTTCCAA GGAATGACC CGGCCATCTC CGGGAGCCAA 900  
 AGCCTTCGCC CACCAAGAG CGAGAGCTCC CTCAACTGGC TGCAAGACCC AGCTTTTGTG 960  
 GCCTCAGCCT ACATTCTCTGA GAGCCTGGGC AGCTTGCAAG CGGATGATGA CAAGATCTAC 1020  
 TTTTCTCTCA GCGAGACTGG CCAGGAATTT GAGTCTCTTG AGAACACCAT TGTGTCCCGC 1080  
 ATTGCCCGCA TCTGCAAGGG CGATGAGGGT GGAGAGCGGG TGCTACAGCA GCGCTGGACC 1140  
 TCCTTCTCTCA AGGCCAGCT GCTGTGCTCA CGGCCGACG ATGGCTTCCC CTCAACGCTG 1200  
 CTGCAGGATG TCTTCAGCT GAGCCCGAGC CCCAGGACT GCGGTGACAC CCTTTTCTAT 1260  
 GGGGTCTTCA CTTCACAGTG GCACAGGGGA ACTACAGAAG GCTCTGCCGT CTGTGTCTTC 1320  
 ACAATGAAGG ATGTGCAGAG AGTCTTCAGC GGCCTCTACA AGGAGGTGAA CCGTGAGACA 1380  
 CAGCAGTGGT ACACCGTGAC CCACCCGGTG CCCACACCCC GGCCTGGAGC GTGCATCACC 1440  
 AACAGTGCCC GGAAGAGAA GATCAACTCA TCCCTGCAGC TCCAGACCG CGTGTGAAC 1500  
 TTCTCAAGG ACCACTTCCT GATGGACGGG CAGGTCCGAA GCCGCATGCT GCTGTGTCAG 1560  
 CCCAGGCTC TCTACAGCG CGTGGCTGTA CACCGCGTCC CTGGCCTGCA CCACACCTAC 1620  
 GATGTCTCT TCTTGGGAC TGGTGACGGC CGGCTCCACA AGGCAGTGAG CGTGGGCCCC 1680  
 CGGGTGACCA TCAATTGAGG GCTGCAGATC TTCTCATCGG GACAGCCCGT GCAGAACTG 1740  
 CTCTGGACA CCCACAGGGG GCTGCTGTAT GCGGCCTCAC ACTCGGCGT AGTCCAGGTG 1800  
 CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGGACT GCCTCTCGC CCGGGACCCC 1860  
 TACTGTGCTT GAGAGCGCTC CAGCTGCAAG CAGCTCAGCC TCTACAGGCC TCAGCTGGCC 1920  
 ACCAGGCCGT GGATCCAGGA CATCGAGGGA GCCAGCGCCA AGGACCTTTG CAGCGCTCT 1980  
 TCGGTTGTGT CCCCGTCTTT TGTACCAACA GGGGAGAAGC CATGTGAGCA AGTCCAGTTC 2040  
 CAGCCCAACA CAGTGAACAC TTTGGCCTGC CCGCTCTCTT CCAACCTGGC GACCCGACTC 2100  
 TGGCTACGCA ACGGGGCCCC CGTCAATGCC TCGGCCCTCT GCCACGTGCT ACCCACTGGG 2160  
 GACCTGTCTG TGGTGGGCAC CCAACAGCTG GGGGAGTTCC AGTGTCTGTC ACTAGAGGAG 2220  
 GGCTTCCAGC AGCTGGTAGC CAGCTACTGC CCAGAGGTGG TGGAGGACCG GGTGGCAGAC 2280  
 CAAACAGATG AGGGTGGCAG TGTACCCGTC ATTATCAGCA CATCGCGTGT GAGTGCACCA 2340  
 GCTGGTGGCA AGGCCAGCTG GGTGTCAGAC AGGTCCCTACT GGAAGGAGTT CTGGTGTATG 2400  
 TGCAGGCTCT TTTGTCTGGC CGTGTGCTC CAGTTTTAT TCTGTCTCTA CCGGACCCGG 2460  
 AACAGCATGA AAGTCTTCCT GAAGCAGGGG GAATGTGCCA GCGTGACCCC CAAGACCTGC 2520  
 CCTGTGGTGC TGCCCCCTGA GACCCGCCCA CTCAACGGCC TAGGGCCCCC TAGCACCCCG 2580  
 CTGCATCACC GAGGGTACCA GTCCCTGTCA GACAGCCCCC CGGGGTCCCC AGTCTTCACT 2640  
 GAGTCAGAGA AGAGGCCACT CAGCATCCAA GACAGCTTCG TGGAGGTATC CCAGTGTGC 2700  
 CCGCGGCCCC GGGTCCGCT TGGCTCGGAG ATCCGTGACT CTGTGGTGTG AGAGCTGACT 2760  
 TCCAGAGGAC GCTGCCCTGG CTTAGGGGCG TGTGAATGCT CGGAGAGGGT CAACTGGACC 2820  
 TCCCTCCGC TCTGCTCTTC GTGGAACACG ACCGTGGTGC CCGGCCCTTG GAGGCTTGG 2880  
 GGCCAGCTGG CCTGCTGCTC TCCAGTCAAG TAGCGAAGCT CCTACCACCC AGACACCCAA 2940  
 ACAGCCGTGG CCCAGAGGT CCTGGCCAAA TATGGGGGCC TGCTAGGTT GGTGGAACAG 3000  
 TGCTCTTAT GTAACCTGAG CCCTTTGTTT AAAAAACAAT TCCAAATGTG AAAGTGAAT 3060  
 GAGAGGGGAG AGATAGCATG GCATGCAGCA CACACGGCTG CTCCAGTTCA TGGCCTCCCA 3120  
 GGGGTGCTGG GATGTCATCC AAAGTGGTTG TCTGAGACAG AGTTGGAAC CCTCACCAAT 3180  
 TGGCTCTTCT ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT 3240  
 CAGGACCAGC TTGGGCTGCG TGCCTTCTGC CTTGCCAGTC AGCCGAGGAT GTAGTTGTTG 3300  
 CTGCCGCTGT CCCACACCT CAGGACCCAG AGGGCTAGGT TGGCACTGCG GCCCTCACCA 3360  
 GGTCTTGGGC TCGGACCCAA CTCCTGGACC TTTCCAGCCT GTATCAGGCT GTGGCCACAC 3420  
 GAGAGGACAG CGCGAGCTCA GGAGAGATT CTGTGCAATG TACGCCTTTC CCTCAGAAAT 3480  
 CAGGGAAGAG ACTGTGCGCT GCCTTCTCTC GTTGTGCGT GAGAACCCTG GTGCCCTTTC 3540  
 CCACCATATC CACCTCGCT CCATCTTGA ACTCAAACAC GAGGAACATA CTCACCCCTG 3600  
 GTCTCTCTCC CAGTCCCCAG TTCACCCCTC ATCCCTCACC TTCCTCCACT CTAGGGGATA 3660  
 TCAACACTGC CAGACAGAG GGCCTGAAT TTATGTGGTT TTTATACATT TTTAATAAAG 3720  
 ATGCACTTTA TGTCATTTTT TAATAAAGTC TGAAGAATTA CTGTTT 3756

Seq ID NO: C49 DNA Sequence  
 Nucleic Acid Accession #: NM\_007019.1  
 Coding sequence: 41..580

1 11 21 31 41 51  
 GGCACGAGCG AGTTCCTGTC TCTCTGCCAA CGCCGCCCGG ATGGCTTCCC AAAACCGCGA 60

```

CCCAGCCGCC ACTAGCGTCG CCGCCGCCCG TAAAGGAGCT GAGCCGAGCG GGGGCGCCGC 120
CCGGGGTCCG GTGGGCAAAA GGCTACAGCA GGAGCTGATG ACCCTCATGA TGTCTGGCGA 180
TAAAGGGATT TCTGCCITCC CTGAATCAGA CAACCTTTTC AAATGGGTAG GGACCATCCA 240
TGGAGCAGCT GGAACAGTAT ATGAAGACCT GAGGTATAAG CTCTCGCTAG AGTTCCCCAG 300
TGGCTACCCCT TACAATGGCG CCACAGTGAA GTTCTCACG CCCTGCTATC ACCCCAACGT 360
GGACACCCAG GGTAAACATAT GCCTGGACAT CCTGAAGGAA AAGTGGTCTG CCCTGTATGA 420
TGTCAAGACC ATTCTGCTCT CCATCCAGAG CCTTCTAGGA GAACCCAACA TTGATAGTCC 480
CTTGAACACA CATGCTGCCG AGCTCTGGAA AAACCCACCA GCTTTTAAGA AGTACCTGCA 540
AGAAACCTAC TCAAAGCAGG TCACAGGCCA GGAGCCCTGA CCCAGGCTGC CCAGCCTGTC 600
CTTGTGTGCT TTTTAAATT TTTCTTAGA TGGTCTGTCC TTTTGTGAT TTCTGTATAG 660
GACTCTTTAT CTTGAGCTGT GGTATTTTGT TTTTGTTTTT GTCTTTTAAA TTAAGCCTCG 720
GTTGAGCCCT TGTATATTAA ATAAATGCAT TTTTGTCTCT TTTTAAAAAA AAAAAAAAAA 780
AAA 783

```

Seq ID NO: C50 DNA Sequence  
Nucleic Acid Accession #: NM\_014584.1  
Coding sequence: 227..1633

```

1 11 21 31 41 51
| | | | |
GCACAGAGCC CGGGCTGCCG GCGCGGGCGC GCGGCGCAGT CCACAGGCTG GGTGCGGAGG 60
TGGCGATCGC TGAGAGGCGAG GAGGGCCGAG GCGGGCCTGG GAGGCGGCCG GGAGGTGGGG 120
CGCCGCTGGG GCCGGCCCGC ACGGGCTTCA TCTGAGGGCG CACGGCCCGC GACCGAGCGT 180
GCGGACTGGC CTCCCAAGCG TGGGGCGACA AGCTGCCGGA GCTGCAATGG GCCGCGGCTG 240
GGGATTTCTG TTTGGCCTCC TGGGGCGCGT GTGGCTGTCT AGCTCGGGCC ACGGAGAGGA 300
GCAGCCCCCG GAGACAGCGG CACAGAGGTG CTTCTGCCAG GTTAGTGGTT ACTTGGATGA 360
TTGTACCTGT GATGTTGAAA CCATTGATAG ATTTAATAAC TACAGGCTTT TCCCAAGACT 420
ACAAAAAATT CTTGAAAGTG ACTACTTTAG GTATTACAAG GTAAACCTGA AGAGGCCGTG 480
TCCTTTCTGG AATGACATCA GCCAGTGTGG AAGAAGGGAC TGTGCTGTCA AACCATGTCA 540
ATCTGATGAA GTTCTGTATG GAATTAAATC TGCGAGCTAC AAGTATTCTG AAGAAGCCAA 600
TAATCTCATT GAAGAATGTG AACAAAGCTG ACGACTTGGG GCAGTGGATG AATCTCTGAG 660
TGAGGAAACA CAGAAGGCTG TTCTTCAGTG GACCAAGCAT GATGATTCTT CAGATAACTT 720
CTGTGAAGCT GATGACATTC AGTCCCCTGA AGCTGAATAT GTAGATTGCG TTCTTAATCC 780
TGAGCGCTAC ACTGGTTACA AGGGACCCAGA TGCTTGGAAA ATATGGAATG TCATCTACGA 840
AGAAACTGT TTTAAGCCAC AGACAATTAA AAGACCTTTA AATCCTTTGG CTTCTGGTCA 900
AGGGACAAGT GAAGAGAAAC CTTTTTACAG TTGGCTAGAA GGTCTCTGTG TAGAAAAAAG 960
AGCATTCTAC AGACTTATAT CTGGCCTACA TGCAAGCATT AATGTGCATT TGAGTGCAAG 1020
ATATCTTTTA CAAGAGACCT GGTTAGAAAA GAAATGGGGA CACAACATTA CAGAAATTTCA 1080
ACAGCGATTT GATGGAATTT TGACTGAAGG AGAAGGTCCA AGAAGGCTTA AGAACTTGTA 1140
TTTTCTCTAC TTAATAGAAC TAAGGGCTTT ATCCAAAGTG TTACCATTCT TCGAGCGCCC 1200
AGATTTTCAA CTCTTTACTG GAAATAAAAT TCAGGATGAG GAAAAACAAA TGTTACTTCT 1260
GGAAATACTT CATGAAATCA AGTCATTTCC TTGCAATTTT GATGAGAAAT CATTTTITGC 1320
TGGGGATAAA AAAGAGCAC ACAAACTAAA GGAGGACTTT CGACTGCATT TTAGAAATAT 1380
TTCAAGAAAT ATGGATTGTG TTGGTTGTTT TAAATGTCGT CTGTGGGGAA AGCTTCAGAC 1440
TCAGGGTTTG GGCAGTGTCT TGAAGATCTT ATTTTCTGAG AAATTGATAG CAAATATGCC 1500
AGAAAGTGA CTAAGTTATG AATTCCATCT AACCAGACAA GAAATAGTAT CATTATTCAA 1560
CGCAATTGGA AGAATTTCTA CAAGTGTGAA AGAATTAGAA AACTTCAGGA ACTTGTGTCA 1620
GAATATTCAT TAAAGAAAAC AAGCTGATAT GTGCCGTGTT CTGGACAATG GAGGCGAAAG 1680
AGTGGAAATT CATTCAAAGG CATAATAGCA ATGACAGTCT TAAGCCAAAC ATTTTATATA 1740
AAGTTGCTTT TGTAAAGGAG AATTATATTG TTTTAAGTAA ACACATTTT TAAAAATGTG 1800
TTAAGTCTAT GTATAATACT ACTGTGAGTA AAAGTAATAC TTTAATAATG TGGTACAAAT 1860
TTTAAAGTTT AATATTGAAT AAAAGGAGGA TTATCAAATT CATATATGAT AAAAGTGAAT 1920
GTTCTAAGTC TCTCAAACCTA GCGTTTTATG TAATAATATG TAATATAAAT AAAACTATGG 1980
TAAATGTGAC AAGCATTTAA TAGGAAAATG CTAAGGAGGC CTCATAAATG ACCCATAATT 2040
ACCAACGTAG AATTTTTCAG TACATTTAGG GTTGCTGGAT TTAGCAATAA AAAATAAAGA 2100
TGGCCAGATT AGATTGGAAT TTCAGATAAA CAATTAGTTT TTTAATATTT TACATGGAAT 2160
ATTTGAAAAA TACTTATACT AAAAAATTAT TTGTTTGAAA TTCACATTTA ACTGGGAGTC 2220
TTGTATTTTA TCTGGCAATC CTAAAATACA TTGGTATGAA ACAAATCACT TTTAGAAGTA 2280
TATTGCTATT TTGATTGGGT TGTTTTTGTG TGTAGAAACG TACAATAACA ACTCAAAGGC 2340
ACAGGAGATT TCTAAACATT GTGAAAAGTT GAATAGATTA TATATTTATT CTCATAATAC 2400
TTTCACTAAT ACTAAATAAA ATTTGGGGAA CACTTTTTAT TTTTATATAA TTTCCAATT 2460
ACAGAAAAGT TTCAAAAATA GTACAAAGAG CTCTCTTACC CAGATTCACT AATTGTTTAT 2520
ACGTGCTTTA TCTTTCATGC TTTCTCTGTA CACACACACA CACACACAAA TTTTCTCTCA 2580
ATCATTTGAA AGTCAGTTAT AGGCATCATG CCCCTTAAAC CCTAATACT TCAAGTGTGA 2640
ATACTGAATA ATTACTAAAA ATGATTTTCT CAGAAAAAAA AACTCCCACA ATTCTGGAAC 2700
TATAACTCTG TAAGCCTTAG AATAAATAAT ACTTTCAAGT TCCAATCTAA AGTTCTTTTT 2760
GAGTTTTGTT GCCCGTTTTA TGCTTGATGT GTATAGTAAT AGGGTAGGCT ATTTATTTTA 2820
TTAAATTTT TTTTAGAGAC AAGGTTTTGC TGTGTTGCCC AAGCTGGAAC TTGAACGACT 2880
GGGCTGAAGT GATCTTCCCA CTCAGCCTC CCAAGTAGCT GGGAAATACG GTGCTGCCA 2940
CCATACCCAG TTTCATTTTT GTTTTTTATA CCCGAAGTTC ATTTCTTTTG TCTCCCTAAA 3000
ACTGAACCTG AATTTTGGGA GGTTTTCATT AGTGGAGGCT CTTCAATTTT AAAGCTATTT 3060
GAAGGGGTTT AGGAATTTAT ATCACATGGT AATTGTAGAG AAAAAGAAAGC TATATACCTC 3120
AAAATCGTGC CCTCTTTACA TATGCTTTAT CAGGTATAAC ATGTTGAAAT GTCACATTAG 3180
TAGTAAAGTG GGGTTTATTT ATATAGTGGT TAAGAAATGT CAGTTTACAC TGCTGTATAC 3240
TTCTTCTTCT GTGTCCCTAA GGCCTGGTAC AGTGCCAAGC ACATACTTGG TATCCAATAA 3300
ATATTTGTTG GATGAAAAAA AAAAAAAAAA AAAA 3334

```

Seq ID NO: C51 DNA Sequence  
Nucleic Acid Accession #: NM\_002888.1  
Coding sequence: 37..723

```

1 11 21 31 41 51
| | | | |

```

CCACGTCCGG GGTGCCGAGC CAACTTTCCT GCGTCCATGC AGCCCCGCGG GCAACGGGCTG 60  
 CCCGCTCCCT GGTCCGGGCC CAGGGGCCCG CGCCCCACCG CCCCGCTGCT GCGCTGCTG 120  
 CTGTGTCTCG CCCCGGTGGC GCGCGCCCGG GGGTCCGGGG GCCCGACGA CCCTGGGCAG 180  
 CCTCAGGATG CTGGGGTCCC GCGCAGGCTC CTGCAGCAGA AGGCGCGCGC GGCGCTTCAC 240  
 TTCTTCAACT TCCGGTCCGG CTCGCCAGC GCGCTGCGAG TGCTGGCCGA GGTGCAGGAG 300  
 GGCCGCGCGT GGATTAATCC AAAAGAGGGA TGTAAGTTC ACGTGGTCTT CAGCACAGAG 360  
 CGCTACAACC CAGAGTCTTT ACTTCAGGAA GGTGAGGGAC GTTTGGGGAA ATGTTCTGCT 420  
 CGAGTGTGTT TCAAGAATCA GAAACCCAGA CCAACCATCA ATGTAAGTTG TACACGGCTC 480  
 ATCGAGAAAA AGAAAGACA ACAAGAGGAT TACCTGCTTT ACAAGCAAAT GAAGCAACTG 540  
 AAAAACCCCT TGGAAATAGT CAGCATACCT GATAATCATG GACATATTGA TCCCTCTCTG 600  
 AGACTCATCT GGGATTGTC TTTCTTGGG AGCTCTTACG TGATGTGGGA AATGACAACA 660  
 CAGGTGTCTC ACTACTACTT GGCACAGCTC ACTAGTGTGA GGCAGTGGGT AAGAAAAACC 720  
 TGAATAATTAA CTGTGCCCAC AAGAGTTACA ATCAAAGTGG TCTCCTTAGA CTGAATTCAT 780  
 GTGAATCTCT AATTTCATAT CAAGAGTTGT AATCACATTT ATTTCAATAA ATATGTGAGT 840  
 TCCTGC 846

Seq ID NO: C52 DNA Sequence  
 Nucleic Acid Accession #: NM\_005409.3  
 Coding sequence: 94..378

1 11 21 31 41 51  
 | | | | |  
 TTCTTTTCAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60  
 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120  
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180  
 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240  
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT 300  
 AAAGGACAAC GATGCTTAAA TCCCAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGTT 360  
 GAAAGAAAAG ATTTTAAAAA ATATCAAAAC ATATGAAGTC CTGGAAAAGG GCATCTGAAA 420  
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480  
 AGACTTTTCT ATGGTTTGTG GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540  
 GGGTGAAGG ACCAAAAACA GAAATACAGT CTCTCTGAAT GAATGACAAT CAGAATTCCA 600  
 CTGCCCAAAG GAGTCCAGCA ATTAATATGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660  
 GGTACCATC GGAGTTTACA AAGTGCTTTT ACGTTCTTAC TTGTTGTATT ATACATTCAT 720  
 GCATTCTTAG GCTAGAGAAC CTCTAGATTT TGATGCTTAC AACTATTCTG TGTGACTAT 780  
 GAGAACATTT CTGCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840  
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900  
 CATCTATGTG TCGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAAATACAC ACTCTTTTCC 960  
 CCAAAATACA TGTAGCACA CAATATGTAG GAAACATTC TTATGCATCA TTTGTTTGT 1020  
 TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080  
 TGGGATACAT GCAACAGTGC ACATATTTCA TAACCAAAAT AGCAGCACCG GTCTTAATTT 1140  
 GATGTTTTT AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200  
 TGTACTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTGGAC ACATTTGAAA 1260  
 TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTTGAAAAA TAAGCAAATG TATACCTAGC 1320  
 AATCACTTTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380  
 TTGTTTCATG CTATATACTG TAAATTTTAG GTATACTCAA GACTAGTTTA AAGAATCAAA 1440  
 GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTCTTTT TTAACAAAAA AAA 1493

Seq ID NO: C53 DNA Sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..609

1 11 21 31 41 51  
 | | | | |  
 ATGCTGCGGC AGGTGCTTCG CAGAGGGCTC CAGTCGTTCT GCCACAGGCT GGGTTTGTGC 60  
 GTGAGCCGGC ACCCGTCTT TTTCTCACC GTGCCGCGAG TCCTGACAAT CACCTTCGGC 120  
 CTCAGCGCGC TCAACCGCTT CCAGCCCGAG GCGCAGCTGG AGCGCCTGGT CGCTCCAGC 180  
 CACAGCCTGG CCAAGATCGA GCGCAGCCTG GCCAGCAGCC TTTTCCCTT GGACCACTCC 240  
 AAAAGCCAGC TCTATTGCGA CTACACACC CCTGGGAGGT ATGGCAGGGT GATCCTCCTC 300  
 TCCCAACCG GGGACAATAT TTTGCTCCAG GCTGAGGGGA TCCTGCAGAC CCACCGAGCC 360  
 GTGCTGGAAG TGAAGGTGAA CCACAAGGGC TATAATTATA CTTTTTCCCA TCTGTGTGTG 420  
 TTGAGAAATC AGGATAAGAA ATGCGTGTCT GATGATATTA TTTCACTGCT AGAGGATCTC 480  
 AGGCAGGCTC CCGTCTCCAA TAAGACAACA GCCAGGCTGC AAGTGAGGTA TCCCAACACT 540  
 AAATTAAGG TATGCTCCTT CTGCATGCTT CTGCCAATTA AAGAGGCAGC ACTTCATTTT 600  
 TTGCCCTAA 609

Seq ID NO: C54 DNA Sequence  
 Nucleic Acid Accession #: NM\_002438.1  
 Coding sequence: 104..4474

1 11 21 31 41 51  
 | | | | |  
 GGGAACTTGG ATTAGGTGGA GAGGCAGTTG GGGGGCCTCG TTGTTTTCG TCTTAGTTCC 60  
 GCCTCTCTGT CCATCAGGAG AAGGAAAGGA TAAACCTGG GCCATGAGGC TACCCCTGCT 120  
 CCTGGTTTTT GCCTCTGTCA TTCCGGGTGC TGTCTCTCTA CTGGACACCA GGCAATTTTT 180  
 AATCTATAAT GAAGATCACA AGCGCTCGT GGATGCAGTG AGTCCAGTGC CCGTCCAAC 240  
 CGCAGCTTGC AACCAAGATG CCGAATCACA GAAATCCGA TGGGTGTCCG AATCTCAGAT 300  
 TATGAGTGTG GCATTTAAAT TATGCCTGGG AGTGCCATCA AAAACAGACT GGGTTGCTAT 360  
 CACTCTCTAT GCCTGTGACT CAAAAAGTGA ATTTTCAAGAA TGGGAGTGCA AAAATGACAC 420  
 ACTTTTGGGG ATCAAAGGAG AAGATTTATT TTTTAACTAC GGCAACAGAC AAGAAAAGAA 480  
 TATTATGCTC TACAAGGGAT CGGGTTTATG GAGCAGGTGG AAGATCTATG GAACACAGAG 540  
 CAATCTGTGC TCCAGAGGTT ATGAAGCCAT GTATACGCTA CTAGGCAATG CCAATGGAGC 600  
 AACCTGTGCA TTCCCGTTCA AGTTTGAAGA CAAGTGGTAC GCAGATTGCA CAGAGTCTGG 660  
 GCGGTGCGAT GGATGGCTCT GGTGCGGAAC CACTACTGAC TATGACACAG ACAAGCTATT 720

5	TGGATATTGT	CCATTGAAAT	TTGAGGGCAG	TGAAAGCTTA	TGGAATAAAG	ACCCGCTGAC	780
	CAGCGTTTCC	TACCAGATAA	ACTCCAAATC	CGCTTTAACG	TGGCACCAAG	CGAGGAAAAG	840
	CTGCCAACAA	CAGAACCGTG	AGCTCCTGAG	CATCACAGAG	ATACATGAGC	AAACATACCT	900
	GACAGGATTA	ACCAGTTTCT	TGACCTCAGG	ACTCTGGATT	GGACTTAACA	GTCTGAGCTT	960
	CAACAGCGGT	TGGCAGTGGG	GTGACCGCAG	TCCTTTCCGA	TATTTGAACT	GGTTACCAGG	1020
	AAGTCCATCA	GCTGAACCTG	GAAAAAGCTG	TGTGTCACTA	AATCCTGGAA	AAAATGCTAA	1080
	ATGGGAAAAA	CTGGAATGTG	TTCAGAAACT	GGGCTATATT	TGCAAAAAGG	GCAACACCCAC	1140
	TTTAAATTCT	TTTGTATTTC	CCTCAGAAAG	TGATGTGCCT	ACTCACTGTC	CTAGTCAGTG	1200
10	GTGGCCGTAT	GCCGGTCAC	GTTACAAGAT	TCACAGAGAT	GAGAAAAAAA	TCCAGAGGGA	1260
	TGCTCTGACC	ACCTGCAGGA	AGGAAGGCGG	TGACCTCACA	AGTATCCACA	CCATCGAGGA	1320
	ATTGGACTTT	ATTATCTCCC	AGCTAGGATA	TGAGCCAAAT	GACGAATTGT	GGATCGGCTT	1380
	AAATGACATT	AAGATTCAAA	TGTACTTTGA	GTGGAGTGAT	GGGACCCCTG	TAACGTTTAC	1440
	CAAATGGCTT	CGTGGAGAAC	CAAGCCATGA	AAACAACAGA	CAGGAGGATT	GTGTGGTGAT	1500
15	GAAAGGCAAG	GATGGGTACT	GGGCAGATCG	GGGCTGTGAG	TGGCCTCTTG	GCTACACTCTG	1560
	CAAGATGAAA	TCACGAAGCC	AAGGTCGAGA	AATAGTGGAA	GTGCAAAAAG	GCTGCAGGAA	1620
	AGGCTGGAAA	AAACATCACT	TTTACTGCTA	TATGATTGGA	CATACGCTTT	CAACATTTCG	1680
	AGAAGCAAA	CAACCTGTGA	ATAATGAGAA	TGCTTATTTA	ACAACATATT	AAGACAGATA	1740
	TGAACAAGCC	TTCTGACTTA	GTTTCGTGGG	CTTAAGGCCT	GAAAAATATT	TCTGGACAGG	1800
20	ACTTTTCAGAT	ATACAAACCA	AAGGGACTTT	TCAGTGGACC	ATCGAGGAAG	AGGTTTCGGTT	1860
	CACCCACTGG	AATTCAGATA	TGCCAGGGCG	AAAGCCAGGG	TGTGTTGCCA	TGAGAACCCG	1920
	GATTGCAGGG	GGCTTATGGG	ATGTTTGA	ATGTGATGAA	AAGGC AAAAT	TTGTGTGCAA	1980
	GCACTGGGCA	GAAGGAGTAA	CCCACCCACC	GAAGCCACAG	ACGACTCCCG	AAACCAATG	2040
	TCCGGAGGAT	TGGGGCGCCA	GCAGTAGAAC	AAGCTTGTGT	TTCAAGCTGT	ATGCAAAAAG	2100
25	AAAACATGAG	AAGAAAAAGT	GGTTTGAATC	TCGAGATTTT	TGTCGAGCTC	TGGGTGGAGA	2160
	CTTAGCTAGC	ATCAATAACA	AAGAGGAACA	GC AAAAATA	TGGCGATTAA	TAACAGCTAG	2220
	TGGAAGCTAC	CACAAACTGT	TTTGGTTGGG	ATTGACATAT	GGGAAGCCCT	CAGAAAGTTT	2280
	TACTTGGAGT	GATGGTTCTC	CTGTTTCATA	TGAAAACCTG	GCTTATGGAG	AACCTAATAA	2340
	TTATCAAAAT	GTTGAATACT	GTGGTGAGCT	GAAAGGTGAC	CCTACTATGT	CTTGGAAATGA	2400
30	TATTAATTGT	GAACACCTTA	ACAACCTGGAT	TTGCCAGATA	CAAAAAGGAC	AAACACCAAA	2460
	ACCTGAGCCA	ACACAGCTC	CTCAAGACAA	TCCACCAAGT	ACTGAAGATG	GGTGGGTTAT	2520
	TTACAAAGAC	TACCAATATT	ATTTCAGCAA	AGAGAAGGAA	ACCATGGACA	ATGCGCGAGC	2580
	GTTTTGCAAG	AGGAATTTTG	GTGATCTTGT	TTCTATTCAA	AGTGAAAGTG	AAAAGAAGTT	2640
	TCATGGAAAA	TATGTAACAA	GAAATGATGC	ACAGTCTGCA	TATTTTATTG	GTTTATTGAT	2700
35	CAGCTTGGAT	AAAAAGTTTG	CTTGGATGGA	TGGAAGCAAA	TGGGATTACG	TGCTCTGGGC	2760
	CACAGGTGAA	CCCAATTTTG	CAAATGAAGA	TGAAAACCTG	GTGACCATGT	ATTCAAATTC	2820
	AGGGTTTTTG	AATGACATTA	ACTGTGGCTA	TCCAAACGCC	TTCAATTTGCC	AGCGACATAA	2880
	CAGTAGTATC	AATGCTACCA	CAGTTATGCC	TACCATGCC	TCGGTCCCAT	CAGGGTGCAA	2940
	GGAAGGTTGG	AATTTCTACA	GCAACAGTG	TTTCAAATC	TTTGGATTTA	TGGAAGAAGA	3000
40	AAGAAAAAAT	TGGCAAGAGG	CACGAAAAGC	TTGTATAGGC	TTTGGAGGGA	ATCTGGTCTC	3060
	CATACAAAAT	GAAAAAGAGC	AAGCATTTCT	TACCTATCAC	ATGAAGGACT	CCACTTTTCAG	3120
	TGCTTGAGCT	GGGCTGAATG	ATGTCAATTC	AGAACACACG	TTCTTTTGGG	CGGATGGACG	3180
	AGGAGTCCAT	TACACAACCT	GGGGGAAAGG	TTACCCCTGG	GGAAGAGAGG	GCAGTCTTTC	3240
	TTATGAAGAT	GCTGACTGTG	TTGTTATTAT	TGGAGGTGCA	TCAATGAAG	CAGGAAAATG	3300
45	GATGGATGAT	ACCTGCGACA	GTAACGAGG	CTACATATGC	CAGACACGAT	CCGACCCCTC	3360
	CTTGACTAAT	CCTTCAGCAA	CGATTCAAA	AGATGGCTTT	GTTAAATATG	GCAAAAAGCAG	3420
	CTATTCACTC	ATGAGACAAA	AATTTCAATG	GCATGAAGCG	GAGACATACT	GCAAGCTTCA	3480
	CAATTCCTCT	ATAGCCAGCA	TTCTGGATCC	CTACAGTAAT	GCATTTGCGT	GGCTGCAGAT	3540
	GGAAACATCT	AATGAACGTG	TGTGGATCGC	CCTGAACAGT	AACTTGACTG	ATAATCAATA	3600
50	CAGTTGGACT	GATAAGTGGG	GGGTGAGGTA	CACATACTGG	GCTGCTGATG	AGCCCCAATT	3660
	GAAATCAGCA	TGTGTTTATC	TGGATCTTGA	TGGCTACTGG	AAGACAGCAC	ATTGCAATGA	3720
	AAGTTTTTAC	TTTCTCTGTA	AAAGATCAGA	TGAAATCCCT	GCTACTGAAC	CCCCACAAC	3780
	GCCTGGCAGA	TGCCCGGAGT	CAGATCACAC	AGCATGGATT	CCTTTCCATG	GTCACTGTTA	3840
	CTATATTGAG	TCTCTCATATA	CAAGAACTG	GGGCCAAGCT	TCTCTGGAAT	GTCTTCGAAT	3900
55	GGGTTCTCTT	CTGGTTTCCA	TTGAAAGTGC	TGCAGAAATC	AGTTTTCTGT	CATATCGGGT	3960
	TGAGCCACTT	AAAAGTAAAA	CCRAATTTTG	GATAGGATTG	TTGAGAAATG	TTGAAGGGAC	4020
	GTGGCTGTGG	ATAAATAACA	GTCGGTCTC	CTTTGTCAAC	TGGAACACAG	GAGATCCCTC	4080
	TGGTGAACGG	AATGATTTGT	TAGCTTTACA	TGCGTCTTCT	GGGTTTTGGA	GTAATATTCA	4140
60	CTGTTCTTCC	TACAAAAGAT	ATATTTGTAA	AAGACCAAAA	ATTATTGATG	CTAAACCTAC	4200
	TCATGAATTA	CTTACAACAA	AAGCTGACAC	AAGGAAGATG	GACCTTCTTA	AACCGTCTTC	4260
	CAACGTGGCC	GGAGTAGTCA	TCATTGTGAT	CCTCCTGATT	TTAACGGGTG	CTGGCCTTGC	4320
	CGCCTATTTC	TTTTATAAGA	AAAGACGTGT	GCACCTACCT	CAAGAGGGCG	CCTTTGAAAA	4380
	CACCTCTGAT	TTTAACAGTC	AGTCAAGCCC	AGGAACACTAG	GATATGAAAG	ATCTCGTGGG	4440
65	CAATATTGAA	CAGAATGAAC	ACTCGGTCA	CTAGTACCTC	AATGCGATTG	TGAGATATT	4500
	GAATTTTATA	AAATTTGTAAC	TGAAATTTAA	AATTTTTAGT	TCAATGTGAT	TGTTTTCTTT	4560
	AAAATGAGTA	CTGAATTTGA	CTGGTCTGTC	CTTTTTTCTT	TTGCCTAATT	GAAGAAATAA	4620
	TTGCTTGTTT	TCTAGCCTGG	CAAGATATTT	TCATAAAAGA	GGGATAACAA	TGCTGATTAC	4680
70	TACCTTTTAA	AATATTTTGA	ATAAATGCAC	AGCACCACAG	CACCACATCT	AAGCATTAGT	4740
	GATGGGTAGC	TGATGTGAGC	TTTATGTGGA	TTTAAAGCAC	TCTAGAAAAC	ATGAGCTTTC	4800
	TTGGCATATT	TTAAGGAGCT	CCCAAAATGT	GTTACCTATT	AAATTGTAA	TCAGCAAGTA	4860
	GAAGACCAT	TGAAAAGTCA	GGTACAAATT	TCCTCAAGTG	GCATAAAAAT	GTAGTCAGTT	4920
	TTCTCTTTTA	CCAGTTTTTA	TTTCCACTCC	AATATTATTAG	AACCTTTATT	GTACATGTGC	4980
	AGAAGAAATA	GGCAGCTGAG	AATCTTGTTC	CCCCAAGAG	AGTTTTACAG	GCTGAGTGTT	5040
75	GCAAAATGTG	TCTTTGTCTT	GTTATATGTA	TATCAGGAAT	ACAAGGATGT	GAAATAAAAC	5100
	TGTAAATTTG	CATAACTGGA	TGTACTTAGA	TAAATGTGAA	TAAACATTAA	AGACAAGGTC	5160
	TATTTTTTAA	AAAAAAAATA	AAAAA				5185

Seq ID NO: C55 DNA Sequence  
Nucleic Acid Accession #: NM\_024574.2  
Coding sequence: 424..2130

80	1	11	21	31	41	51	
	AGTGCAGCTA	GCGGCGGCGG	GCGAAGCCCG	CGCCAGCCCC	GCGGGTCGCT	GCGGCATCCT	60
	CCCGCCGCCC	AGCCCCGCA	CGCTCCCTGC	AGTTTAAAG	GACCTCCCG	CGCTTCTCGG	120

5	CGCTGCCCCG	GGATTCCCCA	GCCCCGCGCG	GCTCCCTACT	CCACTTCGCA	GCAACTTCGG	180
	CGACCGCGCG	CCGCCCCGCC	TCGCCCGCCT	TTGAAAGTTG	CTGTGCCGAC	CGCAAAGTTG	240
	GGACACTTCA	GCGGATTGAA	TTTTTCTCTT	TTATCTGCCT	CCGTCCCCGC	CCTCCAGGCT	300
	TCTCGTTCCT	GGATATTGGT	GCTTAGCATC	TTGGCAGGGT	CCGGGGACGT	GGACTATTTC	360
	GCACACCA	CCACGGGGAG	GGATTTTTTT	CTATTTTCCC	TACGAAAAAC	AGATCTTTTT	420
	AAGGATGGTG	CTGCTCCACT	GGTGCTCGCT	GTGGCTCCTG	TTTCCACTCA	GCTCAAGGAC	480
	CCAGAAGTTA	CCCACCGGG	ATGAGGA	TTTTCAGATG	CAGATCCGGG	ACAAGGCATT	540
	TTTTTCATGAT	TCGTGAGTAA	TTCCAGATGG	AGCTGAAATT	AGCAGTTATC	TCTTTAGAGA	600
10	TACACCTAAA	AGGTATTTCT	TTGTGGTTGA	AGAAGACAAT	ACTCCATTAT	CAGTCACAGT	660
	GACGCCCTGT	GATGCGCCTT	TGGAGTGGAA	GCTGAGCCTC	CAGGAGCTGC	CAGAGGACAG	720
	GAGCGGGGAA	GGCTCAGGTG	ATCTGGAACC	TCTTGAGCAG	CAGAAGCAGC	AGATCATTAA	780
	TGAGGAAGGC	ACTGAGTTAT	TCTCCTACAA	AGGCAATGAT	GTGAGTATT	TTATATCGTC	840
	TAGTTCCCCA	TCCGGTTTAT	ATCAGTTGGA	TCTTCTTTCA	ACAGAGAAAG	ACACACATT	900
15	CAAAGTATAT	GCCACCACAA	CTCCAGAATC	TGATCAGCCA	TACCTTGAGT	TACCTTATGA	960
	CCCAAGAGTA	GATGTGACCT	CACTGGGGCG	CACCACGGTC	ACTTTGGCCT	GGAAACCAAG	1020
	CCCCACTGCC	TCTTTGCTGA	AACAACCCAT	TCAGTACTGT	GTGGTCATCA	ACAAAGAGCA	1080
	CAATTTCAA	AGTCTCTGTG	CAGTGGGAAG	AAAACTGAGT	GCAGATGATG	CTTTTATGAT	1140
	GGCACCGAAA	CTCGTCTCGG	ACTTCAGCCC	CTTTGACTTT	GCCCACTTTG	GATTTCTCTC	1200
20	TGATAATTCA	GGTAAAGAAC	GCAGTTTCCA	GGCAAAGCCT	TCTCCAAAAC	TGGGGCGTCA	1260
	TGTCTACTCC	AGGCCCAAGG	TTGATATTCA	AAAAATCTGC	ATAGGAAAAC	AGAATCATCT	1320
	CACCGTCTCT	GATCTGAAAC	CCGACACGCA	GTACTACTTT	GACGTATTTG	TGGTCAACAT	1380
	CAACAGCAAC	ATGAGCAGCG	CTTATGTAGG	TACCTTTGCC	AGGACCAAGG	AAGAAGCCAA	1440
	ACAGAAGACA	GTCCAGCTCA	AAGATGGGAA	GATAACAGAT	GTATTTGTTA	AAAGGAAGGG	1500
25	AGCAAAGTTT	CTACGGTTTG	CTCCAGTCTC	TTCTCACCAA	AAAGTCACCT	TCTTTATTCA	1560
	CTCTTGTCTG	GATGCTGTCC	AAATCCAAGT	GAGAAGAGAT	GGGAAACTTC	TTCTGTCTCA	1620
	GAATGTGGA	GGCATTTCAGC	AGTTTCAGCT	TAGAGGAAAA	CCTAAAGCTA	AATACCTCGT	1680
	TCGACTGAAA	GGAAACAAGA	AAGGAGCATC	TATGTTGAAA	ATTCTAGCTA	CCACAAGGCC	1740
	TACTAAGCAG	TCATTTCCCT	CTCTTCCTGA	AGACACAAGA	ATCAAAGCCT	TTGACAAGCT	1800
30	CCGTACTCTG	TCTTCGGCCA	CCGTGGCCTG	GCTAGGCACT	CAGGAAAGGA	ACAAAGTTTG	1860
	CATCTACAAA	AAAGAGTGG	ATGATAACTA	CAATGAAGAC	CAGAAGAAAA	GAGAGCAAAA	1920
	CCAATGTCTA	GGACCAGATA	TAAGGAAGAA	GTCAAGAAAG	GTCTCTGTGA	AATATTTC	1980
	CAGTCAAAAC	CTGCAGAAAG	CAGTGACCAC	AGAAACAATT	AAAGGTCTTC	AGCCTGGCAA	2040
	ATCTTACCTG	CTGGATGTTT	ATGTCATAGG	ACATGGGGGG	CACCTCTGTA	AGTATCAGAG	2100
35	TAAAGTTGTG	AAAACTAGAA	AGTTCTGTTA	GTTACCTTCT	TATAGAGATA	TATTATGTAG	2160
	AACTCCAGGA	GGGACATTAA	ATCACTTTAA	GTATAAATCG	ACTACTCCCA	CAGTTGAGAG	2220
	AAGTTGTGAC	CTGTACTTGT	ACTATGGAAG	GAAGGATATC	AACGTGTGTA	TATTGATGTT	2280
	TATATAAGTA	ACTCTTGAAG	GAGACTTGT	CTAGCGTGCC	CCATGGTACC	TAGTGTGTGT	2340
	CTGATGCCGG	TTGGTGTCAA	AGATAGAGGG	CTTCTTGAAG	GAACTTGCCA	TTCTTGTCTT	2400
40	TGACCACTGC	ATGAACCTGT	TCTAAATTAT	TTTATTACCT	AAAAATTAA	AATATGCCAT	2460
	TCATTTGCACA	CACCCACAAA	TGCAAAATCAT	TCCTCTCTAT	AGATGCTAGG	ATATATATAA	2520
	ATTATTTTAT	AAATCTTGT	TTTAAATGTC	AGTGTTTCTA	TGATTGTAAA	CTATTAAATT	2580
	CTTTTCTTAT	TAAAGTACAG	ATCTAATCTA	AGTATTATTA	AGTTGATAGC	CCTCTAGTCA	2640
	GTTATATTGC	TATTGTAAAT	TCTTGTGTTG	TGAGTAAAT	GTTTAAATAC	TATATGTATC	2700
45	TCATGTACAA	AGTTGACATA	CATTATATTC	ATGTACATAA	AATTAAGAG	ATTAGATTAT	2760
	ATACTGTTAA	AAAAA	AAAAA	AAAAA	AAAAA	AAAAA	2808

Seq ID NO: C56 DNA Sequence  
Nucleic Acid Accession #: BC034229.1  
Coding sequence: 373..1422

55	1	11	21	31	41	51	
	ATCCGGCGGT	GGTGACGCGA	GAGGCTGGGG	TCTCCAGGAC	CAACTCCTCT	TCATCTTCGT	60
	CTTCCTCAGC	CTGCTCAATG	TGAAGCCCTT	GATCATGATT	CACCTCCACT	TAATAAATAA	120
	AGTGTTTTACA	AATCAGAATA	ACTTTTAGAC	AATATTAAAG	TGGTAATCAT	GAACAGAAAA	180
	GATTTTGTAG	TTCTTCCATG	GGGAAAACCT	GGAAATTTCTG	TAAAGCTAAA	ATATAGCAAT	240
	GTAATAATTA	AAACAAAGT	CTAAGATTTG	AAGAGATAAT	TTGCTTCAGG	ATTTTGTAGG	300
60	AAGGCAAAAT	CTAACTTTAA	AAACCAGATT	TCGGAGAAAT	ACAAAAGAAA	TAGAAATGCT	360
	CAAGAACTGC	GAATGGAGAA	AGTACAGTTA	GAGTTTGAGA	ACCAAGAGAT	GGAGAAGAAA	420
	CTGCAAGAAT	TCCGATCCAC	AAGAAACAAA	GAAAAGGAAG	ATAGAGAGTC	AAGCGAGTAT	480
	TACTGGAAAT	CTGGAAAAGT	GGGCAAAATTG	GTCAATCAAT	CATATATGAT	GTCACAAAAT	540
	AAAGGAAATG	TTGTTAAGTT	TTCTGCTGGA	AAAGTGAAAT	TAAAATTGCT	GAAGGAACAG	600
65	ATTCAAGAGC	CAGTGAAACC	AACAGTTAAT	TATAAAATGG	CAAATTTCTC	AGAATGTGAA	660
	AAACCAAGA	TAAATGGGAA	AGTTTGTGGA	CAGTGTGAGA	ACAAAGCTGC	TCTACTGGTA	720
	TGCCCTGAAT	GTGGAGAAGA	TTATTGTTCA	GGATGCTTTG	CTAATGTTCA	CCAGAAAGGG	780
	GCACTAAAGC	TCCACAGAAG	AACTCTTTTG	CAGGCAAGAT	CTCAAATATT	ATTCAATGTA	840
	TTGGATGTTG	CCCATCAGTT	TATAAAGGAT	GTTAATCCAG	ATGAACCCAA	AGAGGAGAA	900
70	AAITCTACAA	AGGAAACCA	TAAAATTCAA	CATAAACCCA	AATCTGTACT	TCTCCAGAGG	960
	AGCAGCTCTG	AGGTAGAAAT	TACAACGATG	AAAAGAGCAC	AACGTACAAA	ACCAAGAAAG	1020
	AGTCTGTTGT	GTGAAGGGTC	ATTTCGATGAA	GAAGCTTCTG	CACAGTCTCT	TCAGGAAGTG	1080
	TTAAGTCAAT	GGAGAACCGG	AAATCATGAT	GACAACAAGA	AACAGATTTT	ACATGCAGCA	1140
	GTAAAAGACT	CATTGGAAGA	ATGCGAAGTA	CAGACTAATC	TGAAAAATTTG	GAGAGAACCA	1200
75	CTTAATATTG	AACTTAAAGA	AGACATTCTA	TCCTATATGG	AAAAATTATG	GCTTAAAAAA	1260
	CACAGGAGAA	CTCCACAAGA	GCAACTTTTT	AAATGCTACC	AGATACGTTT	CCCATCCAC	1320
	ATGAACACC	TGGTGATGCA	CAGTGTCTC	AAAAAGAAA	CGATGAAGAT	AGTGATGGTG	1380
	AGGAGACCAA	AGTACAACAC	ACAGCTCTTT	TATTGCCAGT	AGAAACATTA	AACATAGAGA	1440
	GACCTGAACC	ATCTCTGAAG	ATAGTCGAAC	TGGATGATAC	TTATGAAGAG	GAATTTGAAG	1500
80	AAGCAGAAAA	TATTTGTCCT	TACAAAGTTA	AATTAGCTGA	TGCAGACAGT	CAACGAAGTT	1560
	GTGCTTTTCA	TGATTGTGAG	AAGAATAGCT	TTCCATATGA	AAATGGCATC	CATCAACATC	1620
	ATGTTTTCGA	TAAAGGAAAG	AGAGACTTCT	TAAATCTTTG	TCTGAGAAAC	AGCTCTACTT	1680
	ATTATAAAGA	TAATTCAAAA	GGAGAAACTT	CAACACAGA	TTTTGACAAC	ATCGTGGATC	1740
	CTGATGTGTA	TTCTTCTGAC	ATTGAAAAAA	TTGAGGAAAG	CACCTCCTTT	GAAAGAAATT	1800
	TAAAGGAGAA	AAATATAGGT	TTAGAAAGTA	ATCAAAAGTC	TGATGATTCC	TGTGTATCAC	1860

TTGAAAGCAA GGACACTTTG CTAGGTAGAG ATTTAGAAAA AGCTCCCATT GAGGAGAAAT 1920  
 TATCTCAAGA CATCAAAGAA TCCTTGGAAT TGAGCAATCT GTATAAGAGG CCAAGCTTTG 1980  
 AAGAATCAAA AACTACAAAG TCATCACTGT TGTACAAAGA AATAGCCTGC AGAAGTAAGC 2040  
 CTATAACAAA ACAAATATCAA GGACTTGAGA GATTCTTTAT TTTTGATACA AATGAAAGAC 2100  
 TCAACTTACT TCCTTCTCAT CGTTTAGAAT GCAACAATTC CAGTACTAGG ATTACACTTG 2160  
 CAGGTCAGAA ATCAGACAGA CCTTCAACAG CAAATTTTCC ACTTTCCAAC TCTGTTAAAG 2220  
 AAAGCTCCAG TTGCCTTTCA TCCTCTCATC CTCGATCAAG AAGTGCAGCT GCTCAATCAT 2280  
 CATCTAGAGC TGCTTCTGAA ATTTAGAGAA TTGAATATAT TGATATTACT GACCAGAATG 2340  
 AGCTTTCCTT AGATGACACT ACTGATCAAC ATACTTTAGA CAATTTGGAA AAAGAATTAC 2400  
 AAGTGTGAG ATCTCTTGCA GATACTTCAG AAAAGCTTTA CAGCTTAACC TCAGAAGAGT 2460  
 TCCCAGATT CAGCAGCCAA TCACGAAATA TAAGTCAGAT TTCCACAGAT TTCCCTAAGA 2520  
 CCTCACATGT GAGGGGTCCC TGTGGAGTTG AGGAATTGAG CTGTTCTGGA AGAGATACCA 2580  
 AAATTCAGTC TTGCTGTGCA CTTTCTGAGA GCAGTACAGA TGAGGAGGAG GAAGATTTTC 2640  
 TCAACAAGCA ACATGTCATC ACACCTACCGT GGTCAAAGAG TACTTAAAGA TTATTTGTTC 2700  
 ATTACTGTTT CCATTTTGTA CCCAGAGTAA AGCAAACAAC TGAGAAAAGT AACCAAGTGA 2760  
 TTACCTATCC AAGTGCTGGA GATTTTGATT ACTAATGTCT TTGATGTTTC AAGGCTACAA 2820  
 ACTAATAAAA GTAAAAATTAT AAGTTCAAAA AAATTTTATA AAAAAAAT 2876

Seq ID NO: C57 DNA Sequence  
 Nucleic Acid Accession #: NM\_024687.1  
 Coding sequence: 138..1706

1 11 21 31 41 51  
 AAAAAATGA TGACAAACAG AAACAGAAAT TACATGCAGC AGTAAAAGAC TCATTGGAAG 60  
 AATGCGAAGT ACAGACTAAT CTGAAAATTT GGAGAGAACCC ACTTAATATT GAACTTAAAG 120  
 AAGACATTCT ATCCTATATG GAAAAATTAT GGCTTAAAAA ACACAGGAGA ACTCCACAG 180  
 AGCAACTTTT TAAATGCTA TCAGATACGT TCCCACATCC ACATGAAACC ACTGGTGATG 240  
 CACAGTGTTT TCAAAATGAA AACGATGAAG ATAGTGATGG TGAGGAGACC AAAGTACAAC 300  
 ACACAGCTCT TTTATTGCCA GTAGAAACAT TAAACATAGA GAGACCTGAA CCATCTCTGA 360  
 AGATAGTCGA ACTGGATGAT ACTTATGAAG AGGAATTTGA AGAAGCAGAA AATATTGTGC 420  
 CTTACAAAGT TAAATTAGCT GATGCAGACA GTCAACGAAG TTGTGCTTTT CATGATTGTC 480  
 AGAAGAATAG CTTTCCATAT GAAAATGGCA TCCATCAACA TCATGTTTTC GATAAGGGAA 540  
 AGAGAGACTT CTTAAATCTT TGTCTGAGAA ACAGCTCTAC TTATTATAAA GATAATTCAA 600  
 AAGGAGAAAC TTCAAACACA GATTTTGACA ACATCGTGGG TCCTGATGTG TATTCTTCTG 660  
 ACATTGAAAA AATTGAGGAA AGCACCCTCT TTGAAAGAAA TTTAAAGGAG AAAAATATAG 720  
 GTTTAGAAAG TAATCAAAAG TCTGATGATT CCTGTGTATC ACTTGAAAGC AAGGACACTT 780  
 TGCTAGGTAG AGATTTAGAA AAAGCTCCCA TTGAGGAGAA ATTATCTCAA GACATCAAAG 840  
 AATCCTTGGA ATTGAGCAAT CTGTATAAGA GGCCAAAGCT TGAAGAATCA AAAACTACAA 900  
 AGTCATCACT GTTGTACAA GAAATAGCCT GCAGAAGTAA GCCTATAACA AAACAATATC 960  
 AAGGACTTGA GAGATCTTTT ATTTTGTATA CAAATGAAAG ACTCAACTTA CTTCTTCTC 1020  
 ATCGTTTGA ATGCAACAAT TCCAGTACTA GGATTACACT TGCAGAAGAC AGAGAATGGA 1080  
 TTCAGACCA TAGCTTAAGT GAATATGCTG ATAATGCAAT TGTCTTGGGT GTTCTGAGG 1140  
 GTGCTCAGAG TCCATCATCA AGTAGAAAA AGCAAAAGAT GGGTCAGAAA TCACAGAGAC 1200  
 CTTCAACAGC AAATTTTCCA CTTTCCAAC CTGTTAAAGA AAGCTCCAGT TGCCTTTCAT 1260  
 CCTCTCATCC TCGATCAAGA AGTGCAGCTG CTCATCATC ATCTAGAGCT GCTTCTGAAA 1320  
 TTTCAAGAA TGAATATATT GATATTACTG ACCAGAATGA GCTTTCCTTA GATGACACTA 1380  
 CTGATCAACA TACTTTAGAC AATTTGGAAA AAGAATTACA AGTGCTGAGA TCTCTTGACG 1440  
 ATACTTCAGA AAAGCTTTAC AGCTTAACCT CAGAAGAGTT CCCAGATTTT AGCAGCCAAT 1500  
 CACTGAATAT AAGTCAGATT TCCACAGATT TCCTTAAGAC CTCACATGTG AGGGGTCCCT 1560  
 GTGGAGTTGA GGAATTGAGC TGTTCTGAAA GAGATACCAA AATTCAGTCT TTGCTGTGAC 1620  
 TTTCTGAGAG CAGTACAGAT GAGGAGGAGG AAGATTTTCT CAACAAGCAA CATGTCATCA 1680  
 CACTACCGTG GTCAAAGAGT ACTTAAAGAT TATTTGTTC TACTGTTTC CATTTTGTAC 1740  
 CCAGAGTAAA GCAAACAAC TGAATAAGTA ACCAAGTGAT TACCTATCCA AGTGTGGAG 1800  
 ATTTTGATTA CTAATGTCTT TGATGTTTCA AGGCTACAAA CTAATAAAG TAAATTTATA 1860  
 AGTTCAAAA AAAAAAATA AAAA 1884

Seq ID NO: C58 DNA Sequence  
 Nucleic Acid Accession #: NM\_005408.1  
 Coding sequence: 76..372

1 11 21 31 41 51  
 AAAAGGCCGG CGGAACAGCC AGAGGAGCAG AGAGGCAAAG AAACATTGTG AAATCTCCAA 60  
 CTCTTAACCT TCAACATGAA AGTCTCTGCA GTGCTTCTGT GCCTGCTGCT CATGACAGCA 120  
 GCTTTCAACC CCCAGGGACT TGCTCAGCCA GATGCATCA ACGTCCCATC TACTTGCTGC 180  
 TTCACATTGA GCAGTAAGAA GATCTCCTTG CAGAGGCTGA AGAGCTATGT GATCACCACC 240  
 AGCAGGTGTC CCCAGAAGGC TGTCTCTTTC AGAACCAAC TGGGCAAGGA GATCTGTGCT 300  
 GACCCAAAGG AGAAGTGGGT CCAGAATTAT ATGAAACACC TGGGCCGGAA AGCTCACACC 360  
 CTGAAGACTT GAACTCTGCT ACCCCTACTG AAATCAAGCT GGAGTACGTG AAATGACTTT 420  
 TCCATTCTCC TCTGGCTTCC TCTTCTATGC TTTGGAATAC TTCTACCATA ATTTTCAAAT 480  
 AGGATGCATT CGGTTTGTG ATTCAAATG TACTATGTGT TAAGTAATAT TGCTATTAT 540  
 TTGACTTGTT GCTGGTTTGG AGTTTATTG AGTATTGCTG ATCTTTTCTA AAGCAAGGCC 600  
 TTGAGCAAAG AGTTGCTGT CTCTAAGCCC CCTTCCCTTC CACTATGAGC TGCTGGCAGT 660  
 GGGTTTGTAT TCGGTTCCCA GGGGTTGAGA GCATGCCTGT GGGAGTCATG GACATGAAGG 720  
 GATGCTGCAA TGTAGGAAGG AGAGCTCTTT GTGAATGTGA GGTGTGCTA AATATGTTAT 780  
 TGTGAAAGA TGAATGCAAT AGTAGGACTG CTGACATTTT GCAGAAAATA CATTTTATTT 840  
 AAAATCTCCA AAAAAAATA 860

Seq ID NO: C59 DNA Sequence  
 Nucleic Acid Accession #: AK097746.1  
 Coding sequence: 185..2224



	1	11	21	31	41	51	
5	CTTTCATGAC	AGTAACAAAT	CCAAGATTTT	GGAAAAGCGC	CTACGATATT	TAAATGACCA	60
	CTTCACATAC	AACCTATATT	GTAATATATG	CCGATCACTA	TTTGAGAAGG	ACAAGCTGTT	120
	ATTTTCCTTT	TTATTATGTG	CCAATCTTCT	TCTGGCAAGG	AAAGAGATTG	AATACCAGGA	180
	ACTGATGTTT	CTTTTAACTG	GAGGAGTAAG	TCTTAAAAGT	GCTGAGAAAA	ATCCTGATCC	240
	AACCTGGCTA	CAGGACAAAA	GCTGGGAGGA	AATCTGTGCG	GCAAGTGAAT	TTCTGTCCTT	300
10	CAGAGGACTC	AGGCAACATT	TTTGTGAACA	TATATATGAA	TGGCCGAGAA	TCTATGACAG	360
	TAAAGAGCCA	CATAATGCTA	AATTTCACG	ACCAATGGAT	AAGAACCCTA	ATGAACTACA	420
	GAAAATAATA	ATTCTTCGGT	GTTTAAAGACC	TGATAAGATA	ACCCCAGCTA	TAACAAACTA	480
	TGTAACCTGAC	AACTAGGGA	AAAAGTTTGT	AGAGCCTCCA	CCATTGTGAT	TGACAAAGAG	540
	TTACTTGGAT	TCAAATTGCA	CCATTCCTTT	AATTTTGTGT	CTATCTCCAG	GAGCAGATCC	600
15	TATGGCCAGC	CTGCTGAAAT	TTGCAAAATGA	TAAATCTATG	TCTGAAATA	AGTTTCAAGC	660
	TATTTCACTG	GGACAGGGAC	AAGGACCGAT	TGCAGCAAAA	ATGATTAAAG	CAGCAATTGA	720
	AGAAGGAAC	TGGGTGTGCC	TACAGAATTG	CCATCTTGCA	GTGTCTCGGA	TGCCCATGTT	780
	GGAAAAAATA	TGTGAAGATT	TTACCTCTGA	AACCTGTAA	TCATCCTTTA	GGCTTTGGCT	840
	GACAAGCTAT	CCATCTTCAA	AATTCCTCAG	AACAATTCTA	CAGAATGGAG	TAAAAATGAC	900
20	TAATGAACCT	CCCACGGGTC	TTCGGCTGAA	TCTCCTTCAA	TCATATCTCA	CTGATCCAGT	960
	TTCTGATCCT	GAGTTTTTCA	AGGGATGCCG	TGGAAGAGGA	CTGTTATTTA	TCAATGAATA	1020
	TGATACAATT	CCATTGTGA	CTATATCTTA	CCTGACTGGG	GAGTGTAAAT	ATGGAGGAAG	1080
	AGTGACAGAC	GATTGGGACA	GACGCTTCT	ATTAACCATG	CTGGCTGACT	TTTATAATCT	1140
	GTACATAGTT	GAACCCCTC	ATTATAAGTT	TTCCTCCAGT	GGAACTATT	TTGCACCTCC	1200
25	TAAAGGCAC	TATGAGGACT	ACATTGAATT	CATTAAAGAA	CTTCATTTA	CTCAACACCC	1260
	TGAGATATTT	GGATTACATG	AAAAAGTTGA	CATCTCCAAG	GATCTTCAAC	AAACAAAAAC	1320
	CCTCTTTGAG	TCCTTGCTCC	TCACCCAGGG	AGGCTCCAAA	CAGACAGGAG	CCTCAGGAAG	1380
	TACTGATCAG	ATTCTGTTAG	AAATTACCAA	AGATATCCTC	AACAAGCTCC	CTAGTGATT	1440
	CGACATTGAA	ATGGCACTAC	GGAAGTATCC	TGTGAGATAT	GAAGAAAGCA	TGAATACTGT	1500
30	GTTAGTACAA	GAAATGGAAA	GATTTAACAA	TTTAATTATA	ACTATACGTA	ACACTCTACG	1560
	GAGCCTTGAA	AAAGCTATTA	AGGGTGTGGT	TGTGATGGAT	TCTGCATTGG	AGGCACTCTC	1620
	CAGTAGCTTA	CTTGTGTGAA	AGGTTCCAGA	AATATGGGCC	AAACGTTTCA	ACCCAAGCCT	1680
	TAAGCCCTTG	GGAAGTTACA	TCACAGATT	CCTAGCCCGG	TTGAACCTTT	TACAGGACTG	1740
	GTATAATTCA	GGAAACCTT	GTGTGTTTTG	GCTGTGAGT	TTCTTTTTC	CTCAGGCCCT	1800
35	TTTAACCTGA	GCTATGCGA	ATTATGCCAG	AAAATATACC	ACCCCTATTG	ATTGTCTAGG	1860
	ATATGAATTT	GAGGTATATC	CATCTGATAC	ATCTGACACA	TCACCAGAAG	ATGGTGTTTA	1920
	TATCCACGGA	CTGTATCTCG	ATGGCGCACG	CTGGGACCGA	GAAAGTGGAT	TGCTTGCTGA	1980
	ACAATATCCC	AAACTTCTGT	TTGACCTGAT	GCCCATCATA	TGGATAAAAC	CAACTCAAAA	2040
	ATCTCGGATT	ATAAGTACGG	ATGCCCTATG	CTGTCCCTCT	TACAAGACAA	GTGAACGTAA	2100
40	AGGAACCTCT	TTCCACTACG	GACATTCTAC	TAACTTTGTC	ATTGCAATGT	TGTTAAAAAC	2160
	AGACCAACCT	ACTCGGCACT	GGATCAAGCG	CGGGGTTGCT	TTGCTTTGTC	AGTTGGATGA	2220
	CTAAATTGGA	CAAATTTATA	AAACATCCAA	AAGTTT			2256

Seq ID NO: C60 DNA Sequence  
Nucleic Acid Accession #: J02761.1  
Coding sequence: 14..1159

	1	11	21	31	41	51	
50	GAATTCGGGT	GCCATGGCTG	AGTCACACCT	GCTGCAGTGG	CTGCTGCTGC	TGCTGCCAC	60
	GCCTGTGGGC	CCAGGCACTG	CTGCCCTGGAC	CACCTCATCC	TTGGCCTGTG	CCGAGGGCCC	120
	TGAGTTCTCG	TGCCAAAGCC	TGGAGCAAGC	ATTGCACTGC	AGAGCCCTAG	GGCATTGCCT	180
	ACAGGAAGTC	TGGGGACATG	TGGGAGCCGA	TGACCTATGC	CAAGAGTGTG	AGGACATCGT	240
	CCACATCCTT	AACAAGATGG	CCAAGGAGGC	CATTTTCCAG	GACACGATGA	GGAAAGTTCT	300
55	GGAGCAGGAG	TGCAACGCTG	TCCCTTGA	GCTGCTCATG	CCCCAGTGCA	ACCAAGTGCT	360
	TGACGACTAC	TTCCCTCTGG	TCATCGACTA	CTTCCGAAC	CAGACTGACT	CAACCGGCAT	420
	CTGTATGCAC	CTGGGCTGTG	GCAATCCCG	GCAGCCAGAG	CCAGAGCAGG	AGCCAGGGAT	480
	GTACAGCCCC	CTGCCCAAC	CTCTGCGGGA	CCCTCTGCCA	GACCTCTGCT	TGGACAAAGCT	540
	CGTCTCTCCT	GTGCTGCCCG	GGGCCCTCCA	GGCGAGGCC	GGGCCCTACA	CACAGGATCT	600
60	CTCGAGCAG	CAATTCCTCA	TTCTCTCTCC	CTATTGCTGG	CTCTGCAGGG	CTCTGATCAA	660
	GCGGATCCAA	GCCATGATTG	CCAAGGGTGC	GCTAGCTGTG	GCAGTGGCCC	AGGTGTGCCG	720
	CGTGGTACCT	CTGGTGGCCG	GCGGCATCTG	CCAGTGCCTG	GCTGAGCGCT	ACTCCGTCAT	780
	CCTGCTCGAG	ACGCTGCTGG	GCCGCATGCT	GCCCCAGCTG	GTCTGCCGCC	TCGTCCTCCG	840
	GTGCTCCATG	GATGACAGCG	CTGGCCCAAG	GTGCGCGACA	GGAGAATGGC	TGCCGCGAGA	900
65	CTCTGAGTGC	CACCTCTGCA	TGTCCGTGAC	CACCCAGGCC	GGGAACAGCA	GCGAGCAGGC	960
	CATACCACAG	GCAATGTCTC	AGGCCTGTGT	TGGCTCCTGG	CTGGACAGGG	AAAAGTGCAA	1020
	GCAATTTTGT	GAGCAGCAC	CGCCCCAGCT	GCTGACCCTG	GTGCCAGGG	GCTGGGATGC	1080
	CCACACCACT	TGCCAGGCC	TCCGGGTGTG	TGGGACCATG	TCCAGCCCTC	TCCAGTGTAT	1140
	CCACAGCCCC	GACCTTTGAT	GAGAACTCAG	CTGTCCAGCT	GCAAGGAAA	AGCCAAAGTGA	1200
70	GACGGGCTCT	GGGACCATGG	TGACCAGGCT	CTTCCCTTGC	TCCCTGGCCC	TGCGCAGCTG	1260
	CCAGGCTGAA	AAGAAGCCTC	AGCTCCACAC	CCGCCCTCCT	CACCTCCCTT	CCTCGGCAGT	1320
	CACCTTCACT	GGTGGACAC	GGGCCCCAG	CCCTGTGTCG	GCCTTGTCTG	TCTCAGCTCA	1380
	ACCACAGTCT	GACACCAGAG	CCCACTTCCA	TCCTCTCTGG	TGTGAGGCAC	AGCGAGGGCA	1440
	GCATCTGGAG	GAGCTCTGCA	GCCTCCACAC	CTACCACGAC	CTCCCAGGGC	TGGGCTCAGG	1500
75	AAAAACCAAG	CACCTGCTTTA	CAGGACAGGG	GGTTGAAGCT	GAGCCCCGCC	TCACACCCAC	1560
	CCCCATGCAC	TCAAAGATTG	GATTTTACAG	CTACTTGCAA	TTCAAATTC	AGAAGAATAA	1620
	AAAAATGGGAA	CATACAGAA	TCTAAAGAT	AGACATCAGA	AATTGTTAAG	TTAAGCTTTT	1680
	TCAAAAAATC	AGCAATTCCC	CAGCGTAGTC	AAGGGTGGAC	ACTGCACGCT	CTGGCATGAT	1740
	GGGATGGCGA	CCGGGCAAGC	TTTCTTCTC	GAGATGCTCT	GCTGCTTGAG	AGCTATTGCT	1800
80	TTGTTAAGAT	ATAAAAAGGG	GTTTCTTTT	GTCTTCTGT	AAGGTGGACT	TCCAGATTTT	1860
	GATTGAAAGT	CCTAGGGTGA	TTCTATTCT	GCTGTGATTT	ATCTGCTGAA	AGCTCAGCTG	1920
	GGGTTGTGTC	AGCTAGGGAC	CCATTCCTGT	GTAATACAA	GTCTGCACCA	ATGCTAATAA	1980
	AGTCCTATTG	TCTTTTAAAA	AAAAAAAACG	GAATTC			2026

Seq ID NO: C61 DNA Sequence

Nucleic Acid Accession #: NM\_139172.1  
Coding sequence: 19..552

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
      GGGGTC TGGG GAGGTG ACAT GTTGGG CTGT GGGATC CCAG CGCTGG GCCT GTCCTG CTGT 60
      CTGCAG GGCT CCGCAG ACAG AAATGG AATC CAGGAT TCT TCTAC CCATG GAGCTG TGAG 120
      GGTGAC ATAT GGGACC GGA GAGCTG TGGG GGCCAG GCGG CCATCG ATAG CCCCAAC CTC 180
      TGCCTG CGCT TCCGGT GCTG CTACCG CAAT GGGGTG CTGT ACCACC AGCG TCCAGAC GAA 240
      AACGTG CCGA GGAAGC ACAT GTGGGC GTG GTCTGG ACCT GCAGCG GCCT CCTCCT CCTG 300
      AGCTGC AGCA TCTGCT TGT CTGTGG GGCC AAGCGC CCGG ACGTGT CTGA TATGCC CCGT 360
      TTCTGG CCG GTCCGT GTGA CATGTCC AAG TCCGTCT CGC TGCTCT CCAA GCACCG AGGG 420
      ACCAAGA AGA CGCCGT CCAC GGGCAG CGTG CCAGTC GCGC TGTC CCAAGA GTCCAG GGAT 480
      GTGGAG GGAG GCACCG AGGG GGAAGG GACG GAGGAG GGTG AGGAGA CAGA GGGCAG GGAA 540
      GAGGAG GATT AGGGAG GTCC CCGGGG GACT GCTCA ATA GATACG GTG ACG 593

```

Seq ID NO: C62 DNA Sequence  
Nucleic Acid Accession #: NM\_054023.2  
Coding sequence: 98..379

```

20     1      11      21      31      41      51
      |      |      |      |      |      |
      GGGGAC ACTT TGTATG GCAC GTGGA ACCAC TGGCTT GGTG GATTTT GCTA GATTTT TCTG 60
      ATTTTAA AC TCCTGAAA AA TATCCC AGAT AACTGT CATG AAGCTG GTAA CTATCT TCTC 120
      GCTGGT GACC ATCAGC CTTT GTAGTT ACTC TGCTACT GCC TTCCTC ATCA ACAAA GTGCC 180
      CCTTCT GTTT GACAAG TTGG CACCTT TACC TCTGGAC AAC ATTCTT CCTT TTATGG ATCC 240
      ATTAAAG CTT CTTCGT GAAA CTCTGG GCAT TTCTGT TGAG CACCTT GTGG AGGGCT AAG 300
      GAAGTGT GTA AATGAG CTGG GACCAG AGGC TTCTGA AGCT GTGAAG AAAA TGCTGG AGGC 360
      GCTATC ACAC TTGGTG TGAC ATCAAG ATAA AGAGCG AGG TGGATG GGA TGGAAG ATGA 420
      TGCTCT ATC CTCCCT GCCT GAAACCT GTT CTACCA ATTA TAGATC AAAT GCCCTA AAAAT 480
      GTAGTG ACCC GTGAAA AGGA CAAATA AAGC AATGA ATACT AAAAAA AAAA 540
      AAAAAA AAAA 550

```

Seq ID NO: C63 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..2874

```

35     1      11      21      31      41      51
      |      |      |      |      |      |
      ATGCCC CTGT CCTATG CCTA TAAAA ACGCT GAGACC CTAG CAGGCAG ACA CACAAG CAGC 60
      TGGATG TCGA GAGGAG CATG TCAGCG GAGG AACACAC GCGG CAGCTG GACG TCCAGAG GAA 120
      TGCAC TACA GAAACT GGCA TGCTGG CAGA ACACGT GGA TTTGGCTGG GCAGT TGGAG 180
      GAGAG ATGTT CAGATG GTT CCGAGT TTCT TTCTTCTGGT GGGTTC GTGG TCTCGT TGGC 240
      TCAGG AGCG AGCTGC CAGC CTTCAC GCCA GCCCAG GAAG GGGCTC CCAC AGTGCAG CCG 300
      CAGGCT GAAG CGCTCCTCAA GTGCCG CCGAG AGTGGG CGTC CAGGCAG AGG AGGCCCG AG 360
      ACCGAG CGAG CGAGGATGC CAGCATG CTG TCACCTCT CA GTGCTGCC AT GCGAA ACTAC 420
      CCAACG TCCT CTACCATCCC TCCAAGA AGA TCCTACT CTC CAACCG AAA TGTCTACA AG 480
      AGTTACT CCT GCAGCCTTCC AGACATG AAA ATCTCC ATGG CAGAAT CTGG CCCCTCCT TG 540
      GATAGC CTTG ACATTTCTGGA GGATGG CGAG TCTGGG TCAC CATTTCTT GT GACTCAT TTG 600
      TACTTT CTGG GGGTTGT CAC CACTGGG ATG GAACA CTAG ATTTGAAA C AGGACCAA AC 660
      ATATTG GATT TGCAGAT TTA TGTGA AGGAT GAGGTT GGTG TCACAG ACCT GCAAGT CCTG 720
      ACTGTCC AGG TAACAGATGT GAACGAG CCA CTCAGT TTC AAGGCA ACTT GGCAGA AGAT 780
      CATCTCC GTG CAGACC AGCG ACATTT CAAT GCTCAT AGTC ACACGT ACCT GAGGGT AGTG 840
      GCTACTG CAT TGGCCAGG CA CAGGCT TAGA TCTAGCAT TG GTTCCC CCTT CCTGGG CACC 900
      TTCTGT GTTG TGGTGGG CAG GCAGTAT TTC CTGATT CTC CCCCAG AGAG CTTCAAG ATG 960
      TCTGTCA ATG GCACCTCT TT CTCCACA ACA GAATTG GACT TTGAAG CAGG ACACAGA AGT 1020
      TTCCAT CTCG TCGTGG AGGT GAGGGAC AGT GGAGGC CTCA AAGCCT CCAC AGAGCT CCAG 1080
      GTGAAC ATCG TGAACCTCAA CGACGA AGTC CCTCGCT TTA CCAGCCC GAC ACGAGTGT AC 1140
      ACAGTCT CTG AGGAATCT GAG TCCAGGA ACC ATCGTGG CCA ATATCAG CAGC GGAGGAT CCT 1200
      GATGATG AAG GTTTTCCAG CCACTCCTC TACAGCATTA CCACTGT TAG CAAATAT TTT 1260
      ATGATAA ATC AGTTGACT GG TACAAT CCAA GTGGCC CAAA GGATAG ACCG AGATGC AGGT 1320
      GAATTG AGC AAAATCCC AC CATTTCCCTG GAAGTT CTAG TGAAGG ACAG ACCATAT GGG 1380
      GGTCA GAGA ATCGCATCCA GATAACCTTC ATTGTG GAAG ACGTCA ACGA CAATCCTG CC 1440
      ACATGCC AAA AGTTACCTT CAGATCCAGT CTCCACCCTG CTCTGTG CTC CAAGACG CTG 1500
      ACCTGG ATGG ATACCGTATT AGACTGTTTT CATGCTGCTG ATAAAG ATAT ACCTGTG ACT 1560
      GGGCGA TTTA CAAAAGAAAG AGGTTTAATT GGACTTACAG TTCCACATGG CTGGGGAA AGC 1620
      CTCACA ATCA TGGCAGAAAG CAAGGAGGAG CAAGTCA CAT CTTACATGGA TGGCAGC AGG 1680
      CAAAGAG ATA GAGCTTGTG AGGGAA ACTC CTCCTTATA AGCCATCAGA TCTCATGAGA 1740
      CTTAGT CACT ATCAGCAGAA CAACTCAGGA AAGACTTGCC CCCATGATT CATTTCCTCC 1800
      TACCAG GTCC CTCCCA CAAC ATGTAGGAAT TCAAGA ATCC AGGCCACCAA CAACGAAGAC 1860
      ACAAGCT CTG TCACTGT TAC TGTGAACATC CTTGAAGAAA ATGATG AAAA GCCAATTGT 1920
      ACTCCAA ACT CTTATTTCCT GGCCCTCCCA GTGGATCTGA AAGTTGGCAC AAATATT CAG 1980
      AATTTCA AGC TGACATGTAC CGACCTTGAT TCCAGCCCCA GATCTT TCCG TTATTCCATT 2040
      GGCCCA GGTG ACGTCAACAA TCATTT CACC TTCTCTCCCA ATGCTGGTTC CAATGTCACA 2100
      CGCCTG CTG TACATCTCG CTTTGACTAT GCTGGTGGGT TTGATAAGAT CTGGGACTAC 2160
      AAGCTACT GTG TCTACGTAAC TGATGACA AC TTGATGTCTG ACAGGAAGAA AGCGGAGGCT 2220
      CTTGTTGAGA CAGGAACAGT GACACTGAGT ATTAAGTCA TTCCCC ACCC AACCATA TC 2280
      ATCACC AGA CCCCCAGGCC CAGGGTCACC TATCAGGTCC TGAGGAAAAA CGTTTACTCT 2340
      CCATCTG CAT GGTACGTGCC GTTTGT CATC ACTTTGGGCT CCATATTGCT TCTGGGTCTC 2400
      CTCGTGTACC TGGTGTCTCT ATTGGCCAAA GCCATCCACA GACACTGCCC CTGCAAGACT 2460
      GGGAA GAACA AGGAACCTCT GACAAAGAAA GGAGAAACGA AGACTGCAGA GAGAGACGTC 2520
      GTGGTGGAAA CTATCCAGAT GAACACTATC TTTGATGGAG AAGCCATAGA TCCAGAGCCT 2580
      GAGCAAGCTT CACTCGAGCT CTATGCCCTG CTGCCAGCT GCTGCGACCC TAGTCCAGTA 2640
      ACCCTAAGAA AGGTCCAGGT GTGTGGGGAG AGTGAAGAGA CCGGTCA GTG TTCGGGCCAC 2700

```

ATCACACTTC CCGGCAAGAT TCCAGTCGAT GACCCAAAGGA AACAGGAAAC AGGCCTGCAG 2760  
 GGTGATTTCG AGGTCTGGAC TCTATGCCCC GCTGTGAAGG TGGTTGTAGG CAGCCCTCAA 2820  
 GCTGAACGGT GCATTCGATT GGCTCTCAGT CTGAAAAAGT ACAGTTCTGA TTAA 2874

5

Seq ID NO: C64 DNA Sequence  
 Nucleic Acid Accession #: XM\_168571.1  
 Coding sequence: 155..988

10 1 11 21 31 41 51  
 TACACAGTCC TGGAGGAACT GAGTCCAGGA ACCATCGTGG CCAATATCAC AGCGGAGGAT 60  
 CCTGATGATG AAGGTTTTTC CAGCCACCTC CTCTACAGCA TTACCACTGT TAGCAAATAT 120  
 TTTCATGATA ATCAGTTGAC TGGTACAATC CAAGTGGCCC AAAGGATAGA CCGAGATGCA 180  
 15 GGTGAATTGA GACAAAATCC CACCATTTCC CTGGAAGTTC TAGTGAAGGA CAGACCATAT 240  
 GGGGTCAGG AGAATCGCAT CCAGATAACC TTCAATTGTG AAGACGTCAA CGACAATCCT 300  
 GCCACATGCC AAAAGTTCAC CTTTCAGCATT ATGGTGCCGG AAAGAACAGC CAAGGGGACG 360  
 TTGCTTCTTG ACCTAAACAA GTTCTGCTTT GATGATGACA GTGAGGCACC AAACAACAGA 420  
 TTCAACTTCA CCATGCCATC TGGAGTGGGG AGCGGCAGCA GATTTTACA GGATCCAGCT 480  
 20 GGCTCTGGGA AGATTGTGCT GATTGTGAT CTAGACTACG AAAATCCAAG TAACCTAGCA 540  
 GCCGGCAATA AATATACGGT GATAATCCAG GTGCAGGATG TGGCCCCCCC TTACTATAAA 600  
 AATAACGTCT ACCTTTATAT CCTAACAAAG CCAGAAAATG AGTTTCTCTC CATTTTGTAT 660  
 AGGCCATCCT ATGATTTTGA TGTGTGAGAA AGAAGGCCCG CCCAGGGTCA CCTATCAGGT 720  
 CCTGAGGAAA AAGCTTTACT CTCCATCTGC ATGGTACGTG CCGTTTGTCA TCACTTTGGG 780  
 25 CTCCATATTG CTTCTGGGTC TCCTCGTGTA CCTGGTCGTC CTATTGGCCA AAGCCATCCA 840  
 CAGACACTGC CCCTGCAAGA CTGGGAAGAA CAAGGAACCT CTGACAAAGA AAGGAGAAAC 900  
 GAAGACTGCA GAGAGAGACG TCGTGTGGA AACTATCCAG ATGAACACTA TCTTTGATGG 960  
 AGAAGCCATA GATCCAGTGA CCGGGGAAAC ATATGAATTC AACTCAAAAA CTGGAGCCAG 1020  
 AAAGTGGAAG GATCCACTAA CCCAAATGCC AAAATGGAAG GAGTCCAGCC ACCAGGGAGC 1080  
 30 TGCCCCACGC AGAGTCACTG CTGGGGAAGG GATGGGGTCA CTGAGAAGTG CCAACTGGGA 1140  
 AGAAGATGAG CTGAGTGGCA AAGCGTGGGC TGAGGATGCT GGTCTGGGTT CCAGAAATGA 1200  
 GGGTGGCAAG CTGGGCAACC CAAAGAACAG AAATCCAGCC TTCAATGAACA GGGCTTACCC 1260  
 CAAACACAC CCAGGAAAGT AAACGGGGTC TAAGGAGGGG CCTGTCAATC ACTGAGATGC 1320  
 TGCTTCACCC TAAATCTAT GGGGATGGTG TGGGCATGGT GTAGGGGGGA AAATGTGGGC 1380  
 35 TGAGGGGATT CAGACATCCA GGGTCAAAAC TGGGATGTTT GACAAATTTT TAAACAAATA 1440  
 GAAAGGGGTT TGATCACATA GTTGCGTGTG CTGAAATGAT ACAGGAACAT TTTCTATCAG 1500  
 ATTTAGAAGC TACCTGTGCT TCTGATAAGC AAGACTGTTA ACTTTGGGGT GTGGAATTGT 1560  
 TGTGTTTCTT CTTTGCAATT ACTGCTAGGA AGCTCTATTC TGTTCACCAT AGAAAGTTTG 1620  
 TAGGAATTCG TGACATAAAT AGTGAAGACT ATCCTTACAT CTGGTTTCCA CCTTATTTTC 1680  
 40 CTGCCCTCGT TTTAACATCA CCGAGATTTC TTCAGTTATA AATATGCCAT ACACCTTTGT 1740  
 AAGTCACCTC AATCTTCTT CAAAGAAAGC AGAACAGTGA AAAAAACAGA TGAGTAAGTT 1800  
 AAGAGTTGGT CATCTGGAAA GAAGAAAACT CAGTAGGCAC CTTCTTTTGT TTTTCTTGT 1860  
 GGTGTCCGGA TCAGATCTCT GCATGTGAGA TTCATCCACG TTGTCTGTGC TAGCAGTAGT 1920  
 TCAGTTCTCT TCATGGTATT GTCTGGTTTC ATTCTATGAT TATATCACA TTTATCTATT 1980  
 45 CTACACTTGG GTGGCAGCTG CTTCAGATTT TTTACTTTTA AAAAATATAC TTAAGATGTA 2040  
 ACTACAGGCA GGGCATGATG GCTCATGCCT GTAATGCCAG CACTTTGCCA AGGTGGGCAG 2100  
 ATCACCTAAG CTCAGAGATT CAAGATCAGC CTGGCCTAGA TGGCAAAACC CTGTCTCTAC 2160  
 TAAAAAATAC AAAAATTAGC TTGGTGTGGT GGTGGGCACA TGTAAATCCA GCTACTTGGG 2220  
 AGGCTGAGGT AGGAGAGACT GCTTAAACCT GAGAGGTGGA GGTACAGTG AGTTGAGATT 2280  
 50 GTGCCACTGC ACTCTAGCCT GGGTGACAAA GCAAGACTCC ATCTCAGAAA AAAAAAATAA 2340  
 AAGTGAATTA CAACACT 2357

Seq ID NO: C65 DNA Sequence  
 Nucleic Acid Accession #: NM\_005266.3  
 Coding sequence: 122..1198

55

1 11 21 31 41 51  
 GGCACGAGGC CATTTTCAAA CAGTCCCTCC TGGGAGAACA CAGACAGGCA GAGGATTACA 60  
 ACACAAGGCA GCAAGCACTG GGAGACGAAA GTTTTGGCAT CTGTTCCCTG GCTGTGCCAA 120  
 60 GATGGGCCAT TGGAGCTTCC TGGGAAATTT CCTGGAGGAA GTACACAAGC ACTCGACCGT 180  
 GGTAGGCAAG GTCTGGCTCA CTGTCCTCTT CATATTCCGT ATGCTCGTGC TGGGCACAGC 240  
 TGCTGAGTCT TCCTGGGGGG ATGAGCAGGC TGATTCCCGG TGTGATACGA TTCAGCCTGG 300  
 CTGCCAGAAT GTCTGCTACG ACCAGGCTTT CCCATCTCC CACATTCTGT ACTGGGTGCT 360  
 GCAGATCATC TTCGTCTCCA CGCCCTCTCT GGTGTACATG GGCCACGCCA TGCACTGTCT 420  
 65 GCGCATGCAG GAGAAGCGCA AGCTACGGGA GGCCGAGAGG GCCAAAGAGG TCCGGGGCTC 480  
 TGGCTCTTAC GAGTACCCGG TGGCAGAGAA GGCAGAACTG TCCTGCTGGG AGGAAGGGAA 540  
 TGGAGGATT GCCCTCCAGG GCACTCTGCT CAACACCTAT GTGTGCAGCA TCCTGATCCG 600  
 CACCACCATG GAGGTGGGCT TCATTGTGGG CCAGTACTTC ATCTACGGAA TCTTCTTGAC 660  
 70 CACCTGCGAT GTCTGCCGCA GGAGTCCCTG TCCCACCCCG GTCAACTGTT ACGTATCCCG 720  
 GCCACAGAG AAGAATGTCT TCATTGTCTT TATGCTGGCT GTGGCTGCAC TGTCCCTCCT 780  
 CCTTAGCTCG GCTGAACCTC ACCACTGGG CTGGAAGAAG ATCAGACAGC GATTGTCAA 840  
 ACCGGCGGAG CACATGGCTA AGTGCCAGCT TTCTGGCCCC TCTGTGGGCA TAGTCCAGAG 900  
 CTGCACACA CCCCCGACT TTAATCAGTG CCTGGAGAAT GGCCCTGGGG GAAAATTCTT 960  
 75 CAATCCCTTC AGCAATAATA TGGCTCCCA ACAAACACA GACAACCTGG TCACCGAGCA 1020  
 AGTACGAGGT CAGGAGCAGA CTCCTGGGGA AGGTTTCATC CAGGTTCTGT ATGGCCAGAA 1080  
 GCCTGAGGTG CCAATGGAG TCTACCCAGG TCACCGCCTT CCCATGGCT ATCATAGTGA 1140  
 CAAGCGAGCT CTTAGTAAGG CCAGCAGCAA GGCAAGGTCA GATGACCTAT CAGTGTGACC 1200  
 CTCCTTTATG GGAGGATCAG GACCAGGTGG GAACAAAGGA GGCTCAGAGA GGAAGACGT 1260  
 80 GTCCCTCTTG AACTGATGCT TTCTCACTGT CATCACTGCT TGGCTCCTTT GAGCCCGGG 1320  
 TCTCAATGAC GTTGCTCATT AATTCTAGAA ACTATAACCA GGGCTCTGGG ATAGTAAGAG 1380  
 AGGTGACAA CCACCCAGAC TGCAGTTCCC TCCCCACCCT CTACCCAGTA TACGAAGCCT 1440  
 TTCAGATTAC TCATGAAACA GGGTAGAGGG AAAGAAGGGA AGCATGGCAA AAGCTGGCCT 1500  
 GGAAGGGATA GCCAGAGGGA TAGAATGACT CTCTCTCTAC ATACCAGCAG CATACCAAT 1560  
 GCGTTCTCTA AGTTCTTACC TCCTTGACCT GATCAACCTC CCTCTCCAA GGAAGAGCTC 1620

AAAGTTCCCA GCCAATAGAC AGCATGAATC AAGGAACTTG CATTATATGT GCTCTTGAAT 1680  
 CTGTTGTCTC CATGGACCAT TCCTCGGAGT AGTGGTGAGA TGGCCTTGGG TTGCCCTTGG 1740  
 CTTCTCCTCC CTCTACTCAG CCTTAAAAAG GGCTTCTTGG AACTTTACCA GCAGCCTCAG 1800  
 CTTTACAAAT GCCTTGGTAT GTACCTCTGG CAAATGCCCT GGTATGTACC TCTGGCAAAT 1860  
 5 GCCCACCTT GGTGATGTTG CAACCTTTCC TTCTGCTAGG GTGTACACCT AGCCTGTGCA 1920  
 GGTGTACGCC CTGCTAGGGA GTCACGTGAC ACACAAACTC TACTGGAATT CCTGCCAACA 1980  
 TCTGTACACC TGCAGCTCCT TTACAGTTCA ATCCAATGAT AGAAACCATC CCTTCCCTTT 2040  
 CTCCTTGGG TGTTTACCCA GCCATTCCCT GAAGGCCTTA CCAACAGGAA TATCCAAGAA 2100  
 10 GCTGTTGTCC TCTCTCGAAC CCTGACCAGA TCATCAGCCA CTGAGGCCAG TGAATTTCC 2160  
 CCAGGCCCTG TTAATAAAAA AAAAAAATAA 2190

Seq ID NO: C66 DNA Sequence  
 Nucleic Acid Accession #: NM\_014459.2  
 Coding sequence: 738..3407

15  
 1 11 21 31 41 51  
 | | | | |  
 GTAGATGCAG TCCGCCGCGG CCGCTGCCTC AGCCAGCAAT GCAAGATTAG ATCTCTAAAT 60  
 GCAGCAAAAC ACTGCCTGAA AACAGACCCG CCCGCGCAGC AAGCAGACAT TTCACGGTGC 120  
 20 GCTGGGGAAG CTTCAAATA TATCTGTGAC TCTGTCTTCG TTGCTCTTCA TCCCATCAA 180  
 TTTTCATCAG GGAGGCGAGC AGCAAGTAAG AATTTCACTT TCGGATCTGC CTAGAGACAC 240  
 ACCTCCCTGC TCCCTCCCCC ACTCGATGTG AAGAGTATTC CGGAGTCTCC GGGCGGGAGT 300  
 AGATTTGCAG CACCTTAGCG GGAGCGAGGA AAACCTACTG ATTCTTTAGC TCATTATCAT 360  
 25 CTCTCCGAGA CGAGATTTCC TTCTTATCGC CTGCCTCATC GCTCAAGTTT GAGCCTCCCG 420  
 AAGTCCGGGC GGGAGGAGAGC AAACCCCTGG CTCACCCCCA GCGCAGGAA GCCACCGCCT 480  
 TGCTCCAAGC CCTGTGAGCT CTGCTGCACC GCAGCTTCTC ACCCAGTGC GATGCTGTAG 540  
 ATCAACAGGT TCAGGGAAC TTAGCAGAA TAAAGAGAGC CACCGGGTGC CGCAGCTCGG 600  
 GTGCAGAGGG AAAAAAGGAC CCATAGACTT GTGGCTCGCG TCGCGCGCGC ACGCTGCGCC 660  
 30 AGGGCCCCAG GTGGGCGCGC ACTCCCTCTC TGGCTCCTCC AGTCCGATTG CTCCTGCCCC 720  
 CACCTTACAG GTCTGGGATG TACCTTTCCA TCTGTGTGCTG CTTTCTTCTA TGGGCCCCCTG 780  
 CCTCACTCT CAAGAACCTC AACTACTCCG TGCCGGAGGA GCAAGGGGCC GGCACGGTGA 840  
 TCGGGAACAT CGGCAGGGAT GCTCGACTGC AGCCTGGGCT TCCGCTGCA GAGCGCGCG 900  
 GCGGAGGGCG CAGCAAGTCG GGTAGCTACC GGGTGTGGA GAACCTCCGCA CGCACCTGC 960  
 35 TGACATGGA CGCAGACAGC GGGCTCCTCT ACACCAAGCA GCGCATCGAC CGCAGTCCC 1020  
 TGTGCCGCCA CAATGCCAAG TGCCAGCTGT CCTCGAGGT GTTCGCCAAC GACAAGGAGA 1080  
 TCTGCATGAT CAAGGTAGAG ATCCAGGACA TCAACGACAA CGCGCCTTCC TTCTCTCGG 1140  
 ACCAGATCGA AATGGAGTCG TCGGAGAAGC CTGCTCCGGG CACCGCTTC CCCCTCACCA 1200  
 CGCACATGA CCCCAGCGCC GGCAGAAATG GGCTCCGCAC CTACCTGCTC ACGCGCGACG 1260  
 40 ATCAGGCCTT CTTTGGACTC GACGTTAAGT CCGCGGCGCA CGGCACCAAG TTCCAGAAC 1320  
 TGTTCATCCA GAAGGCTCTG GACCGCGAGC AACAGAATCA CCATACGCTC GTGCTGACTG 1380  
 CCTTGGACGG TGGCGAGCCT CCACGTTCCG CCACCGTACA GATCAACGTG AAGGTGATTG 1440  
 ACTCCAACGA CAACAGCCCG GTCTTCGAGG CGCCATCCTA CTTGGTGGAA TTGCCCGAGA 1500  
 ACGCTCCGCT GGTTCAGTGT GTCATCGATC TGAACGCCAC CGACGCCGAT GAAGGTCCCA 1560  
 45 ATGGTGAAGT GCTCTACTCT TTCAGCAGCT ACGTGCTTGA CCGCGTGC GG GAGCTTCTT 1620  
 CCATCGACCC CAAGACCGCG CTAATCCGTG TGAAGGGCAA TCTGGACTAT GAGGAAAACG 1680  
 GGATGTGGA GATTGACGTG CAGGCCCGAG ACCTGGGGCC TAACCTATC CCAGCCACT 1740  
 GCAAAAGTCA GGTCAAGCTC ATCGACGCA ACGACAATGC GCGCTCCATC GGTTCGTCT 1800  
 CCGTGCGCCA GGGGCGCGTG AGCGAGGCCG CCCTCCCGG CACCGTCATC GCCCTGGTGC 1860  
 50 GGGTCACTGA CCGGACTCTT GGCAAGAACG GACAGCTGCA GTGTCGGGTC CTAGGCGGAG 1920  
 GAGGACGGG CGGCGCGCGG GGCCTGGGCG GCGCCGGGGG TTCCGTCCTC TTCAAGCTTG 1980  
 AGGAGAACTA CGACAACCTC TACACGCTGG TGAAGTACCG CCGCTGAGC CGCGAGACAC 2040  
 AAGACAGATA CAACGTGACC ATCGTGGCG GGGACGGGGG CTCTCTCTCC CTCAACTCCA 2100  
 CCAAGTCGTT CGCGATCAAG ATTCTAGACG AGAACGACAA CCGCCTCTCG TTCAACAAAG 2160  
 55 GGTCTTACGT GCTTCAGGTG CACGAGAAC AATCCCGGG AGAGTACCTG GGCTCTGTGC 2220  
 TCGCCAGGA TCCCGACCTG GGCCAGAACG GCACCGTATC CTACTCTATC CTGCCCTCGC 2280  
 ACATCGGCGA CGTGTCTATC TACACCTATG TGTCTGTGAA TCCACGAAC GGGGCCATCT 2340  
 ACGCCCTGCG CTCCTTTAAT TTCCAGCAGA CCAAGGCTTT TGAGTTCAAG GTGCTTGCTA 2400  
 AGGACTCGGG GCGCCCGCGG CACTTGGAGA GCAACGCCAC GGTGAGGGT ACAGTGTAG 2460  
 60 ACGTGAATGA CAACGCGCCA GTGATCGTGT TCCCCAGCT GCAGAACGAC ACCGCGGAGC 2520  
 TGCAAGTGGC GCGCAACGCT GGCTGGGCT ATCTGTTGAG CACTGTGCGC GCCCTAGACA 2580  
 GCGACTTCGG CGAGAGCGGG CGTCTCACCT ACGAGATCGT GGACGGCAAC GACGACCACC 2640  
 TGTTTGAGAT CGACCCGTCC AGCGGCGAGA TCCGACGCT GCACCTTTT TGGGAGGACG 2700  
 TGACGCCCCG GTTGGAGCTG GTGGTGAAGG TGACCGACCA CGGCAAGCCT ACCCTGTCCG 2760  
 65 CAGTGGCCAA GCTCATCATC CGCTCGGTGA GCGGATCCCT TCCGAGGGG GTACCAAGGG 2820  
 TGAATGGCGA GAGCACCAC TGGGACATGT CGCTGCGCT CATCGTACT CTGAGCACTA 2880  
 TCTCCATCAT CCTCTAGCG GCCATGATCA CCAATCGCGT CAAGTGCAAG CGCGAGAACA 2940  
 AGGAGATCCG CACTTACAAC TGCCGATCG CCGAGTACAG CCACCGCAG CTGGGTGGGG 3000  
 70 GCAAGGGCAA GAAGAAGAAG ATCAACAAA ATGATATCAT GCTGGTGCAG AGCGAAGTGG 3060  
 AGGAGAGGAA CGCATGAAC GTCATGAACG TGGTGAGCAG CCCCTCCCTG GCCACCTCCC 3120  
 CCATGTACTT CGACTACGAC ACCCGCTGCG CCTCAGCTC GCGCCGCTCG GAGGTGATGT 3180  
 ATCTCAAAC GGCCTTCAAC AACCTGACTG TCCCTCAGGG GCACGCGGGC TGCCACACCA 3240  
 GCTTCACCGG ACAAGGGACT AATGCAAGCG AGACCCCTGC CACTCGGATG TCCTAATTC 3300  
 75 AGACAGACAA TTTTCCGCA GAGCCCAATT ACATGGGCAG CAGGCAGCAG TTTGTTCAAA 3360  
 GTATTTCAGT AGCTCCACGT TTAAGGACCC AGAAAGAGCC AGCCTGAGAG ACAGTGGGCA 3420  
 CGGGGACAGT GATCAGGCTG ACAGTGACCA AGACACTAAC AAAGGCTCCT GCTGTGACAT 3480  
 GTCTGTAGG GAGGCACTCA AGATGAAAAC TACTTCACT AAAAGCCAAC CACTTGAAAC 3540  
 AGAACCGAAG GAGTGTGTTA ATTGCACAGA TGAATGCCGA GTGCTTGGTC ATTCTGACAG 3600  
 80 GTGCTGGATG CCACAGTTCC CTGCAGCCAA TCAGGCTGAA AATGCAGATT ACCGCACAAA 3660  
 TCTCTTTGTA CTTACAGTGT AAGCTAATGT TGAGACTGAG ACTTACGAAA CTGTGAATCC 3720  
 CACTGGGAAA AAGACTTTT GTACATTTGG AAAAGACAAG CGAGAGCACA CTATTCTCAT 3780  
 TGCCAACTGT AAACCTTATT TAAAGCCAA ACGTGCCCTG AGCCCTCTCC TCCAAGAGGT 3840  
 CCCCTCAGCA TCAAGCAGCC CAACCAAGGC GTGCATCGAG CCTTGACCT CAACAAAAGG 3900  
 CTCCTGGAT GGCTGTGAAG CAAACACAGG AGCCTGGCT GAAGCAGCA CTCAGTACTT 3960  
 GCCCACTGAC AGTCAATATC TGTACCTAG TAAGCAACCA AGAGACCCTC CCTTCATGGC 4020

5 TTCCGATCAG ATGGCAAGGG TCTTTCAGAG TGTGCATTCC AGAGCCAGCC GGGATTCCAG 4080  
 TGAGATGGGT GCTGTTCTTG AGCAGCTTGA CCACCCCAAC AGGATCTGG GCAGAGAGTC 4140  
 TGTGGATGCA GAGGAAGTTG TGAGAGAAAT TGATAAGCTT TTGCAAGACT GCCGGGGAAA 4200  
 CGACCCCTGTG GCTGTGAGAA AGTGAAAAAA GAAAAAAA AAGGCATTGG CATTTTCTTG 4260  
 TCTCTTCTGT TGATTAAAA ATGATCCCTC CTGGTGATAA CCCATTTTAC AGGGATGAAG 4320  
 AAAGACCAAT GCTGCTTTAA GGCTTTTAGT GAACATCTGA AGTGCCACA AGTATGTTCT 4380  
 TTCCACTGCT GATTTCTTTT TCAGAGATAA CAATGGTTTC GTTTTGACCA AACTTGTTAT 4440  
 AGGACAGAAT TAATGATGCT TAAAGAGAAA AGAAAAAAG AGAGAAGAAA AAGGAGAGAT 4500  
 GAAAAAGGAG GATGAGGAGA AGAATTACCT TTTGACAATC TGTAGGAAG GTATGCAGTG 4560  
 10 TGAGAACTGA AGTATTCTTG ATCACTCTCA GACTGTCCTC CGTGATTAT GCTGACTTAA 4620  
 CTGTTTACCT ATAAACCCCA TACAAAGCAG GGTCAATAAT TGTGATCTGT GGTGGATTTC 4680  
 TAGCAGTCAT CACAGGCTTC TACTGAAAGT CCTGAAAAGA CCTTGCACTA GTCCAAGCTA 4740  
 CACCAACAT TAACACATAT TTGTGGTAAA CATTTCTGTA TAAAGTTACC TGACACACAT 4800  
 15 ATAAACACAA GGAACATTCC ATATCATTAG TCGAAAAA AAACAAAAA AAACCTTTG 4860  
 GTCATTGTGA AGACATCTCA TGTCTATATA AAGTTAAATG TAAAAAGATA CAGTCCATT 4920  
 TGTCTCGCAC ACACGTAGAC TAATTCACGT CAAAAA AAAAAA 4966

Seq ID NO: C67 DNA Sequence  
 Nucleic Acid Accession #: NM\_005601.2  
 Coding sequence: 101..598

20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

1 11 21 31 41 51  
 CCCAGGAGTC TGGGTGCACA GCCTCCTTCT CTCTGAGATT CAAGAGTCTG ATCAGCAGCC 60  
 TCTTCCTCCT CCAGGACCCA GAAGCCCTGA GCTTATCCCC ATGGAGCTCT GCCGGTCCCT 120  
 GGCCTCTGCT GGGGGCTCCC TGGGCTGAT GTTCTGCTG ATTGCTTTGA GCACCGATT 180  
 CTGGTTTGA GCTGTGGGTC CCACCCACTC AGCTCACTCG GGCTCTGGC CAACAGGGCA 240  
 TGGGACATC ATATCAGGCT ACATCCACGT GACGCAGACC TTCAGCATT TGGCTGTTCT 300  
 GTGGGCCCTG GTGTCCGTGA GCTTCCTGGT CCTGTCTGCT TCCCTCCAC TGTTCCTCC 360  
 AGGCCACGGC CGCTTGTCT CAACCCACGC AGCCTTGTCT GCAGCCATCT CATGTTGGT 420  
 GGGCATGGCG GTGTACACCA GCGAGCGGTG GGACAGCCT CCACACCCC AGATCCAGAC 480  
 CTTCTTCTCC TGGTCTTCT ACCTGGGCTG GGTCTCAGCT ATCTCTTGC TCTGTACAGG 540  
 TGCCCTGAGC CTGGGTGCTC ACTGTGGCGG TCCCGTCCT GGTATGAAA CTTGTGAGC 600  
 AGAAGGCAAG AGCGGCAAGA TGAGTTTGA GCGTTGTATT CCAGAGCCT CATCTGGAGC 660  
 CTGCGGAAAG TCTGGTCTTA CATTTGCCCG CCCTTCCAGC CCTTCCCAG CCCCTCTCT 720  
 TGTTCCTTCA TTCATTCAAC AAAATTGGC TGGAAAAA AAAAAA AAAAAA 780  
 AAA 783

Seq ID NO: C68 DNA Sequence  
 Nucleic Acid Accession #: NM\_006433.2  
 Coding sequence: 129..566

45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

1 11 21 31 41 51  
 GTATCTGTGG TAAACCCAGT GACACGGGG AGATGACATA CAAAAGGGC AGGACCTGAG 60  
 AAAGATTAAAG CTGCAGGCTC CTGCCCATA AAACAGGGTG TGAAGGCAT CTCAGCGGT 120  
 GCCCACCAT GGTACTCTGG GCCCTCTGCT TCCTTGAGC CATGCTCTG GGCACCCAG 180  
 GTCTGGTCTT CTCTCTGCTG AGCCCTGAGT ACTACGACCT GGCAGAGCC CACCTGCTG 240  
 ATGAGGAGAA ATCCTGCCCC TGCCCTGGCC AGGAGGGCCC CCAGGGTGAC CTGTTGACCA 300  
 AAACACAGGA GCTGGGCGGT GACTACAGGA CCTGTCTGAC GATAGTCAA AACTGAAGA 360  
 AGATGGTGGG TAAGCCACC CAGAGAAGTG TTTCCAATGC TGCAGCCCG GTGTGTAGGA 420  
 CGGGGAGGCT ACAGTGGCGC GACGTCTGCA GAAATTTTCA GAGGAGGTAT CAGCTAGAG 480  
 TTACCCAGGG CCTCGTGGCC GGAGAAACTG CCCAGCAGAT CTGTGAGGAC CTCAGGTTGT 540  
 GTATACCTTC TACAGGTTCC CTCTGAGCCC TCTCACCTTG TCTGTGGAA GAAGCACAGG 600  
 CTCCTGTCTC CAGATCCCGG GAACCTCAGC AACCTCTGCC GGTCTCTCG TTCTCGATC 660  
 CAGAATCCAC TCTCCAGTCT CCCTCCCCTG ACTCCCTCTG CTGTCTCCC CTCTCACAGG 720  
 AATAAAGTGT CAAGCAAG 738

Seq ID NO: C69 DNA Sequence  
 Nucleic Acid Accession #: NM\_002985.2  
 Coding sequence: 69..344

65  
 70  
 75  
 80

1 11 21 31 41 51  
 GCTGCAGAGG ATTCCTGCAG AGGATCAAGA CAGCACGTGG ACCTCGCACA GCCTCTCCA 60  
 CAGGTACCAT GAAGGTCTCC GCGGCAGCCC TCGCTGTCT CCTATTGCT ACTGCCCTCT 120  
 GCGCTCCTGC ATCTGCCTCC CCATATTCTT CCGACACCAC ACCCTGCTGC TTTGCCTACA 180  
 TTGCCCGCCC ACTGCCCGGT GCCCACATCA AGGAGTATTT CTACACCAGT GGCAAGTGCT 240  
 CCAACCCAGC AGTCGTCTTT GTCACCCGAA AGAACCCGCA AGTGTGTGCC AACCAGAGA 300  
 AGAAATGGGT TCGGAGTAGT ATCAACTCTT TGGAGATGAG CTAGGATGGA GAGTCTTGA 360  
 ACCTGAACCT ACACAAATTT GCCTGTTTCT GCTTGCTCTT GTCTAGCTT GGGAGGCTT 420  
 CCCTCACTAT CCTACCCAC CCGCTCCTTG AAGGGCCCAG ATTCTACCAC ACAGCAGCAG 480  
 TTACAAAAAC CTTCCCCAGG CTGACGCTGG TGGCTCACGC CTGTAATCCC AGCACTTTG 540  
 GAGGCCAAGG TGGGTGGATC ACTTGAGGTC AGGAGTTTGA GACCAGCCTG GCCAACATGA 600  
 TGAAACCCCA TCTCTACTAA AAATACAAAA AATTAGCCGG GCGTGGTAGC GGGCGCTGT 660  
 AGTCCAGCT ACTCGGGAGG CTGAGGCAGG AGAATGGCGT GAACCCGGGA GCGCGAGCTT 720  
 GCAGTGAGCC GAGATCGCGC CACTGCATC CAGCCTGGGC GACAGAGCGA GACTCCGTCT 780  
 CAAAAA AAAAAA AAAATACAAA AATTAGCCGG GCGTGGTAGC GCGCGCTGT 840  
 AATCCAGCT ACTCGGGAGG CTAAGGCAGG AAAATGTTT GAACCCAGGA GGTGGAGGCT 900  
 GCAGTGAGCT GAGATTGTGC CACTTCACTC CAGCCTGGGT GACAAAGTGA GACTCCGTCA 960  
 CAACACAAAC AAAAAAAGC TTCCCAACT AAAGCCTAGA AGAGCTTCTG AGGCGCTGCT 1020  
 TTGTCAAAG GAAGTCTCTA GGTCTGAGC TCTGGCTTTG CCTTGGCTTT GCCAGGGCT 1080

TGTGACCAGG AAGGAAGTCA GCATGCCTCT AGAGGCAAGG AGGGGAGGAA CACTGCACTC 1140  
 TTAAGCTTCC GCCGTCTCAA CCCCTCACAG GAGCTTACTG GCAAACATGA AAAATCGGCT 1200  
 TACCATTAAA GTTCTCAATG CAACCATAAA AAAAAAA 1237

5

Seq ID NO: C70 DNA Sequence  
 Nucleic Acid Accession #: NM\_022154.2  
 Coding sequence: 1381..1722

10

1	11	21	31	41	51	
AGTGTGGTTT	TAGTTTTTCC	TAAGAAGTGG	CGTGGTTTGG	GGCTTTATAT	CCGGGAGGAG	60
CATATGTACG	CAAATCCTGG	GGCGTTTGCA	AACCCGGATC	CGGGGCGTCT	GGCCCCATGC	120
CCGGCCGGGC	GTTTGGAGGC	TACTGCCACG	CAGCGTTTCT	GGAGCCTGCC	GGCTGGTGCC	180
CTGGTGGCCT	TTATCTCTGT	CCCCCTTTGT	CCTCTTTATC	TCAGGCTCTC	CAGGAGGCCG	240
GGGGGCCAC	TCCGCTATC	GCTCCCTCG	GCTACGCTGC	CACTCCAATG	CCCGCAGGT	300
CGCGAGCTGC	TGTTCTTTCG	AAGGCGCCGG	AGAACCAGGG	GCCTCCCGCG	CCACCTCTGA	360
CTCGGAGCAG	CGCCGAGCAC	TGACGCTCCC	GCCCTTGGGC	AAGGACGCCA	GTGCGCCCGC	420
GCGCGTCCCT	CTGCGCGGCA	GCCCGTCGCG	GGCCCTCAAG	GGGAAGCCCA	GGCCAGGATG	480
GCCCCGGGTC	GCGCGGTGGC	CGGGCTCCTG	TTGCTGGCGG	CCGCGCGCCT	CGGAGGAGTG	540
GCGGAGGGGC	CAGGGCTAGC	CTTCAGCGAG	GATGTGCTGA	GCGTGTTCGG	CGCGAATCTG	600
AGCCTGTGCG	CGGCCGAGCT	CCAGCACTTG	CTGGAGCAGA	TGGGAGCCGC	CTCCGCGGTG	660
GGCGTCCCGG	AGCCTGGCCA	GCTGCACTTC	AACCAGTGTT	TAAGTCTGTA	AGAGATCTTT	720
TCCCTTCATG	GCTTTTCAAA	TGCTACCCAA	ATAACCAGCT	CCAAATTCTC	TGTCATCTGT	780
CCAGCAGTCT	TACAGCAATT	GAACCTTCAC	CCATGTGAGG	ATCGGCCCAA	GCACAAAACA	840
AGACCAAGTC	ATTCAAGAGT	TTGGGGATAT	GGATTCTCTG	CAGTGACGAT	TATTAATCTG	900
GCATCTCTCC	TGGATTGAT	TTTGACTCCA	CTGATAAAGA	AATCTTATTT	CCCAAGAGAT	960
TTGACCTTTT	TTGTGGGGCT	GGCTATTGGG	ACTCTTTTTT	CAAAATGCAAT	TTTCCAACCT	1020
ATTCCAGAGG	CATTGGGATT	TGATCCCAA	GTGACAGATT	ATGTTGAGAA	GGCAGTTGCT	1080
GTGTTTGGTG	GATTTTACCT	ACTTTTCTTT	TTTGAAGAA	TGCTAAAGAT	GTTATTAAAG	1140
ACATATGGTC	AGAAATGGTCA	TACCACTTT	GGAAATGATA	ACTTTGGTCC	TCAAGAAAAA	1200
ACTCATCAAC	CTAAAGCATT	ACCTGCCATC	AATGGTGTGA	CATGCTATGC	AAATCCTGCT	1260
GTCCAGAAAG	CTAATGGACA	TATCCATTTT	GATAATGTCA	GTGTGGTATC	TCTACAGGAT	1320
GGAAAAAAG	AGCCAAATTC	ATGTACCTGT	TTGAAGGGGC	CCAAACTGTC	AGAAATAGGG	1380
ACGATTGCCT	GGATGATAAC	GCTCTGCGAT	GCCCTCCACA	ATTTTCATCGA	TGGCCTGGCG	1440
ATTGGGGCTT	CCTGCACCTT	GTCTCTCCTT	CAGGGACTCA	GTACTTCCAT	AGCAATCCTA	1500
TGTGAGGAGT	TTCCCCACGA	GTTAGGAGAC	TTTGTGATCC	TACTCAATGC	AGGGATGAGC	1560
ACTGCACAAG	CCTTGCTAAT	CAACTTCCTT	TCTGCTATGT	CCTGCTATGT	TGGGCTAGCT	1620
TTTGGCATT	GGTGGGCAA	CAATTTGCT	CCAAATATTA	TATTTGCACT	TGCTGGAGGC	1680
ATGTTCTCT	ATATTTCTCT	GGCAGATATG	TTTCCAGAGA	TGAATGATAT	GCTGAGAGAA	1740
AAGGTAACTG	GAAGAAAAAC	CGATTTCAAC	TTCTTCATGA	TCAGAATGC	TGGAATGTTA	1800
ACTGGATTCA	CAGCCATTCT	ACTCATTACC	TTGTATGCAG	GAGAAATCGA	ATTGGAGTAA	1860
TAGAAAATGG	AAGATGGTGT	TGTTAATAAA	GGCATTTAAT	AGATAAAAAAC	ATCTCCAAAA	1920
AGGATTTTGA	AGCTGATCCT	ATTTAGTTAA	AAAGATAAAT	TTGCTTTCAA	CTGTAGGTCC	1980
AGAAAATAAA	TTATTGGCAT	CAGTCTGTGA	AATAGTCCAT	TATTTGTGTG	TAAAAATGCT	2040
TCAAAAGGTT	TTCAAGTGTCA	GTCTGAGATG	CCTGGTATAT	AGGAGCCTTT	GGGAAATACT	2100
TATTTTTCAG	TATTTCCATG	ATATTAGATA	TCACCATGAA	GCAAGAGACA	TGCATTCTAT	2160
AATCATGTAG	ACACTCAGAC	TCAGGGGAAA	ATACAAGTTA	TATCCTGAAA	GCCTTTAAAA	2220
CTCTATGGTA	GGATCAAAGA	TTCAAATGGT	TTCAGAGAGG	TTTTATTTCA	ATTAATTTGT	2280
TCTAGTGCTT	TCAAGAGCAA	GTACATCAAA	ATGTAGAAGG	TAAAATGTAT	GCAACACTAA	2340
TATAAATTAT	TCCAAGTCTT	TAAGGAGCCA	AAGAAAAAAA	AGATTCTCTA	CAGCTTTTGT	2400
TTCTGTTTTG	TATTTCAATT	AGGAACCTGC	AGTATTATTT	TGAAAACCAT	TCTAAAAATA	2460
TAGGAGTTAG	GAAATAAATA	AAGTTTGTCT	AGCCCTGCTA	AGTTCAAGCT	TAGAGGCTTA	2520
TCGCTAAGTN	TAAACTTCAC	CAGATTCCAC	GAAAAGCTGG	ATAGCTTTTT	TTCTGACTTA	2580
TGTTGTGGTT	GCACCCCTCA	CAAATGGCAG	AACAGTATGT	AAAGCTGGTA	ACACCTCGGT	2640
TTCAATGTCAC	CATGTGTTTG	CTTTGTGAAG	GTGAAGAATA	TGTTGGTTTA	GAGAAAGAAA	2700
TTGGATGTAA	TTTTATGCAA	TTTACTTTTA	AAGACAAACA	TAACTATTTA	GCAGAGAATA	2760
TTTTATAAAA	TGCAAAACAA	CAGCTGGACT	GCTGTACATC	AAGGACAGAT	TAACTGGAAA	2820
ACATATGTTT	CTTATGTGTG	ATTGAGAGCC	ATTGAGAAAA	GACTTCCTTT	GTGTTTCAGCC	2880
TATACTTTTC	CATATGGTAT	ACCTTGAAAA	AAATTAGCAC	ACCATGGTTA	TTTTTCTACC	2940
TTTTATAAAA	GACAGAGCCT	GTTTACTCAT	TTAGAAGATA	GAGAAAATTG	GTCTAAAAAT	3000
GAACATCCTA	GATTACACAT	CCCAAGTCAC	TTAAGGTGAT	TTGATGGTGA	GGAAAATGAT	3060
TGACAAAGCC	CAACAATGAT	CTCAGGAATT	ACATTTTCCA	ACAGACCAAA	AAATGTTTTT	3120
ATGTAGCAGC	AATGCAGATT	TGGTGAATAT	TTAATATATA	TTTATGATAT	TATTTCACTT	3180
TATGACTGAC	AATTAATAAA	TATTGTTTGG	CCAAATAGTA	AACACCCTTT	TGAAAACCATG	3240
AAAAAA						3246

70

Seq ID NO: C71 DNA Sequence  
 Nucleic Acid Accession #: NM\_004184.2  
 Coding sequence: 188..1603

75

80

1	11	21	31	41	51	
CGAAAAAAGA	GGGGAAGAGT	ATTAAAGACC	ATTTCTGGCT	GGGCAGGGCA	CTCTCAGCAG	60
CTCAACTGCC	CAGCGTGACC	AGTGGCCACC	TCTGCAGTGT	CTTCCCAAC	CTGGCTTTGA	120
CTCGTCTGCT	GAACAAATCC	TCTGACCTCA	GGCCGGCTGT	GAACGTAGTT	CCTGAGAGAT	180
AGCAACATG	CCCACACAGT	AGCCCGCATC	TCTGCTGGAG	CTGTTCAACA	GCATCGCCAC	240
ACAAAGGGAG	CTCGTAAGGT	CCCTCAAAGC	GGGAAATGCG	TCAAAGGATG	AAATGTGATT	300
TGCAATAAAG	ATGTTGGTGT	CATTAAAAAT	GAGCTACAAA	GCTGCGCGCG	GGGAGGATTA	360
CAAGGCTGAG	TGTCTCCAG	GGAACCCAGC	ACCTACCAGT	AATCATGGCC	CAGATGCCAC	420
AGAAGCTGAA	GAGGATTTTG	TGGACCCATG	GACAGTACAG	ACAAGCAGTG	CAAAAGGCAT	480
AGACTACGAT	AAGCTCATTG	TTGCGTTTGG	AAGTAGTAAA	ATTGACAAAG	AGCTAATAAA	540
CCGAATAGAG	AGAGCCACCG	GCCAAAGACC	ACACCCTTTC	CTGCGCAGAG	GCATCTTCTT	600

5	CTCACACAGA GATATGAATC AGGTTCTTGA TGCCTATGAA AATAAGAAGC CATTTTATCT 660
	GTACACGGGC CGGGGCCCTT CTTCTGAAGC AATGCATGTA GGTCACTCA TTCCATTAT 720
	TTTCACAAAG TGGTCCAGG ATGTATTTAA CGTGCCCTTG GTCATCCAGA TGACGGATGA 780
	CGAGAAGTAT CTGTGGAAGG ACCTGACCCT GGACCAGGCC TATGGCGATG CTGTTGAGAA 840
	TGCCAAGGAC ATCATCGCCT GTGGCTTTGA CATCAACAAG ACTTTCATAT TCTCTGACCT 900
	GGACTACATG GGGATGAGCT CAGGTTTCTA CAAAAATGTG GTGAAGATTC AAAAGCATGT 960
	TACCTTCAAC CAAGTGAAAG GCATTTTCGG CTTCACTGAC AGCGACTGCA TTGGGAAGAT 1020
	CAGTTTTCTT GCCATCCAGG CTGCTCCCTC CTTGAGCAAC TCATTTCCAC AGATCTTCCG 1080
10	AGACAGGACG GATATCCAGT GCCTTATCCC ATGTGCCATT GACCAGGATC CTTACTTTAG 1140
	AATGACAAAG GACGTGCGCC CCAGGATCGG CTATCCTAAA CCAGCCCTGT TGCATCCAC 1200
	CTTCTTCCCA GCCCTGCAGG GCGCCAGAC CAAAATGAGT GCCAGCGACC CAAACTCCTC 1260
	CATCTTCTTC ACCGACACGG CCAAGCAGAT CAAAACCAAG GTCATAAGC ATGCGTTTTT 1320
	TGGAGGGAGA GACACCATCG AGGAGCACAG GCAGTTTGGG GGCAACTGTG ATGTGGACGT 1380
15	GTCTTTATG TACCTGACCT TCTTCTCGA GGACGACGAC AAGCTCGAGC AGATCAGGAA 1440
	GGATTACAC AGCGGAGCCA TGCTCACCGG TGAGCTCAAG AAGGCACTCA TAGAGGTTCT 1500
	GCAGCCCTTG ATCGCAGAGC ACCAGGCCCG GCGCAAGGAG GTCACGGATG AGATAGTGAA 1560
	AGAGTTTATG ACTCCCCGGA AGCTGTCTCT CGACTTTTCA TAGCACTCGT TTTACATATG 1620
	CTTATAAAG AAGTATGATA TCAGTAATGT ATCAATAATC CCAGCCCACT CAAAGCACCG 1680
20	CCACTGTAG GCTTCTGTCT CATGGTAATT ACTGGGCTG GCCTCTGTAA GCCTGTGTAT 1740
	GTTATCAATA CTGTTTCTTC CTGTGAGTTC CATTATTTCT ATCTCTTATG GGCAAAAGAT 1800
	TGTGGGTAAT TGGTGTCTGC TAACATTGCA TGGTCGGATA GAGAAGTCCA CGTGTGAGTC 1860
	TCTCCCCAAA GCAGCCCCAG AGTGGAGCCT TCGGCTGGAA GTCCATGGGC CACCTGTTC 1920
	TTGTCCATG AGGACTTCCG AGGTTTCCAA GTATACTCTT AAGACCCACT CTGTTTAAAA 1980
25	ATATATATTC TATGTATGCG TATATGGAAT TGAAATGICA TTATTGTAAC CTAGAAAAGTG 2040
	CTTTGAAATA TTGATGTGGG GAGTTTATT GAGCACAGA TGTATTTTCA CCCATGCCCC 2100
	CTCCCAAAAA GAAATTGATA AGTAAAAGCT TCGTTATACA TTTGACTAAG AAATCACCCA 2160
	GCTTTAAAGC TGCTTTTAA C AATGAAGATT GAACAGAGTT CAGCAATTTT GATTAAATTA 2220
	AGACTTGGGG GTGAAACTTT CCAGTTTACT GAACCTCAGA CCATGCAATG AGTCCACTCC 2280
30	AGAATCATG CTCGCTTCCC TTGGGCACAC AGTGTCTCTC TGCCAAATGA CCCTAGACCC 2340
	TCTGTCTGCG AGAGTCAGGG TGGCTTTTCC CCTGACTGTG TCCGATGCCA AGGAGTCTCT 2400
	GCCTCCGACG ATGCTTCAAT TTGACCTTGG GCTGCAGTGG AAGTCAGCAC AGAGCAGTGC 2460
	CCTGGCTGTG TCCTGGACGG GTGGACTTAG CTAGGGAGAA AGTCGAGGCA GCAGCCCTCG 2520
	AGGCCCTCAC AGATGTCTAG GCAGGCCCTCA TTTTATCAGC CAGCATGTGC AGGCCTGGAA 2580
35	GAGCAAAAGC AAATCTCAGG GAAGTCTCTG GTTGTATGAT CTGGGTCTCC TCTGGAGCAC 2640
	TCTGCCCTCC TGTACCCAG TAGAGTAAAT AAACCTCTCT GGCTCCTAAA AAA 2693

Seq ID NO: C72 DNA Sequence

Nucleic Acid Accession #: NM\_004938.1

Coding sequence: 337..4632

40	1 11 21 31 41 51
	CGGAGGACAG CCGGACCAG CCAACGCCGG GGAATTTGTT CCCTCCACGG AGGGGACTCG 60
45	GCAATCTGCA GCGGCAGGCT CTGGGGCCGG CGCCTGGGAG GGATCTGCGC CCCCCTCTCA 120
	CTCCCTAGCT GTGTTCCTCG CGCCGCCCGG GCTAGTCTCC GGCGCTGGCG CCTATGGTCG 180
	GCCTCCGACA GCGCTCCGGA GGGACCGGGG GAGCTCCAG GCGCCCGGGA CTGGAGACTG 240
	ATGCATGAGG GGCCTACGGA GCGCGAGGAG CGGTGGTGAT GGTCTGGGAA GCGGAGCTGA 300
	AGTCCCTTGG GCTTTGGTGA GGCCTGACAG TTTATCATGA CCGTGTTCAG GCAGGAAAAC 360
50	GTGGATGATT ACTACGACAC CGCGCAGGAA CTTGGCAGTG GACAGTTTGC GGTGTGTAAG 420
	AAATGCCGTG AGAAAAGTAC CGGCCTCCAG TATGCCGCCA AATTTCATCA GAAAAGGAGG 480
	ACTAAGTCCA GCCGCGGGGG TGTGAGCCGC GAGGACATCG AGCGGGAGGT CAGCATCTCT 540
	AAGGAGATCC AGCACCCCAA TGTATCACCC CTGCACGAGG TCTATGAGAA CAAGACGGAC 600
	GTCATCTTGA TCTTGAAGT CGTTGACAGT GGCAGCTGTG TTGACTTCTT AGCTGAAAAG 660
55	GAATCTTTAA CTGAAGAGGA AGCAACTGAA TTTCTCAAAC AAATCTCTAA TGGTGTTTAC 720
	TACCTGCACT CCCTTCAAA CTGCCACTTT GATCTTAAAG CTGAGAACAT AATGCTTTTG 780
	GATAGAAATG TCCCAAAACC TCGGATCAAG ATCATTGACT TTGGGTGGGC CCATAAAAAT 840
	GACTTTGGAA ATGAATTTAA AAACATATTT GGGACTCCAG AGTTTGTGCG TCCTGAGATA 900
	GTCAACTATG AACCTCTTGG TCTTGAGGCA GATATGTGGA GTATCGGGGT AATAACCTAT 960
60	ATCCTCCTAA GTGGGCGCTC CCATTTCTTT GGAGACATA AGCAAGAAAC GTTAGCAAT 1020
	GTATCCGCTG TCAACTACGA ATTTGAGGAT GAATACTTCA GTAATACCAG TGCCCTAGCC 1080
	AAAGATTTCA TAAGAAAGCT TCTGGTCAAG GATCCAAAGA AGAGAATGAC AATTCAAGAT 1140
	AGTTTGCAGC ATCCCTGGAT CAAGCCTAAA GATACACAAC AGGCACCTAG TAGAAAAGCA 1200
	TCAGCAGTAA ACATGGAGAA ATTCAAGAA TTTGCAGCCC GGAAAAAATG GAAACAATCC 1260
65	GTTCGCTTGA TATCACTGTG CCAAAGATTA TCCAGGTCTT TCCTGTCCAG AAGTAACATG 1320
	AGTGTGTGCA GAAGCGATGA TACTCTGGAT GAGGAAGACT CCTTTGTGAT GAAAGCCATC 1380
	ATCCATGCCA TCAACGATGA CAATGTCCCA GGCCTGCAGC ACCTTCTGGG CTCATTATCC 1440
	AACTATGATG TTAACCAACC CAACAAGCAC GGGACACCTC CATTACTCAT TGCTGCTGGC 1500
	TGTGGGAATA TTCAAATACT ACAGTTGCTC ATTTAAAGAG GCTCGAGAAT CGATGTCCAG 1560
70	GATAAGGGCG GGTCCAATGC CGTCTACTGG GCTGCTCGGC ATGGCCACGT CGATACCTTG 1620
	AAATTTCTCA GTGAGAACAA ATGCCCTTTG GATGTGAAAG ACAAGTCTGG AGAGATGGCC 1680
	CTCCACGTGG CAGCTTCGCTA TGGCCATGCT GACGTGGCTC AAGTTACTTG TGCACTTCG 1740
	GCTCAAAATC CAATATCCAG GACAAAGGAA GAAGAAACCC CCCTGCATCT TGCTGCTTGG 1800
	CACGGCTATT ACTCTGTGGC CAAAGCCCTT TGTGAAGCCG GCTGTAAAGT GAACATCAAG 1860
75	AACCGAGAAG GAGAGACGCC CCTCTGACA GCCTCTGCCA GGGGCTACCA CGACATCGTG 1920
	GAGTGTCTGG CCGAACATGG AGCCGACCTT AATGTCTGCG ACAAGGACGG ACACATTGCC 1980
	CTTCACTCTG CTGTAAGACG GTGTCAAGAT GAGGTAATCA AGACTCTCCT CAGCGAAGGG 2040
	TGTTTCTGTG ATTATCAAGA CAGGCACGGC AATACTCCCC TCCATGTGGC ATGTAAGAT 2100
	GGCAACATGC CTATCGTGGT GGCCCTCTGT GAAGCAAACT GCAATTTGGA CATCTCCAAC 2160
80	AAGTATGGGC GAACGCCCTCT GCACCTTGGC GCCAACACG GAATCTTAGA CGTGGTCCGG 2220
	TATCTCTGTC TGATGGGAGC CAGCGTTGAG GCGCTGACCA CGGACGGAAA GACGGCAGAA 2280
	GATCTTGTGA GATCGGAACA GCACGAGCAC GTAGCAGGTC TCTTGTCAAG ACTTCGAAAG 2340
	GATACGCACC GAGGACTCTT CATCCAGCAG CTCCGACCCA CACAGAACCT GCAGCCAAGA 2400
	ATTAAGCTCA AGCTGTTTGG CCACTCGGGA TCCGGGAAAA CCACCCTTGT AGAATCTCTC 2460
	AAGTGTGGGC TGCTGAGGAG CTTTTCAGAA AGGCGTCGGC CCAGACTGTC TTCCACCAAC 2520

5	TCCAGCAGGT	TCCCACCTTC	ACCCCTGGCT	TCTAAGCCCA	CAGTCTCAGT	GAGCATCAAC	2580
	AACCTGTACC	CAGGCTGCGA	GAACGTGAGT	GTGAGGAGCC	GCAGCATGAT	GTTTCGAGCCG	2640
	GGTCTTACCA	AAGGGATGCT	GGAGGTGTTT	GTGGCCCCGA	CCCACCACCC	GCACTGCTCG	2700
	GCCGATGACC	AGTCCACCAA	GGCCATCGAC	ATCCAGAACG	CTTATTTGAA	TGGAGTTGGC	2760
	GATTTACGCG	TGTGGGAGTT	CTCTGGAAAT	CCTGTGTATT	TCTGCTGTTA	TGACTATTTT	2820
	GCTGCAAAATG	ATCCCACGTC	AATCCATGTT	GTTGTCTTTA	GTCTAGAAGA	GCCCTATGAG	2880
	ATCCAGCTGA	ACCCAGTGAT	TTTCTGGCTC	AGTTTCCTGA	AGTCCCTTGT	CCCAGTTGAA	2940
	GAACCCATAG	CCTTCGGTGG	CAAGCTGAAG	AACCCACTCC	AAGTTGTCTT	GGTGGCCACC	3000
10	CACGCTGACA	TCATGAATGT	TCCTCGACCG	GCTGGAGGCG	AGTTTGGATA	TGACAAAGAC	3060
	ACATCGTTGC	TGAAAGAGAT	TAGGAACAGG	TTTGGAAATG	ATCTTCACAT	TTCAAATAAG	3120
	CTGTTTGTTC	TGGATGCTGG	GGCTTCTGGG	TCAAAGGACA	TGAAGGTACT	TCGAAATCAT	3180
	CTGCAAGAAA	TAGCAAGCCA	GATTGTTTCG	GTCTGTCTCT	CCATGACTCA	CCTGTGTGAG	3240
	AAAATCATCT	CCACGCTGCC	TTCTTGAGG	AAGCTCAATG	GACCCAACCA	GCTGATGTCT	3300
15	CTGCAGCAGT	TTGTGTACGA	CGTGACAGGAC	CAGCTGAACC	CCCTGGCCAG	CGAGGAGGAC	3360
	CTCAGGCGCA	TTGCTCAGCA	GCTCCACAGC	ACAGGCGAGA	TCAACATCAT	GCAAAGTGAA	3420
	ACAGTTACAG	ACGTGCTGCT	CCTGGACCCC	CGTGGCTCT	GCACAAACGT	CCTGGGGAAG	3480
	TTGCTGTCCG	TGGAGACCCC	ACGGGCGCTG	CACCACCTACC	GGGGCCGCTA	CACCGTGGAG	3540
	GACATCCAGC	GCTTGGTGCC	CGACAGCGAC	GTGGAGGAGC	TGCTGCAGAT	CCTCGATGCC	3600
20	ATGGACATCT	GCGCCCGGGA	CCTGAGCAGC	GGGACCATGG	TGGACGTCCC	AGCCCTGATC	3660
	AAGACAGACA	ACCTGCACCG	CTCCTGGGCT	GATGAGGAGG	ACGAGGTGAT	GGTGTATGGT	3720
	GGCGTGGCGA	TCGTGCCCGT	GGAACACCTC	ACCCCTTCC	CATGTGGCAT	CTTTCACAAG	3780
	GTCCAGGTGA	ACCTGTGCCG	GTGGATCCAC	CAGCAAAGCA	CAGAGGGCGA	CGCGGACATC	3840
	CGCTGTGGG	TGAATGGCTG	CAAGCTGGCC	AACCGTGGG	CCGAGCTGCT	GGTGTCTGCT	3900
25	GTCAACCACG	GCCAGGGCAT	TGAGGTCCAG	GTCCGTGGCC	TGGAGACGGA	GAAGATCAAG	3960
	TGCTGCCTGC	TGCTGGAATC	GGTGTGCAGC	ACCATTGAGA	ACGTCATGGC	CACCACGCTG	4020
	CCAGGGCTCC	TGACCGTGAA	GCATTACCTG	AGCCCCCAGC	AGCTGCGGGA	GCACCATGAG	4080
	CCCGTCATGA	TCTACCAAGC	ACGGGACTTC	TTCCGGGCAC	AGACTCTGAA	GGAAACCTCA	4140
	CTGACCAACA	CCATGGGGGG	GTACAAGGAA	AGCTTCAGCA	GCATCATGTG	CTTCGGGTGT	4200
30	CACGACGTCT	ATCTCACAGG	CAGCCTCGGC	ATGGACATCC	ATGCATCAGA	CCTGAACTCT	4260
	CTCACTCGGA	GGAAACTGAG	TGCGCTGCTG	GACCCGCCCG	ACCCCTGGG	GAGGAGCTGG	4320
	TGCCCTTCTG	CCATGAACCT	AGGCCTCCCT	GACCTCGTGG	CAAAGTACAA	CACCAATAAC	4380
	GGGGCTCCCA	AGGATTTCCT	CCCCAGCCCC	CTCCACGCCC	TGCTGCGGGA	ATGGACCACC	4440
	TACCCTGAGA	GCACAGTGGG	CACCCTCATG	TCCAACTGA	GGGAGCTGGG	TCGCCGGGAT	4500
35	GCCCGAGACC	TTTTGTCTGA	GGCATCCTCT	GTGTTCAAAA	TCAACCTGGA	TGGCAATGGC	4560
	CAGGAGGCCT	ATGCCTCGAG	CTGCAACAGC	GGCACCTCTT	ACAATTCCAT	TAGCTCTGTT	4620
	GTATCCCGGT	GAGGGCAGCC	TCTGGCTTGG	ACAGGGTCTG	TTTGGACTGC	AGAACCRAAG	4680
	GGGTGATGTA	GCCCATGCTT	CCCTTTGGAG	ATGCTGAGGG	TGTTTCTTCC	TGCACCCACA	4740
	GCCAGGGGGA	TGCCACTCTG	CCCTCCGGCT	TGACCTGTTT	CTCTGCCGCT	ACCTCCCTCC	4800
40	CCGTCTCAAT	CCGTGTGCTG	TGGATGGTCA	TTGCAGTTTA	AGAGCAGAAC	AGATCTTTTA	4860
	CTTTGGCCGC	TTGAAAAGCT	AGTGTACCTC	CTCTCAGTGT	TTTGGACTCC	ATCTCTCATC	4920
	CTCCAGTACC	TGTGTTCTTA	CTGATAATTT	TGCTGGAATT	CCTAACTTTT	CAATGACATT	4980
	TTTTTTAACT	ATCATATTGA	TTGTCCCTTA	AAAAAGAAAA	GTGCATATTT	ATCCAAAATG	5040
	TGTATTTCTT	ATACGCTTTT	CTGTGTTATA	CCATTTCTCT	AGCTTATCTC	TTTTATATTT	5100
45	GTAGGAGAAA	CTCCCATGTA	TGGAATCCCA	CTGTATGATT	TATAAACAGA	CAATATGTGA	5160
	GTGCCCTTTG	CAGAAGAGGG	TGTGTTTGAA	ATCATCGGAG	TCAGCCAGGA	GCTGTCAACA	5220
	AGGAAACGCT	ACCTCTCTGT	CCCTTGCTGT	ATGCTGATCA	TCGCCAGAGG	TGCTTCACCC	5280
	TGAGTTTGT	TTTGTATTGT	TTTCTGACAG	TTTTCTGTTT	TTGTTTGGCA	AGGAAAGGGG	5340
	AGAAGGGAAT	CCTCCTCCAG	GGTGATTTTA	TGATCAGTGT	TGTTGCTCTA	GGAAGACATT	5400
50	TTTCCGTTTG	CTTTTGTTC	AATGTCAATG	TGAACGTCCA	CATGAAACCT	ACACACTGTC	5460
	ATGCTTCATC	ATTCCCTCTC	ATCTCAGGTA	GAAGGTTGAC	ACAGTTGTAG	GGTTACAGAG	5520
	ACCTATGTAA	GAATTCAGAA	GACCCCTGAC	TCATCATTTG	TGGCAGTCCC	TTATAATTGG	5580
	TGCTATGACG	ATGTTTTCAC	CATTAGATC	CTGGTTTCAT	AACTTCCTGT	ACTTGAAGTC	5640
	TAAAAGCAGA	AAATAAAGGA	AGCAAGTTT	CTTCCATGAT	TTTAAATGTT	GATCGAGTTT	5700
55	TAAATTGATA	GGAGGGAACA	TGTCCTAATT	CTTCTGCTCT	GAGAAGCATG	TAATGTTAAT	5760
	GTTATATCAT	ATGTATATAT	ATATATGCAC	TATGTATATA	CATATATATT	AATATGGTA	5820
	TTTTTACTTA	ATCTATAAAA	TGTCGTAAAA	AAGTTGTTTG	TTTTTTTCTT	TTTTTATAAA	5880
	TAAACTGTTG	CTCGTTAAAA	AAAAAATAAA				5910

Seq ID NO: C73 DNA Sequence  
Nucleic Acid Accession #: NM\_002081.1  
Coding sequence: 222..1898

65	1	11	21	31	41	51	
	GGCTGCCCGA	GCGAGCGTTC	GGACCTCGCA	CCCCGCGCGC	CCCCGCGCGC	CGCGCGCGCC	60
	GGCTTTTGT	GTCTCCGCCT	CCTCGGCGGC	CGCGCGCTCT	GGACCGGAG	CCGCGCGCGC	120
	CGGGACCTTG	GCTCTGCCCT	TCGCGGGCGG	GAACTGCGCA	GGACCCGCGC	AGGATCCGAG	180
	AGAGGCGCGG	GCGGGTGGCC	GGGGGCGCCG	CCGGCCCCGC	CATGGAGCTC	CGGGCCCCGAG	240
70	GCTGGTGGCT	GCTATGTGCG	GCCGACGCGC	TGGTCCGCTG	CGCCCCGCGG	GACCCGCGCA	300
	GCAAGAGCCG	GAGCTGCGGC	GAGGTCCGCC	AGATCTACGG	AGCCAAGGGC	TTGAGCCCTGA	360
	GCGACGTGCC	CCAGGCGGAG	ATCTCGGGTG	AGCACTGCGG	GATCTGTCCC	CAGGGCTACA	420
	CCTGCTGACG	CAGCGAGATG	GAGGAGAACC	TGGCCAACCG	CAGCCATGCC	GAGCTGGAGA	480
	CCGCGCTCCG	GGACAGCAGC	CGCGTCTGCG	AGGCCATGCT	TGCCACCCAG	CTGCGCAGCT	540
75	TCGATGACCA	CTTCCAGCAC	CTGCTGAACG	ACTCGGAGCG	GACGCTGCAG	GCCACCTTCC	600
	CCGGCGCCTT	CGGAGAGCTG	TACACGCAGA	ACGCGAGGGC	CTTCCGGGAC	CTGTACTCAG	660
	AGCTGCGCCT	GTACTACGCG	GGTGCCAACC	TGCACCTGGA	GGAGACGCTG	GCCGAGTTCT	720
	GGGCCCGCCT	GCTCGAGCGC	CTCTTCAAGC	AGCTGCACCC	CCAGCTGCTG	CTGCCTGATG	780
	ACTACCTGGA	CTGCCTGGGC	AAGCAGGCGG	AGGCGCTGCG	GCCCTTCGGG	GAGGCCCGCA	840
80	GAGAGCTGCG	CCTGCGGGCC	ACCCGTGCCT	TCGTGGCTGC	TCGCTCCTTT	GTGCAGGGCG	900
	TGGGCGTGGC	CAGCGACGTG	GTCCGGAAG	TGGCTCAGGT	CCCCCTGGGC	CCGGAGTGCT	960
	CGAGAGCTGT	CATGAAGCTG	GTCTACTGTG	CTCACTGCCT	GGGAGTCCCC	GGCGCCAGGC	1020
	CCTGCCCCGA	CTATTGCCGA	AATGTGCTCA	AGGGCTGCCT	TGCCAACCAG	GCCGACCTGG	1080
	ACGCCGAGTG	GAGGAACCTC	CTGGACTCCA	TGGTGCTCAT	CACCGACAAG	TTCCTGGGTA	1140
	CATCGGGTGT	GGAGAGTGTC	ATCGGCACGG	TGCACACGTG	GCTGGCGGAG	GCCATCAACG	1200



5  
10  
15  
20  
25  
30  
35  
40  
45

```

CCCTCCAGGA CAACAGGGAC ACGCTCACGG CCAAGGTCAT CCAGGGCTGC GGGAAACCCCA 1260
AGGTCAACCC CCAGGGCCCT GGGCCCTGAGG AGAAGCGGCG CCGGGGCAAG CTGGCCCCGC 1320
GGGAGAGGCC ACCTTCAGGC ACGCTGGAGA AGCTGGTCTC TGAAGCCAAG GCCCAGCTCC 1380
GCGACGTCCA GGACTTCTGG ATCAGCCTCC CAGGGACACT GTGCAGTGAG AAGATGGCCC 1440
TGAGCACTCG CAGTGATGAC CGCTGCTGGA ACGGGATGGC CAGAGGCCGG TACCTCCCCG 1500
AGGTCAATGG TGACGGCCTG GCCAACCCGA TCAACAACCC CGAGGTGGAG GTGGACATCA 1560
CCAAGCCGGA CATGACCATC CGGCAGCAGA TCATGCAGCT GAAGATCATG ACCAACCCGG 1620
TGCGCAGCGC CTACACGGGC AACGACGTGG ACTTCCAGGA CGCCAGTGAC GACGGCAGCG 1680
GCTCGGGCAG CGGTGATGGC TGTCTGGATG ACCTCTGCGG CCGGAAGGTC AGCAGGAAGA 1740
GCTCCAGCTC CCGGACGCC TTGACCCATG CCCTCCAGG CCTGTACAG CAGGAAGGAC 1800
AGAAGACCTC GGCTGCCAGC TGCCCCCAGC CCCCAGCCTT CCTCTGCCC CTCTCTCTCT 1860
TCCTGGCCCT TACAGTAGCC AGGCCCCGGT GCGGTAACT GCCCAAGGC CCCAGGGACA 1920
GAGGCCAAGG ACTGACTTTG CCAAAAATAC AACACAGACG ATATTTAAT CACCTCAGCC 1980
TGGAGAGGCC TGGGTGGGA CAGGGAGGGC CGGCGCTCT GAGCAGGGGC AGGCGCAGAG 2040
GTCCCAGCCC CAGGCTGCGC CTGCGCTGCC TTCTGCTCTT TTAATTTTGT ATGAGGTCTT 2100
CAGGTACAGT GGGAGCCAGT GTGCCCAAAA GCCATGTATT TCAGGGACCT CAGGGGCACC 2160
TCCGCTGCCC TAGCCCTCCC CCCAGCTCCC TGACCCGCGG CAGAAGCAGC CCCTCGAGGC 2220
CTACAGAGGA GGCCTCAAAG CAACCCGCTG GAGCCACAG CGAGCCTGTG CCTTCTCTCC 2280
CGCCTCTCTC CACTGGGACT CCCAGCAGAG CCCACCAGCC AGCCCCGGCC CACCCCCCAG 2340
CTTCCAGAGA AGCCCCGCAC GGGCTGTCTG GGTGTCCGCC ATCCAGGGTC TGGCAGAGCC 2400
TCTGAGATGA TGCATGATGC CCTCCCCTCA GCGCAGGCTG CAGAGCCCGG CCCACCTCC 2460
CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGGTGACGCC TGAGACAGCA CCACTGCTGA 2520
GGAGTCTGAG GACTGTCTCT CCACAGACCC TGCACTGAGG GGGCTTCCAT GCGCAGATGA 2580
GGGGCCACTG ACCCACTGCG GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCCAG 2640
GAGAGCAGCG TGGGCTCTGC CAATGTGGGC TGCCCCCTCG ACACAGGGCT CACAGGGCAG 2700
GCCTTGCTGG GGTCCAGGGC TGTGGAGGA CCCCAGGGGC TGAGGAGCAG CCAGGACCCG 2760
CCTGCTCCCA TCCTCACCCA GATCAGGAAC CAGGGCTCTC CTGTTACCGG TGACACAGGT 2820
CAGGGCTCAG AGTGACCCCTC GGTGTGCACT TGCTCACAGG GATGCTGGTG GCTGGTGAGA 2880
CCCCGCACTG CACACGGGAA TGCTAGGTC CCTTCCGAC CCAGCCAGCT GCACTGCAGG 2940
GCACGGGGAC CTGGATAGTT AAGGGCTTTT CCAACATGAC ATCCATTAC TGACACTTCC 3000
TGTCCTTGTT CATGGAGAGC TGTTGCTCTC TCCAGATGG CTTCGGAGGC CCGCAGGGCC 3060
CACCTTGGAC CTTGGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120
CTGGAGGGGC CCTCTTCCC TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GAGGGGTGG 3180
TGTGCTGTTG GGAAGGGGTC CTGACGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG 3240
TCCTGAACCG ACTGACCCCTG AGGAGGCCCG TTAGTGTCTG TTTGCTTTTC ATCACCCTCC 3300
CGCACAGTGG ACGAGGAGTCC CCGGTTGCTG GTCAGGTCCC CATGGCTTGT TCTCTGGAAC 3360
CTGACTTTAG ATGTTTTGGG ATCAGGAGCC CCCAACACAG CCAAGTCCAC CCCATAATAA 3420
CCCTGCCAGT GCCAGGGTGG GCTGGGGACT CTGGCACAGT GATGCCGGGC GCCAGGACAG 3480
CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CCTACGCTCA 3540
TCTCTGGAAG GGGCAGCCCT GAGTGGTCAC TGGTCAGGGC AGTGGCCAAG CCTGCTGTGT 3600
CCTTCCCTCA CAAGGTCCCC CCACCGCTCA GTGTCAGCGG GTGACGTGTG TTCTTTGAG 3660
TCCTTGATG AATAAAAGGC TGGAAACCTA AA 3692

```

Seq ID NO: C74 DNA Sequence  
Nucleic Acid Accession #: BC030205.1  
Coding sequence: 45..878

50  
55  
60  
65  
70  
75

```

1 11 21 31 41 51
| | | | |
GTGAGCAGCC CCTAACAGGC TGTACTTCA CTACAACCTGA CGATATGATC ATCTTAATTT 60
ACTTATTTCT CTGCTATGG GAAGACACTC AAGGATGGGG ATTCAAGGAT GGAATTTTTC 120
ATAACTCCAT ATGCTTTGAA CGAGCAGCCG GTGTGTACCA CAGAGAAGCA CGGTCTGGCA 180
AATAACAGCT CACCTACGCA GAAGCTAAGG CGGTGTGTGA ATTTGAAGGC GGCCATCTCG 240
CAACTTACAA GCGCTAGAG GCAGCCAGAA AAATGGATT TCATGTCTGT GCTGCTGGAT 300
GGATGGCTAA GGGCAGAGTT GGATACCCCA TTGTGAAGCC AGGGCCCAAC TGTGGATTG 360
GAAAACTGG CATATTGAT TATGGAATCC GTCTCAATAG GAGTGAAAGA TGGGATGCCT 420
ATTGCTACAA CCCACACGCA AAGGAGTGTG GTGGCGTCTT TACAGATCCA AAGCAAAATTT 480
TTAAATCTCC AGGCTTCCCA AATGAGTACG AAGATAACCA AATCTGTAC TGGCACATTA 540
GACTCAAGTA TGGTCAGCGT ATTCACCTGA GTTTTTTGA TTTTGACCTT GAAGATGACC 600
CAGGTTGCTT GGCTGATTAT GTTGAAATAT ATGACAGTTA CGATGATGTC CATGGCTTTG 660
TGGGAAGATA CTGTGGAGAT GAGCTTCCAG ATGACATCAT CAGTACAGGA AATGTCATGA 720
CCTTGAAGTT TCTAAGTGAT GCTTCAGTGA CAGCTGGAGG TTTCCAAATC AAATATGTTG 780
CAATGGATCC TGTATCCAAA TCCAGTCAAG GAAAAAATAC AAGTACTACT TCTACTGGAA 840
ATAAAAACTT TTTAGCTGGA AGATTTAGCC ACTTATAAAA AAAAAAAAAG GATGATCAAA 900
ACACACAGTG TTTATGTTGG AATCTTTTGG AACTCCTTGT ATCTCACTGT TATTATTAAC 960
ATTTATTTAT TATTTTCTA AATGTGAAG CAATACATAA TTTAGGGAAA ATTGGAAAAT 1020
ATAGGAACTT TTAACGAGA AAATGAAACC TCTCATAATC CCAGTGCATA GAAATAACAA 1080
GCGTTAACAT TTTCAATTTT TTTTCTTTCA GTCATTTTTC TATTTGTGGT ATATGTATAT 1140
ATGTACCTAT ATGTATTTGC ATTTGAAATT TTGGAATCCT GCTCTATGTA CAGTTTGTGA 1200
TTATACTTTT TAAATCTTGA ACTTTATAAA CATTTTCTGA AATCATTGAT TATTCTACAA 1260
AAACATGATT TTAACAGCT GTAAATATT CTATGATATG AATGTTTAT GCATTATTTA 1320
AGCCTGTCTC TATTGTTGGA ATTTCAGGTC ATTTTCATAA ATATTGTTGC AATAAATATC 1380
CTTGAACACA AAAAAAATAA AAAAAAATAA AAAAAAATAA 1430

```

Seq ID NO: C75 DNA Sequence  
Nucleic Acid Accession #: NM\_001982.1  
Coding sequence: 199..4227

80

```

1 11 21 31 41 51
| | | | |
CTCTCACACA CACACACCCC TCCCCTGCCA TCCCTCCCGG GACTCCGGCT CCGGCTCCGA 60
TTGCAATTTG CAACCTCCGC TGCCGTCGCC GCAGCAGCCA CCAATTCGCC AGCGGTTCAG 120

```

	GTGGCTCTTG	CCTCGATGTC	CTAGCCTAGG	GGCCCCCGGG	CCGGACTTGG	CTGGGCTCCC	180
	TTACCCCTCT	CGGGAGTCAT	GAGGGCGAAC	GACGCTCTGC	AGGTGCTGGG	CTTGCTTTTC	240
	AGCCTGGCCC	GGGGCTCCGA	GGTGGGCAAC	TCTCAGGCAG	TGTGTCTCTG	GACTCTGAAT	300
5	GGCCTGAGTG	TGACCGGCCA	TGCTGAGAAC	CAATACCAGA	CACGTACAAA	GCTCTACGAG	360
	AGGTGTGAGG	TGGTATGGG	GAACCTTGAG	ATTGTGCTCA	CGGGACACAA	TGCCGACCTC	420
	TCCTTCCTGC	AGTGGATTGC	AGAAGTGACA	GGCTATGTCC	TCGTGGCCAT	GAATGAATTC	480
	TCTACTCTAC	CATTGCCCAA	CCTCCGCGTG	GTGCGAGGGA	CCCAGGTCTA	CGATGGGAAG	540
	TTTGCCATCT	TCGTATGTT	GAACCTATAAC	ACCAACTCCA	GCCACGCTCT	GCGCCAGCTC	600
10	CGCTTGACTC	AGCTCACCGA	GATTCTGTCA	GGGGGTGTTT	ATATTGAGAA	GAACGATAAG	660
	CTTTGTACAC	TGGACACAAT	TGACTGGAGG	GACATCGTGA	GGGACCGAGA	TGCTGAGATA	720
	GTGGTGAAGG	ACAATGGCAG	AAGCTGTCCC	CCCTGTCATG	AGGTTTGCAA	GGGGCGATGC	780
	TGGGGTCCCTG	GATCAGAAGA	CTGCCAGACA	TTGACCAAGA	CCATCTGTGC	TCCTCAGTGT	840
	AATGGTCACT	GCTTTGGGCC	CAACCCCAAC	CAGTGTCTGC	ATGATGAGTG	TGCCGGGGGC	900
15	TGCTCAGGCC	CTCAGGACAC	AGACTGCTTT	GCCTGCCGGC	ACTTCAATGA	CAGTGGAGCC	960
	TGTGTACCTC	GCTGTCCACA	GCCTCTTGTC	TACAACAAGC	TAACTTTCCA	GCTGGAACCC	1020
	AATCCCCACA	CCAAGTATCA	GTATGGAGGA	GTTTGTGTAG	CCAGCTGTCC	CCATAACTTT	1080
	TGCGTGGATC	AAACATCTTG	TGTCAGGGCC	TGTCCTCCTG	ACAAGATGGA	AGTAGATAAA	1140
	AATGGGCTCA	AGATGTGTGA	GCCTTGTGGG	GGACTATGTC	CCAAGCCCTG	TGAGGGAACA	1200
20	GGCTCTGGGA	GCCGCTTCCA	GACTGTGGAC	TCGAGCAACA	TTGATGGATT	TGTGAACTGC	1260
	ACCAAGATCC	TGGGCAACCT	GGACTTTCCTG	ATCACCGGCC	TCAATGGAGA	CCCCTGGCAC	1320
	AAGATCCCTG	CCCTGGACCC	AGAGAAGCTC	AATGTCTTCC	GGACAGTACG	GGAGATCACA	1380
	GGTTACCTGA	ACATCCAGTC	CTGGCCGCCC	CACATGCACA	ACTTCAGTGT	TTTTTCCAAT	1440
	TTGACAACCA	TTGAGGCGAC	AAGCCTCTAC	AACCGGGGCT	TCTCATGTGT	GATCATGAAG	1500
25	AACTTGAATG	TCACATCTCT	GGGCTTCCGA	TCCCTGAAGG	AAATTAGTGC	TGGGCGTATC	1560
	TATATAAGTG	CCAATAGGCA	GCTCTGCTAC	CACCACCTTT	TGAACCTGGAC	CAAGGTGCTT	1620
	CGGGGGCCTA	CGGAAGAGCG	ACTAGACATC	AAGCATAATC	GGCCGCGCAG	AGACTGCGTG	1680
	GCAGAGGGCA	AAGTGTGTGA	CCCACTGTGC	TCCTCTGGGG	GATGCTGGGG	CCCAGGCCCT	1740
	GGTCAGTGCT	TGTCTGTCTG	AAATTATAGC	CGAGGAGGTG	TCTGTGTGAC	CCAATGCAAC	1800
30	TTTCTGAATG	GGGAGGCTCG	AGAATTGTGC	CATGAGGCGG	AATGCTTCTC	CTGCCACCCG	1860
	GAATGCCAAC	CCATGGGGGG	CACCTGCCACA	TGCAATGGCT	CGGGCTCTGA	TACTTGTGCT	1920
	CAATGTGCCC	ATTTTGCAGA	TGGGCCCCAC	TGTGTGAGCA	GCTGCCCCCA	TGGAGTCCCTA	1980
	GGTGCCAAGG	CCCCAATCTA	CAAGTACCCA	GATGTTTCTA	ATGAATGTCG	GCCCTGCCAT	2040
	GAGAATCGCA	CCCAGGGGTG	TAAAGGACCA	GAGCTTCAAG	ACTGTTTAGG	ACAAACACTG	2100
35	GTGCTGATCG	GCAAAACCCA	TCTGACAATG	GCTTTGACAG	TGATAGCAGG	ATTGGTAGTG	2160
	ATTTTCTATG	TGCTGGGCGG	CACCTTTCTC	TACTGGCGTG	GGCGCCGGAT	TCAGAATAAA	2220
	AGGGCTATGA	GGCGATACTT	GGAACGGGGT	GAGAGCATAG	AGCCTCTGGA	CCCCAGTGAG	2280
	AAGGCTAACA	AAGTCTTGGC	CAGAATCTTC	AAAGAGACAG	AGCTAAGGAA	GCTTAAAGTG	2340
	CTTGGCTCGG	TGCTCTTTGG	AACTGTGCAC	AAAGGAGTGT	GGATCCCTGA	GGGTGAATCA	2400
40	ATCAAGATTC	CAGTCTGCAT	TAAAGTCATT	GAGGACAAGA	TGGACGGCA	GAGTTTTCAT	2460
	GCTGTGACAG	ATCATATGCT	GGCCATTGGC	AGCCTGGACC	ATGCCACAT	TGTAAGGCTG	2520
	CTGGGACTAT	GCCAGGGGTC	ATCTCTGCAG	CTTGTCACTC	AAATTTTGCC	TCTGGGTCTT	2580
	CTGCTGGATC	ATGTGAGACA	ACACCGGGGG	GCACCTGGGC	CACAGCTGCT	GCTCAACTGG	2640
	GGAGTACAAA	TTGCCAAGGG	AATGTACTAC	CTTGAGGAAC	ATGGTATGGT	GCATAGAAAC	2700
45	CTGGCTGCCC	GAAACGTGCT	ACTCAAGTCA	CCCAGTCAGG	TTCAGGTGGC	AGATTTTGGT	2760
	GTGGCTGACC	TGCTGCTCTC	TGATGATAAG	CAGCTGCTAT	ACAGTGAGGC	CAAGACTCCA	2820
	ATTAAGTGGA	TGGCCCTTGA	GAGTATCCAC	TTTGGGAAAT	ACACACACCA	GAGTGAATGC	2880
	TGGAGCTATG	GTGTGACAGT	TTGGGAGTTG	ATGACCTTCG	GGGCAGAGCC	CTATGCAGGG	2940
	CTACGATTGG	CTGAAGTACC	AGACCTGCTA	GAGAAGGGGG	AGCGGTGGGC	ACAGCCCCAG	3000
50	ATCTGCACAA	TTGATGTCTA	CATGGTGATG	GTCAAGTGT	GGATGATTGA	TGAGAACATT	3060
	CGCCCAACCT	TTAAAGAACT	AGCCAAATGAG	TTCAACAGGA	TGGCCCGAGA	CCCAACACGG	3120
	TATCTGGTCA	TAAAGAGAGA	GAGTGGGCCT	GGAATAGCCC	CTGGGCCAGA	GCCCCATGGT	3180
	CTGACAAACA	AGAAGCTAGA	GGAAGTAGAG	CTGGAGCCAG	AACTAGACCT	AGACCTAGAC	3240
	TTTGAAGCAG	AGGAGGACAA	CCTGGCAACC	ACCACACTGG	GCTCCGCCCT	CAGCCTACCA	3300
55	GTGGGAACAC	TTAATCGGCC	ACGTGGGAGC	CAGAGCCTTT	TAAGTCCATC	ATCTGGATAC	3360
	ATGCCCATGA	ACCAGGGTAA	TCTTGGGGGG	TCTTGGCAGG	AGTCTGCAGT	TTCTGGGAGC	3420
	AGTGAACGGT	GGCCCCGTCC	AGTCTCTCTA	CACCCAATGC	CACGGGGATG	CCTGGCATCA	3480
	GAGTCATCAG	AGGGGCATGT	AACAGGCTCT	GAGGCTGAGC	TCCAGGAGAA	AGTGTCAATG	3540
	TGTAGAAGCC	GGAGCAGGAG	CCGGAGCCCA	CGGCCACGCG	GAGATAGCGC	CTACCATTC	3600
60	CAGCGCCACA	GTCTGCTGAC	TCTTGTATCC	CCACTCTCCC	CACCCGGGTT	AGAGGAAGAG	3660
	GATGTCAACG	GTTATGTCTAT	GCCAGATACA	CACCTCAAAG	GTACTCCCTC	CTCCCGGGA	3720
	GGCACCCCTTT	CTTCAGTGGG	TCTCAGTTCT	GTCCTGGGTA	CTGAAGAAGA	AGATGAAGAT	3780
	GAGGAGTATG	AATACATGAA	CCGGAGGAGA	AGGCACAGTC	CACCTCATCC	CCCTAGGCCA	3840
	AGTTCCCTTG	AGGAGCTGGG	TTATGAGTAC	ATGGATGTGG	GGTCAGACCT	CAGTGCCTCT	3900
65	CTGGGCAGCA	CACAGAGTTG	CCCACTCCAC	CCTGTACCCA	TCATGCCCCAC	TGCAGGCACA	3960
	ACTCCAGATG	AAGACTATGA	ATATATGAAT	CGGCAACGAG	ATGGAGGTGG	TCCTGGGGGT	4020
	GATTATGCAG	CCATGGGGGC	CTGCCAGCA	TCTGAGCAAG	GGTATGAAGA	GATGAGAGCT	4080
	TTTCAGGGGC	CTGACATACA	GGCCCCCAT	GTCCATTATG	CCCGCCTAAA	AACTCTACGT	4140
	AGCTTAGAGG	CTACAGACTC	TGCCCTTGAT	AACCTGATT	ACTGGCATAG	CAGGCTTTTC	4200
70	CCCAAGGCTA	ATGCCAGAG	AACGTAATC	CTGCTCCCTG	TGGCACTCAG	GGAGCATTTA	4260
	ATGGCAGCTA	GTGCCCTTAG	AGGGTACCGT	CTTCTCCCTA	TTCCCTCTCT	CTCCAGGTC	4320
	CCAGCCCTTT	TTCCCAAGTC	CCAGACAATT	CCATTCAATC	TTTGGAGGCT	TTTAAACATT	4380
	TTGACACAAA	ATCTTATGAG	TATGTAGCCA	GCTGTGCACT	TTCTTCTCTT	TCCCAACCCC	4440
	AGGAAAGGTT	TTCTTATTTT	TGTGTGCTTT	CCCAGTCCCA	TTCTTCAGCT	TCTTCACAGG	4500
75	CACCTCTGGA	GATATGAAGG	ATTACTCTCC	ATATCCCTTC	CTCTCAGGCT	CTTGACTACT	4560
	TGGAAGTACG	CTCTTATGTG	TGCCCTTGTG	TCCCATCAGA	CTGTCAAGAA	GAGGAAAGGG	4620
	AGGAAACCTG	GCAGAGGAAA	GTGTAATTTT	GGTTTATGAC	TCTTAACCCC	CTAGAAAGAC	4680
	AGAAGCTTAA	AATCTGTGAA	GAAAGAGGTT	AGGAGTAGAT	ATTGATTACT	ATCATAATTC	4740
	AGCACTTAAC	TATGAGCCAG	GCATCATACT	AAACTTCACC	TACATTATCT	CACCTAGTCC	4800
80	TTTATCATCC	TTAAACAAT	TCTGTGACAT	ACATATTATC	TCATTTTACA	CAAAGGGAAG	4860
	TGGGCGATGG	TGGCTCATGC	CTGTAATCTC	AGCACTTTGG	GAGGCTGAGG	CAGAGGAGTT	4920
	ACCTGAGGCA	AGGAGTTTGA	GACCAGCTTA	GCCAACATAG	TAAGACCCCC	ATCTC	4975

Seq ID NO: C76 DNA Sequence

Nucleic Acid Accession #: NM\_001216.1  
Coding sequence: 43..1422

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CTTGTGCCCC 60
AGCCCCTGGC TCCCTCTGTT GATCCCAGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG 120
CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCAGAGGT TGGCCCGGAT GCAGGAGGAT 180
TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGCGGAGGA GGATCTGCCC 240
10 AGTGAAGAGG ATTCACCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAATCAGA AGAAGAGGGC 360
TCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCAG 420
AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480
CCGCCCTGGC CCGGGGTGTC CCCAGCCTGC GCGGGCCGCT TCCAGTCCCC GGTGGATATC 540
15 CGCCCCAGC TCGCCCGCTT CTGCCCGGCC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG 600
CTCCCGCCGC TCCAGAACTC GCGCTGCGC AACAAATGGC ACAGTGTGCA ACTGACCCCTG 660
CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGAGT ACCGGGCTCT GCAGCTGCAT 720
CTGCACTGGG GGGCTGCTGG TCGTCCGGGC TCGGAGCACA CTGTGGAAG CCACCGTTTC 780
20 CCTGCCGAGA TCCACGTGGT TCACCTCAGC ACCGCCTTTG CCAGAGTTGA CGAGGCCCTT 840
GGGCGCCCCG GAGGCTTGGC CGTGTGGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC 900
AGTGCCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAG CTGAGAGACT 960
CAGTCCAGC GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA 1020
TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAA 1080
25 CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCCTCT CTGACACCCT GTGGGGACCT 1140
GGTGACTCTC GGTCTACAGT GAACCTCCGA GCGACGAGC CTTTGAATGG GCGAGTGATT 1200
GAGGCTTCTT TCCCTGCTGG AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGTTT TTGGCCTCCT TTTTGCTGTC 1320
ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380
30 GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA 1440
TGTGAGAAAG CAGCCAGAGG CATCTGAGGG GGAGCCGGTA ACTGTCTCTG CTGCTCATT 1500
ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTATA AT 1552

```

Seq ID NO: C77 DNA Sequence  
Nucleic Acid Accession #: NM\_004207.1  
Coding sequence: 63..1460

```

35      1      11      21      31      41      51
      |      |      |      |      |      |
GGCGAGAGGC GGGCTGAGGC GGCCAGCGG CGGCAGGTGA GGCGAAACCA ACCCTCCTGG 60
40 CCATGGGAGG GGCCTGTGTG GACGAGGGCC CCACAGGCGT CAAGGCCCTT GACGGCGGCT 120
GGGGCTGGGC CGTGCTCTTC GGCTGTTTCG TCATCACTGG CTTTCTCTAC GCCTTCCCCA 180
AGGCCGTGAG TGTCTTCTTC AAGGAGCTCA TACAGGAGTT TGGGATCGGC TACAGCGACA 240
CAGCCTGGAT CTCCTCCATC CTGCTGGCCA TGCTCTACGG GACAGGTCGG CTCTGCAGTG 300
TGTGCGTGAA CCGCTTTGGC TGCCCGCCCG TCATGCTTGT GGGGGGTCTC TTTGCGTCGC 360
45 TGGGCATGGT GGCCTGCGTG TTTTGCCGGA GCATCATCCA GGTCTACCTC ACCACTGGGG 420
TCATCAGGGG GTTGGGTTTG GCACTCAACT TCCAGCCCTC GCTCATCATG CTGAACCGCT 480
ACTTCAGAAA GCGCGCGCCC ATGGCCAACG GGCTGGCGGC AGCAGGTAGC CCGTCTCTCC 540
TGTGTGCCCT GAGCCCGCTG GGGCAGCTGC TGCAGGACCG CTACGGCTGG CGGGCGGCT 600
50 TCCTCATCCT GGGCGGCCTG CTGCTCAACT GCTGCGTGTG TGCCGCACTC ATGAGGCCCC 660
TGGTGGTCAG GCGCCAGCCG GGCTCGGGGC CGCCGCGACC CTCGCGGCGC CTGCTAGACC 720
TGAGCGTCTT CCGGAGCCGC GGCTTTGTGC TTTACGCCGT GGCCGCTCG GTCTGCTGTC 780
TGGGGCTCTT CGTCCCGCCC GTGTTCTGTC TGAGCTACGC CAAGGACCTG GCGTGTCCCG 840
ACACCAAGGC CGCCTTCCTG CTCACCATCC TGGGCTTCAT TGACATCTTC GCGCGGCCGG 900
CGCGGGGCTT CGTGGCGGGG CTGCGGAAGG TGCGGCCCTA CTCGCTCTAC CTCTTCAGCT 960
55 TCTCCATGTT CTTCAACGGC CTCGCGGACC TGGCGGGCTC TACGGCGGGC GACTACGGCG 1020
GCCTCGTGTT CTTCTGCATC TTCTTTGGCA TCTCTACGG CATGGTGGGG GCCCTGCAGT 1080
TCGAGGTGCT CATGGGCATC GTGGGCACCC ACAAGTCTC CAGTGCCATT GGCCTGGTGC 1140
TGTGATGGA GGCCTGTGGC GTGCTCGTGC GGCCCCCTTC GGGAGGCCAA CTCCTGGATG 1200
CGACCCAGCT CTACATGTAC GTGTTTCATC TGGCGGGGGC CGAGGTGCTC ACCTCCTCCC 1260
60 TGATTTTGCT GCTGGGCAAC TTCTTCTGCA TTAGGAAGAA GCCCAAGAG CCACAGCCTG 1320
AGGTGGCGGC CGCGGAGGAG GAGAAGCTCC ACAAGCCTCC TGCAGACTCG GGGGTGGACT 1380
TGCGGGAGGT GGAGCATTTT CTGAAGGCTG AGCCTGAGAA AACGGGGAG GTGGTTTACA 1440
CCCCGAAAC AAGTGTCTGA GTGGCTGGGC GGGGCCGGCA GGCACAGGGA GGAGGTACAG 1500
AAGCCGGCAA CGCTTGCTAT TTATTTTACA AACTGGACTG GCTCAGGCAG GGCCACGGCT 1560
65 GGGCTCCAGC TGCCGGGCCA GCGATCGTC GCCGATCAG TGTTTGAGG GGGAGGGTGG 1620
CGGGGTGGGA ACCGTGTCTT TCCAGAGTGG ATCTGCGGTG AAGCCAAAGC GCAAGGTTAC 1680
AAGGCATCCT CACCAAGGGC CCCGCTCTGT GCTCCAGGT GGCCTGCGGC CACTGCTATG 1740
CTCAAGGACC TGGAAACCCA TGCTTCGAGA CAACGTGACT TTAATGGGAG GGTGGGTGGG 1800
CGCAGACAG GCTGGCAGGG CAGGTGCTGC GTGGGGCCCT CTCCAGCCCG TCCTACCCTG 1860
70 GGCTCACATG GGGCCTGTGC CCACCCCTCT TGAGTGTCTT GGGGACAGCT CTTTCCACCC 1920
CTGGAAGATG GAAATAAAC TCGGTGTGGG TGGAGTGTTC TCGTGCCGAA TTCAAAAAGC 1980
TT

```

Seq ID NO: C78 DNA Sequence  
Nucleic Acid Accession #: NM\_000358.1  
Coding sequence: 48..2099

```

80      1      11      21      31      41      51
      |      |      |      |      |      |
GCTTGCCCGT CGGTCTGCTAG CTCGCTCGGT GCGCGTCGTC CCGCTCCATG GCGCTCTTCG 60
TGCGGCTGCT GGCTCTCGCC CTGGCTCTGG CCCTGGGCCC CGCCGCGACC CTGGCGGGTC 120
CCGCCAAGTC GCCCTACCAG CTGGTGTCTG AGCACAGCAG GCTCCGGGGC CGCCAGCACG 180
GCCCAACGTT GTGTGCTGTG CAGAAGGTTA TTGGCACTAA TAGGAAGTAC TTCACCAACT 240

```

5	GCAAGCAGTG	GTACCAAAAGG	AAAATCTGTG	GCAAATCAAC	AGTCATCAGC	TACGAGTGTCT	300
	GTCTCTGGATA	TGAAAAAGGTC	CCTGGGGGAGA	AGGGCTGTCC	AGCAGCCCTA	CCACTCTCAA	360
	ACCTTTACGA	GACCCCTGGGA	GTGCTTGGAT	CCACCCACCAC	TCAGCTGTAC	ACGGACCGCA	420
	CGGAGAAGCT	GAGGCCCTGAG	ATGGAGGGGC	CCGGCAGCTT	CACCATCTTC	GCCCTTAGCA	480
	ACCAGGGCCTG	GGCCTCCTTG	CCAGCTGAAG	TGCTGGACTC	CCTGGTCAGC	AATGTCAACA	540
	TTGAGCTGTCT	CAATGCCCTC	CGCTACCATA	TGGTGGGCAG	GCGAGTCTGT	ACTGATGAGC	600
	TGAAACACGG	CATGACCCCTC	ACCTCTATGT	ACCAGAATTCT	CAACATCCAG	ATCCACCACT	660
	ATCCTAATGG	GATTGTAACT	GTGAACCTGTG	CCCGGCTCCT	GAAAGCCGAC	CACCATGCAA	720
10	CCAACGGGGT	GGTGCACCTC	ATCGATAAGG	TCATCTCCAC	CATCACCAAC	AACATCCAGC	780
	AGATCATTGA	GATCGAGGAC	ACCTTTGAGA	CCCTTCGGGC	TGCTGTGGCT	GCATCAGGGC	840
	TCAACACGAT	GCTTGAAGGT	AACGGCCAGT	ACACGCTTTT	GGCCCCGACC	AATGAGGCCT	900
	TCGAGAAGAT	CCCTAGTGAG	ACTTTGAACC	GTATCCTGGG	CGACCCAGAA	GCCCTGAGAG	960
	ACCTGCTGAA	CAACCACATC	TTGAAGTCAG	CTATGTGTGC	TGAAGCCATC	GTTGCGGGGC	1020
	TGTCTGTAGA	GACCCCTGGAG	GGCAGGACAC	TGGAGGTGGG	CTGCAGCGGG	GACATGCTCA	1080
15	CTATCAACGG	GAAGGCGATC	ATCTCCAATA	AAGACATCCT	AGCCACCAAC	GGGGTGATCC	1140
	ACTACATTGA	TGAGCTACTC	ATCCCAGACT	CAGCCAAGAC	ACTATTTGAA	TTGGCTGACG	1200
	AGTCTGATGT	GTCCACAGCC	ATTGACCTTT	TCAGACAAGC	CGGCCTCGGC	AATCATCTCT	1260
	CTGGAAGTGA	GCGGTTGACC	CTCCTGGCTC	CCCTGAATTTC	TGTATTCAAA	GATGGAAACCC	1320
20	CTCCAATTGA	TGCCCCATACA	AGGAATTTGC	TTCGGAACCA	CATAATTAAA	GACCAGCTGG	1380
	CCCTTAAGTA	TCTGTACACT	GGACAGACCC	TGGAAACTCT	GGGCGGCAAA	AAACTGAGAG	1440
	TTTTTTGTTTA	TCGTAATAGC	CTCTGCATTG	AGAACAGCTG	CATCGCGGCC	CACGACAAGA	1500
	GGGGGAGGTA	CGGGACCCCTG	TTACAGATGG	ACCGGGTGCT	GACCCCCCA	ATGGGGGACTG	1560
	TCATGGATGT	CCTGAAGGGA	GACAATCGCT	TTAGCATGCT	GGTAGCTGCC	ATCCAGTCTG	1620
25	CAGGACTGAG	GGAGACCCCTC	AACCGGGAAG	GAGTCTACAC	AGTCTTTGCT	CCCAACAAATG	1680
	AAGCCTTCCG	AGCCCTGCCA	CCAAGAGAAC	GGAGCAGACT	CTTGGGAGAT	GCCAAGGAAC	1740
	TTGCCAACAT	CCTGAAATAC	CACATTGGTG	ATGAAATCCT	GGTTAGCGGA	GGCATCGGGG	1800
	CCCTGGTGCG	GCTAAAGTCT	CTCCAAGGTG	ACAAGCTGGA	AGTCAGCTTG	AAAAACAATG	1860
	TGGTGAGTGT	TAACAAGGAG	CCTGTTGCCG	AGCCTGACAT	CATGGCCACA	AATGGCGTGG	1920
30	TCATGTGCAT	CACCAATGTT	CTGCAGCCTC	CAGCCAACAG	ACCTCAGGAA	AGAGGGGATG	1980
	AACTTGCAGA	CTCTGGCCTT	GAGATCTTCA	AACAAGCATC	AGCGTTTTTC	AGGGCTTCCC	2040
	AGAGGTCTGT	GCGACTAGCC	CCTGTCTATC	AAAAGTTATT	AGAGAGGATG	AAGCATTAGC	2100
	TTGAAGCACT	ACAGGAGGAA	TGCACCACGG	CAGCTCTCCG	CCAATTCTTC	TCAGATTTC	2160
	ACAGAGACTG	TTTGAATGTT	TTCAAAACCA	AGTATCACAC	TTTAATGTAC	ATGGGCGCGCA	2220
35	CCATAATGAG	ATGTGAGCCT	TGTGCATGTG	GGGGAGGAGG	GAGAGAGATG	TACTTTTTTA	2280
	ATCATGTTCC	CCCTAAACAT	GGCTGTTAAC	CCACTGCATG	CAGAAACTTG	GATGTCACTG	2340
	CCTGACATTCT	ACTTCCAGAG	AGGACCTATC	CCAAATGTGG	AATTGACTGC	CTATGCCAAG	2400
	TCCTCGGAAA	AGGAGCCTTC	GTATTGTGGG	GCTCATAAAA	CATGAATCAA	GCAATCCAGC	2460
	CTCATGGGAA	GTCCCTGGAC	AGTTTTGTGA	AAGCCCTTGC	ACAGCTGGAG	AAATGGCATC	2520
40	ATTATAAGCT	ATGAGTTGAA	ATGTTCTGTC	AAATGTGTCT	CACATCTACA	CGTGGCTTGG	2580
	AGGCTTTTAT	GGGGCCCTGT	CCAGGTAGAA	AAGAAATGGT	ATGTAGAGCT	TAGATTTCCT	2640
	TATTGTGACA	GAGCCATGGT	GTGTTTGTAA	TAATAAAACC	AAAGAAACAT	A	2691

Seq ID NO: C79 DNA Sequence  
Nucleic Acid Accession #: NM\_006536.2  
Coding sequence: 109..2940

50	1	11	21	31	41	51	
	ACCTAAAACC	TTGCAAGTTC	AGGAAGAAAC	CATCTGCATC	CATATTGAAA	ACCTGACACA	60
	ATGTATGCAG	CAGGCTCAGT	GTGAGTGAAC	TGGAGGCTTC	TCTACAACAT	GACCCAAAGG	120
	AGCATTGCAG	GTCCTATTGG	CAACCTGAAG	TTTGTGACTC	TCCTGGTTGC	CTTAAGTTCA	180
	GAACTCCCAT	TCTCTGGAGC	TGGAGTACAG	CTTCAAGACA	ATGGGTATAA	TGGATTGCTC	240
55	ATTGCAATTA	ATCCTCAGGT	ACCTGAGAA	CAGAACCTCA	TCTCAACAT	TAAGGAAATG	300
	ATAACTGAAG	CTTCATTTTA	CCTATTTAAT	GCTACCAAGA	GAAGAGTATT	TTTCAGAAAT	360
	ATAAAGATT	TAATACCTGC	CACATGGAAA	GCTAATAATA	ACAGCAAAAT	AAAAACAAGAA	420
	TCATATGAAA	AGGCAAAATG	CATAGTGACT	GACTGGTATG	GGGCACATGG	AGATGATCCA	480
	TACACCCATC	AATACAGAGG	GTGTGGAAAA	GAGGGAAAAAT	ACATTCAATT	CACACCTAAT	540
60	TTCTACTGTA	ATGATAAATT	AACAGCTGGC	TACGGATCAC	GAGGCCGAGT	GTTTGTCCAT	600
	GAATGGGCCC	ACCTCCGTTG	GGGTGTGTTT	GATGAGTATA	ACAATGACAA	ACCTTCTCAT	660
	ATAAATGGGC	AAAATCAAA	TAAAGTGACA	AGGTGTTTAT	CTGACATCAC	AGGCATTTTT	720
	GTGTGTGAAA	AAGGTCCTTG	CCCCCAAGAA	AACGTGATTA	TTAGTAAGCT	TTTAAAGAA	780
	GGATGCACCT	TTATCTACAA	TAGCACCCAA	AATGCAACTG	CATCAATAAT	GTTTCATGCA	840
65	AGTTTATCTT	CTGTGGTTGA	ATTTTGTAAT	GCAAGTACCC	ACAACCAAGA	AGCACCAAAAC	900
	CTACAGAACC	AGATGTGCAG	CCTCAGAAGT	GCATGGGATG	TAATCACAGA	CTCTGCTGAC	960
	TTTCACCACA	GCTTTCCCAT	GAATGGGACT	GAGCTTCCAC	CTCCTCCAC	ATTCTCGCTT	1020
	GTACAGGCTG	GTGACAAAGT	GGTCTGTTTA	GTGCTGGATG	TGTCAGCAA	GATGGCAGAG	1080
	GCTGACAGAC	TCCTTCAACT	ACAACAAGCC	GCAGAATTTT	ATTTGATGCA	GATTGTTGAA	1140
70	ATTCATACCT	TCGTGGGCAT	TGCCAGTTTC	GACAGCAAAG	GAGAGATCAG	AGCCCCAGCTA	1200
	CACCAAAATTA	ACAGCAATGA	TGATCGAAAG	TTGCTGGTTT	CATATCTGCC	CACCACTGTA	1260
	TCAGCTAAAA	CAGACATCAG	CATTGTGTCA	GGGCTTAAGA	AAGGATTGTA	GGTGGTTGAA	1320
	AAACTGAATG	GAAGAGCTTA	TGGCTCTGTG	ATGATATTAG	TGACCAGCGG	AGATGATAAG	1380
	CTTCTTGGCA	ATTGCTTTACC	CACGTGTCTC	AGCAGTGGTT	CAACAATTCA	CTCCATTGCC	1440
75	CTGGGTTTAT	CTGCAGCCCC	AAATCTGGAG	GAATTATCAC	GTCTTACAGG	AGGTTTAAAG	1500
	TTCTTTGTTC	CAGATATATC	AAACTCCAAT	AGCATGATTG	ATGCTTTTCA	TAGAAATTTCC	1560
	TCGTGAACTG	GAGACATTTT	CCAGCAACAT	ATTCAGCTTG	AAAGTACAGG	TGAAATGTTC	1620
	AAACCTCACC	ATCAATTGAA	AAACACAGTG	ACTGTGGATA	ATACTGTGGG	CAACGACACT	1680
80	ATGTTTCTAG	TTACGTGGCA	GGCCAGTGGT	CTCCTGAGA	TTATATTAT	TGATCCTGAT	1740
	GGACGAAAAT	ACTACACAAA	TAATTTTATC	ACCAATCTAA	CTTTTGGGAC	AGCTAGTCTT	1800
	TGGATTCCAG	GAACAGCTAA	GCCTGGGCAC	TGGACTTACA	CCCTGAACAA	TACCCATCAT	1860
	TCTCTGCAAG	CCCTGAAAGT	GACAGTGACC	TCTCGGCCT	CCAACCTCAG	TGTGCCCCCA	1920
	GCCACTGTGG	AAGCCTTTGT	GGAAGAGAGC	AGCCTCCATT	TTCTCATCC	TGTGATGATT	1980
	TATGCCAATG	TGAACAGGG	ATTTTATCCC	ATTCTTAATG	CCAATCTCAC	TGCCACAGTT	2040
	GAGCCAGAGA	CTGGAGATCC	TGTTACGCTG	AGACTCCTTG	ATGATGGAGC	AGGTGCTGAT	2100

GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTTTCT CCTTTGCTGC AAATGGTAGA 2160  
 TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCACGC CCACTCTATT 2220  
 CCAGGGAGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280  
 GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC 2340  
 AGCTCAGGAG GCTCCTTTTC AGTGTCTGGGA GTTCCAGCTG GCCCCACCC TGATGTGTTT 2400  
 CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAAGTAG AAGAGGAAT GACCCCTATCT 2460  
 TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG 2520  
 AGTAAAAATC TACAGAATAT CCAAGATGAC TTTAACAAATG CTATTTTAGT AAATACATCA 2580  
 AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTCC 2640  
 ACGAATGGAC CTGAACATCA GCCAAATGGA GAAACACATG AAAGCCACAG AATTTATGTT 2700  
 GCAATACGAG CAATGGATAG GAACTCCTTA CAGTCTGCTG TATCTAACAT TGCCCAGGCG 2760  
 CCTCTGTTTA TTCCCCCAA TTCTGATCCT GTACCTGCCA GAGATTATCT TATATTGAAA 2820  
 GGAGTTTTAA CAGCAATGGG TTTGATAGGA ATCATTGCCC TTATTATAGT TGTGACACAT 2880  
 CATACTTTAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATATA 2940  
 ATAAATATCC AAAGTGTCTT CCTTCTTAGA TATAAGACCC ATGGCCCTCG ACTACAAAAA 3000  
 CATACTAAAC AAGTCAAAAT AACATCAAAA CTGTATTAAA ATGCATTGAG TTTTGTACA 3060  
 ATACAGATAA GATTTTTTACA TGGTAGATCA ACAATTCCTT TTGGGGGTAG ATTAGAAAAAC 3120  
 CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAAGTAAT GTCCTTAAAG 3180  
 GCAGGAGGAA GGGTAAAGTC GGACCAAGTGT CAAGGAAAGT TTGTTTATT GAGGTGGAAA 3240  
 AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACGTCTCT TGTGAAGCAA 3300  
 TCATTTAGTT ACTTTGATTA ATTTTCTTT TCTCCTTATC TGTGCAGTAC AGGTTGCTTG 3360  
 TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAAG CTCTTTACCT 3420  
 CTTGCTATTT TGTTATATAT ATTTAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT 3480  
 TTTCACTGTA AGAGGTAACC TTTAACAATA TGGGTATTAC CTTTGTCTCT TCATACCGGT 3540  
 TTTATGACAA AGGTCTATTG AATTTATTG TMTGTAAGTT TCTACTCCCA TCAAAGCAGC 3600  
 TTTCTAAGTT TATTGCCTTG GGTATTATG GAATGATAGT TATAGCCCCN TATAATGCCT 3660  
 TACCTAGGAA A 3671

Seq ID NO: C80 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1413

1 11 21 31 41 51  
 | | | | |  
 35 ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCCTGAAC 60  
 AGCTCTACAA GCCTGGAAAA AAATAATGTG CTATTTGGTG AAAGATACTT AGAAAAATTT 120  
 TATGGCCTTG AGATAAACAA ACTTCCAGTG ACAAATAATGA AATATAGTGG AAACCTTAATG 180  
 AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240  
 40 ACATCTACCC TGGAGATGAT GCACGCACCT CGATGTGGAG TCCCCGATGT CCATCATTTT 300  
 AGGGAAATGC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT 360  
 TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCCGGAAGC TTTCGAAGTA 420  
 TGGAGTAATG TTACCCCTT GAAATTCAGC AAGATTAAAC CAGGCATGGC TGACATTTTG 480  
 GTGGTTTTG CCCGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540  
 45 CTAGCCCATG CTTTGTGACC TGGATCTGGC ATTGGAGGGG ATGCACATTT CGATGAGGAC 600  
 GAATTCCTGA CTACACATTC AGGAGGCACA AACTTGTTC TCACCTGCTG TCACGAGATT 660  
 GGCCATTCTCT TAGGTCTTGG CCATTCAGT GATCCAAAGG CCGTAATGTT CCCCACCTAC 720  
 AAATATGTTG ACATCAACAC ATTTGCGCTC TCTGCTGATG ACATACGTGG CATTCAGTCC 780  
 CTGTATGGAG ACCCAAAAGA GAACCAACGC TTGCCAAATC CTGACAATTC AGAACCAGCT 840  
 50 CTCTGTGACC CCAATTTGAG TTTTGTGCT GTCACCTACG TGGGAAATAA GATCTTTTTT 900  
 TTCAAAGACA GGTTCCTCTG GCTGAAGGTT TCTGAGAGAC CAAAGACCAG TGTTAATTTA 960  
 ATTTCTTCTT TATGGCCAACT CTGCACTCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020  
 AGAAATCAAG TTTTCTTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080  
 GAGCCAAATT ATCCCAAGAG CATACATTCT TTTGGTTTTT CTAACCTTGT GAAAAAATT 1140  
 55 GATGCACTGT TTTTAAACCC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAACCAGTAT 1200  
 TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCTGCTT ATCCCAACT GATTACCAAG 1260  
 AACTTCCAAG GAATCGGGCC TAAATTTGAT GCAGTCTCT ACTCTAAAA CAATACCTAC 1320  
 TATTTCTTCC AAGGATCTAA CCAATTTGAA TATGACTTCC TACTCCAACG TATACCCAAA 1380  
 ACATGAAAAA GCAATAGCTG GTTTGGTGTG TGA 1413

Seq ID NO: C81 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..1413

1 11 21 31 41 51  
 | | | | |  
 65 ATGAAGTTTC TTCTAATACT GCTCCTGCAG GCCACTGCTT CTGGAGCTCT TCCCCTGAAC 60  
 AGCTCTACAA GCCTGGAAAA AAATAATGTG CTATTTGGTG AAAGATACTT AGAAAAATTT 120  
 TATGGCCTTG AGATAAACAA ACTTCCAGTG ACAAATAATGA AATATAGTGG AAACCTTAATG 180  
 70 AAGGAAAAAA TCCAAGAAAT GCAGCACTTC TTGGGTCTGA AAGTGACCGG GCAACTGGAC 240  
 ACATCTACCC TGGAGATGAT GCACGCACCT CGATGTGGAG TCCCCGATGT CCATCATTTT 300  
 AGGGAAATGC CAGGGGGGCC CGTATGGAGG AAACATTATA TCACCTACAG AATCAATAAT 360  
 TACACACCTG ACATGAACCG TGAGGATGTT GACTACGCAA TCCGGAAGC TTTCGAAGTA 420  
 TGGAGTAATG TTACCCCTT GAAATTCAGC AAGATTAAAC CAGGCATGGC TGACATTTTG 480  
 75 TGGTTTTTG CCCGTGGAGC TCATGGAGAC TTCCATGCTT TTGATGGCAA AGGTGGAATC 540  
 CTAGCCCATG CTTTGTGACC TGGATCTGGC ATTGGAGGGG ATGCACATTT CGATGAGGAC 600  
 GAATTCCTGA CTACACATTC AGGAGGCACA AACTTGTTC TCACCTGCTG TCACGCCATT 660  
 GGCCATTCTCT TAGGTCTTGG CCATTCAGT GATCCAAAGG CCGTAATGTT CCCCACCTAC 720  
 AAATATGTTG ACATCAACAC ATTTGCGCTC TCTGCTGATG ACATACGTGG CATTCAGTCC 780  
 CTGTATGGAG ACCCAAAAGA GAACCAACGC TTGCCAAATC CTGACAATTC AGAACCAGCT 840  
 80 CTCTGTGACC CCAATTTGAG TTTTGTGCT GTCACTACCG TGGGAAATAA GATCTTTTTT 900  
 TTCAAAGACA GGTTCCTCTG GCTGAAGGTT TCTGAGAGAC CAAAGACCAG TGTTAATTTA 960  
 ATTTCTTCTT TATGGCCAACT CTGCACTCT GGCATTGAAG CTGCTTATGA AATTGAAGCC 1020  
 AGAAATCAAG TTTTCTTTTT TAAAGATGAC AAATACTGGT TAATTAGCAA TTTAAGACCA 1080  
 GAGCCAAATT ATCCCAAGAG CATACATTCT TTTGGTTTTT CTAACCTTGT GAAAAAATT 1140

GATGCAGCTG TTTTAAACCC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAACCAGTAT 1200  
 TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCTTGGTT ATCCCAAACT GATTACCAAG 1260  
 AACTTCCAAAG GAATCGGGCC TAAATTTGAT GCAGTCTTCT ACTCTAAAAA CAAATACIAC 1320  
 TATTTCTTCC AAGGATCTAA CCAATTTGAA TATGACTTCC TACTCCAACG TATCACCAAA 1380  
 AACTGAAAA GCAATAGCTG GTTTGGTTGT TGA 1413

Seq ID NO: C82 DNA Sequence  
 Nucleic Acid Accession #: NM\_006952.1  
 Coding sequence: 11..793

1 11 21 31 41 51  
 AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTTCGTTGC TTCCAGGGCC TGCTGATTTT 60  
 TGGAAATGTG ATTATTTGTT GTTTCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120  
 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180  
 GGCTGCCTGG ATCGGCATAT TGTGGGGCAT CTGCCCTCTC TGCTGTCTG TTCTAGGCAT 240  
 TGTAGGCATC ATGAAGTCCA GCAGGAAAAT TCTTCTGGCG TATTTTCATT TGATGTTTAT 300  
 AGTATATGCC TTGGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360  
 ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACCAACGCC CTCCAAACAA 420  
 TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480  
 CAATTGCTGT GGGCTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCCGGAC 540  
 TGAGAAATAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600  
 AGAACCTCTC AACCTGGAGG CTTGTAAACT AGGCGTGCCT GGTTTTATC ACAATCAGGG 660  
 CTGCTATGAA CTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTTG CCTGGTTTGG 720  
 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTCTGGT ACCATGTCTT ACTGGAGCAG 780  
 AATTGAATAT TAAGAA 796

Seq ID NO: C83 DNA Sequence  
 Nucleic Acid Accession #: NM\_001793.2  
 Coding sequence: 71..2560

1 11 21 31 41 51  
 AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCCGTCGC GGCAGCTGCT TCACCCCTCT 60  
 CTCTGCAGCC ATGGGGCTCC CTGCTGGACC TCTCGCGTCT CTCCCTCCTC TCCAGGTTTG 120  
 CTGGCTGCAG TGC CGCGCCTG CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180  
 CTTGAGAGCG GAGGCGCGCG AGCAGGAGCC CCGCCAGGCG CTGGGGAAG TATTATGGG 240  
 CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300  
 TGGCGAGACA GTCCAGGAAA GAAGGTCAC TGAAGGAAAG AATCCATTGA AGATCTTCCC 360  
 ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420  
 TGAAAATGCG AAGGGTCCCT TCCCCAGAG ACTGAATCAG CTCAACTCTA ATAAAGATAG 480  
 AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540  
 CTTCTGCTGA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600  
 GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTGAGG AATGGTGCCT CAGTGGAGGA 660  
 CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720  
 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTTACCA GGTACTTCTG TGATGCAGGT 780  
 GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840  
 CCATAGCCAA GAACCAAGAG ACCCACACGA CCTCATGTTT ACCATTCACC GGAGCACAGG 900  
 CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAGAA GTCCCTGAGT ACACACTGAC 960  
 CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020  
 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080  
 GCCTGAGAAAT CAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCAGTGATC TGGACGCCCC 1140  
 CAACTACCA CGGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200  
 TACCATCACC ACCCACCTTG AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGGA 1260  
 TTTTGAGGCC AAAAACCCAGC ACACCTGTA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320  
 GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380  
 ACCTGTGTTT GTCCCACTGT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440  
 GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAGA TCAGCTACCG 1500  
 CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560  
 TGTGGGCACC TCGACCGTGT AGGATGAGCA GTTTGTGAGG AACAACTATC ATGAAGTCAT 1620  
 GTTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680  
 ACTGATTGAT GTCAATGACC ATGGCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740  
 CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800  
 CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860  
 GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCTTG AAGCAGGATA CATATGACGT 1920  
 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980  
 GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAGGGGAG GTTTCATCCT 2040  
 CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTGTC TTTTGTGGT 2100  
 GAGAAAGAAG CGGAAGATCA AGGAGCCCTT CTTACTCCCA GAAGATGACA CCGTGAACA 2160  
 CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATACCCCA 2220  
 GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGACG TGGACCAAC 2280  
 CATCATCCCC ACACCCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340  
 TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCACAC GCCCCGCTCT ACAGACCCCT 2400  
 CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCTGAGCT CCCTCACTC 2460  
 CTCGCTCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTTCAA 2520  
 GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GGGCCCTGCC TGCAGGGCTG 2580  
 GGGACCAACG CTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCTCC TTCACTGAG 2640  
 GACTTCGAGC GTTGTGAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700  
 ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760  
 AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAAGCC 2820  
 TCTTACTGTC CGTAAATGTC TCAACCTGT GTCTGGGCC TGGGCTGTCT GTGACTGACC 2880  
 TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940  
 TTTTTTTAAAT GCTACTTCCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000  
 GCTGGGCCCA GTGCCCCTCA TGCATTTCTG GTTTCAGAC CCAATGCCT CCATTCGGA 3060

TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTTT TATTTTCCCT 3120  
 GTTGC GTTG TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180  
 TAAAGAACT TTTCCAGAA AAAAA 3205

5

Seq ID NO: C84 DNA Sequence  
 Nucleic Acid Accession #: NM\_005629.1  
 Coding sequence: 639..2546

10 1 11 21 31 41 51  
 | | | | | |  
 TAGTCGGAGC GAGGTGGCGA GTCGCTGAGC CCGCCGCGGC CCCGAGAGCG GCTGCAGCCG 60  
 CCGCCGCGCG GAAGGAGAGG GCGAGGCGCG CCCGAGCCGC CGCCGCGCGC GCCACGCGCG 120  
 CCGCCGCGCAC CACCGCCACC GGAGTCGCGG GCCAGCCGGG CAGCCTCCGC GGGCCCGCGC 180  
 CGGGCGGGGG GCGCGGGGCC ACAGGCCCCCT GCTCCGGCCG TCGTTTGAGC ACCGCGGGCG 240  
 15 CCGATGTGCG CCGCGCCCCG TTAGGATGAG TCTCGGGTCG GCGGAGGAGC CGCCGAGACC 300  
 GCCGCGCGCC GAGCCGCGGG CAGGAGCCTC GGGAGCCGCC GCCGCGCGCG CGCCGCGCCG 360  
 GCCGGGCCCC GAGCGCGCCC GCGCGCCCCC GGGCCCCCGA CACACATGAG ATTCTTCAGG 420  
 CTCACCTTCA AGTGCTTCGT GGACTGCTTC TGACTGCGCC GCCCGCGCCC CGCACCCCGC 480  
 CGTCCGCCCC CGCGCCCGTC CCGCGCCCCG GCGCGCCCCC GGGCCCCGGC CGGCCGCGCG 540  
 20 CCTCGGGGCC CTCCCCGGTG CCGCCCGGTG CCCCCCGCTG ACCGCGCGCC CCCGTGAGGC 600  
 GCCGCGACCC CGGCCGCGCC GTGCGGCCCC CCGGGGCCAT GCGGAAGAAG AGCGCCGAGA 660  
 ACGGCATCTA TAGCGTGTCC GCGGACGAGA AGAAGGGCCC CCTCATCGCG CCGGGGCCCC 720  
 ACGGGGCCCC GCGCAAGGGC GACGGCCCCG TGGCCTGGG GACACCCGGC GGGCGCCTGG 780  
 CCGTGCCGCC GCGGAGAGAC TGGACGCGCC AGATGGACTT CATCATGTCT TCGTGGGCT 840  
 25 TCGCCGTGGG CTTGGGCAAC GTGTGGCGCT TCCCTTACCT GTGCTACAAG AACGGCGGAG 900  
 GTGTGTTCC TATTCCCTAC GTCTGATCG CCCTGGTTGG AGGAATCCCC ATTTTCTTCT 960  
 TAGAGATCTC GCTGGGCCAG TTCTATGAAG CCGGCAGCAT CAATGTCTGG AACATCTGTC 1020  
 CCTGTTCCTA AGGCTGGGGC TACGCTTCCA TGGTGATCGT CTCTACTGTC AACACCTACT 1080  
 ACATCATGGT GCTGGCCTGG GGCTTCTATT ACCTGGTCAA GTCCCTTACC ACCACGCTGC 1140  
 30 CCTGGGCCAC ATGTGGCCAC ACCTGGAACA CTCCCGACTG CGTGGAGATC TTCCGCCATG 1200  
 AAGACTGTGC CAATGCCAGC CTGGCCAACC TCACCTGTGA CCAGCTTGCT GACCGCCGGT 1260  
 CCCTGTCTAT CGAGTTCTGG GAGAACAAAG TCTTGAGGCT GTCTGGGGGA CTGGAGGTGC 1320  
 CAGGGGCCCT AACTGGGAG GTGACCCCTT GTCTGCTGGC CTGCTGGGTG CTGGTCTACT 1380  
 35 TCTGTGTCG GAAGGGGGTC AAATCCACGG GAAAGATCGT GTACTTCACT GCTACATTCC 1440  
 CCTACGTGGT CCTGGTGTGC CTGCTGGTGC GTGGAGTGCT GCTGCTGGC GCCCTGGATG 1500  
 GCATCATTTA CTATCTCAAG CCTGACTGGT CAAAGCTGGG GTCCCTCAG GTGTGGATAG 1560  
 ATGCGGGGAC CCAGATTTTC TTTTCTTACG CCATTGGCCT GGGGGCCCTC ACAGCCCTGG 1620  
 CGAGCTACAA CCCTCTCAAC AACAACCTGT ACAAGGACGC CATCATCTCT GCTCTCATCA 1680  
 40 ACAGTGGGAC GCTGGCTTTT GCTGGCTTCT TGGTCTTCTC CATCCTGGGC TTCTATGGCTG 1740  
 CAGAGCAGGG CGTGACATAT TCCAAGGTGG CAGAGTCAGG GCCGGGCTCG GCCTTCATCG 1800  
 CCTACCCGCG GCGTGTACG CTGATGCCAG TGGCCCACT CTGGGCTGCC CTGTTCTTCT 1860  
 TCATGCTGTT GCTGCTTGGT CTGACAGGCC AGTTTGTAGG TGTGGAGGGC TTCATCACCG 1920  
 GCCTCTCGA CCGCTCTCCG GCCTCTACT ACTTCCGTTT CCAAGGGGAG ATCTCTGTGG 1980  
 45 CCCTCTGTTG TGGCCTCTGC TTTGTCTATG ATCTCTCATG GTTGACTGAT GCGGGGATGT 2040  
 ACGTCTTCCA GCTGTTTGAC TACTACTCGG CCAGCGGCAC CACCTTCTCT TGGCAGGCCT 2100  
 TTTGGGAGTG CGTGGTGGTG GCCTGGGTGT ACGGAGCTGA CCGCTTCATG GACGACATTG 2160  
 CCTGTATGAT CGGGTACCAG CCTTGCCCTT GGATGAAATG GTGCTGGTCC TTCTTACACC 2220  
 CGCTGGTCTG CATGGGCATC TTCTATCTCA ACGTTGTGTA CTACGAGCCG CTGGTCTACA 2280  
 50 ACAACACCTA CGTGTACCCG TGGTGGGGTG AGGCCATGGG CTGGGCTTCT GCCCTGTCTC 2340  
 CCATGCTGTG CGTGCCGCTG CACCTCTCTG GCTGCCTCTC CAGGGCCAGG GGCACCATGG 2400  
 CTGAGCGCTG CAGACCTCTG ACCCAGCCCA TCTGGGGCCT CCACCACTTG GAGTACCGAG 2460  
 CTGAGGACGC AGATGTCTAG GGCCTGACCA CCTGACCCC AGTGTCCGAG AGCAGCAAGG 2520  
 TCGTCTGGT GAGAGTGTC ATGTGACAAC TCAGCTCACA TCACCAGCTC ACCTCTGGTA 2580  
 55 GCCATAGCAG CCCCTGCTTC AGCCCCACCG CACCCCTCCA GGGGGCCTGC CTCTCCCTGA 2640  
 CACTTTTGGG GTCTGCTCTG GGGAGGAGGG GAGAAAGCAC CATGAGTGCT CACTAAAAA 2700  
 ACTTTTCCA TTTTATAATA AACGCCAAAA ATATCACAAAC CCACCAAAAA TAGATGCCTC 2760  
 TCCCCCTCCA GCCCTAGCCG AGCTGGTCTT AGGCCCGGCC TAGTGCCCA CCCCCACCA 2820  
 CAGTGCTGCA CTCCTCTCTG CCCTGCCACG CCCACCCCTT GCCCACTCTT CCAGGCTCTG 2880  
 60 CTCTGCAGCA CACCCGTGGG TGACCCCTCA CCCCAGAGC AGCAGTGGCA GCTTGGGAAA 2940  
 TGTGAGGAAG GGAAGGAGGG AGAGACGGGA GGGAGGAGAG AGAGGAGAAG GGAGGCAGGG 3000  
 GAGGGGAGC AGAACCAAGG CAAATATTTT AGCTGGGCTA TACCCCTCTC CCCATCCCTG 3060  
 TTATAGAAGC TTAGAGAGCC AGCCAGCAAT GGAACCTTCT GGTTCCTGCG CCAATCGCCA 3120  
 CCAGTATCAA TTGGTGTGAG TTGGGTGCGA GTGCACGCGT GCGTGAGTAC GGAGAGTATA 3180  
 65 TATAGATCTC TATCTCTTAG CAAAGGTGAA TGCCAGATGT AAATGGCGCC TCTGGGCAAA 3240  
 GGAGGCTTGT ATTTTGCACA TTTTATAAAA ACTTGAGAGA ATGAGATTTC TGCTTGATATA 3300  
 TTTCTAAAAA GAGGAAGGAG CCCAAACCAT CCTCTCTTCA CCACTCCCAT CCCTGTGAGC 3360  
 CCTACCTTAC CCCTCTGCCC CTAGCCAAAG AGTGTGAATT TATAGATCTA ACTTTCATAG 3420  
 70 GCAAAACAAA AGCTTCGAGC TGTGCGTGT GTGAGTCTGT TGTGTGGATG TCGTGTGTG 3480  
 GTCCCCAGCC CAGACTGGA TTGGAAGAGT GCATGGTGGG GGCTCGGGG CTGTCCCCAC 3540  
 GCTGTCCCTT TGCCACAAGT CTGTGGGGCA AGAGGCTGCA ATATTCGCTC CTGGGTGTCT 3600  
 GGGCTGTCAA CTTGGCTTGC TCAGGCTTCC CACCCGTGTC GGGGCACACC CCGAGGAAGG 3660  
 GACCTCGGAC ACGGCTCCCA CGTCCAGGCT TAAGGTGGAT GCACCTTCCC CACCTCCAGT 3720  
 CTTCTGTGTA CCGACTTTAA CCAAGTTTG TCTGTACGT CCAGTCCCGA GACGGCTGAG 3780  
 75 TGACCCCAAG AAGGCTTCC CCGACACCCA GACAGAGGCT GCAGGGCTGG GGTGGGTGA 3840  
 GGGTGGCGGG CTTGCGGGGA CATTCTACTG TGCTAAAAAG CCACTGCAGA CATAGCAATA 3900  
 AAAACATGTC ACTTTCC 3917

Seq ID NO: C85 DNA Sequence  
 Nucleic Acid Accession #: NM\_006516.1  
 Coding sequence: 180..1658

80

1 11 21 31 41 51  
 | | | | | |  
 TAGTCGCGGG TCCCCGAGTG AGCACGCCAG GGAGCAGGAG ACCAAACGAC GGGGGTTCGGA 60

GTCAGAGTCG CAGTGGGAGT CCCCAGGACG GAGCACGAGC CTGAGCGGGA GAGCGCCGCT 120  
 CGCACGCCCG TCGCCACCCG CGTACCCGGC GCAGCCAGAG CCACCAGCGC AGCGCTGCCA 180  
 TGGAGCCCGC CAGCAAGAAG CTGACGGGTC GCCTCATGCT GGCTGTGGGA GGAGCAGTGC 240  
 TTGGCTCCCT GCAGTTTGGC TACAACACTG GAGTCATCAA TGCCCCCAG AAGGTGATCG 300  
 AGGAGTTCTA CAACCAGACA TGGGTCCACC GCTATGGGGA GAGCATCTG CCCACCACGC 360  
 TCACCACGCT CTGCTCCCTC TCAGTGGCCA TCTTTTCTGT TGGGGGCATG ATTGGCTCCT 420  
 TCTCTGTGGG CCTTTCTGTT AACCGCTTGT GCCGGCGGAA TCAATGCTG ATGATGAACC 480  
 TGCTGGCCTT CGTGTCGCCG GTGCTCATGG GCTTCTCGAA ACTGGGCAAG TCCTTTGAGA 540  
 TGCTGATCCT GGGCGGCTTC ATCATCGGTG TGTACTGCGG CCTGACCACA GGCTTCGTGC 600  
 CCATGTATGT GGGTGAAGTG TCACCACAG CTTTTCGTGG GGCCCTGGGC ACCCTGCACC 660  
 AGCTGGGCAT CGTCTGCGG ATCCTCATCG CCCAGGTGTT CGGCCCTGGAC TCCATCATGG 720  
 GCAACAAGGA CCTGTGGCCC CTGCTGCTGA GCATCATCTT CATCCCGGCC CTGTGTCAGT 780  
 GCATCGTGCT GCCCTTCTGC CCCGAGAGTC CCCGCTTCCT GCTCATCAAC GCCAACGAGG 840  
 AGAACCGGGC CAAGAGTGTG TAAAGAAGC TGCGCGGGAC AGCTGACGTG ACCCATGACC 900  
 TGCAGGAGAT GAAGAGAAGT AGTCGGCAGA TGATGCGGGA GAAGAAGTTC ACCATCTGG 960  
 AGCTGTTCCG CTCGCCCGCC TACCGCCAGC CCATCCTCAT CGCTGTGGTG CTGCAGCTGT 1020  
 CCCAGCAGCT GTCTGGCATC AACCGTGTCT TCTATTACTC CACGAGCATC TTCGAGAAGG 1080  
 CGGGGGTGCA GCAGCTCTGT TATGCCACCA TTGGCTCCGG TATCGTCAAC ACGGCTTTCA 1140  
 CTGTCTGTGTC GCTGTTTGTG GTGGAGCGAG CAGGCCGGCG GACCTTGAC CTCATAGGCC 1200  
 TCGCTGGCAT GGGCGGTTGT GCCATACTCA TGACCATCGC GCTAGCACTG CTGGAGCAGC 1260  
 TACCCTGGAT GTCCATCTGT AGCATCGTGG CCATCTTTGG CTTTGTGGCC TTCTTTGAAG 1320  
 TGGGTCTCTG CCCCATCCCA TGGTTTCATG TGGCTGAAC CTTAGCCAG GGTCCACGTC 1380  
 CAGCTGCCAT TGCCGTGTGA GGCTTCTCCA ACTGGACCTT AAATTTTCATT GTGGGCATGT 1440  
 GCTTCCAGTA TGTGGAGCAA CTGTGTGGTC CCTACGTCTT CATCATCTTC ACTGTGCTCC 1500  
 TGGTTCTGTT CTTCATCTTC ACCTACTTCA AAGTTCTCTG GACTAAAGGC CGGACCTTCG 1560  
 ATGAGATCCG TTCCGGCTTC CGGCAGGGGG GAGCCAGCCA AAGTGATAAG ACACCCGAGG 1620  
 AGCTGTTCCA TCCCTTGGGG GCTGATTCCC AAGTGTGAGT CGCCCCAGAT CACCAGCCCG 1680  
 GCCTGCTCCC AGCAGCCCTA AGGATCTCTC AGGAGCACAG GCAGCTGGAT GAGACTTCCA 1740  
 AACCTGACAG ATGTGAGCCG AGCCGGGCCCT GGGGCTCCCT TCTCCAGCCA GCAATGATGT 1800  
 CCAGAGAAT ATTCAGGACT TAACGGCTCC AGGATTTTAA CAAAAGCAAG ACTGTTGCTC 1860  
 AAATCTATTG AGACAGCAA CAGGTTTTAT AATTTTTTTA TTAAGTATTG TGTATTATTT 1920  
 ATATCAGCCT GAGTCTCTCG TGCCACATC CCAGGCTTCA CCCTGAATGG TTCCATGCCT 1980  
 GAGGGTGGAG ACTAAGCCCT GTGAGACAC TTGCTTCTTT CACCCAGCTA ATCTGTAGGG 2040  
 CTGGACCTAT GTCCTAAGGA CACACTAATC GAACATGAA CTACAAGCT TCTATCCAG 2100  
 GAGGTGGCTG TGGCCACCCG TTCTGCTGGC CTGGATCTCC CCACTCTAGG GGTGAGGCTC 2160  
 CATTAGGATT TGCCCTTCCC CATCTCTTCC TACCCAAACA CTCAAATTAA TCTTTCTTTA 2220  
 CCTGAGACCA GTTGGGAGCA CTGGAGTGCA GGGAGGAGAG GGGAGGGGCC AGTCTGGGCT 2280  
 GCGGGTTCT AGTCTCTTTC GCACTGAGGG CCACACTATT ACCATGAGAA GAGGGCCTGT 2340  
 GGGAGCCTGC AAATCACTG CTCAAGAAGA CATGGAGACT CTGCCCCTGT TGTGTATAGA 2400  
 TGCAAGATAT TTATATATAT TTTTGGTTGT CAATATTAAA TACAGACACT AAGTTATAGT 2460  
 ATATCTGGAC AAGCCAACCT GTAAATACAC CACCTCACTC CTGTTACTTA CCTAAACAGA 2520  
 TATAAATGGC TGGTTTTTAG AAACATGGTT TTGAAATGCT TGTGGATTGA GGGTAGGAGG 2580  
 TTTGGATGGG AGTGAGACAG AAGTAAGTGG GGTGCAACC ACTGCAACCG CTAGACTTTC 2640  
 GACTCAGGAT CCACTCCCTT ACACGTACCT CTATCATGTG TCTCTTGCT CAAAATCTG 2700  
 TTTGATCCCT GTTACCCAGA GAATATATAC ATTCTTTATC TTGACATTCA AGGCATTTCT 2760  
 ATCACAATAT TGATAGTTGG TGTTCAAAAA AACACTAGTT TGTGCCAGC CGTGATGCTC 2820  
 AGGCTTGAAA TCGCATTATT TTGAATGTGA AGGGAA 2886

Seq ID NO: C86 DNA Sequence  
 Nucleic Acid Accession #: XM\_035292.2  
 Coding sequence: 53..1576

1 11 21 31 41 51  
 GCTCGCTGGG CGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60  
 TCGCGGCCCG AAGCGGCGCG CGCTAGCGGC GCCGCGGCC GAGGAGAAGG AAGAGGCGCG 120  
 GGAGAAGATG CTGGCCGCGA AGAGCGCGGA CGGCTCGGCG CCGCAGGCG AGGGCGAGGG 180  
 CGTGACCCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT 240  
 TATCGGCTCG GGCATCTTCG TGACGCCAC GGGCGTGCTC AAGGAGGCG GCTCGCCGGG 300  
 GCTGGCGCTG GTGGTGTGGG CCGCGTGGCG CGTCTTCTCC ATCGTGGGCG CGCTCTGCTA 360  
 CGCGGAGCTC GGCACCAACA TCTCCAAATC GGGCGGCGAC TACGCCTACA TGCTGGAGGT 420  
 CTACGGCTCG CTGCCGCCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCGGCCCTTC 480  
 ATCGCAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAAGCCG TCTTCCCCAC 540  
 CTGCCCCTG CCGAGAGAG CAGCCAAGCT CGTGGCCTGC CTCTGCTGTC TGCTGCTCAC 600  
 GGCCTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCCCGCGC 660  
 CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720  
 TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGACCA AAATGATG TGGGGAACAT 780  
 TGTGTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGGAAATTACT TGAATTTCTG 840  
 CACAGAGGAA ATGATCAACC CCTACAGAAA CTTGCCCTG GCCATCATCA TCTCCCTGCC 900  
 CATCGTGACG CTGGTGTACG TGCTGACCAA CCTGGCCTAC TTCACCACCC TGTCACCCGA 960  
 GCAGATGCTG TCGTCCGAGG CCGTGGCCGT GGACTTCGGG AACTATCACC TGGGCGTCA 1020  
 GTCCTGGATC ATCCCCGTCT TCGTGGGCGT GTCCTGCTTC GGCTCCGTC ATGGGTCCCT 1080  
 GTTCAATCC TCCAGGCTCT TCTTCGTGGG GTCCCGGGA GGCACCTGC CCTCCATCT 1140  
 CTCCATGATC CACCCACAGC TCCTCACCCC CGTGCCGCTC CTCGTGTTCA CGTGTGTGAT 1200  
 GACGCTGCTC TACGCTTCTT CCAAGGACAT CTCTCCGCTC ATCAACTTCT TCAGCTTCT 1260  
 CAACCTGGCTC TAGCTGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAGGCC 1320  
 TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCCTGCCT GTGTTCTTCA TCCTGGCCTG 1380  
 CCTCTTCTG ATGCCGCTCT CCTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTAC 1440  
 CATCATCCTC AGCGGGCTGC CCGTCTACTT CTTGGGGGTC TGGTGGAAAA ACAAGCCCAA 1500  
 GTGGCTCCTC CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAAGTGGT 1560  
 CCCCAGGAG ACATAGCCAG GAGGCCAGT GGTGCGCGGA GGAGCATGC 1609

Seq ID NO: C87 DNA Sequence  
 Nucleic Acid Accession #: NM\_005268.1



Coding sequence: 168..989

	1	11	21	31	41	51	
5	TAAAAAGCAA	AAGAATTCGC	GGCCGCGTCG	ACACGGGCTT	CCCCGAAAAC	CTTCCCCGCT	60
	TCTGGATATG	AAATTCAAGC	TGCTTGCTGA	GTCTTATTGC	CGGCTGCTGG	GAGCCAGGAG	120
	AGCCCTGAGG	AGTAGTCACT	CAGTAGCAGC	TGACGCGTGG	GTCCACCATG	AACTGGAGTA	180
	TCTTTGAGGG	ACTCCTGAGT	GGGGTCAACA	AGTACTCCAC	AGCCTTTGGG	CGCATCTGGC	240
10	TGTCTCTGGT	CTTCATCTTC	CGCGTGCTGG	TGTACTTGGT	GACGGCCGAG	CGTGTGTGGA	300
	GTGATGACCA	CAAGGACTTC	GACTGCAATA	CTCGCCAGCC	CGGCTGCTCC	AACGTCTGCT	360
	TTGATGAGTT	CTTCCCTGTG	TCCCATGTGC	GCCTCTGGGC	CCTGCAGCTT	ATCCTGGTGA	420
	CATGCCCTTC	ACTGCTCGTG	GTCAATGCAG	TGGCCTACCG	GGAGGTTTCA	GAGAAGAGGC	480
	ACCGAGAAGC	CCATGGGGAG	AACAGTGGGC	GCCTCTACCT	GAACCCCGGC	AAGAAGCGGG	540
	GTGGGGCTCTG	GTGGACATAT	GTCTGCAGCC	TAGTGTTCAA	GGCGAGCGTG	GACATCGCCT	600
15	TTCTCTATGT	GTTCCTACTCA	TTCTACCCCA	AATATATCCT	CCCTCCTGTG	GTCAAGTGCC	660
	ACGCAGATCC	ATGTCCCAAT	ATAGTGGACT	GCTTCATCTC	CAAGCCCTCA	GAGAAGAAAC	720
	TTTTTACCCT	CTTCATGGTG	GCCACAGCTG	CCATCTGCAT	CCTGCTCAAC	CTCGTGGAGC	780
	TCATCTACCT	GGTGAGCAAG	AGATGCCACG	AGTGCCTGGC	AGCAAGGAAA	GCTCAAGCCA	840
20	TGTGCACAGG	TCATCACCCC	CACGCTACCA	CCTCTTCCTG	CAAACAAGAC	GACCTCCTTT	900
	CGGGTGACCT	CATCTTTCTG	GGCTCAGACA	GTCACTCTCC	TCTCTTACCA	GACCGCCCCC	960
	GAGACCATGT	GAAGAAAACC	ATCTTGTGAG	GGGCTGCCTG	GACTGTGCTG	GCAGGTTGGG	1020
	CCTGGATGGG	GAGGCTCTAG	CATCTCTCAT	AGGTGCAACC	TGAGAGTGGG	GGAGCTAAGC	1080
	CATGAGGTAG	GGCAGGCAAG	GAGAGAGGAT	TCAGACGCTC	TGGGAGCCAG	TTCTTAGTCC	1140
25	TCAACTCCAG	CCACCTGCCC	CAGCTCGACG	GCACTGGGCC	AGTTCCCCCT	CTGCTCTGCA	1200
	GCTCGGTTTC	CTTTTCTAGA	ATGGAAATAG	TGAGGGCCAA	TGC		1243

Seq ID NO: C88 DNA Sequence  
Nucleic Acid Accession #: NM\_005130  
Coding sequence: 98..802

	1	11	21	31	41	51	
30	CTCTACCTGA	CACAGCTGCA	GCCTGCAATT	CACTCCCCT	GCCTGGGATT	GCACTGGATC	60
	CGTGTGCTCA	GRACAAGGTG	AACGCCCAGC	TGCAGCCATG	AAGATCTGTA	GCCTCACCT	120
35	GCTCTCCTTC	CTCCTACTGG	CTGCTCAGGT	GCTCCTGGTG	GAGGGGAAAA	AAAAAGTGAA	180
	GAATGGACTT	CACAGCAAAG	TGGTCTCAGA	ACAAAAGGAC	ACTCTGGGCA	ACACCCAGAT	240
	TAAGCAGAAA	AGCAGGCCCG	GGAAACAAAG	CAAGTTTGTG	ACCAAAGACC	AAGCCAACTG	300
	CAGATGGGCT	GCTACTGAGC	AGGAGGAGGG	CATCTCTCTC	AAGGTTGAGT	GCACTCAATT	360
40	GGACCATGAA	TTTTCCTGTG	TCTTGTCTGG	CAATCCAACC	TCATGCCTAA	AGCTCAAGGA	420
	TGAGAGAGTC	TATTGGA AAC	AAGTTGCCCG	GAATCTGCGC	TCACAGAAAG	ACATCTGTAG	480
	ATATTTCAAG	ACAGCTGTGA	AAACCAGAGT	GTGCAGAAAG	GATTTTCCAG	AATCCAGTCT	540
	TAAGCTAGTC	AGCTCCACTC	TATTTGGGAA	CACAAAGCCC	AGGAAGGAGA	AAACAGAGAT	600
	GTCCCCCAGG	GAGCAGATCA	AGGGCAAAGA	GACCACCCCC	TCTAGCCTAG	CAGTGACCCA	660
45	GACCATGGCC	ACCAGAGCTC	CCGAGTGTGT	GGAGGACCCA	GATATGGCAA	ACCAGAGGAA	720
	GACTGCCCTG	GAGTTCGTGT	GAGAGACTTG	GAGCTCTCTC	TGCACATTCT	TCTTCAGCAT	780
	AGTGACAGAC	ACGTCTAGTC	AATGAGGTCA	AAAGAGAACG	GGTTCCTTTA	AGAGATGTCA	840
	TGTCTAAGT	CCCTCTGTAT	ACTTTAAAGC	TCTCTACAGT	CCCCCAAAA	TATGAACCTT	900
	TGTGCTTAGT	GAGTGCAACG	AAATATTATA	ACAAGTTTGT	TATTTTGTGC	TTTGTGTTT	960
50	TGGAATTTGC	CTTATTTTTC	TTGGATGCGA	TGTTTCAAGG	CTGTTTCTCG	CAGCATGTAT	1020
	TTCCATGGCC	CACACAGCTA	TGTGTTTGTG	CAGCGAAGAG	TCTTTGAGCT	GAATGAGCCA	1080
	GAGTGATAAT	TTCAAGTGCA	CGAACTTTCT	GCTGAATTAA	TGGTAATAAA	ACTCTGGGTG	1140
	TTTTTCAAAA	AAAAAATAAA	AAA				1163

Seq ID NO: C89 DNA Sequence  
Nucleic Acid Accession #: BC022542  
Coding sequence: 274..927

	1	11	21	31	41	51	
60	ACTTGGTCCC	AGCCGATAAA	TCTGGGGCAG	CGCGCGGTAG	GAGCTGCGGG	CGGCCAGGCC	60
	CCTTCCTGCG	TCCGCACCTG	GCCCCGCGCG	CCCCTCTCGG	GCGTCCGCGT	TCCGGCGTCC	120
	TGGCGGGCTG	GGTGGCGGCG	GTTGCGGGCG	CCGCTCTGGT	GCTCCTCGGG	GCGGCGACGG	180
	GGCTCACGCG	CGGGCCCGCC	ACGGCCTTCA	CCGCCGCGCG	CTCTGACGCC	GGCATAAGGG	240
65	CCATGTGTTT	TGAATATTAT	TTGAGGCAAG	AAGTTTGTAA	AGATGGTTTC	CACAGAGACC	300
	TTTTAATCAA	AGTGAAGTTT	GGGGAAGCA	TTGAGGACTT	GCACACGTGC	CGTCTCTTAA	360
	TTAAACAGGA	CATTCCTGCA	GGACTTTATG	TGGATCCGTA	TGAGTTGGCT	TCATTACGAG	420
	AGAGAAACAT	AACAGAGGCA	GTGATGGTTT	CAGAAAATTT	TGATATAGAG	GCCCCAACT	480
	ATTTGTCCAA	GGAGCTTGAA	GTTTCTATTT	ATGCCAGACG	AGATTACAG	TGCATTGACT	540
70	GTTTTCAAGC	CTTTTTCGCT	GTGCACTGCC	GCTATCATCG	CCGCACAGT	GAAGATGGAG	600
	AAGCCTCGAT	TGTGGTCAAT	AACCCAGATT	TGTTGATGTT	TTGTGACCAA	GAGTTCCTCGA	660
	TTTTGAAGAT	CTGGGCTCAC	TCAGAAAGTG	CAGCCCCCTG	TGCTTTGGAT	AATGAGGATA	720
	TATGCCAATG	GAACAAGATG	AAGTATAAAT	CAGTATATAA	GAATGTGATT	CTACAAGTTC	780
	CAGTGGGACT	CAGTGTACAT	ACCTCTCTAG	TATGTTCTGT	GACTCTGCTC	ATTACAATCC	840
75	TGTGCTCTAC	ATTGATCCTT	GTAGCAGTTT	TCAAATATGG	CCATTTTTC	CTATAAGTTT	900
	TATGTAGTTA	AATGCTTCTT	AGAAACCTAA	ATAAGATCTA	TTAATTTCTG	ACGAGAGGTG	960
	TTCTCTAGTA	ATTAATTACT	TTTATCTTTT	GTCTTCATTT	GTGGCCAAAA	TTATGTTTAC	1020
	TAGAGGAAAT	TTGGGATCAT	TCTCAGCTAA	TTCCAAAATG	TAGTGCTCTA	TTGCATGGAT	1080
	CCTTGGTAAT	CCTCAAGCAT	CAGATGCCAT	AAGGGGAAAC	TTAATTTCTG	TAAATTAATG	1140
80	TTTATTTTGT	GAGAAGTGAC	TTTATCTTCA	TTTGGGGTAG	AAAAATTATT	TCTTTATGTA	1200
	GTAGAGACAA	ATTATTTCTA	TTTTGCAAGT	ACTTTCAATT	TAGACTACAA	ATTGAGAAAA	1260
	CCGTTATAAA	TAAGAAATAA	ATAGGCCAGG	CACAGTGGCT	CACACCTGTA	ATCCCAGCAC	1320
	TTTGGGAGGC	CGAGGTGGGC	GGATCACCAG	AGGTCAAGAG	TTTGAGACCA	GCTTGGTGAA	1380
	ACCTGTCTCT	TACTAAAAAT	ACAAAAGTTA	GCTGGGGCTG	GTGGTGGGCA	TCTGTAGTCC	1440
	CAGCTAATTG	GAAGGGTGAG	GCGGGAGGAT	CGCTTGAAAC	TGGGAGGCGG	AGGTTCCAGA	1500

GAGCCAAGAT CGCACCCTG CACTACAGCC TGGGCGACAG AACGAGACCC TGTCTCCAAA 1560  
 GGAAAAACAA AAAAGAAGAA TAAAAAATT TGGATGAAAA TCATGTTTAT TTAAATAGTA 1620  
 ATGTCAATGAG ACTATTAAAG ATGTGCCAGA GTTTCATGA AAATCATTAA AGTAGGACAG 1680  
 CTAAGAAAT AATATTAAAT TAAAAATTAT TGATAATCTT AAATATTATGA TTATTCCCTTA 1740  
 ACGCACTCCA TTCTCCTTTT ACATTTTATC ATGTTTCTTT TGAATATATG AATTGGCAAA 1800  
 GGACTTGATG AAAGTGAAT CTAAGATTG GTACAGAGTA TGTGAGGAAG ACAACTCAGA 1860  
 TTGCCATTTT AAATAAAGTT GTACATGAAC AAAAAAAAAA AAAAAA 1906

Seq ID NO: C90 DNA Sequence  
 Nucleic Acid Accession #: NM\_004994  
 Coding sequence: 20..2143

1 11 21 31 41 51  
 AGACACCTCT GCCCTCACCA TGAGCCTCTG GCAGCCCTG GTCCTGGTGC TCCTGGTGTCT 60  
 GGGCTGCTGC TTTGCTGCC CAGACAGCG CCAGTCCACC CTGTGCTCT TCCTGGAGA 120  
 CCTGAGAAC AATCTCACC ACAGGCAGCT GGCAGAGGAA TACCTGTACC GCTATGGTTA 180  
 CACTCGGTG GCAGAGATG GTGGAGATC GAAATCTCTG GGGCCTGCGT TGCTGCTTCT 240  
 CCAGAAGCAA CTGTCCCTGC CCGAGACCGG TGAGCTGGAT AGCGCCACGC TGAAGGCCAT 300  
 GCGAACCCCA CGGTGCGGGG TCCAGACCT GGGCAGATTC CAAACCTTTG AGGCGGACCT 360  
 CAAGTGGCAC CACCACAACA TCACCTATTG GATCCAAAAC TACTCGAAG ACTTGCCGCG 420  
 GGCCTGTGAT GACGACGCTT TTGCCGCGC CTTCGCACTG TGGAGCGCGG TGACGCGGCT 480  
 CACCTTCACT CGCGTGTACA GCCGGGACGC AGACATCGTC ATCCAGTTTG GTGTGCGCGA 540  
 GCACGGAGAC GGGTATCCCT TCGACGGGAA GGACGGGCTC CTGGCACACG CCTTCTCTCC 600  
 TGGCCCGCGG ATTCAGGGAG ACGCCCATTT CGACGATGAC GAGTTGTGGT CCCTGGGCAA 660  
 GGGCGTCTGT GTTCCAACTC GGTCTGGAAC CGCAGATGGC GCGGCTGACC ACTTCCCTCT 720  
 CATCTTCGAG GGCCTCTCTT ACTCTGCTTG CACCACCGAC GGTCTGCTCG ACGGCTTGCC 780  
 CTGGTGCAGT ACCACGGCCA ACTACGACAC CGACGACCGG TTTGGCTTCT GCCCAGCGA 840  
 GAGACTCTAC ACCCGGGACG GCAATGCTGA TGGGAAACCC TGCCAGTTTC CATTCATCTT 900  
 CCAAGGCCAA TCTTACTCCG CCTGCACCAC GGACGGTCTG TCCGACGGCT ACCGCTGGTG 960  
 CGCCACCACC GCAACTACG ACCGGGACAA GCTCTTCGGC TTCTGCCGA CCGAGCTGA 1020  
 CTCGACGGTG ATGGGGGGCA ACTCGGCGGG GGAGCTGTGC GTCTTCCCTT TCACTTCTCT 1080  
 GGGTAAGGAG TACTCGACCT GTACGACGCA GGGCCGCGGA GATGGGCGCC TCTGGTGGCG 1140  
 TACCACCTCG AACTTTGACA GCGACAAGAA GTGGGGCTTC TGCCCGGACC AAGGATACAG 1200  
 TTTGTTCTCT GTGGCGGCGC ATGAGTTCTG CCACGCGCTG GGTCTAGATC ATTCTCTAGT 1260  
 GCCGGAGGCG CTCATGTACC CTATGTACCG CTTCACTGAG GGGCCCCCTT TGCATAAGGA 1320  
 CGACGTGAAT GGCATCCGGC ACCTCTATGG TCCTCGCCCT GAACCTGAGC CACGGCTCTC 1380  
 AACCACCAAC ACACCGCAGC CCACGGCTCC CCGCAGCGTC TGCCCCACCG GACCCCCCAC 1440  
 TGTCCACCCC TCAGAGCGCC CCACAGCTGG CCCCACAGGT CCCCCCTCAG CTGGCCCCAC 1500  
 AGGTCCCCCC ACTGCTGGCC CTTCTACGGC CACTACTGTG CCTTTGAGTC CGGTGGACGA 1560  
 TGCCCTGCAAC GTGAACATCT TCGACGCCAT CGCGGAGATT GGGAACACAG TGTATTGTGT 1620  
 CAAGGATGGG AAGTACTGGC GATTCTCTGA GGGCAGGGGG AGCCGGCGCG AGGGCCCTTT 1680  
 CCTTATCGCC GACAGTGGG CCGCGCTGCC CCGCAAGCTG GACTCGGTCT TTGAGGAGCC 1740  
 GCTCTCCAAG AAGCTTTTCT TCTTCTCTGG GCGCCAGGTG TGGGTGTACA CAGGCGCGTC 1800  
 GGTGCTGGGG CCGAGGGGCT TGGACAAGCT GGGCCTGGGA GCGACGCTGG CCGAGGTGAC 1860  
 CGGGGCCCTC CCGAGTGGCA GGGGGAAGAT GCTGCTGTTC AGCGGGCGGC GCCTCTGGAG 1920  
 GTTTCGAGTG AGCGCGCAGA TGGTGGATCC CCGGAGCGCC AGCGAGGTGG ACCGGATGTT 1980  
 CCCCAGGGTG CCTTTGGACA CGCAGCAGCT CTTCCAGTAC CGAGAGAAAG CCTATTCTCT 2040  
 CCAGGACCGC TTCTACTGGC GCGTGAGTTC CCGGAGTGAG TTGAACACAG TGGACCAAGT 2100  
 GGGCTACGCT ACCATGACA TCCTGCACTG CCCTGAGGAC TAGGGCTCCC GTCTGCTTTT 2160  
 GCAGTGCCAT GTAATATCCC ACTGGGACCA ACCCTGGGGA AGGAGCCAGT TTGCCGGATA 2220  
 CAAACTGGTA TTCGTGTTCT GAGGAAAGGG AGGAGTGGAG GTGGGCTGGG CCCTCTCTTC 2280  
 TCACCTTTGT TTTTGTGTTG AGTGTTTCTA ATAAACTTGG ATTCTCTAAC CTTT 2334

Seq ID NO: C91 Sequence  
 Nucleic Acid Accession #: NM\_000213  
 Coding sequence: 188..5656

1 11 21 31 41 51  
 GCGCTGCCCG CCTCGTCCCC ACCCCCCAAC CCCCCGCGCC GCCTCTCGGA CAGTCCCTGC 60  
 TCGCCCGCGC GCTGCAGCCC CATCTCCTAG CGGCAGCCCA GCGCGGAGG GAGCGAGTCC 120  
 GCCCCGAGGT AGGTCCAGGA CGGGCGCACA GCAGCAGCCG AGGCTGGCCG GGAGAGGGAG 180  
 GAAGAGGATG GCAGGGCCAC GCCCCAGCCC ATGGGCCAGG CTGCTCTTGG CAGCCTTGAT 240  
 CAGCGTCAGC CTCTCTGGGA CCTTGGCAAA CCGCTGCAAG AAGGCCCCAG TGAAGAGCTG 300  
 CACGGAGTGT GTCCGTGTGG ATAAGGACTG CGCCTACTGC ACAGACGAGA TGTTCAGGGA 360  
 CCGGCGCTGC AACACCCAGG CGGAGCTGCT GGCCTGCGGC TGCCAGCGGG AGAGCATCGT 420  
 GGTCTATGAG AGCAGCTTCC AAATCACAGA GGAGACCCAG ATTGACACCA CCCTGCGGCG 480  
 CAGCCAGATG TCCCCCAAG GCCTGCGGGT CCGTCTGCGG CCGGTGAGG AGCGGCATTT 540  
 TGAGCTGGAG GTGTTTGAGC CACTGGAGAG CCCCCTGGAC CTGTACATCC TCATGGACTT 600  
 CTCCAACTCC ATGTCCGATG ATCTGGACAA CCTCAAGAAG ATGGGGCAGA ACCTGGCTCG 660  
 GGTCTGAGC CAGCTCACCA GCGACTACAC TATTGGATTT GGCAGTTTGG TGGACAAAGT 720  
 CAGCGTCCCC CAGACGGACA TGAGGCCTGA GAAGCTGAAG GAGCCCTGGC CCAACAGTGA 780  
 CCCCCCTTC TCCTTCAAGA ACGTCATCAG CCGTACAGAA GATGTGGATG AGTTCCGGAA 840  
 TAAACTGAGG GGAGAGCGGA TCTCAGGCAA CCTGGATGCT CTGAGGGGCG GCTTCGATGC 900  
 CATCTCGAG ACAGCTGTGT GCACAGGGGA CATTGGCTGG CGCCCGGACA GCACCCACCT 960  
 GCTGCTCTTC TCCACCGAGT CAGCCTTCCA CTATGAGGCT GATGGCGCCA ACGTGTGCTG 1020  
 TGGCATCATG AGCCGCAACG ATGAACGGTG CCACCTGGAC ACCAGGGGCA CCTACACCCA 1080  
 GTACAGGACA CAGGACTACC CGTCGGTGCC CACCTGGGTG GCGCTGCTCG CCAAGCAAA 1140  
 CATCATCCCC ATCTTTGCTG TCACCAACTA CTCCTATAGC TACTACGAGA AGCTTCACAC 1200  
 CTATTTCCTT GTCTCTCTAC TGGGGGTGCT GCAGGAGGAC TCGTCCAAAC TCGTGGAGCT 1260  
 GCTGGAGGAG GCCTTCAATC GGATCCGCTC CAACCTGGAC ATCCGGGCCC TAGACAGCCC 1320  
 CCGAGGCCTT CGGACAGAGG TCACCTCCAA GATGTTCCAG AAGACGAGGA CTGGGTCTCT 1380  
 TCACATCCGG CGGGGGGAAG TGGGTATATA CCAGGTGCAG CTGCGGGCCC TTGAGCACGT 1440

GGATGGGACG CACGTGTGCC AGCTGCCGGA GGACCAGAAG GGCAACATCC ATCTGAAACC 1500  
TTCCTTCTCC GACGGCCTCA AGATGGACGC GGGCATCATC TGTGATGTGT GCACCTGCGA 1560  
GCTGCAAAAA GAGGTGCGGT CAGCTCGCTG CAGCTTCAAC GGAGACTTCG TGTGCGGACA 1620  
GTGTGTGTGC AGCGAGGGCT GAGGTGGCCA GACCTGCAAC TGCTCCACCG GCTCTCTGAG 1680  
TGACATTGAG CCCTGCTGCT GGGAGGGCGA GGACAAGCCG TGCTCCGGCC GTGGGGAGTG 1740  
CCAGTGCGGG CACTGTGTGT GCTACGGCGA AGGCCGCTAC GAGGGTCAGT TCTGCGAGTA 1800  
TGACAACTTC CAGTGTCCCC GCACCTCCGG GTTCTGTGTC AATGACCGAG GACGCTGCTC 1860  
CATGGGCCAG TGTGTGTGTG AGCCTGGTTG GACAGGCCCA AGCTGTGACT GTCCCCCTAG 1920  
CAATGCCACC TGCATCGACA GCAATGGGGG CATCTGTAAT GGACGTGGCC ACTGTGAGTG 1980  
TGGCCGCTGC CACTGCCACC AGCAGTCGCT CTACACGGAC ACCATCTGCG AGATCAACTA 2040  
CTCGGCGATC CACCCGGGCC TCTGCGAGGA CCTACGCTCC TCGGTGCACT GCCAGGCGTG 2100  
GGGCACCGGC GAGAAGAAGG GGCACACGTG TGAGGAATGC AACTTCAAGG TCAAGATGGT 2160  
GGACGAGCTT AAGAGAGCCG AGGAGGTGGT GGTGCGCTGC TCCTTCCGGG ACGAGGATGA 2220  
CGACTGCACC TACAGCTACA CCATGGAAGG TGACGGCGCC CCTGGGCCCA ACAGCACTGT 2280  
CCTGGTGACAC AAGAAGAAGG ACTGCCCTCC GGGCTCCTTC TGGTGGCTCA TCCCCCTGCT 2340  
CCTCCTCCTC CTGCGGCTCC TGGCCCTGCT ACTGCTGCTA TGCTGGAAGT ACTGTGCCTG 2400  
CTGCAAGGCC TGCTTGGCAG TTCTCCCGTG CTGCAACCGA GGTCACTAGG TGGGCTTTAA 2460  
GGAAGACCAC TACATGCTGC GGGAGAACCT GATGGCCTCT GACCACTTGG ACACGCCCAT 2520  
GCTGCGCAGC GGGAACTTCA AGGGCCGTGA CGTGGTCCGC TGAAGGTCA CCAACAACAT 2580  
CGACGGCGCT GGCCTTGCCA CTCATGCCGC CAGCATCAAC CCCACAGAGC TGGTGCCCTA 2640  
CGGGCTGTCC TTGCGCCTGG CCCGCTTTTG CACCGAGAAC CTGCTGAAGC GTGACACTCG 2700  
GGAGTGCGCC CAGTGCGCC AGGAGGTGGA GGAGAACCTG AACGAGGTCT ACAGGCAGAT 2760  
CTCGGTGTA CTCAGGTTC AGCAGACCAA GTTCCGGCAG CAGCCCAATG CCGGGA AAAA 2820  
GCAAGACCAC ACCATTGTGG ACACAGTGCT GATGGCGCCC CGCTCGGCCA AGCCGGCCCT 2880  
GCTGAAGCTT ACAGAGAAGC AGGTGGAACA GAGGGCCTTC CACGACCTCA AGGTGGCCCC 2940  
CGGCTACTAC ACCTGACTG CAGACCAGGA CGCCCGGGGC ATGGTGGAGT TCCAGGAGGG 3000  
CGTGAGAGTG GTGACGTAC GGGTGCCCTT CTTTATCCGG CCTGAGGATG ACAGCAGAGAA 3060  
CGAGCTGCTG GTGAGGCCA TCGACGTGCC CGCAGGCACT GCCACCTTCG GCCGCGCCCT 3120  
GGTAAACATC ACCATCATCA AGGAGCAAGC CAGAGACGTG GTGTCTTTG AGCAGCCTGA 3180  
GTTCTCGGTC AGCCGCGGGG ACCAGGTGGC CCGCATCCCT GTCTCCGGC GTGTCTTGA 3240  
CGCGGGGAAG TCCAGGTCT CTTACCGCAC ACAGGATGGC ACCGCGCAGG CCAACCGGGA 3300  
CTACATCCCC GTGAGGGTG AGCTGCTGTT CCAGCCTGGG GAGGCCTGGA AAGAGCTGCA 3360  
GGTGAAGCTC CTGAGCTGTC AAGAAGTTGA CTCCTCCTG CGGGGCCGCC AGGTCCGCCG 3420  
TTTCCACGTC CAGCTCAGCA ACCCTAAGTT TGGGGCCAC CTGGGCCAGC CCCACTCCAC 3480  
CACCATCATC ATCAGGGACC CAGATGAACT GGACCGGAGC TTCACGAGTC AGATGTTGTC 3540  
ATCACAGCCA CCCCCTCAG GCGACCTGGG CGCCCCGAG AACCCCAATG CTAAGGCCGC 3600  
TGGGTCCAGG AAGATCCATT TCAACTGGCT GCCCCTTCT GGCAAGCCAA TGGGGTACAG 3660  
GGTAAAGTAC TGGATTACAG GCGACTCCGA ATCCGAAGCC CACCTGTGCG ACAGCAAGGT 3720  
GCCCTCAGTG GAGCTCACCA ACCTGTACCC GTATTGCGAT TATGAGATGA AGGTGTGCGC 3780  
CTACGGGGCT CAGGGCGAGG GACCTACAG CTCCTGCTG TCTTCCGCCA CCCACCAGGA 3840  
AGTGCCACG GAGCCAGGGC GTCTGGCCTT CAATGTCTGC TCCTCCACGG TGACCCAGCT 3900  
GAGCTGGGCT GAGCCGGCTG AGACCAACGG TGAGATCACA GCCTACGAGG TCTGCTATGG 3960  
CCTGTGTAAC GATGACAACC GACCTATTGG GCCCATGAAG AAAGTGCTGG TTGACAACCC 4020  
TAAGAACCGG ATGCTGCTTA TTGAGAACCT TCGGGAGTCC CAGCCCTACC GCTACACGGT 4080  
GAAGGCGCGC AACGGGGCCG GCTGGGGGCC TGAGCGGGAG GCCATCATCA ACCTGGCCAC 4140  
CCAGCCCAAG AGGCCCATGT CCATCCCCAT CATCCCTGAC ATCCCTATCG TGGACGCCCA 4200  
GAGCGGGGAG GACTACGACA GCTTCTTAT GTACAGCGAT GACGTTCTAC GCTCTCCATC 4260  
GGGAGCCAG AGGCCCAGCG TCTCCGATGA CACTGGCTGC GGCTGGAAGT TCGAGCCCTT 4320  
GCTGGGGGAG GAGCTGGACC TGCGGCGCGT CACGTGGCGG CTGCCCCCGG AGCTCATCCC 4380  
GGCCTGTGCG CAGCAGCAGG GCGCTCCTC CGACGCCGAG GCCCCACCG CCCCCCGGAC 4440  
GACGGCGGGG CGGGCGGGAA GGGCGGCAGC CGTGCCCCG AGTGCGACAC CCGGGCCCCC 4500  
CGGAGAGCAC CTGGTGAATG GCCGATGGA CTTTGCCTTC CCGGGCAGCA CCAACTCCCT 4560  
GCACAGGATG ACCACGACCA GTGCTGCTGC CTATGGCACC CACCTGAGCC CACACGTGCC 4620  
CCACCGCGTG CTAAGCACAT CCTCCACCT CACACGGGAC TACAACCTAC TGACCCGCTC 4680  
AGAACTACTA CACTGACCA CACTGCCCCG GGAATACTCC ACCCTCACCT CCGTCTCCTC 4740  
CCACGACTCT CGCCTGACTG CTGGTGTGCC CGACACGCC ACCCGCCTGG TGTTCTCTGC 4800  
CCTGGGGCCC ACATCTCTCA GAGTGAGCTG GCAGGAGCCG CGGTGCGAGC GGCCGCTGCA 4860  
GGGCTACAGT TGGAGTACC AGCTGCTGAA CGGCGGTGAG CTGCATCGGC TCAACATCCC 4920  
CAACCTTGCC CAGACCTCGG TGGTGGTGA AGACCTCCTG CCAACCACT CCTACGTGT 4980  
CCGCGTGGG GCGGAGAGCT AGGAAGGCTG GGGCCGAGAG CGTGAGGGTG TCATCAACAT 5040  
TGAATCCAG GTGCACCCGC AGAGCCCACT GTGTCCCTG CCAGGCTCCG CTTTCACTTT 5100  
GAGCACTCCC AGTGCCCCAG GCCCGCTGGT GTTCACTGCC CTGAGCCAG ACTCGCTGCA 5160  
GCTGAGCTGG GAGCGGCCAC GGAGGCCCAA TGGGGATATC GTCGGCTACC TGGTGACCTG 5220  
TGAGATGGCC CAAGGAGGAG GGCCAGCCAC CGCATTCGG GTGGATGGAG ACAGCCCCGA 5280  
GAGCCGGCTG ACCGTGCCGG GCCTCAGCGA GAACGTGCC TACAAGTTCA AGGTGCAGGC 5340  
CAGGACCACT GAGGGCTTCG GGCCAGAGCG CGAGGGCATC ATCACCATAG AGTCCCAGGA 5400  
TGGAGGACCC TTCCCGCAGC TGGGCGAGCG TGCCGGGCTC TTCCAGCAC CGCTGCAAG 5460  
CGAGTACAGC AGCATACCA CCAACACAC CAGCGCCACC GAGCCCTTCC TAGTGGATGG 5520  
GCTGACCTG GGGGCCAGC ACCTGGAGGC AGGCGGCTCC CTCACCCGGC ATGTGACCCA 5580  
GGAGTTTGTG AGCCGGACAC TGACCACAG CGGAACCTTT AGCACCACA TGGACCAACA 5640  
GTTCTTCAA ACTTGACCGC ACCCTGCCCC ACCCCGCCA TGTCCTACTA GCGCTCTCTC 5700  
CGACTCCTCT CCCGGAGCCT CTTGAGCTAC TCCATCCTTG CACCCCTGGG GGCCAGGCC 5760  
ACCCGATGC ACAGAGCAGG GGCTAGGTGT CTCTGGGAG GCATGAAGGG GGAAGGTCC 5820  
GTCCTCTGTG GGCCAAACC TATTTGTAAC CAAAGAGCTG GGAGCAGCAC AAGGACCCAG 5880  
CCTTTGTCT GCATTAATA ATGGTTTGT CTACTGCTAA AAAAAAAAAA AAAAAAAAAA 5940  
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 5994

Seq ID NO: C92 DNA Sequence  
Nucleic Acid Accession #: NM\_023915  
Coding sequence: 250..1326

1 11 21 31 41 51  
GGCACGAGGG TTTGCTTTTC ATGCTTTACC AGAAAAATCCA CTTCCTGCC GACCTTAGTT 60

TCAAAGCTTA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120  
 GTGAATGGAC AGCCAGCCAC CACAATGAAA GAAATCAAAC CAGGAATAAC CTATGCTGAA 180  
 CCCACGCCTC AATCGTCCCC AAGTGTITTC TGACACGCAT CTTTGCTTAC AGTGCATCAC 240  
 AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GCTGCACGGC 300  
 CAAGAGAGTC ACAATTGAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCTTCAC 360  
 AATGAATTGT ACACAATTGT CTTGCCGGTG CTTTATCTCA TTATATTGT GGCAGCATC 420  
 TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAAC CAGCTTCATA 480  
 TTCTATCTCA AAAACATAGT GGTTCAGAC CTCTAATGA CGCTGACATT TCCATTTCGA 540  
 ATAGTCCATG ATGTCAGATT TGGACCTTGG TACTTCAAGT TTATCTCTCTG CAGATACACT 600  
 TCACTTTTGT TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660  
 GATCGCTATC TGAAGGTGGT CAAGCCATTT GGGGACTCTC GGATGTACAG CATAACCTTC 720  
 ACGAAGGTTT TATCTGTTTG TGTTCGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC 780  
 ATCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAA ACTTAAAGT 840  
 CCTTGGGGG TCAATGGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTGTGGCC 900  
 GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960  
 AGGCAATTCA TAAGTCAGTC AAGCCGAAAG CGAAAAACATA ACCAGAGCAT CAGGGTTGTT 1020  
 GTGCTGTGT TTTTACTCT CTTTCTACCA TATCACTGT GCAGAATTCC TTTTACTTTT 1080  
 AGTCACCTAG ACAGGCTTTT AGATGAATCT GCACAAAAA TCCTATATTA CTGCAAAAGA 1140  
 ATTACACTTT TCTGTCTGTC GTGTAATGTT TGCCTGGATC CAATAATTTA CTTTTTCATG 1200  
 TGTAGGTCAT TTTCAAGAAG GCTGTTCAAA AAATCAAATA TCAGAACCAG GAGTGAAAGC 1260  
 ATCAGATCAC TGCAAAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTACACTGAT 1320  
 GTGTAGGCCT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAATAA AATGTTTCTT 1380  
 TTCATTATCC TAAAAAAA AA 1402

Seq ID NO: C93 DNA Sequence  
 Nucleic Acid Accession #: NM\_020789.1  
 Coding sequence: 208..3699

1 11 21 31 41 51  
 | | | | |  
 GGACAGAGGG TGGAGCCGAG CGGTGCGGAG CAGATCTGGT GGTCTCCGG AGAGCAGCTT 60  
 CCTTGGGTGT TACATGAGCC AAGCCCTCAC TGTACAGAAG AGTGAGAGCT GAAACCTGTT 120  
 CCCTGAGCTG ATCAGAAGGA CATCCCTTGG CCCCTCCATC TGGGCTCCTG TGGATAGGAG 180  
 GGGCTGGGTG AGCAGGGCCAG CTGGGCTATG GTGTGGTGCC TCGGCTGGGC CGTCTCAGC 240  
 CTGCTCATCA GCCAGGGGGC TGACGGTCTGA GGGAGGCTG AGGTGGTATC GGTGGTGGGC 300  
 CGGGCTGAGG AGATGTGGT GCTGGGCTGT GACCTGCTGC CCCGCGCCGG CCGGCCCCCT 360  
 CTGCATGTCA TCAGTGGGCT GCGCTTTGGA TTCTGTCTTC CCATCTTCAT CCAGTTCGGC 420  
 CTCTACTCTC CCCGAATTGA CCCTGATTAC GTGGGACGAG TCCGGCTGCA GAAGGGGGCC 480  
 TCTCTCCAGA TTGAGGGTCT CCGGTGGAA GACCAGGGCT GGTACGAGTG CCGGTGTTT 540  
 TTCTGGGACC AGCATATCCC TGAAGACGAT TTTGCTAACG GCTCCTGGGT GCATCTGACA 600  
 GTCAATTAC CCCCTCAATT CCAGGAGACA CCTCTGCTG TGTGGGAAGT GCAGGAACCTG 660  
 GAGCTGTGTA CCTTGCCTTG TGTGGCCCGT GGCAGCCGCC TGCTCATGT GACGTGGGAG 720  
 CTCGAGGAA AGGACCTTGG CCAGGGCCAG GGCCAGGTGC AAGTGCAGAA CGGGACGCTG 780  
 CGGATCCGCG GGGTAGAGCG AGGCAGCTCT GGGGTCTACA CCTGCCAAGC CTCACGACT 840  
 GAGGGCAGCG CCACCCAGCG CACCCAGCTG CTAGTGCTAG GACCCCGAGT CATCGTGGTG 900  
 CCCCCCAAGA ACAGCAGAGT CAATGCCTCC CAGGATGTTT CATTGGCCTG CCACTGCTGAG 960  
 GCATACCTCG CTACCTCAC CTACAGCTGG TTCCAGGACA ACATCAATGT CTTCCACATT 1020  
 AGCCGCTGCG AGCCCGGGT GCAGATCTCG GTGGACGGGA GCCTGCGGCT GCTGGCCACC 1080  
 CAGCTGATG ATGCCGGCTG CTACACCTGT GTGCCAGCA ATGGCCTCCT GCATCCACCC 1140  
 TCAGCTCTG CCTACCTCAC TGTGCTCTGC ATGCCGGGGG TGATCCGCTG CCGGTTCTG 1200  
 GCCAACCCCG CACTGCTCTT TGTGAGCTGG ACCAAGGATG GAAAGGCCCT GCAGCTGGAC 1260  
 AAGTTCCCTG GCTGTCTCCA GGGCACAGAA GGCTCACTGA TCATCGCCCT GGGGAACGAG 1320  
 GATGCCCTGG GAGAATACTC CTGACCCCC TACAACAGTC TTGGTACGCG CGGGCCCTCT 1380  
 CCTGTGACCC GCGTGTCTGT CAAGGCTCCC CCAGCTTTTA TAGAGCGGCC CAAGGAAGAA 1440  
 TATTTTCAAG AAGTAGGGCG GGAGCTGCTC ATCCCTGCT CCGCCCAAGG GGACCTCCT 1500  
 CCTGTGTCT CTTGAGACAA GGTGGGCCGG GGGCTGCAAG GCCAGGCCCA GGTGGACAGC 1560  
 AACAGCAGCC TCATCTCTCG ACCATTGACC AAGGAGGCCC ACGGCACTG GGAATGCAGT 1620  
 GCCAGCAATG CTGTGGCCCG AGTGGCCACC TCCACGAACG TCTACGTGCT GGGCACTAGC 1680  
 CCTCATGTGT TCACCAATGT GTCCGTGGTG GCTTTGCCCA AGGGTGCCAA TGTCTCCTGG 1740  
 GAGCTGTGCT TTGATGGTGG TTATCTGAG AGATTCACTG TCTGGTACAC CCACTGGCC 1800  
 AAGCTCTCTG ACCGAATGCA CCATGACTGG GTGTCTTGG CAGTGCCTGT GGGGGCTGCT 1860  
 CACCTCTAG TGCCAGGGCT GCAGCCACAC ACCCAGTACC AGTTCAGCGT GCTAGCTCAG 1920  
 AACAGCTGG GAGTGGTCC CTTACGCGAA ATCGTCTTGT CTGCTCCGGA AGGGCTTCTT 1980  
 ACCAGCCAG CTGACCCCGG GCTTCCCCCA ACAGAGATAC CGCTCCCTCT GTCCCTCCG 2040  
 CGGGGTCTGG TGGCAGTAG GACACCCCGG GGGGTACTCC TGCATTGGGA TCCCCAGAG 2100  
 CTGGTCCCTA AGAGACTGGA TGGCTACGTC TTGGAAGGCC GGCAAGGCTC CCAGGGCTGG 2160  
 GAGGTGTGAG ACCCGGCTGT GGCAGGCACA GAAACAGAGC TGCTGTGCTC AGGCTCATC 2220  
 AAGGATGTT TCTACGAGTT CCGCTCGTG GCCTTCGCGG GCAGCTTCGT CAGCGACCCC 2280  
 AGCAACACGG CCAACGTCTC CACTTCCGGT CTGGAGGTCT ACCCTTCGCG CACGAGCTG 2340  
 CCGGGCCTCG TGCTCAGCC CGTGTGCGC GGCCTGGTGG GCGGAGTCTG CTTTCTGGGA 2400  
 GTGGCCGTCC TTGTGAGCAT CTGGCCCGGC TGCCTCCTGA ACCGGCGCAG GCGTCCCGC 2460  
 CGCCGCGCAG AGCGCTCCG CCAAGATCCA CCTCTTATCT TCTCTCCGAC CGGGAAGTCA 2520  
 GCTGCACCT CTGCTCTGGG CTCAGGCAGT CTGACAGCG TGGCGAAGCT GAAGCTCCAG 2580  
 GGATCCCCAG TCCCCAGCCT GCGCCAGAGT CTGCTCTGGG GGGATCTGCT CGGAACCTCC 2640  
 AGCCCCACCC CGGATCTCTC ATCTAGCCGG GGACCTTAC CTCTGGAGCC CATTGCGCG 2700  
 GGCCAGAGCG GCGCTTTTGT GATGGGGCCC ACTGTGGCGG CCCCCAGGA AAGGTCAAGC 2760  
 CGGGAGCAGG CAGAACCTCG GACTCCAGCC CAGCGTCTGG CCCGTCCTT TGAAGTATAG 2820  
 AGCAGCAGCC CCAGTGGGGC ACCCCAGCCC CTCTGCATTG AAGACATCAG CCCTGTGGCA 2880  
 CCCCCCTCAG CAGCCCCACC CAGTCCCTTG CCAGGTCTGT GACCCCTGCT CCAGTACCTG 2940  
 AGCCTGCCCT TCTTCCGAGA GATGAATGTG GATGGGGACT GGCCCCGCT TGAGGAGCCC 3000  
 AGCCTGTGCT CACCCACAGA TTACATGGAT ACCCGCGCT GTCCCACTC ATCTTCTCTT 3060  
 CGTTCTCCAG AAACCCCTCC TGTATCCCC AGGGAATCAC TTCCTGGGGC TGTGTAGGG 3120  
 GCTGGGGCCA CTGCAGAGCC CCCTTACACA GCCCTGGCTG ACTGGACACT GAGGGAGCGG 3180  
 CTGCTGCCAG GCCTTCTCCC TGCTGCCCTT CGAGGCAGCC TCACAGCCA GAGCAGCGG 3240

CGAGGCAGCG CTTCGTTCTT GCGGCCCCCC TCCACAGCCC CCTCTGCAGG AGGCAGCTAC 3300  
 CTCAGCCCTG CTCAGGAGAG CACCAGCAGC TGGGCCAGTG GCCCTGAGAG ATGGCCCCGA 3360  
 AGGGAGCATG TGGTGACAGT CAGCAAGAGG AGGAACACAT CTGTGGACGA GAACTATGAG 3420  
 TGGGACTCAG AATTCCTTGG GGACATGGAA TTGCTGGAGA CTTTGCACCT GGGCTTGGCC 3480  
 AGCTCCCGGC TCAGACCTGA AGCTGAGACA GAGCTAGGTG TGAAGACTCC AGAGGAGGGC 3540  
 TGCCTCCTGA ACACCTGCCA TGTACTGGC CCTGAGGCC GCTGTGCTGC CCTTCGGGAG 3600  
 GAATTCCTGG CCTTCGCGCG CGCCGAGAT GCTACTAGGG CTCGGCTACC AGCCTATCGA 3660  
 CAGCCAGTCC CCCACCCCGA ACAGGCCACT CTGCTGTGAA CATCCCTAAT GTGAGGCTGT 3720  
 GAAAAGGATC ATGACCTGTC AAAGGAGGCC CCCAACGAGA CAGACCTAGT TTCAAAACGAG 3780  
 GGCACTGCCC CTGCTGCCCC CTTTGGTGCC CAGGCACAGA CCCTGATAGT GGGTTTGGGT 3840  
 CACCTTGGTA TGGAAATGTAT GTGCTGACCC CCTAGGTGAG TCTGGGGATT GGAACAGGGA 3900  
 TCTTAGGTCT GCCTCTCTCT CTCTCTCTCT CTCTCTCTCT CTCTCTCTGT GTGTGTGTGT 3960  
 GTGTGTGAAG TTTTTCACAG GTGAATAAAC AAAGTTTGAA AGAAAAAATA AAAAAAATAA 4020  
 AAAA 4024

Seq ID NO: C94 DNA Sequence  
 Nucleic Acid Accession #: NM\_006875  
 Coding sequence: 186..1190

1 11 21 31 41 51  
 | | | | |  
 GAATTCGGCA CGAGCGCGCG GCGAATCTCA ACGCTGCGCC GTCTGCGGGC GCTTCCGGGC 60  
 CACCAGTTTC TCTGCTTTCC ACCCTGGCGC CCCCAGCCCC TGGCTCCCCA GCTGCGCTGC 120  
 CCCGGGCGTC CACGCCCTGC GGGCTTAGCG GGTTCAGTGG GCTCAATCTG CGCAGCGCCA 180  
 CCTCCATGTT GACCAAGCCT CTACAGGGGGC CTCCCGCGCC CCCCAGGACC CCCACGCGCC 240  
 CGCCAGGAGG CAAGGATCGG GAAGCGTTCC AGGCCGAGTA TCGACTCGCG CCCCCTCTGG 300  
 GTAAGGGGGG CTTTGGCACG GTCTTCGCGA GACACCGCCT CACAGATCGA CTCCAGGTGG 360  
 CCATCAAGT GATTCCCGCG AATCGTGTGC TGGGCTGGTC CCCCTTGTCA GACTCAGTCA 420  
 CATGCCCACT CGAAGTCGCA CTGCTATGGA AAGTGGGTGC AGGTGGTGGG CACCCTGGCG 480  
 TGATCCCGCT GCTTGACTGG TTTGAGACAC AGGAAGGCTT CATGCTGGTC CTGAGCGGGC 540  
 CTTTGGCCGC CCAGGATCTC TTTGACTATA TCACAGAGAA GGGCCCACTG GGTGAAGGCC 600  
 CAAGCCGCTG CTTCTTTGGC CAAGTAGTGG CAGCCATCCA GCACCTGCCAT TCCCGTGGAG 660  
 TTGTCCATCG TGACATCAAG GATGAGAAC A TCCTGATAGA CCTACGCCGT GGTGTGCCA 720  
 AACTCATTGA TTTTGGTTCT GGTGCCCTGC TTCATGATGA ACCCTACACT GACTTTGATG 780  
 GGACAAGGGT GTACAGCCCC CCAGAGTGG A TCTCTCGACA CCAGTACCAT GCACCTCCCG 840  
 CCCTGTCTGT TCACTGGGCG ATCTCCTCT ATGACATGGT GTGTGGGGAC ATTCCCTTTG 900  
 AGAGGGACCA GGAGATTCTG GAAGCTGAGC TCCACTTCCC AGCCCATGTC TCCCAGACT 960  
 GCTGTGCCCT AATCCGCGCG TGCCTGGCCC CCAAACCTTC TTCCCGACCC TCACTGGAAG 1020  
 AGATCCTGCT GGACCCCTGG ATGCAAAAC CAGCCGAGGA TGTACCCCT CAACCCCTCC 1080  
 AAAGGAGGCC CTGCCCTTTT GGCCTGTGCC TTGCTACCTT AAGCTTGACC TGGCCTGGCC 1140  
 TGGCCCCAAG TGGTCAGAAG AGCCATCCCA TGGCCATGTC ACAGGGATAG ATGGACATTT 1200  
 GTTGACTTGG TTTTACAGGT CATTACCACT CATTAAAGTC CAGTATTACT AAGGTAAGGG 1260  
 ATTAGGATC AGGGGTTAGA AGACATAAAC CAAGTTTGCC CAGTTCCTTT CCCAATCCTA 1320  
 CAAAGGAGCC TTCTTCCCG AACCTGTGGT CCCTGATTTT GGAGGGGGAA CTTCTTGCTT 1380  
 CTCATTTTGC TAAGGAAGTT TATTTTGGTG AAGTTGTGCC CATTTTGAGC CCCGGGACTC 1440  
 TTATTTGAT GATGTGTAC CCCACATTGG CACCTCCTAC TACCACCACA CAACTTAGT 1500  
 TCATATGCTT TACTTGGGC AAGGGTGCTT TCCTTCCAAT ACCCCAGTAG CTTTATTTT 1560  
 AGTAAAGGGA CCCTTTCCCC TAGCCTAGGG TCCCATATG GGTCAAGCTG CTTACCTGCC 1620  
 TCAGCCCAGG ATTTTATTTT TTGGGGGAGG TAATGCCCTG TTGTTACCCC AAGGCTTCTT 1680  
 TTTTTTTTTT GGTGAGGGGA CCGTACTTTG TTATCCCAAG TGCTCTTATT 1740  
 CTGGTGAGAA GAACCTTAAT TCCATAAATT GGGAGGAAT GGAAGATGGA CACCACCGGA 1800  
 CACCACGAGA CAATAGGATG GGATGGATGG TTTTGTGGG GATGGGCTAG GGGAAATAAG 1860  
 GCTTGCTGTT TGTTTTCTG GGGCGCTCCC TCCAATTTG CAGATTTTGG CAACCTCCTC 1920  
 CTGAGCCGGG ATGTGCAAT TACTAAAATG TAAATAATCA CGTATTGTGG GGAGGGGAGT 1980  
 TCCAAGTGTG CCCTCCTTTT TTTTCTGCC TGGATTATTT AAAAAGCCAT GTGTGGAAC 2040  
 CCACATTTTA ATAAAAGTAA TAGAATCAGA AAAAAAATA AAAAAAATA 2088

Seq ID NO: C95 DNA Sequence  
 Nucleic Acid Accession #: NM\_002510.1  
 Coding sequence: 92..1774

1 11 21 31 41 51  
 | | | | |  
 CAGATGCCAG AAGAACTACT TTGCTCTTGG TGGACGGGCC CAGAGGAATT CAGAGTTAAA 60  
 CCTTGAGTGC CTGCGTCCGT GAGAAATCAG CATGGAATGT CTCTACTATT TCCTGGGATT 120  
 TCTGCTCCTG GCTGCAAGAT TGCCACTTGA TGCCGCCAAA CGATTTCATG ATGTGCTGGG 180  
 CAATGAAAGA CCTTCTGCTT ACATGAGGGA GCACAATCAA TTAATGGCT GGTCTTCTGA 240  
 TGAAAATGAC TGGAAATGAA AACTCTACCC AGTGTGGAAG CGGGGAGACA TGAGGTGGAA 300  
 AAACCTCTGG AAGGGAGGCC GTGTGCAGGC GGTCTGACC AGTGACTCAC CAGCCCTCGT 360  
 GGGCTCAAT ATAACATTG CGGTGAACCT GATATTCCCT AGATGCCAAA AGGAAGATGC 420  
 CAATGGCAAC ATAGTCTATG AGAAGAACTG CAGAAATGAG GCTGGTTTAT CTGCTGATCC 480  
 ATATGTTTAC AACTGACACG CATGGTCAGA GGACAGTGAC GGGGAAAATG GCACCGGCCA 540  
 AAGCATCAT AACCTCTTCC CTGATGGGAA ACCTTTTCCCT CACCACCCCG GATGGAGAAG 600  
 ATGGAATTTT ATCTACGTCT TCCACACACT TGGTCAGTAT TTCCAGAAAT TGGGACGATG 660  
 TTCAGTGAGA GTTCTGTGTA ACACAGCCAA TGTGACACTT GGGCCTCAAC TCATGGAAGT 720  
 GACTGTCTAC AGAAGACATG GACGGGCATA TGTTCACATC GCACAAGTGA AAGATGTGTA 780  
 CGTGGTAACA GATCAGATTCT CTGTGTTTGT GACTATGTTT CAGAAGAACG ATCGAAATTC 840  
 ATCCGACGAA ACCTTCTCCA AAGATCTCCC CATTATGTTT GATGTCTTGA TTCATGATCC 900  
 TAGCCACTTC CTCAATTATT CTACCAATTA CTACAAGTGG AGCTTCGGGG ATAATACTGG 960  
 CCTGTTTGT TCCACCAAT ATACTGTGAA TCACACGTAT GTGCTCAATG GAACCTTCAG 1020  
 CCTTAACCTC ACTGTGAAAG CTGCAGCACC AGGACCTTGT CCGCCACCGC CACCACACC 1080  
 CAGACCTTCA AAACCCACCC CTCTTTTAGG ACCTGCTGGT GACAACCCCC TGGAGCTGAG 1140  
 TAGGATTCCT GATGAAAAC GCCAGATTAA CAGATATGGC CACTTTCAG CCACCATCAC 1200  
 AATTGTAGAG GGAATCTTAG AGGTAAACAT CATCCAGATG ACAGACGTCC TGATGCCGT 1260

	GCCATGGCCT	GAAAGCTCCC	TAATAGACTT	TGTCGTGACC	TGCCAAGGGA	GCATTCCCAC	1320
	GGAGGTCTGT	ACCATCATTT	CTGACCCAC	CTGCAGATC	ACCCAGAACA	CAGTCTGCAG	1380
	CCCTGTGGAT	GTGGATGAGA	TGTGTCTGCT	GACTGTGAGA	CGAACCTTCA	ATGGGTCTGG	1440
5	GACGTACTGT	GTGAACCTCA	CCCTGGGGGA	TGACACAAGC	CTGGCTCTCA	CGAGCACCCCT	1500
	GATTTCTGTT	CCTGACAGAG	ACCCAGCCTC	GCCTTTAAGG	ATGGCAAACA	GTGCCCTGAT	1560
	CTCCGTTGGC	TGCTTGCCCA	TATTTGTCC	TGTGATCTCC	CTCTTGGTGT	ACAAAAACA	1620
	CAAGGAATAC	AACCCAATAG	AAAATAGTCC	TGGGAATGTG	GTCAGAAGCA	AAGCCCTGAG	1680
	TGTCCTTTCTC	AACCGTGCAA	AAGCCGTGTT	CTTCCCGGGA	AACCAAGAAA	AGGATCCGCT	1740
10	ACTCAAAAC	CAAGAATTTA	AAGGAGTTTC	TTAAATTTCC	ACCTTGTGTT	TGAAGCTCAC	1800
	TTTTCACTGC	CATTTGATGT	AGATGTGCTG	GAGTGGCTAT	TAACCTTTTT	TTCTAAAGA	1860
	TTATTGTTAA	ATAGATATTG	TGTTTTGGGG	AAGTTGAATT	TTTTATAGGT	TAAATGTCAT	1920
	TTTAGAGATG	GGGAGAGGGA	TTATACTGCA	GGCAGCTTCA	GCCATGTTGT	GAAACTGATA	1980
	AAAGCAACTT	AGCAAGGCTT	CTTTTCATTA	TTTTTTATGT	TTCACTTATA	AAGTCTTAGG	2040
15	TAAC TAGTAG	GATAGAAACA	CTGTGTCCTG	AGAGTAAGGA	GAGAAGCTAC	TATTGATTAG	2100
	AGCCTAACCC	AGGTTAACTG	CAAGAAGAGG	CGGGATACTT	TCAGCTTTCC	ATGTAACGTG	2160
	ATGCATAAAG	CCAACTGAGT	CCAGTTTCTA	AGATCATGTT	CCAAGCTAAC	TGAATCCAC	2220
	TTCAATACAC	ACATCATGAAC	TCCTGATGGA	ACAATAACAG	GCCCAAGCCT	GTGGTATGAT	2280
	GTGCACACTT	GCTAGACTCA	GAAAAAATAC	TACTCTCATA	AATGGGTGGG	AGTATTTTGG	2340
20	TGACAACCTA	CTTTGCTTGG	CTGAGTGAAG	GAATGATATT	CATATATTCA	TTTATTCCAT	2400
	GGACATTAG	TTAGTGCTTT	TTATATACCA	GGCATGATGC	TGAGTGACAC	TCTTGTGAT	2460
	ATTTCCAAAT	TTTTGTATAG	TCGCTGCACA	TATTTGAAAT	CATATATTAA	GACTTTCCAA	2520
	AGATGAGGTC	CCTGGTTTTT	CATGGCAACT	TGATCAGTAA	GGATTTCAAC	TCTGTTTGTA	2580
	ACTAAACCA	TCTACTATAT	GTTAGACATG	ACATTCCTTT	TCTCTCCTTC	CTGAAAAATA	2640
25	AAGTGTGGGA	AGAGACAAAA	AAAAAATA				2669

Seq ID NO: C96 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..4247

30	1	11	21	31	41	51	
	ATGCGAATCC	TAAAGCGTTT	CCTCGCTTGC	ATTGAGCTCC	TCTGTGTTTG	CCGCCTGGAT	60
	TGGGCTAATG	GACTACTACAG	ACAACAGAGA	AACTTGTGTG	AAGAGATTGG	CTGGTCTCTAT	120
	ACAGGAGCAC	TGAATCAAAA	AAATTGGGGA	AAGAAATATC	CAACATGTAA	TAGCCCAAAA	180
35	CAATCTCCTA	TCAATATTGA	TGAAGATCTT	ACACAAGTAA	ATGTGAATCT	TAAGAAACTT	240
	AAATTTCCAGG	GTTGGGATAA	AACATCATTT	GAAAAACAT	TCATTCTATA	CACTGGGAAA	300
	ACAGTGGAAA	TTAATCTCAC	TAATGACTAC	CGTGTGAGCG	GAGGAGTTTC	AGAAATGGTG	360
	TTTAAAGCAA	GCAAGATAAC	TTTTCACTGG	GGAAAAATGCA	ATATGTGATC	TGATGGATCA	420
	GAGCATACTT	TAGAAGGACA	AAAATTTCCA	CTTGAGATGC	AAATCTACTG	CTTTGATGCA	480
40	GACCGATTTT	CAAGTTTGTG	GGAAGCAGTC	AAAGGAAAAG	GGAAGTTAAG	AGCTTTATCC	540
	ATTTTGTGTT	AGGTTGGGAC	AGAAGAAAAT	TTGGATTTC	AAGCGATTAT	TGATGGAGTC	600
	GAAAGTGTGA	GTCGTTTGGG	GAAAGCAGCT	GCTTTAGATC	CATTCTACT	GTTGAACCTT	660
	CTGCCAAACT	CAACTGACAA	GTATTACATT	TACAATGGCT	CATTGACATC	TCTTCCCTGC	720
	ACAGACACAG	TTGACTGGAT	TGTTTTTAAA	GATACAGTTA	GCATCTCTGA	AAGCCAGTTG	780
45	GCTGTTTTTT	GTGAAGTCT	TACAATGCAA	CAATCTGGTT	ATGTCATGCT	GATGGACTAC	840
	TTACAAAACA	ATTTTCGAGA	GCAACAGTAC	AAGTTCTCTA	GACAGGTGTT	TTCTCTATAC	900
	ACTGGAAAGG	AAGAGATTCA	TGAAGCAGTT	TGTAGTTTCA	AACCAAGAAA	TGTTCAAGCT	960
	GACCCAGAGA	ATTATACCAG	CCTTCTTGT	ACATGGGAAA	GACCTCGAGT	CGTTTATGAT	1020
50	ACCATGATTG	AGAAGTTTGG	AGTTTGTGAC	CAGCAGTTGG	ATGGAGAGGA	CCAAACCAAG	1080
	CATGAATTTT	TGACAGATGG	CTATCAAGAC	TTGGGTGCTA	TTCTCAATAA	TTTGCTACCC	1140
	AATATGAGTT	ATGTTCTTCA	GATAGTAGCC	ATATGCACTA	ATGGCTTATA	TGGAAAATAC	1200
	AGCGACCAAC	TGATTGTGCA	CATGCCTACT	GATAATCTCT	AACTTGATCT	TTTCCCTGAA	1260
	TTAATTTGAA	CTGAAGAAAT	AATCAAGGAG	GAGGAAGAGG	GAAAAGACAT	TGAAGAAGGC	1320
55	GCTATTTGTA	ATCCTGGTGA	AGACAGTGCT	ACAACCAAAA	TCAGGAAAAA	GGAAACCCAG	1380
	ATTTCTACCA	CAACACATGA	CAATCGCATA	GGGACGAAAT	ACAATGAAGC	CAAGACTAAC	1440
	CGATCCCCAA	CAAGAGGAAG	TGAATTTCTT	GGAAAGGGTG	ATGTTCCCAA	TACATCTTTA	1500
	AATTCACACT	CCCAACCACT	CACATAAATTA	GCCACAGAAA	AAGATATTTT	CTTGACTTCT	1560
	CAGACTGTGA	CTGAAGTCCG	ACCTCACACT	GTGGAAGGTA	CTTCAGCCTC	TTTAAATGAT	1620
	GGCTCTAAAT	CTGTTCTTAG	ATCTCCACAT	ATGAACCTGT	CGGGGACTGC	AGAATCCCTA	1680
60	AATACAGTTT	CTATAACAGA	ATATGAGGAG	GAGAGTTTAT	TGACCAAGTT	CAAGCTTGAT	1740
	ACTGGAGCTG	AAGATTCTTC	AGGCTCCAGT	CCCGCAACTT	CTGCTATCCC	ATTCATCTCT	1800
	GAGAACATAT	CCCAAGGGTA	TATATTTTCC	TCCGAAAACC	CAGAGACAAT	AACATATGAT	1860
	GTCCCTATAT	CAGAATCTGC	TAGAAATGCT	TCCGAAGATT	CAACTTTCAT	AGGTTTCAAG	1920
65	GAATCACTAA	AGGATCCTTC	TATGGAGGGA	AATGTGTGGT	TTCCTAGCTC	TACAGACATA	1980
	ACAGCACAGC	CCGATGTTGG	ATCAGGCAGA	GAGAGCTTTT	TCCAGACTAA	TTACACTGAG	2040
	ATACGTGTTG	ATGAATCTGA	GAAGACAACC	AAGTCTTTT	CTGCAGGCC	AGTGATGTCA	2100
	CAGGGTCCCT	CAGTTACAGA	TCTGGAAATG	CCACATTATT	CTACCTTTGC	CTACTTCCCA	2160
	ACTGAGGTAA	CACCTTATGC	TTTTACCCCA	TCTCCAGAC	AACAGGATTT	GGTCTCCAG	2220
70	GTCAACGTGG	TATACTCGCA	GACAACCCAA	CCGGTATACA	ATGAGGCCAG	TAATAGTAGC	2280
	CATGAGTCTC	GTATTGGTCT	AGCTGAGGGG	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	2340
	CTTGTGATCG	TGTCAGCCCT	GACTTTTATC	TGCTTAGTGG	TTCTTGTGGG	TATTTCTCATC	2400
	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	TTTACTTAG	AGGACAGTAC	ATCCCTTAGA	2460
	GTTATATCCA	CACCTTCCA	ACCTATCTTT	CCAATTTTCA	ATGATGTGCG	AGCAATTCCA	2520
75	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	2580
	TTTGAGGAAG	TGCAGAGCTG	TACTGTTGAC	TTAGGTATTA	CAGCAGACAG	CTCCAACCCAC	2640
	CCAGACAACA	AGCAACAAGAA	TGATATCGTT	CCTATGATCA	TAGCAGGGTT		2700
	AAGCTAGCAC	AGCTTGCTGA	AAAGGATGGC	AACTGACTG	ATTATATCAA	TGCCAATTAT	2760
	GTTGATGGCT	ACAACAGACC	AAAAGCTTAT	ATTGCTGCCC	AAGGCCCACT	GAAATCCACA	2820
80	GCTGAAGATT	CTGTGAGAA	GATATGGGAA	CATAATGTGG	AAGTTATTGT	CATGATAACA	2880
	AACCTCGTGG	AGAAAGGAAG	GAGAAAATGT	GATCAGTACT	GGCCTGCCGA	TGGGAGTGAG	2940
	GAGTACGGGA	ACTTCTGGT	CACCTCAGAAG	AGTGTGCAAG	TGCTTGCCCTA	TTATACTGTG	3000
	AGGAATTTTA	CTCTAAGAAA	CACAAAATA	AAAAAGGGCT	CCCAGAAAGG	AAGACCCAGT	3060
	GGACGTGTGG	TCACACAGTA	TCACTACACG	CAGTGGCCTG	ACATGGGAGT	ACCAGAGTAC	3120
	TCCTGACCAG	TGCTGACCTT	TGTGAGAAAG	GCAGCCTATG	CCAAGGCCCA	TGCAGTGGGG	3180

CCTGTTGTCG TCCACTGCAG TGCTGGAGTT GGAAGAACAG GCACATATAT TGTGCTAGAC 3240  
 AGTATGTTGC AGCAGATTCA ACACGAAGGA ACTGTCAACA TATTTGGCTT CTTAAAAACAC 3300  
 ATCCGTTTAC AAAGAAATTA TTTGGTACAA ACTGAGGAGC AATATGTCTT CATTTCATGAT 3360  
 5 ACACGTGTTG AGGCCATAC TTAGTAAAGAA ACTGAGGTGC TGGACAGTCA TATTCATGCC 3420  
 TATGTTAATG CACTCTCAT TCCTGGACCA GCAGGCAAAA CAAAGCTAGA GAAACAATTC 3480  
 CAGCTCCTGA GCCAGTCAAA TATACAGCAG AGTGACTATT CTGCAGCCCT AAAGCAATGC 3540  
 AACAGGGAAA AGAATCGAAC TTCTTCTATC ATCCCTGTGG AAAGATCAAG GGTGGCATT 3600  
 TCATCCCTGA GTGGAGAAGG CACAGACTAC ATCAATGCCT CCTATATCAT GGGCTATTAC 3660  
 10 CAGAGCAATG AATTTCATCAT TACCCAGCAC CCTCTCCTTC ATACCATCAA GGATTTCTGG 3720  
 AGGATGATAT GGGACCATAA TGCCCAACTG GTGGTTATGA TTCCTGATGG CCAAAACATG 3780  
 GCAGAGATG AATTGTTTGA CTGGCCAAAT AAAGATGAGC CTATAAATG TGAGAGCTTT 3840  
 AAGGTCACCT TTATGGCTGA AGAACACAAA TGTCATCTTA ATGAGGAAAA ACTTATAATT 3900  
 CAGGACTTTA TCTTAGAAGC TACACAGGAT GATTATGTAC TTGAAGTGAG GCACTTTCAG 3960  
 15 GTGCTCTAAT GGCCAAATCC AGATAGCCCC ATTAGTAAAA CTTTGAACCT TATAAGTGT 4020  
 ATAAAAAGAG AAGCTGCCAA TAGGGATGGG CCTATGATTG TTCATGATGA GCATGGAGGA 4080  
 GTGACGGCAG GAACTTTCTG TGCTCTGACA ACCCTTATGC ACCAACTAGA AAAAGAAAAAT 4140  
 TCCGTGGATG TTTACCAGGT AGCCAAAGAT ATCAATCTGA TGAGGCCAGG AGTCTTTGCT 4200  
 GACATTGAGC AGTATCAGTT TCTCTACAAA GTGATCCTCA GCCTTGTGAG CACAAGGCAG 4260  
 20 GAAGAGAATC CATCCACCTC TCTGGACAGT AATGGTGCAG CATTGCCTGA TGGAAATATA 4320  
 GCTGAGAGCT TAGAGTCTTT AGTTTAA 4347

Seq ID NO: C97 DNA Sequence  
 Nucleic Acid Accession #: XM\_031379  
 Coding sequence: 148..7095

1 11 21 31 41 51  
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60  
 CAAAAAAAC ATTTCTCTCG CTCCTCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120  
 30 CGGCGAGGGG CGCAGACCGG TCTGGAATAG CGAATCCTAA AGCGTTTCCT CGCTTGCAAT 180  
 CAGCTCCTCT GTGTTTGGCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTTGTTGAAG AGATTGGCTG GTCTTATACA GGAGCACTGA ATCAAAAAAA TTGGGGAAAG 300  
 AAATATCCAA CATGTAATAG CCAAAAAACA TCTCTATCA ATATTGATGA AGATCTTACA 360  
 35 CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA 420  
 AACACATTC AATCATAACG TGGGAAAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT 480  
 GTCAGCGGAG AGGTTTCAGA AATGGTGTTC AAAGCAAGCA AGATAACTTT TCACTGGGGA 540  
 AAATGCAATA TGTCATCTGA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600  
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAA 660  
 40 GGAAGAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGGAG TTGGGACAGA AGAAATTTTG 720  
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTTAGTC GTTTTGGGAA GCAGGCTGCT 780  
 TTAGATCCAT TCATCTGTTT GAACCTTCTG CCAAACTCAA CTGACAAGTA TTACATTTAC 840  
 AATGGCTCAT TGACATCTCC TCCTTGACCA GACACAGTTG ACTGGATTGT TTTTAAAGAT 900  
 ACAGTTAGCA TCTCTGAAAG CCAAGTTGGCT GTTTTTTGTG AAGTTCTTAC AATGCAACAA 960  
 45 TCTGTTATG TCATGCTGAT GGACTACTTA CAAAACAATT TTCGAGAGCA ACAGTACAAG 1020  
 TTCTCTAGAC AGGTGTTTTT CTCATACACT GGAAGGAAG AGATTCATGA AGCAGTTTGT 1080  
 AGTTTCAAGC CAGAAATGTG TCAGGCTGAC CCAGAGAATT ATACCAGCCT TCTTGTAC 1140  
 TGGGAAAGAG CTGAGTTCGT TTATGATACC ATGATTGAGA AGTTTGAGT TTTGTACCAG 1200  
 CAGTTGGATG GAGAGGACCA AACCAAGCAT GAATTTTGA CAGATGGCTA TCAAGACTTG 1260  
 50 GGTGCTATTG TCAATAATTT GCTACCCAAT ATGAGTTATG TTCTTCAGAT AGTAGCCATA 1320  
 TGCACTAATG GCTTATATGG AAAATACAGC GACCAACTGA TTGTCGACAT GCCTACTGAT 1380  
 AATCCTGAAC TTGATCTTTT CCCTGAATTA ATTGGAAGTG AAGAAATAAT CAAGGAGGAG 1440  
 GAAGAGGGAA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGCTAGAGA CAGTGCTACA 1500  
 AACCAATCA GGAAGGAAG ACCCCAGATT TCTACCACAA CACACTACAA TCGCATAGGG 1560  
 55 ACAGAAATCA ATGAAGCCAA GACTAACCGA TCCCCAACAA GAGGAAGTGA ATTCTCTGGA 1620  
 AAGGGTATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCAGTCAC TAAATTAGCC 1680  
 ACAGAAAAAG ATATTTCTTT GACTTCTCAG ACTGTGACTG AACTGCCACC TCACACTGTG 1740  
 GAAGGTACTT CAGCTCTTTT AAATGATGGC TCTAAAAC TGTTTATGAT TCCACATATG 1800  
 AACTTGTGCG GGACTGCGAGA ATCTTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG 1860  
 60 AGTTTATTGA CCAAGTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCAGTCCC 1920  
 GCAACTTCTG CTATCCCAT TCTCTGAG AACATATCCC AAGGGTATAT ATTTCTCTCC 1980  
 GAAACCCAG AGACAATTAAC ATATGATGTC CTATACCCAG AATCTGCTAG AAATGCTTCC 2040  
 GAAGATTCAA CTTTCATCAG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAAT 2100  
 GTGTGGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG 2160  
 65 AGCTTTCTCC AGACTAATTA CACTGAGATA CGTGTGATG AATCTGAGAA GACAACCAAG 2220  
 TCCTTTCTG CAGGCCAGT GATGTCACAG GGTCCCTCAG TTACAGATCT GGAATGCCA 2280  
 CATTATTCTA CCTTTGCCTA CTTCCCAACT GAGGTAACAC CTCATGCTTT TACCCCATCC 2340  
 TCCAGACAAC AGGATTTGGT CTCCACGGTC AACGTGGTAT ACTCGCAGAC AACCCAAACC 2400  
 70 GTATACAATG GTGAGACACC TCTTCAACCT TCCTACAGTA GTGAAGTCTT TCCTCTAGTC 2460  
 ACCCTTTGT TGCTTGACAA TCAGATCTCT AACACTACCC CTGCTGCTTC AAGTAGTGAT 2520  
 TCGGCCTTGC ATGCTACGCC TGTATTTCCC AGTGTGATG TGTCTTTGA ATCCATCTCT 2580  
 TCTTCTATG ATGTTGCAAC TTTGCTTCCA TTTTCTCTG CTTCCTTCAG TAGTGAATTG 2640  
 TTTGCGCAAT TGCATACAGT TTCTCAAATC CTTCCACAAG TTACTTTCAG TACCGAGAGT 2700  
 75 GATAAGGTGC CCTTGCATG TCTCTGCCA GTGGCTGGGG GTGATTGTCT ATTAGAGCCC 2760  
 AGCCTTGCTC AGTATTCTGA TGTGCTGICC ACTACTCATG CTGCTTCAGA GACGCTGGAA 2820  
 TTTGGTAGTG AATCTGGTGT TCTTTATAAA ACGCTTATGT TTTCTCAAGT TGAACACCC 2880  
 AGCAGTGATG CCATGATGCA TGACGTTCT TCAGGGCCTG AACCTTCTTA TGCCTTGTCT 2940  
 GATAATGAGG GCTCCCAACA CATCTTCACT GTTTCTTACA GTTCTGCAAT ACCTGTGCAT 3000  
 GATTCTGTGG GTTAACCTTA TCAGGGTTCC TTATTTAGCG GCCCTAGCCA TATACCAATA 3060  
 80 CCTAAGTCTT CGTTAATAAC CCCAACTGCA TCATTACTGC AGCCTACTCA TGCCCTCTCT 3120  
 GGTGATGGGG AATGGTCTGG AGCCTCTTCT GATAGTGAAT TTCTTTTACC TGACACAGAT 3180  
 GGGCTGACAG CTTTAAACAT TTCTTCACT GTTCTGTAG CTGAATTAC ATATACAACA 3240  
 TCTGTGTTTG GTGATGATAA TAAGGCGCTT TCTAAAAGTG AAATAATATA TGGAAATGAG 3300  
 ACTGAAGTGC AAATTCCTTC TTTCAATGAG ATGGTTTACC CTTCTGAAAG CACAGTCATG 3360  
 CCAACATGAT ATGATAATGT AAATAAGTTG AATGCGTCTT TACAAGAAAC CTCTGTTTCC 3420

ATTTCTAGCA CCAAGGGCAT GTTTCAGGG TCCCTTGCTC ATACCACCAC TAAGGTTTTT 3480  
 GATCATGAGA TTAGTCAAGT TCCAGAAAAT AACTTTTCAG TCAACCTAC ACATACGTGC 3540  
 TCTCAAGCAT CTGGTGACAC TTCGCTTAAA CCTGTGCTTA GTGCAAACTC AGAGCCAGCA 3600  
 5 TCCTCTGACC CTGCTTCTAG TGAAATGTTA TCTCCTTCAA CTCAGCTCTT ATTTTATGAG 3660  
 ACCTCAGCTT CTTTGTAGTAC TGAAGTATTG CTACAACCTT CCTTTCAGGC TTCTGATGTT 3720  
 GACACCTTGC TTAATACTGT TCTTCCAGCT GTGCCCAGTG ATCCAATATT GGGTGAAACC 3780  
 CCCAAAGTTG ATAAAATTAG TTCTACAATG TTGCATCTCA TTGTATCAAA TTCTGCTTCA 3840  
 AGTGAAAACA TGCTGCACTC TACATCTGTA CCAGTTTTTG ATGTGTCGCC TACTTCTCAT 3900  
 10 ATGCACTCTG CTTCACCTCA AGGTTTGACC ATTTCTATG CAAGTGAGAA ATATGAACCA 3960  
 GTTTTGTAA AAAGTGAAAG TTCCCAACCA GTGGTACCTT CTTTGTACAG TAATGATGAG 4020  
 TTGTTCCAAA CGGCCAATTT GGAGATTAAC CAGGCCCATC CCCCAAAAGG AAGGCATGTA 4080  
 TTTGCTACAC CTGTTTTATC AATTGATGAA CCATTAAATA CACTAATAAA TAAGCTTATA 4140  
 CATTCCGATG AAATTTTAACT CTCCACCAA AGTTCTGTTA CTGGTAAGGT ATTTGCTGGT 4200  
 15 ATTCCAACAG TTGCTTCTGA TACATTTGTA TCTACTGATC ATTCTGTCTC TATAGGAAAT 4260  
 GGGCATGTTG CCATTACAGC TGTTTCTCCC CACAGAGATG GTTCTGTAAC CTCACAAAG 4320  
 TTGCTGTTTC CTCTAAGGC AACTTCTGAG CTGAGTCATA GTGCCAAATC TGATGCCGGT 4380  
 TTAGTGGGTG GTGGTGAGAA TGGTGACACT GATGATGATG GTGATGATGA TGATGATGAC 4440  
 AGAGGTAGTG ATGGCTTATC CATTCTAAG TGTATGTCAT GCTCATCCTA TAGAGAATCA 4500  
 20 CAGGAAAAGG TAATGAATGA TTCAGACACC CACGAAAACA GTCTTATGGA TCAGAATAAT 4560  
 CCAATCTCAT ACTCACTATC TGAGAAATCT GAAGAAGATA ATAGAGTCAC AAGTGTATCC 4620  
 TCAGACAGTC AAACCTGGTAT GGACAGAAAT CCTGGTAAAT CACCATCAGC AAATGGGCTA 4680  
 TCCCAAAAGC ACAATGATGG AAAAGAGGAA AATGACATT CAGACTGGTAG TGCTCTGCTT 4740  
 CCTCTCAGCC CTGAATCTCA AGCATGGGCA GTTCTGACAA GTGATGAAGA AAGTGGATCA 4800  
 25 GGGCAAGGTA CCTCAGATAG CCTTAATGAG AATGAGACTT CCACAGATTT CAGTTTTGCA 4860  
 GACACTAATG AAAAAGATGC TGATGGGATC CTGGCAGCAG GTGACTCAGA AATAACTCCT 4920  
 GGATTCACAG AGTCCCCAAC ATCATCTGTT ACTAGCGAGA ACTCAGAAAT GTTCCACGTT 4980  
 TCAGAGGCAG AGGCCAGTAA TAGTAGCCAT GAGTCTCGTA TTGGTCTAGC TGAGGGGTTG 5040  
 GAATCCGAGA AGAAGGCAGT TATACCCCTT GTGATCGTGT CAGCCCTGAC TTTTATCTGT 5100  
 30 CTAGTGGTTT TGTGGGTAT TCTCATCTAC TGGAGGAAAT GCTTCCAGAC TGCACACTTT 5160  
 TACTTAGAGG ACAGTACATC CCTTAGAGTT ATATCCACAC CTCCAACACC TATCTTTCCA 5220  
 ATTTAGATG ATGTCGGAGC AATTCCAATA AAGCACTTTC CAAAGCATGT TGCAGATTTA 5280  
 CATGCAAGTA GTGGGTTTAC TGAAGAATTT GAGACACTGA AAGAGTTTTA CCAGGAAGTG 5340  
 CAGAGCTGTA CTGTTGACTT AGGTATTACA GCAGACAGCT CCAACCACCC AGACAACAAG 5400  
 35 CACAAGAATC GATACATAAA TATCGTTGCC TATGATCATA GCAGGGTTAA GCTAGCACAG 5460  
 CTGTCTGAAA AGGATGGCAA ACTGACTGAT TATATCAATG CCAATTATGT TGATGGCTAC 5520  
 AACAGACCAA AAGCTTATAT TGCTGCCCAA GGCCCATGTA AATCCACAGC TGAAGATTTT 5580  
 TGGAGAATGA TATGGGAACA TAATGTGGAA GTTATTGTCA TGATAACAAA CCTCGTGGAG 5640  
 AAAGGAAGGA GAAATGTGTA TCAGTACTGG CCTGCCGATG GGAGTGAGGA GTACGGGAAC 5700  
 40 TTTCTGGTCA CTCAGAAGAG TGTGCAAGTG CTGCGCTATT ATACTGTGAG GAATTTTACT 5760  
 CTAAGAAACA CAAAAATAAA AAAGGGCTCC CAGAAAGGAA GACCCAGTGG ACGTGTGGTC 5820  
 ACACAGTATC ACTACACGCA GTGGCCTGAC ATGGGAGTAC CAGAGTACTC CCTGCCAGTG 5880  
 CTGACCTTTG TGAGAAAGGC AGCCTATGCC AAGCGCCATG CAGTGGGGCC TGTGTGCTGC 5940  
 CACTGCACTG CTGGAGTTGG AAGAACAGGC ACATATATTG TGCTAGACAG TATGTTGCAAG 6000  
 45 CAGATTCAAC ACGAAGGAAC TGTCAACATA TTTGCTTCT TAAACACAT CCGTTCCACA 6060  
 AGAAATTATT TGGTACAAAC TGAGGAGCAA TATGTCTTCA TTCATGATAC ACTGGTTGAG 6120  
 GCCATACCTTA GTAAAGAAAC TGAGGTGCTG GACAGTCATA TTCATGCCTA TGTTAATGCA 6180  
 CTCTCATTC CTCAGAGATG AGGCCAAACA AAGCTAGAGA AACAATTCCA GCTCCTGAGC 6240  
 CAGTCAATAA TACAGCAGAG TGAATATTCT GCAGCCCTAA AGCAATGCAA CAGGGAAAAG 6300  
 50 AATCGAACTT CTCTATCAT CCCTGTGGAA AGATCAAGGG TTGGCATTTC ATCCCTGAGT 6360  
 GGAGAAGGCA CAGACTACAT CAATGCCCTCC TATATCATGG GCTATTACCA GAGCAATGAA 6420  
 TTCATCATTA CCCAGCACCC TCTCCTTCAT ACCATCAAGG ATTTCTGGAG GATGATATGG 6480  
 GACCATTAATG CCAACTGGT GGTATGATT CCTGATGGCC AAAACATGGC AGAAGATGAA 6540  
 TTTGTTTACT GGCCTAATAA AGATGAGCCT ATAAATTGTG AGAGCTTTAA GGTCACTCTT 6600  
 55 ATGGCTGAAG AACACAAATG TCTATCTAAT GAGGAAAAAC TTATAATTCA GGACTTTATC 6660  
 TTAGAAGCTA CACAGATGTA TTATGTACTT GAAAGTGAGG ACTTTCAGTG TCCTAAATGG 6720  
 CCAATCCAG ATAGCCCCAT TAGTAAAACT TTTGAACTTA TAAGTGTTAT AAAAGAAGAA 6780  
 GCTGCCAATA GGGATGGGCC TATGATTGTT CATGATGAGC ATGGAGGAGT GACGGCAGGA 6840  
 ACTTTCTGTG CTCTGACCAAC CCTTATGCAC CAACTAGAAA AAGAAAATT CCGTGGATGT 6900  
 60 TACCAGTAG CCAAGATGAT CAATCTGATG AGGCCAGGAG TCTTTGCTGA CATTGAGCAG 6960  
 TATCAGTTTC TCTACAAAGT GATCCTCAGC CTTGTGAGCA CAGGCCAGGA AGAGAATCCA 7020  
 TCCACCTCTC TGGACAGTAA TGGTGACGCA TTGCTGATG GAAATATAGC TGAGAGCTTA 7080  
 GAGTCTTTAG TTTAACACAG AAAGGGGTGG GGGGACTCAC ATCTGAGCAT TGTTTTCTCT 7140  
 TTCTTAAAT TAGGCAGGAA AATCAGTCTA GTTCTGTTAT CTGTTGATTT CCCATCACCT 7200  
 65 GACAGTAAT TCTATGACAT AGGATTCTGC CGCCAAATTT ATATCATTA CAAATGTGTG 7260  
 CTTTTTGC AA GACTTGTAA TTTACTTATTA TGTGTAAGT AAAATGATTG AATTTTACAG 7320  
 TATTTCTAAG AATGGAATTG TGGTATTTTT TTCTGTATTG ATTTTAAACAG AAAATTTCAA 7380  
 TTTATAGAGG TTAGGAATTC CAAACTACAG AAAATGTTTG TTTTATAGTG CAAATTTTAA 7440  
 70 GCTGTATTGG TAGCAATTAT CAGGTTTGGT AGAAATATAA CTTTAAATAC AGTAGCCTGT 7500  
 AAATAAAACA CTCTCCATA TGATATTCAA CATTTTACAA CTGCAGTATT CACCTAAAGT 7560  
 AGAAATAATC TGTACTTAT TGTAATAACT GCCCTAGTGT CTCCATGGAC CAAATTTATA 7620  
 TTTATAATTG TAGATTATTA TATTTTACTA CTGAGTCAAG TTTTCTAGTT CTGTGTAATT 7680  
 GTTTAGTTTA ATGACGTAGT TCATTAGCTG GTCTTACTCT ACCAGTTTTT TGACATTGTA 7740  
 75 TTGTTTACC TAAGTCATTA ACTTGTTC AGCATGTAAT TTTAACTTTT GTGGAATAA 7800  
 GAAATACCTT CATTTTGAAA GAAGTTTTTA TGAGAATAAC ACCTTACCAA ACATTGTTCA 7860  
 AATGGTTTTT ATCCAAGGAA TTGCAAAAAT AAATATAAAT ATTGCCATTA AAAAAAATAA 7920  
 AAAAAAATAA AAAAAAATAA AAAA 7944

Seq ID NO: C98 DNA Sequence  
 Nucleic Acid Accession #: NM\_002851  
 Coding sequence: 77..4518

1 11 21 31 41 51  
 | | | | |  
 CACACATACG CACGCACGAT CTCACCTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60



	CAAAAAAAAAAC	ATTTCTCTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
	CGCGAGGGGG	CCGCAGACCG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
5	CTTGTGGAAG	AGATTGGCTG	GTCTATACAC	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTGAGCGGAG	GAGTTTCAGA	AATGGTGTTC	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
10	AAATGCAATA	TGTCTATCTA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTGTAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTCAAAG	CGATTATTGA	TGGAGTCGAA	AGTGTTAGTC	GTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACCTTCTG	CCAAACTCAA	CTGACAAGTA	TTACATTTC	840
15	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
	ACAGTTAGCA	TCTCTGAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTCTTAC	AATGCAACAA	960
	TCTGGTTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGCA	ACAGTACAAG	1020
	TTCTCTAGAC	AGGTGTTTTC	CTCATACACT	GGAAAGGAAG	AGATTTCATGA	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAGCCT	TCTTGTTACA	1140
20	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCACT	TTTGTACCAG	1200
	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTTC	TCAATAATTT	GCTACCCAAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACATAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTGCGCAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACCT	AAGAAATAAT	CAAGGAGGAG	1440
25	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500
	AACCAAAATCA	GGAAAAAGGA	ACCCAGATT	TCTACCACAA	CACACTACAA	TGCGATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACAGTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCTCT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
30	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCTG	TTCTTAGATC	TCCACATATG	1800
	AACCTTGTGCG	GGACTGCGACA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCAACTTCTG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGTATAT	ATTTTCTCTC	1980
35	GAAGAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTTCTCC	AGACTAATTA	CACTGAGATA	CGTGTTGATG	AATCTGAGAA	GACAACCAAG	2220
40	TCTTTTCTG	CAGGCCACGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTTCA	CCGTTGCTTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGTGT	CTCCACGGTC	AACGTGGTAT	ACTCGCAGAC	AACCCAAACC	2400
	GTATACAATG	CAGAGGCCAG	TAATAGTAGC	CATGAGTCTC	GTTATTGGTCT	AGCTGAGGGG	2460
	TTGGAATCCG	AGAAGAAGGC	AGTTATACCC	CTTGTGATCG	TGTCAGCCCT	GACTTTTATC	2520
45	TGTTCTAGTG	TCTTTGTGGG	TATTTCTATC	TACTGGAGGA	AATGCTTCCA	GACTGCACAC	2580
	TTTTACTTAG	AGGACAGTAC	ATCCCCTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
	CCAATTTTCA	ATGATGTCGG	AGCAATTCCA	ATAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700
	TTACATGCAA	GTAGTGGGTT	TACTGAAGAA	TTTGAGACAC	TGAAAGAGTT	TTACCAGGAA	2760
50	GTGACAGACT	GTACTGTTGA	CTTAGGTATT	ACAGCAGACA	GCTCCAACCA	CCCAGACAAC	2820
	AAGCACAGAA	ATCGATTACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGCTAGCA	2880
	CAGCTTGCTG	AAAAGGATGG	CAAACTGACT	GATTATATCA	ATGCCAATTA	TGTTGATGGC	2940
	TACAACAGAC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCAC	TGAAATCCAC	AGCTGAAGAT	3000
	TTCTGGAGAA	TGATATGGGA	ACATAATGTG	GAAATTATTG	TCATGATAAC	AAACCTCGTG	3060
55	GAGAAAGGAA	GGAGAAAATG	TGATCAGTAC	TGGCCTGCCG	ATGGGAGTGA	GGAGTACGGG	3120
	AACTTTCTGG	TCACTCAGAA	GAGTGTGCAA	GTGCTTGCTT	ATTATACTGT	GAGGAATTTT	3180
	ACTCTAAGAA	ACACAAAAAT	AAAAAAGGGC	TCCCAGAAAG	GAAGACCCAG	TGGACGTGTG	3240
	GTCAACAGT	ATCACTACAC	GCAGTGGCCT	GACATGGGAG	TACCAGAGTA	CTCCCTGCCA	3300
	GTGCTGACCT	TTGTGAGAAA	GGCAGCCTAT	GCCAAGCGCC	ATGCAGTGGG	GCCTGTTGTC	3360
	GTCCACTGCA	GTGCTGGAGT	TGGAAGAACAA	GGCACATATA	TTGTGCTAGA	CAGTATGTTG	3420
60	CAGCAGATTC	AACACGAAAG	AACTGTCAAC	ATATTTGGCT	TCTTAAACAA	CATCCGTTCA	3480
	CAAGAGAAAT	ATTGGTGA	AACTGAGGAG	CAATATGTCT	TCATTTCATGA	TACACTGGTT	3540
	GAGGCCATAC	TTAGTAAAGA	AACTGAGGTG	CTGGACAGTC	ATATTTCATGC	CTATGTTAAT	3600
	GCATCTCTCA	TTCTTGAGCC	AGCAGGCCAA	ACAAAGCTAG	AGAAACAATT	CCAGCTCCTG	3660
	AGCCAGTCAA	ATATACAGCA	GAGTGACTAT	TCTGCAGCCC	TAAAGCAATG	CAACAGGGAA	3720
65	AAGAATCGAA	CTTCTTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTTGGCAT	TTTATCCCTG	3780
	AGTGGAGAAG	GCACAGACTA	CATCAATGCC	TCCTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
	GAATTTCATCA	TTACCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTTCTG	GAGGATGATA	3900
	TGGGACCATA	ATGCCCAACT	GGTGGTTATG	ATTCTGTATG	GCCAAAACAT	GGCAGAAGAT	3960
70	GAATTTGTTT	ACTGGCCAAA	TAAAGATGAG	CCTATAAATT	GTGAGAGCTT	TAAGGTCACT	4020
	CTTATGGCTG	AAGAACACAA	ATGTCATCT	AATGAGGAAA	AACTTATAAT	TCAGGACTTT	4080
	ATCTTAGAAG	CTACACAGGA	TGATTATGTA	CTTGAAGTGA	GGCACTTTCA	GTGTCCTAAA	4140
	TGGCCAAATC	CAGATAGCCC	CATTAGTAAA	ACTTTTGAAC	TTATAAGTGT	TATAAAAGAA	4200
	GAAGCTGCCA	ATAGGGATGG	GCCTATGATT	GTTTCATGATG	AGCATGGAGG	AGTGACGGCA	4260
75	GGAACTTTCT	GTGCTCTGAC	AACCCTTATG	CACCAACTAG	AAAAAGAAAA	TTCCGTGGAT	4320
	GTTTACCAGG	TAGCCAAGAT	GATCAATCTG	ATGAGGCCAG	GAGTCTTTGC	TGACATTGAG	4380
	CAGTATCAGT	TTCTCTACAA	AGTGATCCTC	AGCCTTGTTGA	GCACAAGGCA	GGAAGAGAAT	4440
	CCATCCACCT	CTCTGGACAG	TAATGGTGCA	GCATTGCTGTG	ATGGAAATAT	AGCTGAGAGC	4500
	TTAGAGTCTT	TAGTTTAAACA	CAGAAAGGGG	TGGGGGGACT	CACATCTGAG	CATTGTTTTC	4560
80	CTCTTCTTCA	AATTAGCCAG	GAAATCAGT	CTAGTCTGTG	TATCTGTTGA	TTTCCCATCA	4620
	CCTGACAGTA	ACTTTTCATGA	CATAGGATTC	TGCCGCCAAA	TTTATATCAT	TAACAATGTG	4680
	TGCCTTTTTG	CAGAGCTTGT	AATTTACTTA	TTATGTTTGA	ACTAAAATGA	TTGAATTTTA	4740
	CAGTATTTCT	AAGAATGGAA	TTGTTGTTAT	TTTTCTGTGA	TTGATTTTAA	CAGAAAAATT	4800
	CAATTTATAG	AGGTTAGGAA	TTCCAAACTA	CAGAAAATGT	TTGTTTTTAG	TGTCAAAATT	4860
	TTAGCTGTAT	TTGTAGCAAT	TATCAGGTTT	GCTAGAAATA	TAACTTTTAA	TACAGTAGCC	4920
	TGTAAATAAA	ACACTCTTCC	ATATGATATT	CAACATTTTA	CAACTGCAGT	ATTCACCTAA	4980
	AGTAGAAATA	ATCTGTTACT	TATTGTAAAT	ACTGCCCTAG	TGCTCTCATG	GACCAAAATT	5040
	ATATTTATAA	TTGTAGATTT	TTATATTTTA	CTACTGAGTC	AAGTTTTCTA	GTTCTGTGTA	5100

ATTGTTTAGT TTAATGACGT AGTTCATTAG CTGGTCTTAC TCTACCAGTT TTCTGACATT 5160  
 GTATTGTGTT ACCTAAGTCA TTAACTTTGT TTCAGCATGT AATTTTAACT TTGTGGGAAA 5220  
 ATAGAAATAC CTTCAATTTT AAAGAAGTTT TTATGAGAAT AACACCTTAC CAAACATTGT 5280  
 TCAAAATGGT TTTATCCAAG GAATTGCAAA AATAAATATA AATATTGCCA TTAACAAAAA 5340  
 AAAAAA AAAA AAAA 5367

Seq ID NO: C99 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 501..4514

	1	11	21	31	41	51	
	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
	CAAAAAAAC	ATTTCCTTCG	CTCCCCCTCC	CTCTCCACTC	TGAGAAGCAG	AGGAGCCGCA	120
15	CGGCGAGGGG	CCGCAGAGTG	TCTGGAAATG	CGAATCCTAA	AGCGTTTCCT	CGCTTGCAAT	180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTGAAG	AGATTGGCTG	GTCCTATACA	GGAGCACTGA	ATCAAAAAAT	TGGGGGAAAG	300
	AAATATCCAAC	ATGTAATAGC	CCAAAACAAT	CTCCTATCAA	TATTGATGAA	GATCTTACAC	360
	AAGTAAATGT	GAATCTTAAG	AAACTTAAAT	TTCAGGGTTG	GGATAAAACA	TCATTGGAAA	420
20	ACACATTCAT	TCATAACACT	GGGAAAACAG	TGGAAATTAA	TCCTACTAAT	GACTACCGTG	480
	TCAGCGGAGG	AGTTTCAGAA	ATGGTGTTTA	AAGCAAGCAA	GATAACTTTT	CACCTGGGAA	540
	AATGCAATAT	GTCACTCGAT	GGATCAGAGC	ATAGTTTAGA	AGGACAAAAA	TTTCCACTTG	600
	AGATGCAAAAT	CTACTGCTTT	GATGCGGACC	GATTTTCAAG	TTTTGAGGAA	GCAGTCAAAG	660
	GAAAAGGGAA	GTTAAGAGCT	TTATCCATTT	TGTTTGAGGT	TGGGACAGAA	GAAAATTTGG	720
25	ATTTCAAAGC	GATTATTGAT	GGAGTCGAAA	GTGTTAGTCG	TTTTGGGAAG	CAGGCTGCCT	780
	TAGATCCATT	CATACTGTGG	AACCTTCTGC	CAAACTCAAC	TGACAAGTAT	TACATTTACA	840
	ATGGCTCATT	GACATCTCCT	CCCTGCACAG	ACACAGTTGA	CTGGATTGTT	TTTAAAGATA	900
	CAGTTAGCAT	CTCTGAAAGC	CAGTTGGCTG	TTTTTTGTGA	AGTTCCTACA	ATGCAACAAT	960
30	CTGGTTATGT	CATGCTGATG	GACTACTTAC	AAAACAATTT	TCGAGAGCAA	CAGTACAAGT	1020
	TCTCTAGACA	GGGTTTTTCC	TCATACACTG	GAAAGGAAGA	GATTTCATGAA	GCAGTTTGTA	1080
	GTTTCAGAAC	AGAAAATGTT	CAGGCTGACC	CAGAGAATTA	TACCAAGCCT	CTTGTTACAT	1140
	GGGAAAGACC	TCGAGTCGTT	TATGATACCA	TGATTGAGAA	GTTTGCAGTT	TTGTACCAGC	1200
	AGTTGGATGG	AGAGGACCAA	ACCAAGCATG	AATTTTGGAC	AGATGGCTAT	CAAGACTTGG	1260
	GTGCTATTCT	CAATAATTTG	CTACCCAATA	TGAGTTATGT	TCTTCAGATA	GTAGCCATAT	1320
35	GCCTAATG	CTTATATGGA	AAATACAGCG	ACCAACTGAT	TGTCGACATG	CCTACTGATA	1380
	ATCCTGAAT	TGATCTTTTC	CCTGAATTAA	TTGGAAGTGA	AGAAATAATC	AAGGAGGAGG	1440
	AAGAGGGAAA	AGACATTGAA	GAAGGCGCTA	TTGTGAATCC	TGGTAGAGAC	AGTGCTACAA	1500
	ACCAAAATCAG	GAAAAAGGAA	CCCCAGATTT	CTACCAACAAC	ACACTACAAT	CGCATAGGGA	1560
40	CGAAATACAA	TGAAGCCAA	ACTAACCGAT	CCCCAACAAAG	AGGAAGTGAA	TTCTCTGGAA	1620
	AGGGTGATGT	TCCCAATACA	TCTTTAAATT	CCACTTCCCA	ACCAGTCACT	AAATTAGCCA	1680
	CAGAAAAAGA	TATTTCTCTG	ACTTCTCAGA	CTGTGACTGA	ACTGCCACCT	CACACTGTGG	1740
	AAGGTACTTC	AGCCTCTTTA	AATGATGGCT	CTAAAACTGT	TCTTAGATCT	CCCATATGTA	1800
	ACTTGTCCGG	GAGTCGAGAA	TCCTTAATAA	CAGTTTCTAT	AAACAGATAT	GAGGAGGAGA	1860
45	GTTTATTGAC	CAGTTTCAAG	CTTGATCTG	GAGCTGAAGA	TTCTTCAGGC	TCCAGTCCCG	1920
	CAACTTCTGC	TATCCCATTG	ATCTCTGAGA	ACATATCCCA	AGGGTATATA	TTTTCTCCCG	1980
	AAAACCCAGA	GACAAATAAC	TATGATGTCC	TTATACCAGA	ATCTGCTAGA	AATGCTTCCG	2040
	AAGATTCAAC	TTCAATCAGT	TCAGAAAGAA	CACATAAGGA	TCCTTCTATG	GAGGGAATG	2100
	TGTGGTTTCC	TAGCTCTACA	GACATAACAG	CACAGCCCGA	TGTTGGATCA	GGCAGAGAGA	2160
50	GCTTTCTCCA	GACTAATTAC	ACTGAGATAC	GTGTTGATGA	ATCTGAGAAG	ACAACCAAGT	2220
	CCTTTTCTCG	AGGCCCAATG	ATGTCACAGG	GTCCCTCAGT	TACAGATCTG	GAAATGCCAC	2280
	ATTATTTCTAC	CTTTGCCCTAC	TTCCCAACTG	AGGTAACACC	TCATGCTTTT	ACCCCATCCT	2340
	CCAGACAACA	GGATTGTGTC	TCCACGGTCA	ACGTGGTATA	CTCGCAGACA	ACCCCAACCGG	2400
	TATACAATGA	GGCCAGTAAT	AGTAGCCATG	AGTCTCGTAT	TGGTCTAGCT	GAGGGGTTGG	2460
55	AATCCGAGAA	GAAGGCAGTT	ATACCCCTTG	TGATCGTGTC	AGCCCTGACT	TTTATCTGTC	2520
	TAGTGGTTCT	TGTGGGTAAT	CTCATCTACT	GGAGGAAATG	CTTCCAGACT	GCACACTTTT	2580
	ACTTAGAGGA	CAGTACATCC	CCTAGAGTTA	TATCCACACC	TCCAACACCT	ATCTTTCCAA	2640
	TTTCAGATGA	TGTCGGAGCA	ATTCCAATAA	AGCACTTTCC	AAAGCATGTT	GCAGATTTAC	2700
	ATGCAAGTAG	TGGGTTTACT	GAAGAATTGG	AGCACTGAA	AGAGTTTAC	CAGGAAGTGC	2760
	AGAGCTGTAC	TGTTGACTTA	GGTATTACAG	CAGACAGCTC	CAACCACCCA	GACAACAAGC	2820
60	ACAAGAATCG	ATACATAAAT	ATCGTTGCCT	ATGATCATAG	CAGGGTTAAG	CTAGCACAGC	2880
	TTGCTGAAAA	GGATGGCAAA	CTGACTGATT	ATATCAATGC	CAATTATGTT	GATGGCTACA	2940
	ACAGACCAAA	AGCTTATATT	GCTGCCCAAG	GCCCACTGAA	ATCCACAGCT	GAAGATTCTT	3000
	GGAGAATGAT	ATGGGAACAT	AATGTGGAAG	TTATTGTGAT	GATAACAAAC	CTCGTGGAGA	3060
	AAGGAAGGAG	AAAATGTGAT	CAGTACTGGC	CTGCCGATGG	GAGTGAGGAG	TACGGGAAGT	3120
65	TTCTGGTCC	TCAGAAAGAT	GTGCAAGTGC	TTGCCATTTA	TACTGTGAGG	AATTTTACTC	3180
	TAAGAAACAC	AAAAATAAAA	AAGGGCTCCC	AGAAAGGAAG	ACCCAGTGGA	CGTGTGGTCA	3240
	CACAGTATCA	CTACACGCAG	TGGCCTGACA	TGGGAGTACC	AGAGTACTCC	CTGCCAGTGC	3300
	TGACCTTTGT	GAGAAAGGCA	GCCTATGCCA	AGCGCCATGC	AGTGGGGCCT	GTTGTGCTCC	3360
70	ACTGCAGTGC	TGGAGTTGGA	AGAACAGGCA	CATATATTGT	GCTAGACAGT	ATGTTGCAGC	3420
	AGATTCAACA	CGAAGGAAGT	GTCAACATAT	TTGGCTTCTT	AAAAACATC	CGTTTCAAAA	3480
	GAAATTTATT	GGTACAAACT	GAGGAGCAAT	ATGCTTTCAT	TCATGATACA	CTGGTTGAGG	3540
	CCATACCTTAC	TAAAGAAACT	GAGGTGCTGG	ACAGTCATAT	TCATGCCTAT	GTTAATGCAC	3600
	TCCTCATTTG	TGGACACGCA	GGCAAAACAA	AGCTAGAGAA	ACAATTCAG	CTCCTGAGCC	3660
	AGTCAAAATAT	ACAGCAGAGT	GACTATTCTG	CAGCCCTAAA	GCAATGCAAC	AGGGAAAAGA	3720
75	ATCGAACTTC	TTCTATCATC	CCTGTGAAAA	GATCAAGGGT	TGGCATTTCA	TCCCTGAGTG	3780
	GAGAAAGGCAC	AGACTACATC	AATGCCCTCT	ATATCATGGG	CTATTACCAG	AGCAATGAAT	3840
	TCATCATTTAC	CCAGCACCCCT	CTCCTTCATA	CCATCAAGGA	TTTCTGGAGG	ATGATATGGG	3900
	ACCATAATGC	CCAATGGGTG	GTTATGATTG	CTGATGGCCA	AAACATGGCA	GAAGATGAAT	3960
80	TTGTTTACTG	GCCAAATAAA	GATGAGCCTA	TAAATGTGTA	GAGCTTTAAG	GTCACCTTTA	4020
	TGGCTGAAAG	ACACAATATG	CTATCTAATG	AGGAAAAACT	TATAATTGAG	GACTTTATCT	4080
	TAGAAGCTAC	ACAGGATGAT	TATGTACTTG	AAGTGAGGCA	CTTTCAGTGT	CCTAAATGGC	4140
	CAAATCCAGA	TAGCCCCATT	AGTAAACCTT	TTGAACCTAT	AAGTGTTATA	AAAGAAGAAG	4200
	CTGCCAATAG	GGATGGGCCT	ATGATGTTTC	ATGATGAGCA	TGGAGGAGTG	ACGGCAGGAA	4260
	CTTTCTGTGC	TCTGACAACC	CTTATGCACC	AACTAGAAAA	AGAAAATTCC	GTGGATGTTT	4320

ACCAGGTAGC CAAGATGATC AATCTGATGA GGCCAGGAGT CTTTGCTGAC ATTGAGCAGT 4380  
 ATCAGTTTCT CTACAAAGTG ATCCTCAGCC TTGTGAGCAC AAGGCAGGAA GAGAATCCAT 4440  
 CCACCTCTCT GGACAGTAAT GGTGCAGCAT TGCCCTGATGG AAATATAGCT GAGAGCTTAG 4500  
 AGTCTTTAGT TTAACACAGA AAGGGGTGGG GGGACTCACA TCTGAGCATT GTTTTCCTCT 4560  
 TCCTAAAAAT AGGCAGGAAA ATCAGTCTAG TTCTGTTATC TGTTGATTTC CCATCACCTG 4620  
 ACAGTAACTT TCATGACATA GGATTCTGCC GCCAAATTTA TATCATTAAC AATGTGTGCC 4680  
 TTTTGTCAAG ACTTGTAAAT TACTTATTAT GTTTGAACATA AAATGATTGA ATTTTACAGT 4740  
 ATTTCTAAGA ATGGAATTGT GGTATTTTTT TCTGTATTGA TTTTAACAGA AAATTTCAAT 4800  
 TTATAGAGGT TAGGAATTCC AAACACAGA AAATGTTTGT TTTTAGTGTC AAATTTTAG 4860  
 CTGTATTTGT AGCAATTATC AGGTTTGCTA GAAATATAAC TTTTAATACA GTAGCTGTGA 4920  
 AATAAAACAC TCTTCCATAT GATATTCAAC ATTTTACAAC TGCAGTATTC ACCTAAAGTA 4980  
 GAAATAATCT GTTACTTATT GTAAATACAG CCCTAGTGTC TCCATGGACC AAATTTATAT 5040  
 TTATAATTGT AGATTTTAT ATTTTACTAC TGAGTCAAGT TTTCTAGTTC TGTGTAATTG 5100  
 TTTAGTTTAA TGACGTAGTT CATTAGCTGG TCTTACTCTA CCAGTTTCT GACATTGTAT 5160  
 TGTGTTACCT AGCTCATTAA CTTTGTTCAT GCATGTAATT TTAACCTTTG TGGAAAATAG 5220  
 AAATACCTTC ATTTTGAAAG AAGTTTATAT GAGAATAACA CCTTACCAA CATTGTTCAA 5280  
 ATGGTTTTTA TCCAAGGAAT TGCAAAAATA AATATAAATA TTGCCATTAA AAAAAAATA 5340  
 AAAAAAATA AAA 5363

Seq ID NO: C100 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 148..4362

1 11 21 31 41 51  
 CACACATACG CACGCACGAT CTCACTTCGA TCTATACACT GGAGGATTAA AACAAACAAA 60  
 CAAAAAAAC ATTTCCCTCG CTCCCCTCC CTCTCCACTC TGAGAAGCAG AGGAGCCGCA 120  
 CGGCGAGGGG CCGCAGACCG TCTGGAATG CGAATCCTAA AACGTTTCCT CGCTTGCAAT 180  
 CAGCTCCTCT GTGTTTGGCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240  
 CTGTGTTGAAG AGATTGGCTG GTCCTATACA GGAGCACTGA ATCAAAAAAA TTGGGGAAAG 300  
 AAATATCCAA CATGTAATAG CCCAAACAAA TCTCCTATCA ATATTGATGA AGATCTTACA 360  
 CAAGTAAATG TGAATCTTAA GAACTTAA TTTAGGGTT GGGATAAAC ATCATTGGAA 420  
 AACACATTCA TTCATAACAC TGGGAAAACA GTGGAAATTA ATCTCACTAA TGACTACCGT 480  
 GTCAGCGGAG GAGTTTTCAGA AATGGTGTTC AAAGCAAGCA AGATAACTTT TCACTGGGGA 540  
 AAATGCAATA TGTCATCTGA TGGATCAGAG CATAGTTTAG AAGGACAAAA ATTTCCACTT 600  
 GAGATGCAAA TCTACTGCTT TGATGCGGAC CGATTTTCAA GTTTTGAGGA AGCAGTCAA 660  
 GGAAAAGGGA AGTTAAGAGC TTTATCCATT TTGTTTGAGG TTGGGACAGA AGAAAATTTG 720  
 GATTTCAAAG CGATTATTGA TGGAGTCGAA AGTGTGTAGT GTTTTGGGAA GCAGGCTGCT 780  
 TTAGATCCAT TCATACTGTT GAACCTTCTG CCAACTCAA CTGACAGATA TTACATTAC 840  
 AATGGCTCAT TGACATCTCC TCCCTGCACA GACACAGTTG ACTGGATTGT TTTAAAGAT 900  
 ACAGTTAGCA TCTCTGAAAG CCAGTTGGCT GTTTTTTGT GAAGTTCTTA CAATGCAACA 960  
 ATCTGTTTAT TGCATGCTGA TGGACTACTT ACAAAACAAT TTTCGAGAGC AACAGTACAA 1020  
 GTTCTCTAGA CAGGTGTTTT CCTCATACAC TGGAAAGGAA GAGATTTCATG AAGCAGTTTG 1080  
 TAGTTTCAAA CCGAGAAATG TTCAGGCTGA CCCAGAGAA TATACCAGCC TTTCTGTTAC 1140  
 ATGGGAAAGA CCTCGAGTCG TTTATGATAC CATGATTGAG AAGTTTGAGG TTTTGATACCA 1200  
 GCAGTTGGAT GGAGAGGACC AAACCAAGCA TGAATTTTGG ACAGATTGGCT ATCAAGACTT 1260  
 GGGTGCTATT CTCAATAATT TGCTACCCAA TATGAGTTAT GTTCTTCAGA TAGTAGCCAT 1320  
 ATGCACTAAT GGCTTATATG GAAATACAG CGACCAACTG ATTGTGACGA TGCTACTGTA 1380  
 TAATCCTGAA CTGTGATCTT TCCCTGAATT AATTGGAAT GAAGAAATAA TCAAGGAGGA 1440  
 GGAAGAGGGA AAGACATTG AAGAAGGCGC TATTTGTAAT CCTGGTAGAG ACAGTGCTAC 1500  
 AAACCAATATC AGGAAAAGG AACCACAGAT TTCTACCACA ACACACTACA ATCGCATAGG 1560  
 GACGAAATAC AATGAAGCCA AGACTAACCG ATCCCCAACA AGAGGAGTGA AATCTCTGG 1620  
 AAAGGGTGAT GTTCCCAATA CATCTTTTAA TTTCACTTCC CAACCACTCA CTAAATTAGC 1680  
 CACAGAAAAA GATATTTTCT TGACTTCTCA GACTGTGACT GAAGTGGCAC CTCACACTGT 1740  
 GGAAGGTACT TCGAGCTTCT TAAATGATGG CTCTAAACT GTTCTTAGAT CTCACATAT 1800  
 GAACCTGTGCG GGGACTGCAG AATCCTTAAA TACAGTTTCT ATAACAGAA ATGAGGAGGA 1860  
 GAGTTTATTG ACCAGTTTCA AGCTTGATAC TGGAGCTGAA GATTTCTCAG GCTCCAGTCC 1920  
 CGCAACTTCT GCTATCCCTA TCTATCTGTA GAACATATCC CAAGGGTATA TATTTTCTCT 1980  
 CGAAAAACCA GAGACAATAA CATATGATGT CCTTATACCA GAATCTGCTA GAAATGCTTC 2040  
 CGAAGATTCA ACTTCATCAG GTTCAGAAGA ATCACTAAAG GATCCTTCTA TGGAGGGAAA 2100  
 TGTGTGGTTT CCTAGCTCTA CAGACATAAC AGCACAGCCC GATGTTGGAT CAGGCAGAGA 2160  
 GAGCTTTCTC CAGACTAATT ACATGAGAT ACGTGTGAT GAATCTGAGA AGACAACCAA 2220  
 GTCCTTTTCT CGAGGCCAGG TGATGTCACA GGGTCCCTCA GTTACAGATC TGGAAATGCC 2280  
 ACATTATCTT ACCTTTGCTT ACTTCCCAAC TGAGGTAACA CCTCATGCTT TTACCCCATC 2340  
 CTCAGACCAA CAGGATTTGG TCTCCACGGT CAACGTGGTA TACTGCAGA CAACCCAACT 2400  
 GGTATACAAT GAGGCCAGTA ATAGTAGCCA TGAGTCTCGT ATTTGCTAG CTGAGGGGTT 2460  
 GGAATCCGAG AAGAAGGCAG TTATACCCCT TGTGATCGTG TCAGCCCTGA CTTTATCTG 2520  
 TCTAGTGGTT CTTGTGGGTA TTCTCATCTA CTGGAGGAAA TGCTTCCAGA CTGCACACTT 2580  
 TTACTTAGAG GACAGTACAT CCCCTAGAGT TATATCCACA CCTCCAACAC CTATCTTCTC 2640  
 AATTTTCAGT GATGTCGGAG CAATTCCAAT AAAGCACTTT CCAAAGCATG TTGCGAGATT 2700  
 ACATGCAAGT AGTGGGTTTA CTGAAGAATT TGAGACACTG AAAGAGTTT ACCAGGAAGT 2760  
 GCAGAGCTGT ACTGTGACT TAGGTATTAC AGCAGACAGC TCCAACCAAC CAGACAACAA 2820  
 GCACAAGAA CTATACATAA ATATCGTTGC CTATGATCAT AGCAGGTTA AGTAGCACA 2880  
 GCTTGTGTA AGGATGGCAA ACTGACTGAT TATATCAATG CCAATTATGT TGATGGCTAC 2940  
 AACAGACCAA AAGCTTATAT TGCTGCCCAA GGCCCACTGA AATCCACAGC TGAAGATTTC 3000  
 TGGAGAAATG TATGGGAACA TAATGTGGAA GTTATTGTCA TGATAACAAA CCTCGTGGAG 3060  
 AAAGGAAGGA GAAATGTGA TCAGTACTGG CCTGCCGATG GGAGTGAGGA GTACGGGAAC 3120  
 TTTCTGGTCA CTCAGAAGAG TGTGCAAGTG CTGCTTATT ATACTGTGAG GAATTTTACT 3180  
 CTAAGAAACA CAATAAATAA AAAGGCTCC CAGAAAGGAA GACCCAGTGG ACGTGTGGTC 3240  
 ACACAGTATC ACTACACGCA GTGGCCTGAC ATGGGAGTAC CAGAGTACTC CCTGCCAGTG 3300  
 CTGACCTTTG TGAGAAAGGC AGCCTATGCC AAGCGCATG CAGTGGGGCC TGTGTCTGTC 3360  
 CACTGCAGTG CTGGAGTTGG AAGAACAGGC ACATATATTG TGCTAGACAG TATGTTGCAG 3420  
 CAGATTCAAC ACGAAGGAAC TGTCAACATA TTTGGCTTCT TAAACACAT CCGTTCACAA 3480  
 AGAATTATAT TGGTACAAC TGAGGAGCAA TATGCTTCA TTCATGATAC ACTGGTTGAG 3540

5	GCCATACTTA GTAAAGAAAC TGAGGTGCTG GACAGTCATA TTCATGCCTA TGTTAATGCA 3600
	CTCCTCATTC CTGGACCAGC AGGC AAAACA AAGCTAGAGA AACAAATCCA GGGCTCCTACT 3660
	CTGTCAACCA GGCTGGAGTG CAGAGGCACA ATCTCGGCTC ACTGCAACCT TCCTCTCCCT 3720
	GGCTTAACATG ATCCTCTCTAC CTCAGGCTCC CGAGTGGCTG GGACTATACT CCTGAGCCAG 3780
	TCAAATATAC AGCAGATGA CTATTCTGCA GCCCTAAAGC AATGCAACAG GGAAAAGAAT 3840
	CGAACTTCTT CTATCATCCC TGTGGAAAGA TCAAGGGTTG GCATTTCAATC CCTGAGTGGA 3900
	GAAGGCACAG ACTACATCAA TGCCCTCTAT ATCATGGGCT ATTACCAGAG CAATGAATTC 3960
	ATCATTACCC AGCACCTCT CTTCATACC ATCAAGGATT TCTGGAGGAT GATATGGGAC 4020
10	CATAATGCCG AACTGGTGGT TATGATTCCCT GATGGCCAAA ACATGGCAGA AGATGAATTT 4080
	GTTTACTGGC CAAATAAAGA TGAGCCTATA AATTGTGAGA GCTTTAAGGT CACTCTTATG 4140
	GCTGAAGAAC ACAAATGTCT ATCTAATGAG GAAAACTTA TAATTCAGGA CTTTATCTTA 4200
	GAAGCTACAC AGGATGATTA TGTACTTGAA GTGAGGCCTT TTCAGTGTCC TAAATGGCCA 4260
	AATCCAGATA GCCCCATTAG TAAAACTTTT GAACCTATAA GTGTTATAAA AGAAGAAGCT 4320
15	GCCAAATAGG ATGGGCTTAT GATTGTTTCT GATGAGCATG GAGGAGTGAC GGCAGGAATC 4380
	TTCTGTGCTC TGACAACCCCT TATGCACCAA CTAGAAAAAG AAAATTCCGT GGATGTTTAC 4440
	CAGGTAGCCA AGATGATCAA TCTGATGAGG CCAGGAGTCT TTGCTGACAT TGAGCAGTAT 4500
	CAGTTTCTCT ACAAAGTGAT CCTCAGCCTT GTGGGCACAA GGCAGGAAGA GAATCCATCC 4560
	ACCTCTCTGG ACAGTAATGG TGCAGCATTG CCTGATGGAA ATATAGCTGA GAGCTTAGAG 4620
20	TCCTTTAGTTT AACACAGAAA GGGGTGGGGG GACTCACATC TGAGCATTGT TTCTCTCTTC 4680
	CTAAAAATTAG GCAGGAAAAAT CAGTCTAGTT CTGTTATCTG TTGATTTCCC ATCACCTGAC 4740
	AGTAACCTTC ATGACATAGG ATTCTGCCGC CAAATTATA TCATTACAA TGTGTGCCCT 4800
	TTTGCAAGAC TGTAAATTTA CTTATTATGT TTGAACATAA ATGATTGAAT TTTACAGTAT 4860
	TTCTAAGAAT GGAATTGTGG TATTTTTTTC TGTATTGATT TTAACAGAAA ATTTCAATT 4920
25	ATAGAGGTTA GGAATTCCAA ACTACAGAAA ATGTTTGTGT TTAGTGTCAA ATTTTATAGCT 4980
	GTATTGTAG CAATTATCAG GTTTGCTAGA AATATAACTT TTAATACAGT AGCCTGTAAA 5040
	TAAACACTC TTCCATAGTA TATTCAACAT TTTACAACCT CAGTATTCAC CTAAGTAGA 5100
	AATAATCTGT TACTTATGT AAATACTGCC CTAGTGTCTC CATGGACCAA ATTTATATTT 5160
	ATAATTGTAG ATTTTTATAT TTTACTACTG AGTCAAGTTT TCTAGTCTG TGTAAATGTT 5220
30	TAGTTTAATG ACCTAGTTCA TTAGCTGCTC TTACTCTACC AGTTTCTCGA CATTGTATTG 5280
	TGTTACCTAA GTCATTAATC TTGTTTCAGC ATGTAATTTT AACTTTTGTG GAAAAATAGAA 5340
	ATACCTTCAT TTTGAAAGAA GTTTTTATGA GAATAACACC TTACCAACA TTGTTCAAA 5400
	GGTTTTTATC CAAGGAATTG CAAAAATAA TATAAATATT GCCATTAAAA AAAAAAATA 5460
	AAAAAATAA AAAAAAATA A 5481

Seq ID NO: C101 DNA Sequence  
Nucleic Acid Accession #: Eos sequence  
Coding sequence: 1..3340

40	1	11	21	31	41	51	
	ATGCGAATCC	TAAAGCGTTT	CCTCGCTTGC	ATTCAAGTCC	TCTGTGTTTG	CCGCCTGGAT	60
	TGGGCTAATG	GATACCTACAG	ACAAACAGAGA	AAACTTGTGT	AAGAGATTGG	CTGGTCCCTAT	120
	ACAGGAGCAC	TGAATCAAAA	AAATTGGGGA	AAGAAATATC	CAACATGTAA	TAGCCCAAAA	180
45	CAATCTCCTA	TCAATATTGA	TGAAGATCTT	ACACAAGTAA	ATGTGAATCT	TAAGAAACTT	240
	AAATTTGAGG	GTGTTGGGATAA	AACATCATTTG	GAAAACACAT	TGATTCTATAA	CACTGGGAAA	300
	ACAGTGGAAA	TTAATCTCAC	TAATGACTAC	CGTGTCAGCG	CAGAGGTTTC	AGAAATGGTG	360
	TTTAAAGCAA	GCAAGATAAC	TTTTCACTGG	GGAAAATGCA	ATATGTCTATC	TGTATGGATCA	420
	GAGCATAGTT	TAGAAGGACA	AAAATTTCCA	CTTGAGATGC	AAATCTACTG	CTTGTTATGCG	480
50	GACCGATTTT	CAAGTTTTGA	GGAAGCAGTC	AAAGGAAAAG	GGAAGTTAAG	AGCTTTATCC	540
	ATTTTGTGTT	AGGTTGGGAC	AGAAAGAAAAT	TGGAATTTCA	AAGCGATTAT	TGATGGAGTC	600
	GAAAGTGTTA	GTCGTTTTGG	GAAGCAGGCT	GCTTTAGATC	CATTCTACTC	GTTGAACCTT	660
	CTGCCAAACT	CAACTGACAA	GTATTACATT	TACAATGGCT	CATTGACATC	TCCTCCCTGC	720
	ACAGACACAG	TTGACTGGAT	TGTTTTTAAA	GATACAGTTA	GCATCTCTGA	AAGCCAGTTG	780
55	GCTGTTTTTT	GTGAAGTTCT	TACAATGCAA	CAATCTGGTT	ATGTCTATGCT	GATGGACTAC	840
	TTACAAAAAC	ATTTTCGAGA	GCAACAGTAC	AAGTTCTCTA	GACAGGTTGT	TTCTCTCATC	900
	ACTGGAAAGG	AAGAGATTCA	TGAAGCAGTT	TGTAGTTTCA	AACCAGAAAA	TGTTCAAGCT	960
	GACCCAGAGA	ATTATACCAG	CCTTCTTGTT	ACATGGGAAA	GACCTCGAGT	CGTTTATGAT	1020
	ACCATGATTG	AGAAGTTTGC	AGTTTGTGAC	CAGCAGTTGG	ATGGAGAGGA	CCAAACCAAG	1080
60	CATGAATTTT	TGACAGATGG	CTATCAAGAC	TTGGGTGCTA	TTCTCAATAA	TTTGCTACCC	1140
	AATATGAGTT	ATGTTCTTCA	GATAGTAGCC	ATATGCACTA	ATGGCTTATA	TGGAAAAATC	1200
	AGCGACCAAC	TGATTGTCTGA	CATGCCTACT	GATAATCCTG	AGGCCAGTAA	TAGTAGCCAT	1260
	GAGTCTCTGA	TTGTTCTAGC	TGAGGGGTTG	GAATCCGAGA	AGAAGGCAGT	TATACCCCTT	1320
	GTGATCGTGT	CAGCCCTGAC	TTTTTATCTGT	CTAGTGGTTC	TTGTGGGTAT	TCTCATCTAC	1380
65	TGGAGGAAAT	GCTTCCAGAC	TGCACACTTT	TACTTAGAGG	ACAGTACATC	CCCTAGAGTT	1440
	ATATCCACAC	CTCCAACACC	TATCTTTCCA	ATTTCAAGAT	ATGTCGGAGC	AATTCCAATA	1500
	AAGCACTTTC	CAAAGCATGT	TGCAGATTTA	CATGCAAGTA	GTGGGTTTAC	TGAAGAATTT	1560
	GAGACACTGA	AAGAGTTTTA	CCAGGAAGTG	CAGAGCTGTA	CTGTTGACTT	AGGTATTACA	1620
	GCAGACAGCT	CCAACCAACC	AGACAACAAG	CACAAGAATC	GATACATAAA	TATCGTTGCC	1680
70	TATGATCATA	GCAGGGTTAA	GCTAGCACAG	CTGTCTGAAA	AGGATGGCAA	ACTGACTGAT	1740
	TATATCAATG	CCAATTATGT	TGATGGCTAC	AACAGACCAA	AAGCTTATAT	TGCTGCCCAA	1800
	GGCCCACTGA	AATCCACAGC	TGAAGATTTT	TGGAGAATGA	TATGGGAACA	TAATGTGGAA	1860
	GTTATTGTCA	TGATAACAAA	CCTCGTGGAG	AAAGGAAGGA	GAAAATGTGA	TCAGTACTGG	1920
	CCTGCCGATG	GGAGTGAGGA	GTAACGGGAAC	TTTCTGGTCA	CTCAGAAGAG	TGTGCAAGTG	1980
75	CTTGCCCTATT	ATACTGTGAG	GAATTTTACT	CTAAGAAACA	CAAAAATAA	AAAGGGCTCC	2040
	CAGAAAGGAA	GACCCAGTGG	ACGTGTGGTC	ACACAGTATC	ACTACACGCA	GTGGCCTGAC	2100
	ATGGGAGTAC	CAGAGTACTC	CCTGCCAGTG	CTGACCTTTG	TGAGAAGGCG	AGCCTATGCC	2160
	AAGCGCCATG	CAGTGGGGCC	TGTTGTGCTC	CAGTGCAGTG	CTGGAGTTGG	AAGAACAGGC	2220
	ACATATATTG	TGCTAGACAG	TATGTTGCAG	GAGATTCAAC	ACGAAGGAAC	TGTCAACATA	2280
	TTTGGCTTCT	TAAAACACAT	CCGTTACAAA	AGAAATTAAT	TGGTACAAAC	TGAGGAGCAA	2340
80	TATGTCTTCA	TTCATGATAC	ACTGGTTGAG	GCCATACTTA	GTAAGAAAC	TGAGGTGCTG	2400
	GACAGTCATA	TTCAATGCTTA	TGTTAATGCA	CTCCTCATTC	CTGACCAGCG	AGGCCAAACA	2460
	AAGCTAGAGA	AACAATTCOA	GTCCTGAGC	CAGTCAAATA	TACAGCAGAG	TGACTATTCT	2520
	GCAGCCCTAA	AGCAATGCAA	CAGGGAAGAG	AATCGAACTT	CTTCTATCAT	CCCTGTGGAA	2580
	AGATCAAGGG	TTGGCATTTT	ATCCCTGAGT	GGAGAAGGCA	CAGACTACAT	CAATGCCTCC	2640

TATATCATGG GCTATTACCA GAGCAATGAA TTCATCATT CTCAGCACCC TCTCCTTCAT 2700  
 ACCATCAAGG ATTTCTGGAG GATGATATGG GACCATAATG CCCAACTGGT GGTATGATT 2760  
 CCTGATGGCC AAAACATGGC AGAAGATGAA TTGTGTTACT GGCCAAATAA AGATGAGCCT 2820  
 ATAAATTGTG AGAGCTTTAA GGTCACTCTT ATGGCTGAAG AACACAAATG TCTATCTAAT 2880  
 GAGGAAAAAC TTATAATTCA GGACTTTATC TTAGAAGCTA CACAGGATGA TTATGTACTT 2940  
 GAAGTGAGGC ACTTTTCAGT TCCTAAATGG CCAATCCAG ATAGCCCCAT TAGTAAAACT 3000  
 TTTGAACCTA TAAGTGTTAT AAAAGAAGAA GCTGCCAATA GGGATGGGCC TATGATTGTT 3060  
 CATGATGAGC ATGGAGGAGT GACGGCAGGA ACTTTCTGTG CTCTGACAC CTTTATGCAC 3120  
 CAACTAGAAA AAGAAAAATC CGTGGATGTT TACCAGGTAG CCAAGATGAT CAATCTGATG 3180  
 AGGCCAGGAG TCTTTGCTGA CATTGAGCAG TATCAGTTTC TCTACAAAGT GATCCTCAGC 3240  
 CTTGTGAGCA CAAGGAGGA AGAGAATCCA TCTACCTCTC TGGACAGTAA TGGTGACGCA 3300  
 TTGCTGATG GAAATATAGC TGAGAGCTTA GAGTCTTTAG 3340

Seq ID NO: C102 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..4480

1 11 21 31 41 51  
 20 ATGCGAATCC TAAAGCGTTT CCTCGCTTGC ATTACGCTCC TCTGTGTTTG CCGCCTGGAT 60  
 TGGGCTAATG GATACCTACAG ACAACAGAGA AAACCTGTTG AAGAGATTGG CTGGTCTTAT 120  
 ACAGGAGCAC TGAATCAAAA AAATTTGGGA AAGAAATATC CAACATGTAA TAGCCCCAAA 180  
 CAATCTCCTA TCAATATTGA TGAAGATCTT ACACAAGTAA ATGTGAATCT TAAGAAACTT 240  
 25 AAATTTTCAGG GTTGGGATAA AACATCATTG GAAACACAT TCATTATAA CACTGGGAAA 300  
 ACAGTGGAAA TTAATCTCAC TAATGACTAC CGTGTACGCG GAGGAGTTTC AGAAATGGTG 360  
 TTTAAAGCAA GCAAGATAAC TTTTCACTGG GAAAAATGCA ATATGTCAATC TAGGGATCA 420  
 GAGCATAGTT TAGAAGGACA AAAATTTCCA CTTGAGATGC AAATCTACTG CTTTGATGCA 480  
 GACCGATTTT CAAGTTTTGA GGAAGCAGTC AAAGGAAAAG GGAAGTTAAG AGCTTTATCC 540  
 30 ATTTTGTGTT AGGTTGGGAC AGAAGAAAAT TTGGATTCA AAGCGATTAT TGATGGAGTC 600  
 GAAAGTGTTA GTCGTTTTGG GAAGCAGGCT GCTTTAGATC CATTCACTAT GTTGAACCTT 660  
 CTGCCAAACT CAACCTGACA GTATTACATT TACAATGGTT CATTGACATC TCCTCCCTGC 720  
 ACAGACACAG TTGACTGGAT TGTTTTTAAA GATACAGTTA GCATCTCTGA AAGCCAGTTG 780  
 GCTGTTTTTT GTGAAGTTCT TACAATGCAA CAATCTGGTT ATGTCATGCT GATGGACTAC 840  
 35 TTACAAAACA ATTTTCGAGA GCAACAGTAC AAGTTCTCTA GACAGGTGTT TTCCTCATAC 900  
 ACTGGAAAGG AAGAGATTCA TGAAGCAGTT TGTAAGTTCAG AACCAGAAAA TGTTCAAGCT 960  
 GACCCAGAGA ATTATACAG CTTTCTGTT ACATGGGAAA GACCTCGAGT CGTTTATGAT 1020  
 ACCATGATTG AGAAGTTTGC AGTTTTGTAC CAGCAGTTGG ATGGAGAGGA CCAAAACCAAG 1080  
 CATGAATTTT TGACAGATGG CTATCAAGAC TTGGGTGCTA TTCTCAATAA TTTGCTACCC 1140  
 40 AATATGAGTT ATGTTCTTCA GATAGTAGCC ATATGCACTA ATGGCTTATA TGGAAATATC 1200  
 AGCGACCAAC TGATTGTGCA CATGCCCTACT GATAATCCTG AACTTGATCT TTTCCCTGAA 1260  
 TTAATTGGAA CTGAAGAAAT AATCAAGGAG GAGGAAGAGG GAAAGACAT TGAAGAAGGC 1320  
 GCTATTGTGA ATCCTGGTAG AGACAGTACT ACAAACCAA TCAGGAAAAA GGAACCCAG 1380  
 ATTTCTACCA CAACACACTA CAATCGCATA GGGACGAAAT ACAATGAAGC CAAGACTAAC 1440  
 CGATCCCAA CAAGAGGAAG TGAATTCTCT GGAAGGGTGT ATGTTCCCAA TACATCTTTA 1500  
 45 AATCCACTT CCCAACAGT CACTAAATTA GCCACAGAAA AAGATATTTT CTTGACTTCT 1560  
 CAGACTGTGA CTGAACCTGCC ACCTCACACT GTGGAAGGTA CTTGAGCCTC TTTAAATGAT 1620  
 GGCTCTAAAA CTGTCTTAG ATCTCCACAT ATGAACCTGT CGGGGACTGC AGAATCCTTA 1680  
 AATACAGTTT CTATACAGCA ATATGAGGAG GAGAGTTTAT TGACCAGTTT CAAGCTTGAT 1740  
 50 ACTGGAGCTG AAGATTCTTC AGGCTCCAGT CCCGCAACTT CTGCTATCCC ATTCATCTCT 1800  
 GAGAACATAT CCCAAGGGTA TATATTTTCC TCCGAAAACC CAGAGACAA AACTATATGAT 1860  
 GTCCTTATAC CAGATCTGTC TAGAAATGCT TCCGAAGATT CAACCTCATC AGGTTTCAGAA 1920  
 GAATCACTAA AGGATCTCTT TATGGAGGGA AATGTGTGGT TTCTTAGCTC TACAGACATA 1980  
 ACAGCACAGC CCGATGTTGG ATCAGGCAGA GAGAGCTTTC TCCAGACTAA TTACACTGAG 2040  
 55 ATACGTGTTG ATGAATCTGA GAAGACAACC AAGTCTCTTT CTGCAGGCCC AGTGATGTCA 2100  
 CAGGGTCCCT CAGTTTACAGA TCTGGAAATG CCACATTATT CTACCTTTGC CTACTTCCCA 2160  
 ACTGAGGTAA CACCTCATGC TTTTATCCCA TCCTCCAGAC AACAGGATTT GGTCTCCACG 2220  
 GTCAACGTGG TATACCTGCA GACAACCCAA CCGGTATACA ATGAGGCCAG TAATAGTAGC 2280  
 CATGAGTCTC GTATTGGTCT AGCTGAGGGG TTGGAATCCG AGAAGAAGGC AGTTATACCC 2340  
 CTTGTGATCG TGTGAGCCCT GACTTTTATC TGTCTAGTGG TTCTTGTGGG TATTCTCATC 2400  
 60 TACTGGAGGA AATGCTTCCA GACTGCACAC TTTTACTTAG AGGACAGTAC ATCCCTTAGA 2460  
 GTTATATCCA CACCTCCAAC ACCTATCTTT CCAATTTTCA ATGATGTGCG AGCAATTCCA 2520  
 ATAAAGCACT TTCCAAAGCA TGTTCAGAT TTACATGCAA GTAGTGGGTT TACTGAAGAA 2580  
 TTTGAGACAC TGAAAGAGTT TTACCAGGAA GTGCAGAGCT GTACTGTTGA CTTAGGTATT 2640  
 65 ACAGCAGACA GCTCCAACCA CCCAGACAAC AAGCAACAAG ATCGATACAT AAATATCGTT 2700  
 GCCATGATC ATAGCAGGGT TAAGCTAGCA CAGCTTGCTG AAAAGGATGG CAAACTGACT 2760  
 GATTATATCA ATGCCAATTA TGTGATGGC TACAACAGAC CAAAAGCTTA TATTGCTGCC 2820  
 CAAGGCCAC TGAAATCCAC AGCTGAAGAT TTCTGGAGAA TGATATGGGA ACATAATGTG 2880  
 70 GAAGTTATTG TCATGATAAC AAACCTCGTG GAGAAAGGAA GGAGAAAATG TGATCAGTAC 2940  
 TGGCCTGCGG ATGGGAGTGA GGAGTACGGG AACTTTCTGG TCACTCAGAA GAGTGTGCAA 3000  
 GTGCTTGCCT ATTATACTGT GAGGAATTTT ACTCTAAGAA ACACAAAAAT AAAAAAGGGC 3060  
 TCCAGAAAAG GAAGACCCAG TGGACGTGTG GTCACACAGT ATCACTACAC GCAGTGGCCT 3120  
 GACATGGGAG TACCAGAGTA CTCCTTGCCA GTGCTGACCT TTTGTAGAAA GGCAGCCTAT 3180  
 75 GCCAAGCGCC ATGCAAGTGG GCCTGTTGTC GTCCACTGCA GTGCTGGAGT TGGAAAGAA 3240  
 GGCACATATA TTGTGCTAGA CAGTATGTTG CAGCAGATTC AACACGAAAG AACTGTCAAC 3300  
 ATATTTGGCT TCTTAAACA CATCCGTTCA CAAAGAAATT ATTTGTACA AACTGAGGAG 3360  
 CAATATGTCT TCATTCTAGA TACACTGGTT GAGGCCATAC TTAGTAAAGA AACTGAGGTG 3420  
 CTGGACAGTC ATATTCATGC CTATGTTAAT GCACTCCTCA TTCTTGAGCC AGCAGGCAAA 3480  
 80 ACAAAGCTAG AGAACAATTT CCAGGTCTC ACTCTGTAC CCAGGCTGGA GTGCAGAGGC 3540  
 ACAATCTCGG CTCACCTGCA CCTTCTCTC CTTGGCTTAA CTGATCTCTC TACCTCAGCC 3600  
 TCCGAGGTGG CTAGGACTAT ACTCCTGAGC CAGTCAAATA TACAGCAGAG TGACTATTCT 3660  
 GCAGCCCTAA AGCAATGCAA CAGGGAAGAA AATCGAAGTT CTTCTATCAT CCCTGTGGAA 3720  
 AGATCAAGGG TTGCAATTTT ATCCCTGAGT GGAGAAGGCA CAGACTACAT CAATGCCTCC 3780  
 TATATCATGG GCTATTACCA GAGCAATGAA TTCAATCATTA CCGACACCC TCTCCTTCAT 3840  
 ACCATCAAGG ATTTCTGGAG GATGATATGG GACCATAATG CCCAACTGGT GGTATGATT 3900

CCTGATGGCC AAAACATGGC AGAAGATGAA TTTGTTTACT GGCCAAATAA AGATGAGCCT 3960  
 ATAAATTGTG AGAGCTTTAA GGTCACTCTT ATGGCTGAAG AACACAAATG TCTATCTAAT 4020  
 GAGGAAAAAC TTATAATTCA GGACTTTATC TTAGAAGCTA CACAGGATGA TTATGTACTT 4080  
 GAAGTGAGGC ACTTTTCAGT TCCTAAATGG CCAATCCAG ATAGCCCCAT TAGTAAACT 4140  
 TTTGAACCTA TAAGTGTAT AAAAGAAGAA GCTGCCAATA GGGATGGGCC TATGATTGTT 4200  
 CATGATGAGC ATGGAGGAGT GACGGCAGGA ACTTTCTGTG CTCTGACAAC CCTTATGCAC 4260  
 CAAC TAGAAA AAGAAATTC CGTGGATGTT TACCAGGTAG CCAAGATGAT CAATCTGATG 4320  
 AGGCCAGGAG TCTTTGCTGA CATTGAGCAG TATCAGTTTC TCTACAAAGT GATCCTCAGC 4380  
 CTGTGAGCA CAAGGCAGGA AGAGAATCCA TCCACCTCTC TGGACAGTAA TGGTGACGA 4440  
 TTGCTGATG GAAATATAGC TGAGAGCTTA GAGTCTTTAG 4480

Seq ID NO: C103 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..4220

1 11 21 31 41 51  
 ATGCGAATCC TAAAGCGTTT CCTCGCTTGC ATTGAGCTCC TCTGTGTTTG CCGCCTGGAT 60  
 TGGGCTAATG GATACACAG ACAACAGAGA AAACCTGTGG AAGAGATTGG CTGGTCTTAT 120  
 ACAGGAGCAC TGAATCAAAA AAATTGGGGA AAGAAATATC CAACATGTAA TAGCCCAAAA 180  
 CAATCTCCTA TCAATATTGA TGAAGATCTT ACACAAGTAA ATGTGAATCT TAAGAAACTT 240  
 AAATTTTCAGG GTTGGGATAA AACATCATTT GAAAAACAT TCATTCTATA CACTGGGAAA 300  
 ACAGTGGAAA TTAATCTCAC TAATGACTAC CGTGTACGG GAGGAGTTTC AGAAATGGTG 360  
 TTTAAAGCAA GCAAGATAAC TTTTCACTGG GGAATGCA ATATGTATC TGATGGATCA 420  
 GAGCATAGTT TAGAAGGACA AAAATTTCCA CTGAGATGC AAATCTACTG CTTTGATGCG 480  
 GACCGATTTT CAAATTTTGA GGAAGCAGTC AAAGGAAAAG GGAAGTTAAG AGCTTTATCC 540  
 ATTTTGTGTT AGGTTGGGAC AGAAGAAAAT TTGGATTCCA AAGCGATTAT TGATGGAGTC 600  
 GAAAGTGTTA GTCGTTTGG GAAGCAGGCT GCTTTAGATC CATTCTACT GTTGAACCTT 660  
 CTGCCAAACT CAACAGACAA GTATTACATT TACAATGGCT CATTGACATC TCCTCCCTGC 720  
 ACAGACACAG TTGACTGGAT TGTTTTAA GATACAGTTA GCATCTCTGA AAGCCAGTTG 780  
 GCTGTTTTTT GTGAAGTTCT TACAATGCAA CAATCTGGTT ATGTCATGCT GATGGACTAC 840  
 TTACAAAACA ATTTTCGAGA GCAACAGTAC AAGTCTCTA GACAGGTGTT TTCCTCATAC 900  
 ATCGGAAAGG AAGAGATTCA TGAAGCAGTT TGTAGTTCAG AACCAGAAA TGTTCAGGCT 960  
 GACCCAGAGA ATTATACCAG CCTTCTTGT ACATGGGAAA GACCTCGAGT CGTTTATGAT 1020  
 ACCATGATTG AGAAGTTTGC AGTTTGTGAC CAGCAGTTGG ATGGAGAGGA CCAAAACCAAG 1080  
 CATGAATTTT TGACAGATGG CTATCAAGAC TTGGGTGCTA TTCTCAATAA TTTGCTACCC 1140  
 AATATGAGTT ATGTTCTTCA GATAGTAGCC ATATGCACTA ATGGCTTATA TGGAAAATAC 1200  
 AGCGACCAAC TGATTGTGCA CATGCCCTACT GATAATCCTG AACTTGATCT TTTCCCTGAA 1260  
 TTAATTGGAA CTGAAGAAAT AATCAAGGAG GAGGAAGAGG GAAAAGACAT TGAAGAAGGC 1320  
 GCTATTGTGA ATCTGTGTAG AGACAGTCTC ACAAACCAA TCAGGAAAAA GGAACCCAG 1380  
 ATTTCTACCA CAACACACTA CAATCGCATA GGGACGAAAT ACAATGAAGC CAAGACTAAC 1440  
 CGATCCCAAA CAAGAGGAAG TGAATCTCT GGAAGGGTGT ATGTTCCCAA TACATCTTTA 1500  
 AATTCCACTT CCCAACCACT CACTAAATTA GCCACAGAAA AAGATATTTC CTTGACTTCT 1560  
 CAGACTGTGA CTGAATCGCC ACCTCACACT GTGGAAGGTA CTTGAGCCTC TTTAAATGAT 1620  
 GGCTCTAAAA CTGTTCTTAG ATCTCCACAT ATGAACTTGT CGGGGACTGC AGAATCCTTA 1680  
 AATACAGTTT CTATAACAGA ATATGAGGAG GAGAGTTTAT TGACCAGTTT CAAGCTTGAT 1740  
 ACTGGAGCTG AAGATTCTTC AGGCTCCAGT CCCGCAACTT CTGCTATCCC ATTCATCTCT 1800  
 GAGAACATAT CCCAAGGGTA TATATTTTCC TCCGAAAACC CAGAGACAAT AACATATGAT 1860  
 GTCTTTATAC CAGAATCTGC TAGAAATGCT TCCGAAGATT CAACTTCATC AGGTTTCAAG 1920  
 GAATCACTAA AGGATCCTTC TATGGAGGGA AATGTGTGGT TTCCTAGCTC TACAGACATA 1980  
 ACAGCACAGC CCGATGTTGG ATCAGGCAGA GAGAGCTTTC TCCAGACTAA TTACTACTGAG 2040  
 ATACGTGTTG ATGAATCTGA GAAGACAACC AAGTCTTTT CTGCAAGGCC AGTGATGTCA 2100  
 CAGGGTCCCT CAGTTACAGA TCTGGAATG CCACATTATT CTACCTTTGC CTACTTCCCA 2160  
 ACTGAGGTAA CACCTCATGC TTTTACCCCA TCCTCCAGAC AACAGGATTG GGTCTCCAGC 2220  
 GTCAACGTGG TATACCTGCA GACAACCCAA CCGGTATACA ATGAGGCCAG TAATAGTAGC 2280  
 CATGAGTCTC GTATTGGTCT AGCTGAGGGG TTGGAATCCG AGAAGAAAGC AGTTATACCC 2340  
 CTTGTGATCG TGTGAGCCTT GACTTTTATC TGTCTAGTGG TTCTGTGGG TATTCTCATC 2400  
 TACTGGAGGA AATGCTTCCA GACTGCACAC TTTTACTTAG AGGACAGTAC ATCCCTTAGA 2460  
 GTTATATCCA CACCTCCAAC ACCTATCTTT CCAATTTTCA ATGATGTGCG AGCAATTTCA 2520  
 ATAAAGCACT TTCCAAGAGT TGTTCAGAT TTACATGCAA GTAGTGGGTT TACTGAAGAA 2580  
 TTTGAGACAC TGAAGAGT TTACCAAGGA GTGCAGAGCT GTACTGTTGA CTTAGGTATT 2640  
 ACAGCAGACA GCTCCAACCA CCCAGACAAC AAGCACAAGA ATCGATACAT AAATATCGTT 2700  
 GCCTATGATC ATAGCAGGGT TAAGCTAGCA CAGCTTGCTG AAAAGGATGG CAAACTGACT 2760  
 GATTATATCA ATGCCAATTA TGTGTATGGC TACAACAGAC CAAAAGCTTA TATTGCTGCC 2820  
 CAAGGCCCACT TGAATTCAC AGCTGAAGAT TTCTGGAGAA TGATATGGGA ACATAATGTG 2880  
 GAAGTTATTG TCAATGATAAC AAACCTCGTG GAGAAAGGAA GGAGAAAATG TGATCAGTAC 2940  
 TGGCCTGCCG ATGGGAGTGA GGAGTACGGG AACTTTCTGG TCACTCAGAA GAGTGTGCAA 3000  
 GTGCTTGCTT ATTATACCTG GAGGAATTTT ACTCTAAGAA ACACAAAAAT AAAAAAGGCG 3060  
 TCCAGAAAG GAAGACCCAG TGGACGTGTG GTACACAGAT ATCACTACAC GCAGTGGCCT 3120  
 GACATGGGAG TACCAGAGTA CTCCTGCCA GTGCTGACCT TTGTGAGAAA GCGAGCCTAT 3180  
 GCCAAGCGCC ATGCAGTGGG GCCTGTTGTC GTCCACTGCA GTGCTGGAGT TGAAGAACA 3240  
 GGCACATATA TTTGTGCTAGA CAGTATGTTG CAGCAGATTC AACACGAAGG AACTGTCAAC 3300  
 ATATTTGGCT TCTTAAACA CATCCGTTCA CAAAGAAATT ATTTGTGACA AACTGAGGAG 3360  
 CAATATGTCT TCATTATGTA TACACTGGTT GAGGCCATAC TTAGTAAAGA AACTGAGGTG 3420  
 CTGGACAGTC ATATTATATC CTATGTTAAT GCACTCCTCA TTCTTGAGCC AGCAGGCAAA 3480  
 ACAAAGCTAG AGAAACAAT CCAGCTCTG AGCCAGTCAA ATATACAGCA GAGTGACTAT 3540  
 TCTGCAGCCC TAAAGCAATG CAACAGGGAA AAGAAATCGAA CTCTTCTAT CATCCCTGTG 3600  
 GAAAGATCAA GGGTTGGCAT TTCATCCCTG AGTGAGAGAG GCACAGACTA CATCAATGCC 3660  
 TCCTATATCA TGGGCTATTA CCAGAGCAAT GAATTCATCA TTACCCAGCA CCTCTCCTT 3720  
 CATACCATCA AGGATTTCTG GAGGATGATA TGGGACCATA ATGCCCAACT GGTGGTTATG 3780  
 ATTCCTGATG GCCAAAACAT GGCAGAAGAT GAATTTGTTT ACTGGCCAAA TAAAGATGAG 3840  
 CCTATAAATT GTGAGAGCTT TAAGGTCACT CTTATGGCTG AAGAACACAA ATGCTATCT 3900  
 AATGAGGAAA AACTTATAAT TCAGGACTTT ATCTTAGAAG CTACACAGGC ATGGAGGAGT 3960  
 GACGCAGGA ACTTCTGTG CTCTGACAAC CCTTATGCAC CAACAGAAA AAGAAAATTC 4020

CGTGGATGTT TACCAGGTAG CCAAGATGAT CAATCTGATG AGGCCAGGAG TCTTTGCTGA 4080  
 CATTGAGCAG TATCAGTTTC TCTACAAAGT GATCCTCAGC CTGTGTGAGCA CAAGGCAGGA 4140  
 AGAGAATCCA TCCACCTCTC TGGACAGTAA TGGTGCAGCA TTGCCCTGATG GAAATATAGC 4200  
 TGAGAGCTTA GAGTCTTTAG 4220

Seq ID NO: C104 DNA Sequence  
 Nucleic Acid Accession #: XM\_002914.6  
 Coding sequence: 1..4314

10 1 11 21 31 41 51  
 | | | | | |  
 ATGAAGGATA TCGACATAGG AAAAGAGTAT ATCATCCCCA GTCCTGGGTA TAGAAGTGTG 60  
 AGGGAGAGAA CCAGCACTTC TGGGACGCAC AGAGACCGTG AAGATTCCAA GTTCAGGAGA 120  
 15 ACTCGACCGT TGGAAATGCCA AGATGCCCTT GAAACAGCAG CCCGAGCCGA GGGCCTCTCT 180  
 CTTGATGCCT CCATGCATTC TCAGCTCAGA ATCCTGGATG AGGAGCATCC CAAGGGAAAG 240  
 TACCATCATG GCTTGAGTGC TCTGAAGCCC ATCCGGACTA CTTCCAAACA CCAGCACCCA 300  
 GTGGCAATG CTGGGCTTTT TTCTGTATG ACTTTTTCGT GGCTTTCTTC TCTGGCCCCG 360  
 GTGGCCCCACA AGAAGGGGGA GCTCTCAATG GAAGACGTGT GGTCTCTGTC CAAGCACGAG 420  
 20 TCTTCTGACG TGAACATGAG AAGACTAGAG AGACTGTGGC AAGAAGAGCT GAATGAAGTT 480  
 GGGCCAGACG CTGCTTCCCT GCGAAGGGTT GTGTGGATCT TCTGCCGCAC CAGGCTCATC 540  
 CTGTCCATCG TGTGCCCTGAT GATCACGCAG CTGGCTGGCT TCAGTGGACC AGCCTTCATG 600  
 GTGAAACACC TCTTGGAGTA TACCCAGGCA ACAGAGTCTA ACCTGCAGTA CAGCTTGTGT 660  
 TTAGTGTGGG GCTCCTCTCT GACGGAATC GTGCGTCTT GGTCTGTGCT ACTGACTTGG 720  
 25 GCATTGAATT ACCGAACCGG TGTCCGCTTG CGGGGGGCCA TCCTAACCAT GGCATTTAAG 780  
 AAGATCCTTA AGTTAAAGAA CATTAAAGAG AAATCCCTGG GTGAGCTCAT CAACATTTCG 840  
 TCCAACGATG GGCAGAGAA GTTTGAGGCA GCAGCCGTG GCAGCCTGCT GGCTGGAGGA 900  
 CCGTGTGTG CCATCTTAGG CATGATTAT AATGTAATTA TTCTGGGACC AACAGGCTTC 960  
 CTGGGATCAG CTGTTTTTAT CCTCTTTTAC CCAGCAATGA TGTTCATC ACAGGCTCACA 1020  
 30 GCATATTTCA GAGAAAATG CGTGCCGCC ACAGGATGAAC GTGTCCAGAA GATGAATGAA 1080  
 GTTCTTACTT ACATTAATAT TATCAAATG TATGCCCTGG TCAAAGCATT TTCTCAGAGT 1140  
 GTTCAAAAAA TCCCGAGGGA GGAGCGTCGG ATATTGGAAA AAGCTGGGTA CTTCAGAGC 1200  
 ATCACTGTGG GTGTGGTCC CATGTGGTG GTGATTGCCA GCGTGGTGAC CTTCTCTGTT 1260  
 CATATGACCC TGGGCTTCGA TCTGACAGCA GCACAGGCTT TCACAGTGGT GACAGTCTTC 1320  
 35 AATTCCATGA CTTTGTCTTT GAAAGTAACA CCGTTTTTTCG TAAAGTCCCT CTCAGAGGCC 1380  
 TCAGTGGCTG TTGACAGATT TAAGAGTTTG TTTCTAATGG AAGAGGTTCA CATGATAAAG 1440  
 AACAAACCCG CCACTCCTCA CATCAAGATA GAGATGAAAA ATGCCACCTT GGCATGGGAC 1500  
 TCCTCCCACT CCAGTATCCA GAACTCGCCC AAGCTGACCC CCAAAATGAA AAAAGACAAG 1560  
 AGGGCTTCCA GGGGCAAGAA AGAGAAGGTG AGGCAGCTGC AGCGCACTGA GCATCAGGCG 1620  
 40 GTGCTGGCAG AGCAGAAAGG CCACCTCTC CTGGACAGTG ACGAGCGGCC CAGTCCCGAA 1680  
 GAGGAAGAAG GCAAGCACAT CCACCTGGGC CACCTGCGCT TACAGAGGAC ACTGCACAGC 1740  
 ATCGATCTGG AGATCCAAGA GGGTAAACTG GTTGAATCT GCGGCAGTGT GGGGAAGTGA 1800  
 AAAACCTCTC TCATTTTCAGC CATTTTAGGC CAGATGACGC TTCTAGAGGG CAGCATTGCA 1860  
 ATCAGTGGAA CCTTCGCTTA TGTGGCCAG CAGGCCTGGA TCCTCAATGC TACTCTGAGA 1920  
 45 GACAACATCC TGTTTGGGAA GGAATATGAT GAAGAAGAT ACAACTCTGT GCTGAACAGC 1980  
 TGCTGCCTGA GGCCTGACCT GGCATTTCTT CCCAGCAGCG ACCTGACGGA GATTGGAGAG 2040  
 CGAGGAGCCA ACCTGAGCGG TGGGCAGCGC CAGAGGATCA GCCTTGCCCG GGCCTTGTAT 2100  
 AGTGACAGGA GCTCTACAT CCTGGACGAC CCCCTCAGTG CCTTAGATGC CCATGTGGGC 2160  
 AACCACATCT TCAATAGTGC TATCCGGAAG CATCTCAAGT CCAAGACAGT TCTGTTTGT 2220  
 50 ACCCACCAGT TACAGTACCT GGTGACTGT GATGAAGTGA TCTTCATGAA AGAGGGCTGT 2280  
 ATTACGGAAA GAGGCAACCA TGAGGAATCT ATGAATTTAA ATGGTGACTA TGCTACCAT 2340  
 TTTAATAAAC TGTGTCTGGG AGAGACACCG CCAAGTGAGA TCAATTCAA AAAGGAAACC 2400  
 AGTGGTTTCA AGAAGAAGTC ACAAGACAAG GGTCTTAAAA CAGGATCAGT AAAGAAGGAA 2460  
 AAAGCAGTAA AGCCAGAGGA AGGCGAGCTT GTGCAGCTGG AAGAAAAGG GCAGGGTTCA 2520  
 55 GTGCCCTGGT CAGTATATGG TGTCTACATC CAGGCTGCTG GGGGCCCTT GGCATTCTGT 2580  
 GTTATTATGG CCTTTTTCAT GCTGAATGTA GGCAGCACCG CCTTCAGCAC CTGGTGGTTG 2640  
 AGTTACTTGA TCAAGCAAGG AAGCGGGAAC ACCACTGTGA CTCGAGGGAA CGAGACCTCG 2700  
 GTGAGTGACA GCATGAAGGA CAATCCTCAT ATGCAGTACT ATGCCAGCAT CTACGCCCTC 2760  
 60 TCCATGGCAG TCATGCTGAT CCTGAAAGCC ATTCGAGGAG TTGCTTTTGT CAAGGGCAGC 2820  
 CTGCGAGCTT CCTCCCGGCT GCATGACGAG CTTTCCGAA GATCCTTCG AAGCCCTATG 2880  
 AAGTTTTTTT ACACGACCCC CACAGGGAGG ATTCTCAACA GGTTTTCCAA AGACATGGAT 2940  
 GAAGTTGACG TGGGCTGCC GTTCCAGGCC GAGATGTTCA TCCAGAACGT TATCCTGGTG 3000  
 TTTCTCTGTG TGGGAATGAT CGCAGGAGTC TTCCCGTGGT TCCTTGTGGC AGTGGGGCCC 3060  
 CTTGTCTATC TCTTTTCAGT CCTGCACATT GTCTCCAGGG TCCTGATTCT GGAGCTGAAG 3120  
 65 CGTCTGAGCA ATATCAGCCA GTACCTTTTC CTCTCCACA TCACGTCCAG CATACAGGGC 3180  
 CTTGCCACCA TCCAGCCCTA CAATAAAGGG CAGGAGTTTC TGACAGATA CCAGGAGCTG 3240  
 CTGGATGACA ACCAAGCTTC TTTTTTTTTT TTTACGTGTG CGATGCGGTG GCTGGCTGTG 3300  
 CGGCTGGACC TCATCAGCAT CGCCCTCATC ACCACCACGG GGCCTGATGAT CGTCTCTATG 3360  
 70 CACGGGCAGA TTCCCCGAG CTATGCGGGT CTCGCCATCT CTTATGCTGT CCAGTTAAGC 3420  
 GGGCTGTTC AGTTTACGGT CAGACTGGCA TCTGAGACAG AAGCTCGATT CACCTCGGTG 3480  
 GAGAGGATCA ATCACTACAT TAAGACTCTG TCCTTGGGAG CACCTGCCAG AATTAAGAAC 3540  
 AAGGCTCCCT CTTCTGACTG GCCCCAGGAG GGAGAGGTGA CCTTTGAGAA CGCAGAGATG 3600  
 AGGTACCGAG AAAACCTCCC TCTCGTCTTA AAGAAAGTAT CCTTCAGAT CAAACCTAAA 3660  
 GAGAAGATTG GATTTGTGGG GCGGACAGGA TCAGGGAAGT CTCTGCTGGG GATGGCCCTC 3720  
 75 TTCCGTCTGG TGGAGTTATC TGGAGGCTGC ATCAAGATTG ATGGAGTGAG AATCAGTGAT 3780  
 ATTGGCCTTG CCGACCTCCG AAGCAAATCT TCTATCATTC CTCAAGAGCC GGTGCTGTTC 3840  
 AGTGGCACTG TCAGATCAAA TTTGGACCCC TTCAACCAGT ACACCTGAAGA CCAGATTGGG 3900  
 GATGCCCTGG AGAGGACACA CATGAAAGAA TGTATTGCTC AGTACTCTCT GAAACTTGAA 3960  
 80 TCTGAAGTGA TGGAGAATGG GGATAACTTC TCAGTGGGGG AACGGCAGCT CTTGTGCATA 4020  
 GCTAGAGCCC TGTCCGCCA CTGTAAGATT CTGATTTTAG ATGAAGCCAC AGCTGCCATG 4080  
 GACACAGAGA CAGACTTATG GATTCAAGAG ACCATCCGAG AAGCATTTGC AGACTGTACC 4140  
 ATGCTGACCA TGTCCCATCG CCTGCACACG GTTCTAGGCT CCGATAGGAT TATGGTCTG 4200  
 GCCCAGGGAC AGGTGGTGGG GTTTGACACC CCAATCGTCC TTCTGTCCAA CGACAGTTCC 4260  
 CGATTCTATG CCAATGTTTG TGCTGCAGAG AACAGGTGCT CTGTCAAGGG CTAG 4314

Seq ID NO: C105 DNA Sequence  
Nucleic Acid Accession #: NM\_005688.1  
Coding sequence: 126..4439

5	1	11	21	31	41	51	
	CCGGGCAGGT	GGCTCATGCT	CGGGAGCGTG	GTTGAGCGGC	TGGCGCGGTT	GTCTTGGAGC	60
	AGGGGCGCAG	GAATTCCTGAT	GTGAAACTAA	CAGTCTGTGA	GCCCTGGAAC	CTCCGCTCAG	120
	AGAAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCCCT	GGGTATAGAA	180
10	GTGTGAGGGA	GAGAACACAGC	ACTTCTGGGA	CGCACAGAGA	CCGTGAAGAT	TCCAAGTTCA	240
	GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
	TCTCTCTTGA	TGCTTCCATG	CATTCTCAGC	TCAGAATCCT	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TCATGGCTTG	AGTGCTCTGA	AGCCCATCCG	GACTACTTCC	AAACACCAGC	420
15	ACCCAGTGGG	CAATGCTGGG	CTTTTCTCCT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
	CCCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGAGCTGAAC	TGCAGAAGAC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGGTGTGTGT	GATCTTCTGC	CGCACCAGGC	660
	TCATCTGTGC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAGCCT	720
20	TCATGGTGAA	ACACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
	TGTTGTAGT	GCTGGGCTCT	CTCCTGACGG	AAATCGTGCG	GTCTTGGTCG	CTTGCACTGA	840
	CTTGGGCATT	GAATTACGAA	ACCGGTGTCC	GCTTGCGGGG	GGCCATCCTA	ACCATGGCAT	900
	TTAAGAAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGCTCCAA	CGATGGGCAG	AGAAATGTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
25	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
	GCTTCTCTGG	ATCAGCTGTT	TTTATCCTCT	TTTACCCAGC	AATGATGTTT	GCATCACCGC	1140
	TCACAGCATA	TTTCAGGAGA	AAATGCGTGG	CCGCCACGGA	TGAACGTGTC	CAGAAGATGA	1200
	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
	AGAGTGTTC	AAAAATCCGC	GAGGAGGAGC	GTCCGATATT	GGAAAAAGCC	GGGTACTTCC	1320
30	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTT	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
	CTGTTTCATAT	GACCTTGGGC	TTCGATCTGA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
	TCTTCAATT	CATGACTTTT	GCTTTGAAAG	TAACACCGTT	TTCAGTAAAG	TCCCTCTCAG	1500
	AAGCCTCAGT	GGCTGTTGAC	AGATTTAAGA	GTTTGTCTCT	AATGGAAGAG	GTTTACATGA	1560
	TAAAGAACAA	ACCAGCCAGT	CCTCACATCA	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
35	GGGACTCCTC	CCACTCCAGT	ATCCAGAACT	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
	ACAAGAGGGC	TTCCAGGGGC	AAGAAGAGA	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
	AGGCGGTGCT	GGCAGAGCAG	AAAGGCCACC	TCTCTCTGGA	CAGTGACGAG	CGGCCACGTC	1800
	CCGAGAGGGA	AGAAGGCAAG	CACATCCACC	TGGGCCACCT	GCGCTTACAG	AGGACACTGC	1860
	ACAGCATCGA	CTTGGAGATC	CAAGAGGGTA	AACTGGTTGG	AATCTGCGGC	AGTGTGGGAA	1920
40	GTGGAAAAAC	CTCTCTCAT	TCAGCCATT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
	TGAGAGACAA	CATCCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
	ACAGCTGCTG	CTCGAGGCTG	GACCTGGCCA	TTCTTCCAG	CAGCGACCTG	ACGGAGATTG	2160
	GAGAGCGAGG	AGCCAACCTG	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	GCCCGGGCCT	2220
45	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTT	CAGTGCCCTA	GATGCCCATG	2280
	TGGGCAACCA	CATCTTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
	TTGTTACCCA	CCAGTTACAG	TACCTGGTTG	ACTGTGATGA	AGTGATCTTC	ATGAAAGAGG	2400
	GCTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AACTGATGAA	TTTAAATGGT	GACTATGCTA	2460
	CCATTTTAA	TAACCTGTTG	CTGGGAGAGA	CACCGCCAGT	TGAGATCAAT	TCAAAAAAGG	2520
50	AAACCAAGTG	TTACAGAGA	AAGTCACAAG	ACAAGGGTCC	TAAACAGGA	TCAGTAAAGA	2580
	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
	GTTTCAGTGC	CTGGTCACTA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
	TCTCTGGTTAT	TATGGCCCTT	TTTATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
	GGTTGAGTTA	CTGGATCAAG	CAAGGAAGCG	GGAAACCCAC	TGTGACTCGA	GGGAACGAGA	2820
55	CCTCGGTGAG	TGACAGCATG	AAGGACAATC	CTCATATGCA	GTAATATGCC	AGCATCTACG	2880
	CCCTCTCCAT	GGCAGTCTAG	CTGATCCTGA	AAGCCATTCT	AGGAGTTGTC	TTTGTCAAGG	2940
	GCACGCTGCG	AGCTTCTCTC	CGGCTGCATG	ACGAGCTTTT	CCGAAGGATC	CTTCGAAGCC	3000
	CTATGAAGTT	TTTTCAGACG	ACCCCCACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
	TGGATGAAGT	TGCTGTGCGG	CTGCCGTTCC	AGGCCGAGAT	GTTTATCCAG	AAAGTTATCC	3120
60	TGTTGTTCTT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCCTT	GTGGCAGTGG	3180
	GGCCCTTGT	CATCTCTTTT	TCAGTCTCTC	ACATTGTCTC	CAGGGTCTCT	ATTCCGGAGC	3240
	TGAAGCGTCT	GGACAATATC	ACGCAGTCAC	CTTTCCTCTC	CCACATCACG	TCCAGCATAC	3300
	AGGGCCTTGC	CACCATCCAC	GCCTACATA	AAGGGCAGGA	GTTTCTGCAC	AGATACCAGG	3360
	AGCTGCTGGA	TGACAACCAA	GCTCCTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
65	CTGTGCGGCT	GGACCTCATC	AGCATCGCCC	TCATCACCAC	CACGGGGCTG	ATGATCGTTC	3480
	TTATGCACGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
	TAACGGGGCT	GTTCCAGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTACCTT	3600
	CGGTGGAGAG	GATCAATCAC	TACATTAAGA	CTCTGTCTCT	GGAAGCACCT	GCCAGAATTA	3660
70	AGAACCAAGC	TCCCTCCCTC	GACTGGCCCC	AGGAGGGAGA	GGTGACCTTT	GAGAACGCAG	3720
	AGATGAGGTA	CCGAGAAAAC	CTCCCTCTTG	TCCTAAAGAA	AGTATCCTTC	ACGATCAAAC	3780
	CTAAAGAGAA	GATTGGCATT	GTGGGGCGGA	CAGGATCAGG	GAAGTCTCTG	CTGGGGATGG	3840
	CCCTCTCCCG	TCTGGTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
	GTGATATTGG	CCTTGGCCGAC	CTCCGAAGCA	AACTCTCTAT	CATTCTCTCA	GAGCCGGTGC	3960
	TGTTTCAGTG	CACGTGCAGA	TCAAATTTGG	ACCCCTTCAA	CCAGTACACT	GAAGACCAGA	4020
75	TTTGGGATGC	CCTGGAGAGG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
	TTGAATCTAG	AGTGTGGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTGTG	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTAGATGAA	GCCACAGCTG	4200
	CCATGGACAC	AGAGACAGAC	TTATTGATTG	AAGAGACCAT	CCGAGAAGCA	TTTGCAGACT	4260
	GTACCATGCT	GACCATTGCC	CATCGCCTGC	ACACGGTTCT	AGGCTCCGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTCTCTG	TCCAACGACA	4380
80	GTTCCCGATT	CTATGCCATG	TTTGCTGCTG	CAGAGAACAA	GGTCGCTGTC	AAGGGCTGAC	4440
	TCCTCCCTGT	TGACGAAGTG	TCTTTCTTTT	AGAGCATTTG	CATTCCCTGC	CTGGGGCGGG	4500
	CCCCCATCG	CGTCTCTCTA	CGGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TCGCACAGCA	4560
	GTTCCGGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATT	4620
	ATTCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTCTA	ATTGCACTCT	AAAAGGTTCA	4680



5  
 10  
 15  
 20

```

GGGAACCGTT ATTATAATTG TATCAGAGGC CTATAATGAA GCTTTATACG TGTAGCTATA 4740
TCTATATATA ATTCTGTACA TAGCCTATAT TTACAGTGAA AATGTAAGCT GTTTATTTTA 4800
TATTAAAAATA AGCACTGTGC TAATAACAGT GCATATTCCT TTCTATCATT TTTGTACAGT 4860
TTGCTGTACT AGAGATCTGG TTTTGCTATT AGACTGTAGG AAGAGTAGCA TTTTCTCTT 4920
CTCTAGCTGG TGGTTTCACG GTGCCAGGTT TTCTGGGTGT CCAAAGGAAG ACGTGTGGCA 4980
ATAGTGGGCC CTCGAGCAGC CCCCTCTGCC GCCTCCCCAC AGCCGCTCCA GGGGTGGCTG 5040
GAGACGGGTG GGCCTGTGGA GACCATGCAG AGCGCCGTGA GTTCTCAGGG CTCTGCCTT 5100
CTGTCCCTGT GTCACTTACT GTTTCTGTCA GGAGAGCAGC GGGGCGAAGC CCAGGCCCTT 5160
TTTCACTCCC TCCATCAAGA ATGGGGATCA CAGAGACATT CCTCCGAGCC GGGGAGTTTC 5220
TTTCTGCTCT TCTTCTTTT GCTGTTGTTT CTAAACAAGA ATCAGTCTAT CCACAGAGAG 5280
TCCCACTGCC TCAGGTTTCT ATGGCTGGCC ACTGCACAGA GCTCTCCAGC TCCAAGACCT 5340
GTTGGTTCCA AGCCCTGGAG CCAACTGCTG CTTTTTGAGG TGGCACTTTT TCATTTGCCT 5400
ATTCCACAC CTCCACAGTT CAGTGGCAGG GCTCAGGATT TCGTGGGTCT GTTTTCCTTT 5460
CTCACCGCAG TCGTCGCACA GTCTCTCTCT CTCTCTCCCC TCAAAGTCTG CAACTTTAAG 5520
CAGCTCTTGC TAATCAGTGT CTCACACTGG CGTAGAAGTT TTTGTACTGT AAAGAGACCT 5580
ACCTCAGGTT GCTGGTTGCT GTGTGGTTTG GTGTGTTCCC GCAAACCCCT TTTGTGCTGT 5640
GGGCTGGTA GCTCAGGTGG GCGTGGTCC TGCTGTATC AGTTGAATGG TCAGCGTTGC 5700
ATGTCGTGAC CAACATAGACA TTCTGTGCC TTAGCATGTT TGCTGAACAC CTTGTGGAAG 5760
CAAAAATCTG AAAATGTGAA TAAATTATT TTGGATTTTG TAAAAAATA AAAAAAATA 5820
AAAAAATA AAAAAAATA 5838
  
```

Seq ID NO: C106 DNA Sequence  
 Nucleic Acid Accession #: NM\_005562  
 Coding sequence: 90..3671

25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

```

1 11 21 31 41 51
ACAGCGGAGC GCAGAGTGAG AACCACCAAC CGAGGCGCGG GGCAGCGACC CCTGCAGCGG 60
AGACAGAGAC TGAGCGGCCC GGCACCGCCA TGCTGCGCT CTGGCTGGGC TGCTGCCTCT 120
GCTTCTCGCT CCTCCTGCCC GCAGCCCGGG CCACCTCCAG GAGGGAAGTC TGTGATTGCA 180
ATGGGAAGTC CAGGCAGTGT ATCTTTGATC GGAACCTTCA CAGACAAACT GTGTAATGGAT 240
TCCGCTGCCT CAACTGCAAT GACAACACTG ATGGCATTCA CTGCGAGAAG TGCAAGAATG 300
GCTTTTACCG GCACAGAGAA AGGGACCGCT GTTTGCCCTG CAATTGTAACT TCCAAAGGTT 360
CTCTTAGTGC TCGATGTGAC AACTCTGGAC GGTGCAGCTG TAAACCAGGT GTGACAGGAG 420
CCAGATGCGA CCGATGTCTG CCAGGCTTCC ACATGCTCAC GGATGCGGGG TGCACCCCAAG 480
ACCAAGAGAT GCTAGACTCC AAGTGTGACT GTGACCCAGC TGGCATCGCA GGGCCCTGTG 540
ACGCGGGCCG CTGTGTCTGC AAGCCAGCTG TTACTGGAGA ACGTGTGAT AGGTGTGAT 600
CAGGTTACTA TAATCTGGAT GGGGGGAACC CTGAGGCGTG TACCCAGTGT TTCTGCTATG 660
GGCATTACAG CAGCTGCCCG AGCTCTGCAG AATACAGTGT CCATAAGATC ACCTCTACCT 720
TTCATCAAGA TGTGTATGCG TGGAAGGCTG TCCAACGAAA TGGGTCTCCT GCAAAGCTCC 780
AATGGTCACA GCGCATCAA GATGTGTTTA GCTCAGCCCA ACGACTAGAC CCTGTCTATT 840
TTGTGGCTCC TGCCAAATTT CTGGAATC AACAGGTGAG CTATGGGCAA AGCCTGTCTT 900
TTGACTACCG TGTGGACAGA GGAGGCAGAC ACCCATCTGC CCATGATGTG ATTTCTGGAAG 960
GTGCTGGTCT ACGGATCACA GCTCCCTTGA TGCCACTTGG CAAGACACTG CCTGTGGGC 1020
TCACCAAGAC TTACACATTG AGGTTAAATG AGCATCCAAG CAATAATTGG AGCCCCCAGC 1080
TGAGTTACTT TGAGTATCGA AGGTTACTGC GGAATCTCAC AGCCCTCCGC ATCCGAGCTA 1140
CATATGGAGA ATACAGTACT GGGTACATTG ACAATGTGAC CCTGATTTC GCGGCCCTG 1200
TCTCTGGAGC CCCAGCACCC TGGGTGAAAC AGTGTATATG TCCTGTTGGG TACAGGGGC 1260
AATTTCTGCA GAGTTGTGCT TCTGGCTACA AGAGAGATTG AGCGAGACTG GGGCCTTTTG 1320
GCACCTGTAT TCCTTGTAACT TGTCAAGGGG GAGGGGCCCT TGATCCAGAC ACAGGAGATT 1380
GTTATTCAGG GGATGAGAAT CCTGACATTG AGTGTGCTGA CTGCCCAATT GGTTTCTACA 1440
ACGATCCGCA CACCCCCCGC AGCTGCAAGC CATGTCCCTG TCATAACGGG TTCAGCTGCT 1500
CAGTGATGCC GAGAGCGGAG GAGGTGGTGT GCAATAACTG CCCTCCCGGG GTCACCGGTG 1560
CCGCTGTGA GCTCTGTGCT GATGGCTACT TTGGGGACCC CTTTGGTGAA CATGGCCAG 1620
TGAGGCCTTG TCAGCCCTGT CAATGCAACA ACAATGTGGA CCCCAGTGCC TCTGGGAATT 1680
GTGACCGGCT GACAGCGCAG TGTTTGAAAT GTATCCACAA CACAGCCGGC ATCTACTGCG 1740
ACCAAGTCAG ACGAGCTTAC TTCGGGGACC CATTGGCTCC CAACCCAGCA GACAAGTGTG 1800
GAGCTTGCAA CTGTAACCCC ATGGGCTCAG AGCCTGTAGG ATGTGGAAGT GATGGCACCT 1860
GTGTTTGCAA GCCAGGATTG GGTGGCCCCA ACTGTGAGCA TGGAGCATTC AGCTGTCCAG 1920
CTTGCTATAA TCAAGTGAAG ATTCAGATGG ATCAGTTTAT GCAGCAGCTT CAGAGAATGG 1980
AGGCCCTGAT TTCAAAGGCT CAGGGTGGTG ATGGAGTAGT ACCTGATACA GAGCTGGAAG 2040
GCAGGATGCA GCAGGCTGAG CAGGCCCTTC AGGACATTCT GAGAGATGCC CAGATTTCAG 2100
AAGGTGCTAG CAGATCCCTT GGTCTCCAGT TGGCCAAGGT GAGGAGCCAA GAGAACAGCT 2160
ACCAAGCCG CCTGGATGAC CTCAGATGTA CTGTGGAAAG AGTTCGGGCT CTGGGAAGTG 2220
AGTACCAGAA CCGAGTTCGG GATACTCACA GGCTCATCAC TCAGATGCAG CTGAGCCTGG 2280
CAGAAAGTGA AGCTTCTCTG GGAACAACATA ACATTCCTGC CTCAGACCAC TACGTGGGGC 2340
CAATGGCTT TAAAGTCTG GCTCAGGAG CCACAAGATT AGCAGAAAGC CACGTTGAGT 2400
CAGCCAGTAA CATGGAGCAA CTGACAAGGG AACTGAGGA CTATTCCAAA CAAGCCCTCT 2460
CACTGTGCGC AAGGCCCTG CATGAAGGAG TCGGAAGCGG AAGCGGTAGC CCGGACGGTG 2520
CTGTGGTGCA AGGGCTTGTG GAAAAATTGG AGAAAAACCA GTCCCTGGCC CAGCAGTTGA 2580
CAAGGGAGGC CACTCAAGCG GAAATTGAAG CAGATAGGTC TTATCAGCAC AGTCTCCGCC 2640
TCCTGGATTC AGTGTCTCGG CTTCAGGGAG TCAGTGATCA GTCCCTTCAG GTGGAAGAAG 2700
CAAAGAGGAT CAAACAAAAA GCGGATTTC TCTCAACGCT GGTAACCAAG CATATGGATG 2760
AGTTCAAGCG TACACAAAAG AATCTGGGAA ACTGGAAGA AGAAGCACAG CAGCTCTTAC 2820
AGAATGGAAG AAGTGGGAGA GAGAAATCAG ATCAGCTGCT TTCCCGTGCC AATCTTGCTA 2880
AAAGCAGAGC CAAAGAAGCA CTGAGTATGG GCAATGCCAC TTTTATGAA GTTGAGAGCA 2940
TCCTTAAAAA CCTCAGAGAG TTTGACCTGC AGGTGGACAA CAGAAAAGCA GAAGCTGAAG 3000
AAGCATGAAA GAGACTCTCC TACATCAGCC AGAAGGTTTC AGATGCCAGT GACAAGACCC 3060
AGCAAGCAGA AAGAGCCCTG GGGAGCGCTG CTGCTGATGC ACAGAGGGCA AAGAATGGGG 3120
CCGGGGAGGC CCTGGAATAT TCCAGTGAGA TTGAACAGGA GATTGGGAGT CTGAACTTGG 3180
AAGCAATGAT GACAGCATAT GGAGCCTTGG CCATGGAAAA GGGACTGGCC TCTCTGAAGA 3240
GTGAGATGAG GGAAGTGGAA GGAGAGCTGG AAAGGAAGGA GCTGGAGTTT GACACGAATA 3300
TGATGTCAGT ACAGATGGTG ATTACAGAAG CCCAGAAGGT TGATACCAGA GCCAAGAAGC 3360
CTGGGGTTAC AATCCAAGAC AACTCAACA CATTAGACGG CTCTCTGCAT CTGATGGACC 3420
  
```

AGCCTCTCAG TGATAGTAA GAGGGGCTGG TCTTACTGGA GCAGAAGCTT TCCCGAGCCA 3480  
 AGACCCAGAT CAACAGCCAA CTGCGGCCCA TGATGTGAGA GCTGGAAGAG AGGGCAGGTC 3540  
 AGCAGAGGGG CCACCTCCAT TTGCTGGAGA CAAGCATAGA TGGGATTCTG GCTGATGTGA 3600  
 5 AGAACTTGA GAACATTAGG GACAACCTGC CCCCAGGCTG CTACAATACC CAGGCTCTTG 3660  
 AGCAACAGTG AAGCTGCCAT AAATATTTCT CAACTGAGGT TCTTGGGATA CAGATCTCAG 3720  
 GGCTCGGGAG CCATGTCTATG TGAGTGGGTG GGATGGGGAC ATTTGAACAT GTTTAATGGG 3780  
 TATGCTCAGG TCAACTGACC TGACCCCATT CCTGATCCCA TGGCCAGGTG GTTGTCTTAT 3840  
 TGCACCATAC TCCTTGCTTC CTGATGCTGG GCAATGAGGC AGATAGCACT GGGTGTGAGA 3900  
 10 ATGATCAAGG ATCTGGACCC CAAAGAAATG ACTGGATGGA AAGACAACT GCACAGGCAG 3960  
 ATGTTTGCCCT CATAATATGC GTAAGTGGAG TCCTGGAAAT TGGACAAGTG CTGTTGGGAT 4020  
 ATAGTCAACT TATTCTTTGA GTAATGTGAC TAAAGGAAAA AACTTTGACT TTGCCAGGC 4080  
 ATGAAATTTCT TCCTAATGTC AGAACAGAGT GCAACCCAGT CACACTGTGG CCAGTAAAT 4140  
 ACTATTGGCT CATATTGTCC TCTGCAAGCT TCTTGCTGAT CAGAGTTTCTT CCTACTTACA 4200  
 15 ACCCAGGGTG TGAACATGTT CTCCATTTTC AAGCTGGAAG AAGTGAGCAG TGTTGGAGTG 4260  
 AGGACCTGTA AGGCAGGCC ATTCAGAGCT ATGGTGCTTG CTGGTGCCTG CCACCTTCAA 4320  
 GTTCTGGACC TGGGCATGAC ATCTTTTCTT TTAATGATGC CATGGCACT TAGAGATTGC 4380  
 ATTTTATATTA AAGCATTTCC TACCAGCAAA GCAATATGTT GGAAGATATT TACTTTTTCG 4440  
 GTTCAAAGT GATAGAAAAA TGTGGCTTGG GCATTGAAAG AGGTAAAAAT CTCTAGATTT 4500  
 20 ATTAGTCCCTA ATTCATCTCT ACTTTTCGAA CACCAAAAAT GATGCGCATC AATGTATTTT 4560  
 ATCTTATTTT CTCAATCTCC TCTCTCTTTC CTCCACCCAT AATAAGAGAA TGTTCTTACT 4620  
 CACACTTCAG CTGGTTCACA TCCATCCCTC CATTATCCCT TCCATCCATC TTTCCTTACA 4680  
 TTACCTCCAT CCATCCTTCC AACATATATT TATTGAGTAC CTACTGTGTG CCAGGGGCTG 4740  
 GTGGGACATG GGTGACATG TCTCTGCCCT CATAGAGTTG ATTGTCTAGT GAGGAAGACA 4800  
 25 AGCATTTTTA AAAATAAAT TTAACCTTAC AAACCTTGT TGTCACAAGT GGTGTTTATT 4860  
 GCAATAACCG CTGTTGTTGC AACCTCTTTC CTCAACAGAA CATATGTTGC AAGACCTTCC 4920  
 CATGGGGGCA CTTAGTTTTC GGCAAGGCTG ACAGAGCTCT GGGTTGTGCA CATTCTTTG 4980  
 CATTCCAGCT GTCACCTCTG GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA 5040  
 TAACACCACT GGAATTGCTT GGAGGAACCA GAGGCACCTC CACCTTGGCT GGAAGACTA 5100  
 30 TGGTGTGCTC TTGCTTCTGT ATTTCTTGG ATTTTCCTGA AAGTGTTTT AAATAAGAA 5160  
 CAATTGTTAG ATGCC 5175

Seq ID NO: C107 DNA Sequence  
 Nucleic Acid Accession #: NM\_021101  
 Coding sequence: 221..856

1 11 21 31 41 51  
 | | | | |  
 GAATTCGGCA CGAGGCCTCG TGCCGGGGAG CAACCTCAGC TTCTAGTATC CAGACTCCAG 60  
 CGCCGCCCCG GCGCGGGACC CCAACCCCGA CCCAGAGCTT CTCCAGCGGC GGCGCAGCGA 120  
 40 GCAGGGCTCC CCGCCTTAAC TTCTCCCGCG GGGCCAGGCC ACCTTCGGGA GTCCGGGTG 180  
 CCCACCTGCA AACTCTCCGC CTCTGCAACC TGCCACCCCT GAGCCAGCGC GGGCGCCCGA 240  
 GCGAGTCATG GCGCAGCGCG GGCTGCAGCT GTTGGGCTTC ATTCTCGCCT TCTGGGATG 300  
 GATCGGCGCC ATCGTCAGCA CTGCCCTGCC CCAGTGGAGG ATTTACTCCT ATGCGGCGCA 360  
 45 CAACATCGTG ACCGCCCAGG CCATGTACGA GGGGCTGTGG ATGTCCTGCG TGTGCGCAG 420  
 CACCGGGCAG ATCCAGTGCA AAGTCTTTGA CTCTTGCTG AATCTGAGCA GCACATTGCA 480  
 AGCAACCCCTG GCCTTGATGG TGGTTGGCAT CCTCTGGGA GTGATAGCAA TCTTTGTGGC 540  
 CACCGTTGGC ATGAAGTGTG TGAAGTGCCT GGAAGACGAT GAGGTGCAGA AGATGAGGAT 600  
 GGCTGTCAAT GGGGGCGCGA TATTTCTTCT TGCAGGTCTG GCTATTTTAG TTGCCACAGC 660  
 50 ATGGTATGCG AATAGAATCG TTCAAGAATT CTATGACCCT ATGACCCAG TCAATGCCAG 720  
 GTACGAATTG GTTCACTGCT TCTTCACTGG CTGGGCTGCT GCTTCTCTCT GCCTTCTGGG 780  
 AGGTGCCCCA CTTTGTCTGT CTGTCCCCG AAAAACAACC TCTTACCCAA CACCAAGGCC 840  
 CTATCCAAA CTTGCACCTT CCAGCGGGAA AGACTACGTG TGACACAGAG GCAAAAGGAG 900  
 AAAATCATGT TGAACAAAC CGAAAATGGA CATTGAGATA CTATCATTAA CATTAGGACC 960  
 55 TTAGAATTTT GGGTATTGTA ATCTAAAGTA TGTATTACA AAACAAACAA ACAACAAAA 1020  
 AACCCATGTG TTAATAACT CAGTGCTAAA CATGGCTTAA TCTTATTTA TCTTCTTCC 1080  
 TCAATATAGG AGGGAAGATT TTTCATTG TATTACTGCT TCCCATGAG TAATCATACT 1140  
 CAAATGGGGG AAGGGGTGCT CCTTAAATAT ATATAGATAT GTATATATAC ATGTTTTTCT 1200  
 ATTAATAATA GCCAGTAAAA AAAAAAATA AAAAAA 1237

Seq ID NO: C108 DNA Sequence  
 Nucleic Acid Accession #: AF508964.1  
 Coding sequence: 98..1531

1 11 21 31 41 51  
 | | | | |  
 CAGAGCCGCA AGCGCAGGGA AGGCCTCCCC GCACGGTGGG GGAAGCGGC CGGTGCAGCG 60  
 CGGGGACAGG CACTCGGGCT GGCACCTGGT GCTAGGGATG TCGTCTGGA TAAGTGGCA 120  
 TGGACCGGCC ATGGCGCGGC TCTGGGGCTT CTGCTGGCTG GTTGTGGGCT TCTGGAGGCG 180  
 70 CGCTTTCGCC TGTCCACGCT CCTGCAAATG CAGTGCCTCT CGGATCTGGT GCAGCGACCC 240  
 TTCTCTGGC ATCGTGGCAT TTCCGAGATT GGAGCCTAAC AGTGTAGATC CTGAGAACAT 300  
 CACCGAAATT TTCACTGCAA ACCAGAAAAG GTTAGAAATC ATCAACGAAG ATGATGTTGA 360  
 AGCTTATGTG GGAAGTGAAT ATCTGACAAT TGTGGATTCT GGATTAATAAT TTGTGGCTCA 420  
 TAAAGCATT CTGAATAACA GCAACCTGCA GCACATCAAT TTTACCCGAA ACAAACTGAC 480  
 75 GAGTTTGTCT AGGAAACATT TCCGTACCTT TGACTTGTCT GAACTGATCC TGGTGGGCAA 540  
 TCCATTTACA TGCTCCTGTG ACATTATGTG GATCAAGACT CTCCAAGAGG CTAATCCAG 600  
 TCCAGACACT CAGGATTGTG ACTGCCTGAA TGAAGCAGC AAGAATATTC CCCTGGCAAA 660  
 CCTGCAGATA CCCAATGTGT GTTTGCCATC TGCAAATCTG GCCGCACCTA ACCTCACTGT 720  
 GGAGGAAGGA AAGTCTATCA CATTATCTCT TAGTGTGGCA GGTGATCCGG TTCTAATAT 780  
 80 GTATTGGGAT GTTGGTAACC TGGTTTCCAA ACATATGAAT GAAACAAGCC ACACACAGGG 840  
 CTCCTTAAGG ATAACTAACA TTTTCATCCG TGACAGTGGG AAGCAGATCT CTTGTGTGGC 900  
 GGAATAATCT GTAGAGAGAAG ATCAAGATTG TGTCAACCTC ACTGTGCATT TTGCACCAAC 960  
 TATCACATTT CTGAAATCTC CAACCTCAGA CCACCACTGG TGCAATCCAT TCACTGTGAA 1020  
 AGGCAACCCC AAACAGCGCG TTCAGTGGTT CTATAACGGG GCAATATGTA ATGAGTCCAA 1080  
 ATACATCTGT ACTAAATATC ATGTTACCAA TCACACGGAG TACCACGGCT GCCTCCAGCT 1140

	GGATAATCCC	ACTCACATGA	ACAAATGGGGA	CTACACTCTA	ATAGCCCAAG	ATGAGTATGG	1200
	GAAGGATGAG	AAACAGATTT	CTGCTCACTT	CATGGGCTGG	CCTGGAATG	ACGATGGTGC	1260
	AAACCCAAAT	TATCCTGATG	TAAATTTATG	AGATTATGGA	ACTGCAGCGA	ATGACATCGG	1320
5	GGACACCACG	AACAGAAAGT	ATGAAATCCC	TTCCACAGAC	GTCACTGATA	AAACCGGTCC	1380
	GGAAACATCTC	TCCGCTGATG	CTGTGGTGGT	GATTGCGTCT	GTGGTGGGAT	TTTGCCTTTT	1440
	GGTAATGCTG	TTTCTGCTTA	AGTTGGCAAG	ACACTCCAAG	TTTGGCATGA	AAGGTTTTGT	1500
	TTTGTTCAT	AAGATCCAC	TGGATGGGTA	GCTGAAATAA	AGGAAAAGAC	AGAGAAAAGG	1560
	GCTGTGGTGC	TTGTGTGGTG	ATGCTGCCAT	GTAAGCTGGA	CTCCTGGGAC	TGCTGTGGC	1620
10	TTATCCCGGG	AAGTGTGCT	TATCTGGGGT	TTTCTGGTAG	ATGTGGGCGG	TGTTTGGAGG	1680
	CTGTACTATA	TGAAGCCTGC	ATATACTGTG	AGCTGTGATT	GGGGAACACC	AATGCAGAGG	1740
	TAACTCTCAG	GCAGCTAAGC	AGCACCTCAA	GAACAACTGT	TAAATTAATG	CTTCTCTCT	1800
	TACAGTAGTT	CAAAATACAA	ACTGAAATGA	AATCCCATTG	GATTGTACTT	CTCTTCTGAA	1860
	AAGTGTGCTT	TTTGACCCCTA	CTGGACATTT	ATTGACTTAA	TTGCTTCTGT	TTATTAATAAT	1920
15	TGACCTGCAA	AGTTAAATAA	AAATTAAGT	TGAGAACAGG	TATAAGTGCA	CACCTGAATG	1980
	TCTAATCTAC	ATGTAACACA	TATTTTAGTA	TGATTTTCTA	TACTCTAATC	AGCACTGAAT	2040
	TCAGAGGGTT	TGACTTTTTT	ATCTATAACA	CAGTGACTAA	AAGAGTTAAG	GGTATATATA	2100
	CCATCACTTT	GGGACTTGGT	AGTATTATTA	AAAGGTTATT	TCCTTCACTG	TCAATATAAG	2160
	TCCAAATGTT	TAGCTTAGGT	CTGAGAGTCA	AACAATGTTA	AGGATTGTCT	TAAAGTTCTT	2220
20	TAGCCAGCAA	AACAAAACAA	AACAAAACAA	ACAAATGAAA	AACGTTTAAA	AAGAAGAAGA	2280
	AGAAAAAATA	CAAGAACAAG	CAGCAACAGC	TGTTTTGTGG	GGGCTATAGA	TTTAAGTTAG	2340
	GCATAGTCAA	TTTCAGATA	ACTAAGAGTG	GAATATATGC	ATATGGTGAA	ATTATAACCT	2400
	TGCCCTTTTT	TATTTGCCCT	CTGCGATCCA	CCTGGCTTTT	TAGAAGTCTG	CCGAGTGAGA	2460
	AGGCCACAGT	ATCTCATGCT	GTTTGCATTA	CAGAAGTCCA	GCTTTTCTAC	TCTGAAAAGG	2520
25	CCTGGGAGCA	GAATGGCTGG	CCTGCTGTGA	GCAGGAGAGG	AGATTCTAAG	AAGGATAGTC	2580
	CCCCCTACAA	CATAGTGTCA	TACTGCTGGG	TTTTCATGGG	TAGGAAAGCT	TGCTCTGACC	2640
	CCAGCAGCAA	AGAGGTGGCA	GGTCGCTAAT	GAATATATGC	TTTATAATGT	CCTTCTTCT	2700
	TGCTGAGAGG	GCAGCCTTAG	AGCTGTGGAT	TTCTGCATCC	CCCCTGAGTC	TGACCCATGG	2760
	ACACCTGTTT	CATTCACTTT	AGCATCACAG	TGACCTTTGT	ATGCTCTGTT	CAGTCTGTGT	2820
30	CAGGCAGTAT	GCTTGTCTTG	AAGAGAGGTT	TGGCTATCCC	CCACCCACCC	CACCCACCTT	2880
	GTTCTTTTTT	TATCAGGAGG	ACTTCAGAGC	CAGGCCCTGA	GCATTTTGTG	TGAAAACACA	2940
	ATCAGCTCTG	ACAGTTAGAG	ATGCACACAG	ACGCCATAGC	TGGATTGGAA	ACATTGATGT	3000
	TTTAAAAATT	TATTTTTTTT	GGAAATAGTT	GCACAAATGC	TGCAATTTAG	CTTTAAGGTT	3060
	CTATAGATTT	TAACTAGTCT	CAACACAGTC	AGAAACATTG	TTTTGAATCC	TCTGTAAACC	3120
35	AAGGCATTAA	TCTTAATAAA	CCAGGATCCA	TTTAGGTACC	ACTTGATATA	AAAAGGATAT	3180
	CCATAATGAA	TATTTTATAC	TGCATCCTTT	ACATTAGCCA	CTAAATACGT	TATTTGCTGA	3240
	TGAAGACCTT	TCACAGAATC	CTATGGATTG	CAGCATTTCA	CTTGGCTACT	TCATACCCAT	3300
	GCCTTAAAGA	GGGGCAGTTT	CTCAAAAGCA	GAACATGCC	GCCAGTTCTC	AAGTTTTCCT	3360
	CCTAATCTCA	TTTGAATCTA	AGGGCAGCTG	GCCCCCAATG	TGGGGAGGTC	CGAACATTTT	3420
40	CTGAATTCCT	ATTTTCTTGT	TGCGGCTAA	ATGACAGTTT	CTGTCTTATC	TTAGATTCCG	3480
	ATCTTTCCCA	AAGGTGTTGA	TTTACAAAGA	GGCCAGCTAA	TAGCAGAAAT	CATGACCCCT	3540
	AAAGAGAGAT	GAAATTCAGG	CTGTGAGCCA	GGCAGGAGCT	CAGTATGGCA	AAGGTTCTTG	3600
	AGAATCAGCC	ATTTGTGACA	AAAAAGATTT	TTAAAGCTTT	TATGTTATAC	CATGGAGCCA	3660
	TAGAAAGGCT	ATGGATTTGT	TAAAGACTAT	TTTAAAGTGT	TCCAGACCCA	AAAAGGAAAA	3720
45	ATAAAAAATA	AGGAAATATT	GTACCCACAC	GCTAGAAGGA	TTGCAAGGTA	GATTTTGTGT	3780
	TTAAAAATGA	GAGAAGTGGA	CAGATAAGGC	CATTTAATAT	ATCAAAGATC	AGTTGACATC	3840
	TCTAGGGAAT	GATGAAACAG	CAGGCTATTA	GAAAAATTAT	TCATATAGTT	CTCGTGTCTT	3900
	TTTCTTTTTT	TTAATCCCTG	AAGGGAGATC	AGTAACATAG	CTTCTTTTTT	CTGTACTCTA	3960
	GACCACCCCT	TTTCATCATT	TTGCTTTTTA	TGTCTCCCAT	AAGAAATGTG	CTTTTGTAGG	4020
50	CTTCTTAATG	CAITGTGTGC	ATTATTGCAG	CATTAGAAAA	GGAGAGGTAG	CATTTTGTCT	4080
	GAATCCGGGC	CTGTCACTCT	CCAATAAAGG	TTCTGGCACT	TCAATGCCAG	CGAGGTCTCC	4140
	TAAATGAACA	GAATGATCTG	TGTGAGCCGA	TGCCTGCCCT	TCCAGAGGGG	CCACTGTCCC	4200
	CAGCCGCAGC	CACTGTGTCT	CCACAGGAAT	GGGAGCCTAG	GTTTCCAAAT	CTTGTGATTG	4260
	TTTAGGAGAA	ACATGAAACC	TGGATTTCGT	GTGAAATGTC	CCGATTGTTA	AAAAGTTGGC	4320
	TCAATTATTT	TTAAAAACAT	TTGTAAGCCA	ACAAAAGTCT	GTGGGCTGCC	AGTTTATTAC	4380
55	TTTGTCTCTA	AAACATGATC	ATTGTTCTCT	CACGGTATCC	TTCTGTCTTC	CCGTTGCAAA	4440
	TTCACTTTTC	TTTCTTCTGT	ACATTGCCAT	TGAGGGCTTT	GTTACCAACA	GCTAAGAAAC	4500
	TGAGTTTAA	AGCCCACTTA	TCTGCAACAT	GTCAATTACC	TTTGTCTCTC	TCCTGTGATT	4560
	CCCACCATGC	TGTGACCCCT	AGCTGTCTCC	CTTGTCTGGG	AATTCTGCAC	CAATGTCTTC	4620
60	CCCTCAACCC	ATTCCCTGGT	TGCTCCTACT	CCCGTGTGGC	CAGAGACATC	CTAGCAAAATC	4680
	CTTCTCTCTA	TTATATCTGA	CACATAATTT	TTTTCAACAG	CGCTCATGTC	TCTTGGCCCA	4740
	GTCAGGTGCT	GCCAGGTTTA	GATAGGAAG	TACATGTCCC	ATTTTCATGG	GTGCCCTTAA	4800
	TGTGGTCCAG	GTCTATATAT	TTATTATATT	TACTCATGGC	TCAATGGGGG	CCTCCAGAGA	4860
	CCCTCTCAGG	CTGCTGAGCT	AGACTAAGGA	ATGCATCCAC	TGTCTATACA	TGAGACACTG	4920
65	ACTCTGTGAC	GCAAAAAGTA	CAACAGTCT	GAGGCTAAGA	AAGGTTTATC	TCACAAACAG	4980
	AAAAACAAAT	CTCAACACAC	ATTAGAGATA	ATTGATTACG	GGGTTTTCTC	TCCCAGTCTC	5040
	CCAGCAGGGA	CTGATTTTCT	TTCTGACCCA	CTAGGTTTTC	TTTCCAGAAA	TAGGTAGCAA	5100
	GGACAAGAAC	TAAACAATCC	CAGCCCCACC	CAGCAACACA	GAACACAGGA	GTTTGTCTTT	5160
	GGCTTCTCAC	TCTCCAAGTA	ACCCTGAATT	AGGCCAGAAA	TGGCTGAGGC	TTGGAGCATC	5220
70	TCCTCAGACA	GAGCAGAGGC	GACACCTCTT	CAGGGGTGTG	TGGAGTAAAT	AGCTCGAAGA	5280
	GCTGAAGACA	GAACACAGT	TTTACGCCAG	GTGCGAGAGA	GAGCATAATG	GAGGGAAGCC	5340
	CGCTTTCTCT	CTCTCTTCTT	TTTCTTTTGA	TTTCTTTTGA	GCATTTGACT	TTTTTTTCTC	5400
	TCTCTCTCTA	GTATTTCTAAA	CTGACCCCAT	GACCAACTGA	GAATTTATTT	TTGTTTCTAT	5460
	GGTTGTTTCA	CAGAATTAGA	ACACACACGA	CTTTTATATC	CTCCATTGCA	AAATGGAATC	5520
75	AAGATACTAC	ACAAGACCTG	TGCTTTCTTC	CTTTGCATGA	TTTACACCTC	CGCCTGTTTT	5580
	GGTGCTAGCT	GTCTAGAAGT	TCTCTCTTGG	TTTGAATCTG	ATTCCTTCAC	ACTACACTAG	5640
	AAGTTTATTT	CATCTGTGTT	TGTCTAGACT	CCAGATACAG	AGGGACAGCT	GGACTGAGGA	5700
	CAAGCAATTC	CATCTAGCAT	AGGGTCTCTC	AGGGTTGGTG	CATCCAGCCA	CATGGGCAGG	5760
	GCCAGTCACA	TCTAGTCTAT	GTCCCCAGAG	CCCTTGGAGT	TGCGCAGCTT	AGCTGACTTG	5820
80	ACTCCAAGGA	AATTAGTACA	GAAGTAACCA	CTCTATTAA	TGTGTTCTGC	TATGTTTACA	5880
	TGCCCTGTAGT	ACCTGCAACG	CATGCCAGGT	TCATCTAAGG	ACATAGGGGA	AGATTAAAGG	5940
	CTCTTTTGGG	CAGACCATGA	ATTGAATTG	CTGCCAGGTG	CTGCCAGACT	GAATTTGGCT	6000
	GACAGAACTC	CCAGCCCAGG	AAAGTTCCAT	GACAAATGACT	GTGCGAGAAG	GAAATTTCCC	6060
	ACTAAAGTCA	GTCCATTTTC	AAGTTTGGT	CTTCAGAGAC	AAAAGAACGT	CCCAGCCACC	6120
	TGATTTTGAT	GGTGAGGTAA	CTCTAAGTTG	AATTCAGGCT	AGTGTGTCAG	TATAGCTTTG	6180

GCATGTTTCAT GAGTGAACAC CCAGAATGTG TTGAACCAAC CCCCACCCCT AACTACTGAC 6240  
 TATGACTGCA GTGGGTTTTT ATGGGGAAAA AAAGTGTGAA AAGCAAAAAG AAAGGAACAG 6300  
 AGATTTTTTA TCACCTTTAT TGTAAACAG TCCATTTATG AATTGAGTAT AAACACATAC 6360  
 AAAGTAACAA GAGATTCCTA AGAAACGCAA ATCCTTGAGT TTCACGCAT TCATGTTCAA 6420  
 CCATTTGCTG TAATCCAGAG GCAGCCTGTG AATCATTCTC ATGCCCTGTT TTTTTTTTTT 6480  
 TTTTCTTATA ATGTTCTGGG TTTAAAGGCC ATCTTTTCCA CATTTTCTGT AAATAATGGA 6540  
 TAATCATTTT AAAAAGTTT ATTTTATGTG CTGTTTAAAC AATGTAGATA GATCATAAAT 6600  
 GTACTTGTG AATTCAATCA TTTTAAACAA GCCAATAAAG TTTGATAATT CAAAAAATAA 6660  
 AAAAAAATAA AAAAAAATAA 6679

Seq ID NO: C109 DNA Sequence  
 Nucleic Acid Accession #: NM\_006180.1  
 Coding sequence: 352..2820

1 11 21 31 41 51  
 CCCCCATTTC CATCTAACAA GGAATCTGCG CCCCAGAGAG TCCCGGACGC CGCCGGTCCG 60  
 TGCCCGGCGC GCCCGGCCAT GCAGCGACGG CCGCCGCGGA GCTCCGAGCA GCGGTAGCGC 120  
 CCCCTGTAA AGCGGTTGCG TATGCCGGGA CCACTGTGAA CCCTGCCGCC TGCCGGAACA 180  
 CTCTTCGCTC CGGACGAGCT CAGCCTCTGA TAAGCTGGAC TCGGCACGCC CGCAACAAGC 240  
 ACCGAGGAGT TAAGAGAGCC GCAAGCGCAG GGAAGGCCTC CCGGCACGGG TGGGGGAAAG 300  
 CGGCCGGTGC AGCGCGGGGA CAGGCACTCG GGCTGGCACT GGCTGTAGG GATGTCGTCC 360  
 TGGATAAGGT GGCATGGACC CGCCATGGCG CGGCTCTGGG GCTTCTGCTG GCTGGTTGTG 420  
 GGCTTCTGGA GGGCCGCTTT CGCCTGTCCC ACCTCTGCTA AATGCAGTGC CTCTCGGATC 480  
 TGGTGCAGCG ACCCTTCTCC TGGCATCGTG GCATTTCCGA GATTGGAGCC TAACAGTGTA 540  
 GATCCTGAGA ACATCACCGA AATTTCATC GCAAAACAGA AAAGGTTAGA AATCATCAAC 600  
 GAAGATGATG TTGAAGCTTA TGTGGGACTG AGAAATCTGA CAATTGTGGA TTCTGGATTA 660  
 AAATTTGTGG CTCATAAAGC ATTTCTGAAA AACAGCAACC TGCAGCATAT CAATTTTACC 720  
 CGAAACAAC TGACGAGTTT GTCTAGGAAA CATTTCCGTC ACCTTGACTT GTCTGAACTG 780  
 ATCCTGGTGG GCAATCCATT TACATGCTCC TGTGACATTA TGTGGATCAA GACTCTCCAA 840  
 GAGGCTAAAT CCAGTCCAGA CACTCAGGAT TTGTAAGTCC TGAATGAAAG CAGCAAGAAAT 900  
 ATTCCTCTGG CAAACCTGCA GATACCCAAT TGTGGTTTGC CATCTGCAAA TCTGGCCGCA 960  
 CCTAACCTCA CTGTGGAGGA AGGAAAGTCT ATCACATTAT CCTGTAGTGT GGCAGGTGAT 1020  
 CCGGTTCCCTA ATATGTATTG GGATGTTGGT AACCTGGTTT CCAAACATAT GAATGAAACA 1080  
 AGCCACACAC AGGCTCCTT AAGGATAACT AACATTTTCA CCGATGACAG TGGGAAGCAG 1140  
 ATCTCTTGTG TGGCGGAAAA TCTTGTAGGA GAAGATCAAG ATTCTGTCAA CTCACGTGTG 1200  
 CATTTTGAC CAACTATCAC ATTTCTCGAA TCTCCAACT CAGACCACCA CTGGTGCATT 1260  
 CCATTCACTG TGAAGGCAAA CCCCACCAAC GCGCTTCAGT GGTTCATATA CCGGGCAATA 1320  
 TTGAATGAGT CCAATACAT CTGTACTAAA ATACATGTTA CCAATCACAC GGAGTACCAC 1380  
 GGCTGCCTCC AGCTGGATAA TCCCACTCAC ATGAACAATG GGGACTACAC TCTAATAGCC 1440  
 AAGAATGAGT ATGGGAAGGA TGAGAAACAG ATTTCTGCTC ACTTCATGGG CTGGCCTGGA 1500  
 ATTGACGATG GTGCAACCC AAATTATCCT GATGTAATTT ATGAAGATTA TGGAACTGCA 1560  
 GCGAATGACA TCGGGGACAC CACGAACAGA AGTAATGAAA TCCCTTCCAC AGACGTCACT 1620  
 GATAAAACCG GTCCGGAAACA TCTCTCGTTC TATGCTGTGG TGGTGTATGC GTCTGTGGTG 1680  
 GGATTTTGCC TTTTGGTAAT GCTGTTTCTG CTTAAGTTGG CAAGACATC CAAGTTTGGC 1740  
 ATGAAAGGCC CAGCCTCCGT TATCAGCAAT GATGATGACT CTGCCAGCCC ACTCCATCAC 1800  
 ATCTCCAATG GGAGTAACAC TCCATCTTCT TCGGAAGGTG GCCCAGATGC GTGCATTATT 1860  
 GGAATGACCA AGATCCCTGT CATTGAAAT CCCCAGTACT TTGGCATCAC CAACAGTCAG 1920  
 CTCAGCCAG ACACATTTGT TCAGCACATC AAGCGACATA ACATTGTCTT GAAAGGGAG 1980  
 CTAGGCGAAG GAGCCTTTGG AAAAGTGTTC CTAGCTGAAT GCTATAACCT CTGTCTGAG 2040  
 CAGGACAAGA TCTTGGTGGC AGTGAAGACC CTGAAGGATG CCAGTGACAA TGCACGCAAG 2100  
 GACTTCCACC GTGAGGCCGA GCTCCTGACC AACCTCCAGC ATGAGCACAT CGTCAAGTTC 2160  
 TATGGCGTCT GCGTGGAGGG CGACCCCTC ATCATGCTCT TTGAGTACAT GAAGCATGGG 2220  
 GACCTCAACA AGTTCCCTCAG GGCACACGGC CCTGATGCCG TGCTGATGGC TGAGGGCAAC 2280  
 CCGCCCAAGG AACGTACAGC GTCGAGATG CTGCATATAG CCCAGCAGAT CGCCGCGGGC 2340  
 ATGCTCTACC TGGCGTCCCA GCACCTTCGT CACCGCGATT TGGCCACCAG GAAGTGCCTG 2400  
 GTCCGGGAGA ACTTGTCTGT GAAATCGGG GACTTTGGGA TGTCCCGGGA CGTGTACAGC 2460  
 ACTGACTACT ACAGGTCGCG TGGCCACACA ATGCTGCCCA TTCGCTGGAT GCCTCCAGAG 2520  
 AGCATCATGT ACAGGAAATT CACGACGGAA AGCGACGCTT GGAGCCTGGG GGTCTGTGTT 2580  
 TGGGAGATTT TCACCTATGG CAAACAGCCC TGGTACCAGC TGTCAAACAA TGAGGTGATA 2640  
 GAGTGTATCA CTCAGGGCCG AGTCTGCGAG CGACCCCGCA CGTGCCCGCA GGAGGTGTAT 2700  
 GAGCTGATGC TGGGGTCTG GCAAGGAGAG CCCCACATGA GGAAGAACAT CAAGGGCATC 2760  
 CATACCTTCC TTCAGAACTT GGCCAAGGCA TCTCCGGTCT ACCTGGACAT TCTAGGCTAG 2820  
 GGCCCTTTTC CCCAGACCGA TCCTTCCCAA CGTACTCTCT AGACGGGCTG AGAGGATGAA 2880  
 CATCTTTTAA CTGCCGCTGG AGGCCACCAA GCTGCTCTCC TTCACTTGA CAGTATTAAC 2940  
 ATCAAAGACT CCGAGAAGCT CTCGAGGGAA GCAGTGTGTA CTTCTTCATC CATAGACACA 3000  
 GTATTGACTT CTTTGTGGCA TTATCTCTTT CTCTCTTTCC ATCTCCCTTG GTTGTCTCTT 3060  
 TTTCTTTTTT TAAATTTTCT TTTTCTTCTT TTTTTCGTC TTCCCTGCTT CAGGATTCTT 3120  
 ACCCTTTCTT TTGAATCAAT CTGGCTTCTG CATTACTATT AACTCTGCAT AGACAAAGGC 3180  
 CTTAACAAC GTAATTTGTT ATATCAGCAG ACACCTCCAG TTGCCACCA CACTAACAA 3240  
 TGCCTTGTG TATTCCTGCC TTTGATGTGG ATGAAAAAAA GGGAAAAACA ATATTTCACT 3300  
 TAAACTTTGT CACTTCTGCT GTACAGATAT CGAGAGTTTC TATGGATTCA CTTCTATTTA 3360  
 TTTATTATTA TTACTGTCTT TATTGTTTTT GGATGGCTTA AGCCTGTGTA TAAAAAGAA 3420  
 AACTTGTGTT CAATCTGTGA AGCCTTTATC TATGGGAGAT TAAACACAGA GAGAAAGAAG 3480  
 ATTTATTATG AACCGCAATA TGGGAGGAAC AAAGACAACC ACTGGGATCA GCTGGTGTCA 3540  
 GTCCCTACTT AGGAATACT CAGCAACTGT TAGCTGGGAA GAATGTATTC GGCACCTTCC 3600  
 CCTGAGGACC TTTCTGAGGA GTAAAAAGAC TACTGGCCTC TGTGCCATGG ATGATTCTTT 3660  
 TCCCATCACC AGAAATGATA GCGTGCAGTA GAGAGCAAAG ATGGCTT 3707

Seq ID NO: C110 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 939..2372

1 11 21 31 41 51

	AAGACGGATT	CTCAGACAAG	GCTTGCAAAT	GCCCCGACG	CATCATTTAA	CTGCACCCGC	60
	AGAAATAGTTA	CGGTTTGTCA	CCCAGCCCTC	CCGGATCGCC	TAATTTGTCC	CTAGTGAGAC	120
5	CCCGAGGCTC	TGCCCGCGCC	TGGCTTCTTC	GTAGCTGGAT	GCATATCGTG	CTCCGGGCG	180
	CGCGGCGCA	GGGACGCGT	TCGCGCACAC	CCTAGCACAC	ATGAACACGC	GCAAGAGCTG	240
	AACCAAGCAC	GGTTTCCATT	TCAAAAAGGG	AGACAGCCCT	TACCGCGATT	GTAGAAGAGA	300
	CTGTGGTGTG	AATTAGGGAC	CGGGAGGCGT	CGAACGGAGG	AACGGTTTAT	CTTAGAGACT	360
	AATTTTCTGG	AGTTTCTGCC	CCTGCTCTGC	GTAGCCCTTC	ACGTCACTTC	GCCAGCAGTA	420
10	GCAGAGGCGG	CGCGGCGCGC	TCCCGGAATT	GGGTTGGAGC	AGGAGCCCTG	CTGGCTGCTT	480
	CGCTCGCGCT	CTACGCGCTC	AGTCCCGGCG	GGTAGCAGGA	GCCTGGACCC	AGGCGCCGCC	540
	GGCGGCGCTG	AGGCGCGCGA	GCCCGGCCCTC	GAGGTGCATA	CCGGACCCCC	ATTCGCATCT	600
	AACAAGGAAT	CTGCGCCCCA	GAGAGTCCCG	GGAGCGCCGC	CGGTGCGTGC	CCGGCGCGCC	660
	GGGCCATGCA	GCGACGCGCC	CCGCGGAGCT	CCGAGCAGCG	GTAGCGCCCC	CCTGTAAAGC	720
	GGTTCGCTAT	GCCGGGGCCA	CTGTGAACCC	TGCCGCGCTG	CGGAACACTC	TTCGCTCCGG	780
15	ACCAGCTCAG	CTCTGTATAA	GCTGGACTCG	GCACGCCCGC	AACAAGCACC	GAGGAGTTAA	840
	GAGAGCCGCA	AGCGCAGGGA	AGGCCCTCCCC	GCACGGGTGG	GGGAAAGCGG	CCGGTGCAGC	900
	CGCGGGACAG	GCACCTCGGG	TGGCACTGGC	TGCTAGGGAT	GTCTGCTGCT	ATAAGGTGGC	960
	ATGGACCCGC	CATGGCGCGG	CTCTGGGGCT	TCTGCTGGCT	GGTTGTGGGC	TCTGTGAGGG	1020
20	CCGCTTTCCG	CTGTCCACAG	TCTTGCAAAT	GCAGTGCCTC	TCGGATCTGG	TGCAGCGACC	1080
	CTTCTCCTGG	CATCGTGGCA	TTTCCGAGAT	TGGAGCCCTAA	CAGTGTAGAT	CCTGAGAACA	1140
	TACCCGAAAT	TTTCATCGCA	AACCAAGAAA	GGTTAGAAAT	CATCAACGAA	GATGATGTTG	1200
	AAGCTTATGT	GGGACTGAGA	AATCTGACAA	TTGTGGATTTC	TGGATTAAAA	TTTGTGGCTC	1260
	ATAAAGCATT	TCTGAAAAAC	AGCAACCTGC	AGCACATCAA	TTTTACCCGA	AACAAACTGA	1320
25	CGAGTTTGTC	TAGGAAACAT	TTCCTGCACC	TTGACTTGTC	TGAAGTATC	CTGGTGGGCA	1380
	ATCCATTTAC	ATGCTCCTGT	GACATTATGT	GGATCAAGAC	TCTCCAAGAG	GCTAAATCCA	1440
	ATCCAGACAC	TAGGATTTTG	TACTGCCTGA	ATGAAAGCAG	CAAGAATATT	CCCCTGGCAA	1500
	ACCTGCAGAT	ACCCAATTGT	GGTTTGCCAT	CTGCAAACTC	GGCCGCACCT	AACCTCACTG	1560
	TGGAGGAAGG	AAAGTCTATC	ACATTATCCT	GTAGTGTGGC	AGGTGATCCG	GTTCCCTAAT	1620
30	TGTATTGGGA	TGTTGTGAAC	CTGGTTTCCA	AACATATGAA	TGAAACAAGC	CACACACAGG	1680
	GCTCCTTAAG	GATAACTAAC	ATTTTCATCCG	ATGACAGTGG	GAAGCAGATC	TCTTGTGTGG	1740
	CGGAAATCT	TGTAGGAGAA	GATCAAGATT	CTGTCAACCT	CACCTGTGCAT	TTTGACCCAA	1800
	CTATCACATT	TCTCGAATCT	CCAACCTCAG	ACCACCACTG	GTGCATTCCA	TTCATGTGTA	1860
	AAGGCAACCC	CAAACAGCGG	CTTCAGTGGT	TCTATAACCG	GGCAATATTG	AATGAGTCCA	1920
35	AATACATCTG	TACTAAAAAT	CATGTTACCA	ATCACACGGA	GTACCACGGC	TGCCTCCAGC	1980
	TGGATAATCC	CACTCACATG	AACAATGGGG	ACTACACTCT	AATAGCCAAG	AATGAGTATG	2040
	GGAAGGATGA	GAAACAGATT	TCTGCTCACT	TCAATGGGCTG	GCCTGGAATT	GACGATGGTG	2100
	CAAACCCAAA	TTATCTGTAT	GTAATTTATG	AAGATTATGG	AACCTGCAGC	AATGACATCG	2160
	GGGACACCCG	GAAACAGAGT	AATGAAATCC	CTTCCACAGA	CGTCACTGAT	AAAAACGGTC	2220
40	GGGAACATCT	CTCGGTCTAT	GCTGTGGTGG	TGATTGCGCT	TGTGGTGGGA	TTTTCCTTTT	2280
	TGGTAATGCT	GTTTCTGCTT	AAGTTGGCAA	GACACTCCAA	GTTTGGCATG	AAAGGTTTTG	2340
	TTTTGTTTCA	TAAGATCCCA	CTGGATGGGT	AGCTGAAATA	AAGGAAAAGA	CAGAGAAAGG	2400
	GGCTGTGGTG	CTTGTGGGTT	GATGCTGCCA	TGTAAGCTGG	ACTCCTGGGA	CTGCTGTTGG	2460
	CTTATCCCGG	GAAAGCTGCT	TTATCTGGGG	TTTTCTGGTA	GATGTGGGCG	GTGTTTGGAG	2520
45	GCTGTACTAT	ATGAAGCCTG	CATATACTGT	GAGCTGTGAT	TGGGGAACAC	CAATGCAGAG	2580
	GTAACCTCTA	GGCAGCTAAG	CAGCACCTCA	AGAAAACATG	TTAAATTAAT	GCTTCTCTTC	2640
	TTACAGTAGT	TCAAAATACAA	AACGTAAATG	AAATCCCATT	GGATTGTACT	TCTCTCTCTA	2700
	AAAGTGTGCT	TTTTGACCTT	ACTGGACATT	TATTGACTTA	ATTGCTTCTG	TTTATTAATA	2760
	TTGACCTGCA	AAGTTAAAAA	AAAATTAAG	TTGAGAACAG	GTATAAGTGC	ACACTGAATA	2820
50	GTCTAATCTA	CATGTAACAC	ATATTTTAGT	GTGATTTTCT	ATACTCTAAT	CAGCACTGAA	2880
	TTCAGAGGGT	TTGACTTTT	CATCTATAAC	ACAGTGACTA	AAAGAGTTAA	GGGTATATAT	2940
	ACCATCACTT	TGGGACTTGG	TAGTATTATT	AAAAGGTTAT	TTCTTCACT	GTCAATAAAA	3000
	GTCCAAATGT	TTAGCTTTAG	TCTGAGAGTC	AAACAATGTT	AAGGATTGTC	TTAAAGTTCC	3060
	TTAGCCAGCA	AAACAAAACA	AAACAAATGAA	AAACGTTTAA	AAAGAGAAG	3120	
55	AAAGAAAAAA	ACAAGAACAA	GCAGCAACAG	CTGTTTGTGT	GGGGCTATAG	ATTTAAGTTA	3180
	GGCATAGTCA	ATTTAGAAAT	AACATAAGAGT	GGAAATATATG	CATATGGTGA	AATTATAACC	3240
	TTGCCCTTTT	TTATTTGCCC	TCTGCGATCC	ACCTGCTTTT	TAGAAGTCTG	CCGAGTGAGA	3300
	AGGCCACAGT	ATCTCATGCT	GTTTGCATTA	CAGAAGTCA	GCTTTTCTAC	TCTGAAAAGG	3360
	CCTGGGAGCA	GAATGGCTGG	CCTGCTGTGA	GCAGGAGAGG	AGATTCTAAG	AAGGATAGTG	3420
60	CCCCCTACAA	CATACTGTCA	TACTGCTGGG	TTTTCATGGG	TAGGAAAGCT	TGCTCTGACC	3480
	CCAGCAGCAA	AGAGGTGGCA	GGTGGCTAAT	GAATATATGC	TTTATAATGT	CCTTCTTCAT	3540
	TGCTGAGAGG	GCAGCCTTAG	AGCTGTGGAT	TTCTGCATCC	CCCCTGAGTC	TGACCCATGG	3600
	ACACCTGTTT	CATTCACTTT	AGCATCACAG	TGACCTTTGT	ATGCTCTGTT	CAGTCTGTGT	3660
	CAGGCAATAT	GCTTGTCTCT	AAGAGAGGTT	TGGCTATCCC	CACCCCAACC	CACCCCAACC	3720
	TGTTCTCTTT	TTATCAGGAG	GACTTCAGAG	CCAGGCCTGC	AGCATTTTGT	TTGAAAACAC	3780
65	AATCAGCTCT	GACAGTTAGA	CATGCACACA	GACGCCATAG	CTGGATTGGA	AACATTGATG	3840
	TTTTAAAAAT	TTATTTTTTT	TGGAAATAGT	TGCACAAATG	CTGCAATTTA	GCTTTAAGGT	3900
	TCTATAGATT	TTTAACTAGT	CCAACACAGT	CAGAAACATT	GTTTGTGAATC	CTCTGTAAAC	3960
	CAAGGCATTA	ATCTTAATAA	ACCAGGATCC	ATTTAGGTAC	CACCTTGATAT	AAAAAGGATA	4020
70	TCCATAATGA	ATATTTTATA	CTGCATCCTT	TACATTAGCC	ACTAAATACG	TTATTGCTTG	4080
	ATGAAGACCT	TTACAGAAAT	CCTATGGATT	GCAGCATTTT	ACTTGGCTAC	TTCATACCCA	4140
	TGCCCTTAAAG	ATGGGGCAGTT	TCTCAAAAGC	AGAAACATGC	CGCCAGTTCT	CAAGTTTTC	4200
	TCCTAACTCC	ATTTGAATGT	AAGGGCAGCT	GGCCCCCAAT	GTGGGGAGGT	CCGAACATTT	4260
	TCTGAATTCC	ATTTTCTTGT	TTCCGGGCTA	AATGACAGTT	TCTGTCTATTA	CTTAGATTCC	4320
75	GATCTTTCCC	AAAGGTGTTG	ATTTACAAAG	AGGCCAGCTA	ATAGCAGAAA	TCATGACCCT	4380
	GAAAGAGAGA	TGAAATTCAA	GCTGTGAGCC	AGGCAGGAGC	TCAGTATGGC	AAAGGTTCTT	4440
	GAGAAATCAG	CATTGTGTAC	AAAAAAGATT	TTTAAAGCTT	TTATGTATATA	CCATGGAGCC	4500
	ATAGAAAGGC	TATGGATTGT	TTAAGAAGCTA	TTTAAAGTG	TTCCAGACCC	AAAAAGGAAA	4560
	AATAAAAAAA	AAGGAATATT	TGTACCCAAC	AGCTAGAAGG	ATTGCAAGGT	AGATTTTGTG	4620
80	TTTAAATAGG	AGAGAAGTGG	ACAGATAAGG	CCATTTAATA	TATCAAGAT	CAGTTGACAT	4680
	CTCCTAGGGA	ATGATGAAAA	CAGCAGGCTA	T			4711

Seq ID NO: C111 DNA Sequence  
Nucleic Acid Accession #: NM\_130830.1  
Coding sequence: 1..1746

```

1      11      21      31      41      51
|      |      |      |      |      |
5  ATGCCACTGA AGCATTATCT CCTTTTGTCTG GTGGGCTGCC AAGCCTGGGG TGCAGGGTTG 60
GCCTACCATG GCTGCCCTAG CGAGTGTACC TGTCCAGGG CCTCCAGGT GGAGTGCAAC 120
GGGGCAGCGA TTGTGGCGGT GCCCACCCTT CTGCCCTGGA ACGCCATGAG CCTGCAGATC 180
CTCAACACGC ACATCACTGA ACTCAATGAG TCCCCGTTCC TCAATATCTC AGCCCTCATC 240
GCCCTGAGGA TTGAGAAGAA TGAGCTGTCTG CGCATCACGC CTGGGGCCTT CCGAAACCTG 300
GGCTCGCTGC GCTATCTCAG CCTCGCCAAC AACAGCTGC AGGTTCTGCC CATCGGCCCTC 360
10 TTCCAGGGCC TGGAGCTCTC TGAGTCTCTC CTTCGTCCA GTAACCAGCT GTTGCAATC 420
CAGCCGCCCC ACTTCTCCCA GTGCAGCAAC CTCAAGGAGC TGCAGTTGCA CGGCAACCAC 480
CTGGAATACA TCCCTGACGG AGCCTTCGAC CACCTGGTAG GACTCACGAA GCTCAATCTG 540
GGCAAGAATA GCCTCACCCA CATCTCACCC AGGGTCTTCC AGCACCTGGG CAATCTCCAG 600
GTCCTCCGGC TGTATGAGAA CAGGCTCAGC GATATCCCCA TGGGCACTTT TGATGGGCTT 660
15 GTTAACCTGC AGGAACCTGC TCTACAGCAG AACCAAGATTG GACTGCTCTC CCCTGGTCTC 720
TTCCACAACA ACCACAACCT CCAGAGACTC TACCTGTCCA ACAACCACAT CTCCAGCTG 780
CCACCCAGCA TCTTCATGCA GCTGCCCCAG CTCAACCGTC TTACTCTCTT TGGGAATTCC 840
CTGAAGGAGC TCTCTCTGGG GATCTTCGGG CCCATGCCCCA ACCTGCGGGA GCTTTGGCTC 900
TATGACAACC ACATCTCTTC TCTACCGAC AATGTCTTCA GCAACCTCCG CCAGTTGCAG 960
20 GTCTGTATTC TTAGCCGCAA TCAGATCAGC TTCATCTCCC CGGGTGCCTT CAACGGGCTA 1020
ACGGAGCTTC GGGAGCTGTC CCTCCACACC AACGCACTGC AGGACCTGGA CGGGAATGTC 1080
TTCCGCATGT TGGCCAACCT GCAGAACATC TCCCTGCAGA ACAATCGCCT CAGACAGCTC 1140
CCAGGGAATA TCTTCGCCAA CGTCAATGGC CTCATGGCCA TCCAGCTGCA GAACAACCA 1200
CTGAGAACT TGCCCTCGG CATCTTCGAT CACCTGGGGA AACTGTGTGA GCTGCGGTG 1260
25 TATGACAATC CCTGGAGTG TGACTCAGAC ATCCTTCCGC TCCGCAACTG GCTCCTGCTC 1320
AACCCAGCTA GGTAGGGAC GGACACTGTA CCTGTGTGTT TCAGCCAGC CAATGTCCA 1380
GGCCAGTCCC TCAATATCAT CAATGTCAAC GTTGCTGTTT CAAGCGTCCA TGTCCCTGAG 1440
GTGCTAGTTT ACCAGAAAC ACCATGGTAC CCAGACACAC CCAGTTACCC TGACCAACA 1500
30 TCCGTCTCTT CTACCACTGA GCTAACGAGC CCTGTGGAAG ACTACACTGA TCTGACTACC 1560
ATTCCAGTCA CTGATGACCC CAGCGTTTGG GGCATGACCC AGGCCAGAG CGGGCTGGCC 1620
ATTGCCGCGA TTGTAATTGG CATGTGCGCC CTGGCTGCTC CCCTGGCTGC CTGCGTCGGC 1680
TGTGTGCTGT GCAAGAAGAG GAGCCAAGCT GTCCTGATGC AGATGAAGGC ACCCAATGAG 1740
TGTTAA 1746

```

Seq ID NO: C112 DNA Sequence  
Nucleic Acid Accession #: NM\_002658.1  
Coding sequence: 77..1372

```

1      11      21      31      41      51
|      |      |      |      |      |
40 GTCCCCGCGC GCGCGTCGCG CCTCCTGCC GCAGGCCACC GAGGCCGCGG CCGTCTAGCG 60
CCCCGACCTC GCCACCATGA GAGCCTGCT GGCAGCGCTG CTCTCTGCG TCCTGGTCTG 120
GAGCGACTCC AAAGGCAGCA ATGAACCTCA TCAAGTTCCA TCGAACTGTG ACTGTCTAAA 180
45 TGAGGAACA TGTGTGTCCA ACAAGTACTT CTCCAACATT CACTGGTGCA ACTGCCCAA 240
GAAATTCGGA GGGCAGCACT GTGAAATAGA TAAGTCAAAA ACCTGCTATG AGGGGAATGG 300
TCACCTTTAC CGAGGAAAGG CCAGCACTGA CACCATGGGC CGGCCCTGCC TGCCTGGAA 360
CTCTGCCACT GTCCTTCAGC AAACGTACCA TGCCCAAGA TCTGATGCTC TTCAGCTGGG 420
CCTGGGAAAA CATAATTACT GCAGGAACCC AGACAACCGG AGGCGACCTT GGTGCTATGT 480
GCAGGTGGGC CTAAGCGCGC TTGTCCAAGA GTGCATGGTG CATGACTGCG CATGAGGAA 540
50 AAAGCCCTCC TCTCTCCAG AAGAATTAAA ATTTAGTGT GGCCTAAAAG CTCTGAGGCC 600
CCGCTTTAAG ATTATTGGGG GAGAATTCAC CACCATCGAG AACCCAGCCT GGTTCGCGG 660
CATCTACAGG AGGCACCGGG GGGCTCTGCT CACCTACGTG TGTGGAGGCA GCCTCATCAG 720
CCCTTGCTGG GTGATCAGCG CCACACACTG CTTTATTGAT TACCCAAAGA AGGAGGACTA 780
CATCGTCTAC CTGGGTCTCT CAAGGCTTAA CTCCAACACG CAAGGGGAGA TGAAGTTTGA 840
55 GGTGGAAGAC CTCATCTTAC ACAAGGACTA CAGCGCTGAC ACGCTTGCTC ACCACAACGA 900
CATTGCCCTT CTGAAGATCC GTTCCAAGGA GGGCAGGTGT GCGCAGCCAT CCCGGACTAT 960
ACAGACCATC TGCCTGCCCT CGATGTATAA CGATCCCCAG TTTGGCACAA GCTGTGAGAT 1020
CACTGGCTTT GGAAGAGAGA ATTCTACCGA CTATCTCTAT CCGGAGCAGC TGAAGATGAC 1080
60 TGTGTGAAG CTGATTTCCT ACCGGGAGTG TCAGCAGCCC CACTACTACG GCTCTGAAGT 1140
CACCACCAAA ATGCTATGTG CTGCTGACCC CCAATGGAAA ACAGATTCTT GCCAGGGAGA 1200
CTCAGGGGGA CCCCTCGTCT GTTCCCTCCA AGGCCGATG ACTTTGACTG GAATTGTGAG 1260
TGGGGCCGT GATGTGCCC TGAAGGACAA GCCAGGCTC TACACGAGAG TCTCACACTT 1320
CTTACCCTGG ATCCGCACTC ACACCAAGGA AGAGAATGGC CTGGCCCTCT GAGGGTCCCC 1380
AGGGAGGAAA CGGGCACCAC CCGCTTTCTT GCTGGTTGTC ATTTTTCAG TAGAGTCATC 1440
65 TCCATCAGCT GTAAGAAGAG ACTGGGAAGA TAGGCTCTGC ACAGATGGAT TTGCCTGTGG 1500
CACCACAGG GTGAACGACA ATAGCTTTAC CCTCACGGAT AGGCCTGGGT GCTGGCTGCC 1560
CAGACCTCTT GGCCAGGATG GAGGGGTGGT CCTGACTCAA CATGTTACTG ACCAGCAACT 1620
TGTCTTTTTC TGGACTGAAG CCTGCAGGAG TTAAGGAGGG CAGGGCATCT CCTGTGCATG 1680
GGCTCGAAGG GAGAGCCAGC TCCCCCGACC GGTGGGCATT TGTGAGGCCC ATGGTTGAGA 1740
70 AATGAATAAT TTCCCAATTA GGAAGTGTAA GCAGCTGAGG TCTCTGAGG GAGCTTAGCC 1800
AATGTGGGAG CAGCGGTTTG GGGAGCAGAG AACTAACGCA CTTGAGGCA GGGCTCTGAT 1860
ATTCCATGAA TGTATCAGGA AATATATATG TGTGTGTATG TTTGCACACT TGTGTGTG 1920
GCTGTGAGTG TAAGTGTGAG TAAGAGCTGG TGTCTGATTG TTAAGTCTAA ATATTTCTT 1980
AACTGTGTG GACTGTGATG CCACACAGAG TGGTCTTCTT GGAGAGGTTA TAGGTCACTC 2040
75 CTGGGCCCTT TTGGTCCCC CACGTGACAG TGCCTGGGAA TGTACTTATT CTGCAGCATG 2100
ACCTGTGACC AGCACTGTCT CAGTTTCACT TTCACATAGA TGTCCCTTTC TTGGCCAGTT 2160
ATCCCTTCTT TTTAGCCTAG TTCATCCAAT CCTCACTGGG TGGGGTGAGG ACCACTCCTT 2220
ACACTGAATA TTTATATTTC ACTATTTTTC TTTATATTTT TGTATTTTTC AATAAAGTGT 2280
80 ATCAATAAAA TGTGATTTTTC CTGA 2304

```

Seq ID NO: C113 DNA Sequence  
Nucleic Acid Accession #: XM\_087254.1  
Coding sequence: 47..2332

1	11	21	31	41	51	
AGAGTACGTG	TTTACAGATA	AAACTGGTAC	ACTGACAGAA	AATGAGATGC	AGTTTCGGGA	60
ATGTTCAATT	AATGGCATGA	AATACCAAGA	AATTAATGGT	AGACTTGTAC	CCGAAGGACC	120
AAACCCAGAC	TCTTCAGAAG	GAAACTTATC	TTATCTTAGT	AGTTTATCCC	ATCTTAACAA	180
CTTATCCCAT	CTTACAACCA	GTTCTCTTT	CAGAACCAGT	CCTGAAAAATG	AAACTGAACT	240
AATTAAGAA	CATGATCTCT	TCTTTAAAGC	AGTCAGTCTC	TGTCACACTG	TACAGATTAG	300
CAATGTTCAA	ACTGACTGCA	CTGGTGATGG	TCCCTGGCAA	TCCAACCTGG	CACCATCGCA	360
GTGGAGTAC	TATGCATCTT	CACCAGATGA	AAAGGCTCTA	GTAGAAGCTG	CTGCAAGGAT	420
TGGTATTGTG	TTTATTGGCA	ATTCTGAAGA	AACTATGGAG	GTTAAAACTC	TTGGAAAACT	480
GGAACGGTAC	AAACTGCTTC	ATATTCTGGA	ATTTGATTCA	GATCGTAGGA	GAATGAGTGT	540
AATTGTTTCA	GCACCTTCAG	GTGAGAAAGT	ATTATTGCT	AAAGGAGCTG	AGTCATCAAT	600
TCTCCCTAAA	TGTATAGGTG	GAGAAATAGA	AAAAACCAGA	ATTCTATGTAG	ATGAATTTGC	660
TTTGAAAGGG	CTAAGAACTC	TGTGTATAGC	ATATAGAAAA	TTTACATCAA	AAGAGTATGA	720
GGAAATAGAT	AAACGCATAT	TTGAAGCCAG	GACTGCCTTG	CAGCAGCGGG	AAGAGAAATT	780
GGCAGCTGTT	TTCCAGTTCA	TAGAGAAAGA	CCTGATATTA	CTTGGAGCCA	CAGCAGTAGA	840
AGACAGACTA	CAAGACTGTA	TTGAGAAAC	TATTGAAGCA	TTGAGAATGG	CTGGTATCAA	900
AGTATGGGTA	CTTACTGGGG	ATAAACATGA	AACAGCTGTT	AGTGTGAGTT	TATCATGTGG	960
CCATTTTCAT	AGAACCATGA	ACATCCTTGA	ACTTATAAAC	CAGAAATCAG	ACACGAGTGG	1020
TGCTGAACAA	TTGAGGCAGC	TTGCCAGAAG	AATTACAGAG	GATCATGTGA	TTGAGCATGG	1080
GGTGGTAGTG	GATGGGACCA	GCCTATCTCT	TGCACCTCAG	GAGCATGAAA	AACTATTTAT	1140
GGAAAGTTTG	AGAAATTTGT	CAGCTGTATT	ATGCTGTCGT	ATGGCTCCAC	TGCAGAAAGC	1200
AAAAGTAATA	AGACTAATAA	AAATATCACC	TGAGAAACCT	ATAACATTGG	CTGTTGGTGA	1260
TGGTGCTAAT	GACGTAAGCA	TGATACAAGA	AGCCCCATGT	GGCATAGGAA	TCATGGGTAA	1320
AGAAGGAAGA	CAGGCTGCAA	GAAACAGTGA	CTATGCAATA	GCCAGATTTA	AGTTCTCTCT	1380
CAAAATGCTT	TTTGTTCATG	GTCATTTTAA	TTATATTAGA	ATAGCTACCC	TTGTACAGTA	1440
TTTTTTTTAT	AAGAATGTGT	GCTTTATCAC	ACCCCACTTT	TTATATCAGT	TCTACTGTTT	1500
GTTTTCTCAG	CAAACATTGT	ATGACAGCGT	GTACCTGACT	TTATACAATA	TTTGTTTTAC	1560
TTCCCTACCT	ATTCTGATAT	ATAGTCTTTT	GGAACAGCAT	GTACGCCCTC	ATGTGTTACA	1620
AAATAAGCCC	ACCCCTTATC	GAGACATTAG	TAAAAACCGC	CTCTTAAGTA	TTAAAAACAT	1680
TCTTTATTGG	ACCATCCTGG	GCTTCAGTCA	TGCCCTTTAT	TTCTTTTTTG	GATCCTATTT	1740
ACTAATAGGG	AAAGATACAT	CTCTGCTTGG	AAATGGCCAG	ATGTTTGGAA	ACTGGACATT	1800
TGGCACTTTG	GTCTTCACAG	TCATGGTTAT	TACAGTCACA	GTAAAGATGG	CTCTGGAAAC	1860
TCATTTTGG	ACTTGGATCA	ACCATCTCGT	TACCTGGGGA	TCTATTATAT	TTTATTTTGT	1920
ATTTTCCCTG	TTTTATGGAG	GGATTCTCTG	GCCATTTTGG	GGCTCCCAGA	ATATGTATTT	1980
TGTGTTTATT	CAGCTCCTGT	CAAGTGGTTC	TGCTTGGTTT	GCCATAATCC	TCATGGTTGT	2040
TACATGTCTA	TTTCTTGATA	TCATAAAGAA	GGTCTTTGAC	CGACACCTCC	ACCCTACAAG	2100
TACTGAAAAG	GCACAGCTTA	CTGAAACAAA	TGCAGGTATC	AAGTGTCTGG	ACTCCATGTG	2160
CTGTTTCCCG	GAAGGAGAAAG	CAGCGTGTGC	ATCTGTTGGA	AGAATGCTGG	AACGAGTTAT	2220
AGGAAGATGT	AGTCCAACCC	ACATCAGCAG	ATCATGGAGT	GCATCGGATC	CTTTCTATAC	2280
CAACGACAGG	AGCATCTTGA	CTCTCTCCAC	AATGGACTCA	TCTACTTGTG	AAAGGGGCAG	2340
TAGTACTTTG	TGGGAGCCAG	TTCACTCTCT	TTCTTAAAT	TCAGTGTGAT	CACCTGTGTA	2400
ATGGCCACAC	TAGCTCTGAA	ATTAATTTCC	AAAACTTTG	TAGTAGTTCA	TACCCACTCA	2460
GAGTTATAAT	GGCAAAACAA	CAGAAAGCAT	TAGTACAAGC	CCCTCCCAAC	ACCCTTAATT	2520
TGAATCTGAA	CATGTTAAAA	TTTGAGAATA	AAGAGACATT	TTTCATCTCT	TTGTCTGGTT	2580
TGTCCTCTGT	GCTTATGGGA	CTCCTAATGG	CATTTTCAGT	TGTTGTCTGAG	GCCATTATAT	2640
TTTAATATAA	ATGTAGAAAA	AAGAGAGAAA	TCTTAGTAAA	GAGTATTTTT	TAGTATTAGC	2700
TTGATTATTG	ACTCTCTAT	TTAATCTGTC	TTCTGTAAAT	TATGCTGAAA	GTTTGCCTTG	2760
AGAATCTTAT	TTTTTTATTA	GAGTTATATT	TAAAGCTTTT	CATGGGAAAA	GTTAATGTGA	2820
ATACTGAGGA	ATTTTGGTCC	CTCAGTGACC	TGTGTTGTTA	ATTCAATTAAT	GCATTCTGAG	2880
TTACAGAGC	AAATTAGGAG	AATCATTTC	AACCATTTAT	TACTGCAGTA	TGGGGAGTAA	2940
ATTTATACCA	ATTCCTCTAA	CTGTACTGTA	ACACAGCCTG	TAAAGTTAGC	CATATAAATG	3000
CAAGGGTATA	TCATATATAC	AAATCAGGAA	TCAGGTCCGT	TCACCGAACT	TCAAATTTGAT	3060
GTTTACTAAT	ATTTTGTGGA	CAGAGTATAA	AGACCTTATA	GTGGGTAAAT	TAGATACTAT	3120
TAGCATATTA	TTAATTTAAT	GTCCTTATCA	TTGGATCTTT	TGCATGCTTT	AATCTGGTTA	3180
ACATATTTAA	ATTGCTTTT	TTTCTCTTTA	CCTGAAGGCT	CTGTGTATAG	TATTTTCATGA	3240
CATCGTTGTA	CAGTTTAACT	ATATCAATAA	AAAGTTTGGA	CAGTATTTAA	ATATTGCAAA	3300
TATGTTTAAAT	TATACAAATC	AGAATAGTAT	GGGTAAATTA	ATGAATACAA	AAAGAAGAGC	3360
CTCTTCTGTC	AGCCGACTTA	GACATGCTCT	TCCCTTTCTA	TAAGCTAGAT	TTTGAATAAA	3420
AGGGTTTCAG	TTAATAATCT	TATTTTCAGG	TTATGTCATC	TAACTTTATAG	CAAACTACCA	3480
CAATACAGTG	AGTTCTGCCA	GTGTCCCACT	ACAAGGCATA	TTTCAGGTGT	GGCTGTGGAA	3540
TGTAATAAATG	CTCAACTTGT	ATCAGGTAAT	GTTAGCAATA	AATTAATATG	TAAGAATGAT	3600
TAATCGGGTA	CATGTTACTG	TAATTAACCT	ATTGCACCTC	AAAACCTAAC	TTCCATCCTG	3660
AATTTATCAA	GTAGTTCAGT	ATTGTCAATT	GTTTTGTGTT	TATTGAAAAG	TAATGTTGTC	3720
TTAAGATTTA	GAAGTGATTA	TTAGCTTGAG	AACTATTACC	CAGCTCTAAG	CAATAAATGA	3780
TTGTATACAT	ATTAAGATAA	TGGTTAAATG	CGGTTTTACC	AAGTTTTCCC	TTGAAAATGT	3840
AATTCCTTTA	TGGAGATTTA	TTGTGCAGCC	CTAAGCTTCC	TTCCCATTTT	ATGAATATAA	3900
GGCTTCTAGA	ATTGGACTGG	CAGGGGAAAG	AATGGTAGAG	ACAGAAATTA	AGACTTTATC	3960
CTTGTTTGCT	TGTAAACTAT	TATTTTCTTG	CTAATGTAAC	ATTTGTCTGT	TCCAGTGATG	4020
TAAGGATATT	AAGTTATTAA	GCTAAATATT	AATTTTCAAA	AATAGTCTCT	CTTTAACTTA	4080
GATATTTTAT	AGCTGGATTT	AGGAAGATCT	GTTATTCTGG	AAGTACTAAA	AAGAATAATA	4140
CAACGTACAA	TGCTGTCAAT	CACATAATCA	TGTTCCAGAA	GAGGAAATAA	TGAAGATATA	4200
CTCAGTAGAG	TACTAGGTGG	GAGGATATGG	AAATTTGCTC	ATAAAAATCT	TTATAAAACG	4260
TGCATATAAC	AAAATGACAC	CCAGTAGGCC	TGCATTACAT	TTACATGACC	GTGTTTATTT	4320
GCCATCAAA	AAACTGAGTA	CTGACACCAG	ACAAAGACTC	CAAGTTCATA	AAATAGCCTA	4380
TGACCAACTG	CAGCAAGACA	GGAGGTGAGC	TCGCCTATAA	TGGTGCTTAA	AGTGTGATTG	4440
ATGTAATTTT	CTGTACTCAC	CATTGGAAGT	TAGTTAAGGA	GAACCTTATT	TTTTTAAAAA	4500
AAGTAAATGG	CAACCACTAG	TGTGCTCATC	CTGAAGTGT	ACTCCAAATC	CACCTCGTTT	4560
TTAAAGCAAA	ATTATCTTGT	GATTTTAAAG	AAAGAGTTT	CTATTATATT	AAGAAAGTAA	4620
CAATGCAGTC	TGCAAGCTTT	CAGTAGTTT	CTAGTGCTAT	ATTCTCCTGT	TAAAACCTCT	4680
ACTACGTAAC	CAGTAATCAC	AAGGAAAGTG	TCCCTTTTGC	ATATTCTCTT	AAAATTCTTT	4740
CTTTGGAAG	TATGATGTTG	ATAATTAAC	TACCTTTATC	TGCCAAAACC	AGAGCAAAAT	4800
GCTAAATACG	TTATTGCTAA	TCAGTGGTCT	CAAATCGATT	TGCTCTCTCT	TGCTCTGCTC	4860
GAGGGCTGTA	AGGCTGAAGA	TAGTGGCAAG	CACCAAGTCA	GTTTCCAAAA	TTGCCCTCTCA	4920

GCTGCTTTAA GTGACTCAGC ACCCTGCCTC AGCTTCAGCA GCGTAGGCT CACCCCTGGGC 4980  
 GGAGCAAAGT ATGGGCCAGG GAGAAGTACA GCTACGAAGA CCTGCTGTCG AGTTGAGAAA 5040  
 AGGGGAGAAT TTAGTGTCTG AATTTTCTAA CTGTCTCTCT TCTTGGGTCT AAAGCTCATA 5100  
 5 ATACACAAAG GCTTCCAGAC CTGAGCCACA CCCAGGCCCT ATCCTGAACA GGAGACTAAA 5160  
 CAGAGGCAAA TCACAACTAG GAAATACTTG CATTCGCCCC TACGGTTAGT ACCAGGACTG 5220  
 AGGTCAATTC TACTGGAAAA GATTGTGAGA TTGAACCTAT CTGATCGCTT GAGACTCCTA 5280  
 ATAGGCAGGA GTCAAGGCCA CTAGAAATT GACAGTTAAG AGCCAAAAGT TTTTAAATA 5340  
 TGCTACTCTG AAAAATCTCG TGAAGGCTGT AGGAAAAGGG AGAATCTTCC ATGTTGGTGT 5400  
 10 TTTTCCTGTA AAGATCAGTT TGGGGTATGA TATAAGCAGG TATTAATAAA AATAACACAC 5460  
 CAAAGAGTTA CGTAAACAT GTTTTATTAA TTTTGTCTCC CACGTACAGA CATTTTATT 5520  
 CTATTTTGAA ATGAGTTATC TATTTTCATA AAAGTAAAC ACTATTAAAG TGCTGTTTTA 5580  
 TGTGAAATAA CTTGAATGTT GTTCTTATAA AAAATAGATC ATAACCTATG ATATGTTTGT 5640  
 AATCATGGTA ATTTAGATTT TTATGAGGAA TGAGTATCTG GAAATATTGT AGCAATACTT 5700  
 15 GGTTTAAAAA TTTGGACCTG AGACACTGTG GCTGTCTAAT GTAATCCTTT AAAAATCTTC 5760  
 TGCATTGTCA GTAAATGTAG TATATTATTG TACAGCTACT CATAATTTT TAAAGTTTAT 5820  
 GAAGTTATAT TTATCAAATA AAAACTTTCC TATAT 5855

Seq ID NO: C114 DNA Sequence  
 Nucleic Acid Accession #: XM\_087461.1  
 Coding sequence: 236..1138

1 11 21 31 41 51  
 | | | | |  
 25 CCGCGCGCGG GGGCGGCGGG GAACCCCAAA CGCAACCGGG TCTGGAGGGA TCCCGCGCGC 60  
 GAGCCAGCCG CCGTACCCGC CTCGCGCGCG CCCCTGCGGG CTGGGAGGCG GCCCGGCGCG 120  
 CCGCACTGCG CCGCCGCGCG CGGCTCCCGC GGTCCCAACC TGAGCTCGCC GGCCGCTCGC 180  
 CCGCTCGCCA TGAACCGGCC GCGCGCTCGC CGCGCTAGG CGCCCGCGCG AGGCCATGCT 240  
 GCGCCTGCTC GCGCGCTCC TGGCGCGCGC CTGCCCCGCT CCGCCCGTCC GCGGCGGGGC 300  
 30 CGCGGACGCG CCGCGCTCC TCGGGGTGCC CTCCAATGCT TCAGTCAACG CGTCTCCGC 360  
 GGGCAGCCCA TCGCCCGCGC GCTGCTGGCC TCGGCGGCCC CCGGGCCCCC CGAGCGCCCC 420  
 GGGCCGAGAG AGCGCGCGGC GCGCGCGGCG CCTGTGCAAC ATCAGCGTGC AGCGGCAGAT 480  
 GCTGAGCTCG CTGCTCGTGC GCTGGGGCGC CCGCGGGGCG TTCCAGTGCG ACCTACTGCT 540  
 CTCTCCACC AACCGCACG GCGCGCTTTT CTTCGCGGCC GCCTTCCACC GCGTCGGGCC 600  
 35 GCGCTGCTC ATCGAGCACC TGGGGCTGGC GCGCGGCGCG GCGCAGCAGG ACCTGCGCCT 660  
 CTGCGTGGG TGGCGTGGG TGC CGCGCTCG CCGCACCGGC CGCCTCCGCG CCGCGCGCGC 720  
 CCGCAGCGCC GCGCGCGCA CCGCGGGGCG GCCACCGCG CTGCAGCCT ACCCGCGCGC 780  
 CGAGCCGCCC GGGCGCTGT GGTGCGAGGG CGAGCGCTG CATTTCTGCT GCCTAGACTT 840  
 CAGCCTGGAG GAGCTGCGG GCGAGCGGG CTGGCGGCTG AACCGTAAGC CCATTGAGTC 900  
 40 CAGCTGGTG GCTGCTTCA TGACCTGGT CATCGTGGT TGAGCGTGG CCGCCCTCAT 960  
 CTGGCGGTG CCATCATCG CCGCTTCTT GCCCAACGCG ATGGAACAGC GCCGGACCAC 1020  
 CGCCAGCACC ACCCGAGCCA CCGCGCGCGC AGTGCCCGCA GGGACACCG CAGCCGCGCG 1080  
 CGCGCGCGCC GCTGCGCGCG CCGCGCGGCG CGTCACTTCG GGGGTGGCGA CCAAGTGACC 1140  
 CGCTCCGCTC CTCCTGTGT CCGTCTGTG TCCGCGCGCG CCGGTGCCCT TCCCGCGCGA 1200  
 45 GACTCGGCGG GTGTGCTTCG TGTGTAGTT ATCGTTAGTT CCTCTTCCCG AGATGGGGCC 1260  
 GCCGAGAGAC CCCAGCGCCT TTGAAAAGCA AGGTTTGTGC TGGCTTCCA GTTCCGAAAA 1320  
 GCAGATGTTT AAGCCCTTGG ACTGAGGGTG GGTATCGAGC TCCGAGAGAG GAGAGGAGGG 1380  
 AAATGGGGCG CTTTCCCTTC TATTGCATCC CCGTGCCCGA CTCCTTCCCC GCACCCACGT 1440  
 50 GCCTAGATT CATGGCAGAA AATGACCAA TCCTGTGTAT TTGTTTATA TATTTAATAA 1500  
 CTGTTTAAA TGAAGTTT AGTAAAAAAA ATACAAAACA AAAAGATTAA ATTGCTATTG 1560  
 CTGTAGTAAG AGAAGCTCTT TGTATCTGAA CATAGTTGTA TTTGAAATTT GTGTTTATT 1620  
 AATTTATTTA AATTTGGGGG GAGGGCATGG GAAGGATTAA ACACCGATAT ATTGTTACCG 1680  
 CTGAAAATGA ACTTTATGAA CCTTTTCCAA GTTGATCTAT CCAGTGACGT GGCTGTGTG 1740  
 GCGTTTCTTC TTGTACTTAT GTGGTTTTTT GCGTTTTAAT ACAGACATTT TCCTCC 1796

Seq ID NO: C115 DNA Sequence  
 Nucleic Acid Accession #: XM\_051522.4  
 Coding sequence: 127..1215

1 11 21 31 41 51  
 | | | | |  
 60 ACAGTTGTTG CAAAGTGCTC AGCACTAAGG GAGCCAGCGC ACAGCACAGC CAGGAAGGCG 60  
 AGCGAGCCCA GCCAGCCAG CAGCCCGAGC CAGCCCGGAG GTCATTGAT TGCCCGCCTC 120  
 AGAACGATGG ATCTGCATCT CTTGACTAC TCAGAGCCAG GGAACCTCTC GGACATCAGC 180  
 65 TGGCCATGCA ACAGCAGCGA CTGCATCGTG GTGGACACGG TGATGTGTCC CAACATGCCC 240  
 AACAAAAGCG TCCTGTCTCA CACGCTCTCC TTCAATTACA TTTTCTCTCT CGTCATCGGC 300  
 ATGATTGCCA ACTCCGTGGT GGTCTGGGTG AATATCCAGG CCAAGACCAC AGGCTATGAC 360  
 ACGCACTGCT ACATCTTGAA CCTGGCCATT GCCGACCTGT GGGTTGTCTT CACCATCCCA 420  
 70 GTCTGGGTGG TCAGTCTCGT GCAGCACAAC CAGTGGCCCA TGGGCGAGCT CACGTGCAAA 480  
 GTCACACACC TCATCTTCTC CATCAACCTC TTCGGCAGCA TTTCTTCTCT CAGTGCATG 540  
 AGCGTGAGCC GCTACCTCTC CATCACCTAC TTCACCAACA CCCCCAGCAG CAGGAAGAAG 600  
 ATGGTACGCC GTGTCTCTGT CATCTGGTG TGGCTGCTGG CCTTCTGCGT GTCTCTGCTT 660  
 GACACCTACT ACCTGAAGAG CGTCACGTCT GCGTCCAACA ATGAGACCTA CTGCCGCTCC 720  
 75 TTCTACCCCG AGCACAGCAT CAAGGAGTGG CTGATCGGCA TGGAGCTGGT CTCCGTTGTC 780  
 TTGGGCTTTG CCGTTCCCTT CTCCATTATC GCTGTCTTCT ACTTCTGCTT GGCAGAGCC 840  
 ATCTCGGGGT CCAAGTGACA GGAGAAGCAC AGCAGCCGGA AGATCATCTT CTCTACGTG 900  
 GTGGTCTTCC TTGTCTCTGT GCTGCCCTAC CACGTGGCGG TGCTGTGGA CATCTTCTCC 960  
 ATCTGCACT ACATCCCTTT CACCTGCCGG CTGGAGCAGC CCCTCTTCA CAGCCTGCAT 1020  
 80 GTCACACAGT GCCTGTCTGT GGTGCACTGC TGCCTCAACC CTGTCTCTA CAGCTTCATC 1080  
 AATCGCAACT ACAGGTACGA GCTGATGAAG GCCTTCATCT TCAAGTACTC GGCCAAAACA 1140  
 GGGCTCACA AGCTCATCGA TGCCCTCCAGA GTCTCAGAGA CGGAGTACTC TGCCCTGGAG 1200  
 CAGAGCACA AATGATCTGC CCTGGAGAGG CTCTGGGACG GGTTACTTGT TTTTGAACA 1260  
 GGGTGATGGG CCTTATGTTT TTCTAGAGCA AAGCAAAGTA GCTTCGGGTC TTGATGCTT 1320  
 AGTAGAGTGA AGAGGGGAGC ACGTGCCCCC TGCTATCCATT CTCTCTTCT CTGTGATGAC 1380  
 CAGCTGTCTAT TTGGTGTGTC GTGCTGACAG TTTTGCAACA GGCAGAGCTG TGTGACACG 1440



CAGTGCTGTG CGTCAGAGCC AGCTGAGGAC AGGCTTGCCCT GGACTTCTGT AAGATAGGAT 1500  
 TTTCTGTGTT TCCTGAATTT TTTATATGGT GATTGTGATT TAAATTTTAA GACTTTATTT 1560  
 TCTCACTATT GGTGTACCTT ATAAATGTAT TTGAAAGTTA AATATATTTT AAATATTGTT 1620  
 TGGGAGGCAT AGTGCTGACA TATATTGAGA GTGTTGTAGT TTTAAGGTTA GCGTGACTTC 1680  
 AGTTTGGACT AAGGATGACA CTAATTGTTA GCTGTTTGA AATTATATAT ATATAAATAT 1740  
 ATATAAATAT ATAAATATAT GCCAGTCTTG GCTGAAATGT TTTATTTACC ATAGTTTAT 1800  
 ATCTGTGTGG TGTTTTGTAC CGGCACGGGA TATGGAACGA AAACGTGCTT GTAAATGCAGT 1860  
 TTGTGACATT AATAGTATTG TAAAGTTACA TTTTAAATA AACAAAAAAC TGTCTCGAC 1920  
 TGCAAACTCG CACACACAAC GAACAGTTGC ATTTGAGAGA GTTCTCTCAA TTTGTAAGTT 1980  
 ATTTTTTTTT AATAAGATT TTTGTTTCCT 2010

Seq ID NO: C116 DNA Sequence  
 Nucleic Acid Accession #: NM\_000350.1  
 Coding sequence: 82..6903

1 11 21 31 41 51  
 CTGGCTCTTA ACGGCGTTTA TGTCCTTTGC TGTCTGAGGG GCCTCAGCTC TGACCAATCT 60  
 GGTCTTCGTG TGGTCATTAG CATGGGCTTC GTGAGACAGA TACAGCTTTT GCTCTGGAAG 120  
 AACTGGAGCC TGCGGAAAAG GCAAAAGATT CGCTTTGTGG TGGAACTCGT GTGGCCCTTTA 180  
 TCTTTATTTC TGGTCTTGAT CTGGTTAAGG AATGCCAACC CGCTCTACAG CCATCATGAA 240  
 TGCCATTTCC CCAACAAGGC GATGCCCTCA GCAGGAATGC TGCCGTGGCT CCAGGGGATC 300  
 TTCTGCAATG TGAACAATCC CTGTTTTCAA AGCCCCACCC CAGGAGAATC TCCTGGAATT 360  
 GTGTCAAAC ATAACAACTC CATCTTGGCA AGGGTATATC GAGATTTTCA AGAACTCCTC 420  
 ATGAATGCAC CAGAGAGCCA GCACCTTGGC CGTATTTGGA CAGAGCTACA CATCTTGTCC 480  
 CAATTCAATG ACACCTCCG GACTCACCG GAGAGAATTG CAGGAAGAGG AATACGAATA 540  
 AGGGATATCT TGAAGATGA AGAAACACTG ACACATTTTC TCATTAATAA CATCGGCCCTG 600  
 TCTGACTCAG TGGTCTACCT TCTGATCAAC TCTCAAGTCC GTCCAGAGCA GTTCGCTCAT 660  
 GGAGTCCCGG ACCTGGCGCT GAAGGACATC GCCTGCAGCG AGGCCCTCCT GGAGCGCTTC 720  
 ATCATCTTCA GCCAGAGACG CGGGGCAAG ACGGTGCCTG ATGCCCTGTG CTCCTCTCTC 780  
 CAGGGCACCC TACAGTGGAT AGAAGACACT CTGTATGCCA ACGTGGACTT CTTCAAGCTC 840  
 TTCCGTGTGC TTCCACACT CCTAGACAGC CGTCTCTAAG GTATCAATCT GAGATCTTGG 900  
 GGAGGAATAT TATCTGATAT GTCCACAGA ATTCAGAGT TTATCCATCG GCCGAGTATG 960  
 CAGGACTTGC TGTGGGTGAC CAGGCCCTC ATGCAGAAAT GTGGTCCAGA GACCTTTTACA 1020  
 AAGCTGATGG GCATCTGTG TGACCTCTCG TGTGGCTACC CCGAGGGAGG TGGCTCTCGG 1080  
 GTGCTCTCCT TCAACTGGTA TGAAGACAAT AACTATAAGG CCTTTCTGGG GATTGACTCC 1140  
 ACAAGGAAGG ATCCTATCTA TTCTTATGAC AGAAGAACA CATCCTTTTG TAATGCATFG 1200  
 ATCCAGAGCC TGGAGTCAAA TCCTTTAACC AAAATCGCTT GGAGGGCGCG AAAGCCTTTG 1260  
 CTGATGGGAA AATCCTGTGA CACTCTGAT TCACCTGCAG CACGAAGGAT ACTGAAGAA 1320  
 GCCAACTCAA CTTTGAAGA ACTGGAACAC GTTAGGAAGT TGGTCAAAGC CTGGAAGAA 1380  
 GTAGGGCCCC AGATCTGGTA CTCTTTGAC AACAGCACAC AGATGAACAT GATCAGAGAT 1440  
 ACCCTGGGGA ACCCAACAGT AAAAGACTTT TTGAATAGGC AGCTTGGTGA AGAAGGTATT 1500  
 ACTGTGAAG CCATCTCAA CTCTCTTAC AAGGGCCCTC GGGAAAGCCA GGCTGACGAC 1560  
 ATGGCCAAC TCGACTGGAG GGACATATTT AACATCACTG ATCGCACCTT CCGCTGGTTC 1620  
 AATCAATACC TGGAGTGTCT GGTCTGGAT AAGTTTGAAA GCTACAATGA TGAAGCTCAG 1680  
 CTCACCAAC GTGCCCTCTC TCTACTGGAG GAAACATGT TCTGGGCGCG AGTGGTATTG 1740  
 CCTGACATGT ATCCCTGGAC CAGCTCTCTA CCACCCACG TGAAGTATAA GATCCGAATG 1800  
 GACATAGACG TGGTGGAGAA AACCATAAAG ATTAAAGACA GGTATTGGGA TTCTGGTCCC 1860  
 AGAGCTGATC CCGTGAAGA TTTCCGGTAC ATCTGGGGCG GGTTCGCCTA TCTGCAGGAC 1920  
 ATGGTTGAAC AGGGGATCAC AAGGAGCCAG GTGACGGCGG AGGCTCCAGT TGGAACTTAC 1980  
 CTCACGAGA TGCCCTACCC CTGCTTCGTG GACGATTCTT TCATGATCAT CCTGAACCGC 2040  
 TGTTCCTCTA TCTTCATGGT GCTGGCATGG ATCTACTCTG TCTCCATGAC TGTGAAGAGC 2100  
 ATCGTCTTGG AGAAGGAGTT GCGACTGAAG GAGACCTTGA AAAATCAGGG TGTCTCCAAT 2160  
 GCAGTGATTT GGTGTACCTG GTCTCTGGAC AGCTTCTCCA TCATGTGATG GAGCATCTTC 2220  
 CTCTGACGA TATTACATAT GCATGGAAGA ATCTTACATT ACAGCGACCC ATTATCCTC 2280  
 TTCTGTCTCT TGTGTGCTTT CTCCACTGCC ACCATCATGC TGTGCTTTCT GCTCAGCACC 2340  
 TTCTTCTCCA AGGCCAGTCT GGCAGCAGCC TGTAGTGGTG TCATCTATTT CACCTCTTAC 2400  
 CTGCCACACA TCTGTGCTT CGCCTGGCAG GACCCGATGA CCGCTGAGCT GAAGAAGGCT 2460  
 GTGAGCTTAC TGTCTCCGGT GGCATTGGGA TTTGGCACTG AGTACCTGGT TCGCTTTGAA 2520  
 GAGCAAGGCC TGGGGCTGCA GTGGAGCAAC ATCGGGAACA GTCCACGGA AGGGGACGAA 2580  
 TTCAGCTTCC TGCTGTCCAT GCAGATGATG CTCCTTGATG CTGCGTGTGA TGGCTTACTC 2640  
 GCTTGGTACC TTGATCAGGT GTTTCAGGA GACTATGGAA CCCCACCTTC TTGGTACTTT 2700  
 CTTCTACAAG AGTCGTATTG GCTTAGCGGT GAAGGGTGTT CAACCAAGGA AGAAGAGGCC 2760  
 CTGGAAGAAG CCGAGCCCTT AACAGAGGAA ACGGAGGATC CAGAGCACCC AGAAGGAATA 2820  
 CACGACTCCT TCTTTGAACG TGAGCATCCA GGGTGGGTTT CTGGGGTATG CGTGAAGAAT 2880  
 CTGGTAAAGA TTTTGTAGCC CTGTGGCCGG CCAGCTGTGG ACCGTCTGAA CATCACCTTC 2940  
 TACGAGAACC AGATCACCGC ATTCTGGGGC CACAATGGAG CTGGGAAAAC CACCACCTTG 3000  
 TCCATCTCTA CCGGTCTGTT GCCACCAACC TCTGGGACTG TGCTCGTTGG GGGAGGGAC 3060  
 ATTGAACCA GCCTGGATGC AGTCCGCGAG AGCCTTGGCA TGTGTCCACA GCACAACATC 3120  
 CTGTTCACAC ACCTCACGGT GGCTGAGCAC ATGCTGTCTT ATGCCCAGCT GAAAGGAAAG 3180  
 TCCCAGGAGG AGGCCACGCT GGAGATGGAA GCCATGTGG AGGACACAGG CCTCCACACC 3240  
 AAGCGGAATG AAGAGGCTCA GGACCTATCA GGTGGCATGC AGAGAAAGCT GTCGGTTGCC 3300  
 ATTGCCPTTG TGGGAGATGC CAAGGTGGTG ATTCTGGACG AACCCACCTC TGGGGTGGAC 3360  
 CCTTACTCGA GACGCTCAAT CTGGGATCTG CTCTTGAAGT ATCGCTCAGG CAGAACCATC 3420  
 ATCATGCCCA CTCACCAATG GGACGAGGCC GACCACCAAG GGGACCGCAT TGCCATCATT 3480  
 GCCCAGGAAA GGTCTTACTG CTCAGGCACC CCACTCTTCC TGAAGAACTG CTTTGGCACA 3540  
 GGCTTGTACT TAACCTTGGT GCGCAAGATG AAAACATATC AGAGCCAAAG GAAAGGCAGT 3600  
 GAGGGGACCT GCAGCTGCTC GTCTAAGGGT TTCTCCACCA CGTGTCCAGC CCACGTCGAT 3660  
 GACCTAACTC CAGAACAAGT CCTGGATGGG GATGTAAATG AGCTGATGGA TGTAGTTCTC 3720  
 CACCATGTTT CAGAGGCAAA GCTGGTGGAG TGCATTGGTC AAGAACTTAT CTTCTTCTT 3780  
 CCAATAAGA ACTTCAAGCA CAGAGCATAT GCCAGCTTTT TCAGAGAGCT GGAGGAGACG 3840  
 CTGGCTGACC TTGGTCTCAG CAGTTTGGGA ATTTCTGACA CTCCTCTGGA AGAGATTTTT 3900  
 CTGAAGGTCA CCGAGGATTC TGATTGAGGA CCTCTGTTTG CGGGTGGCGC TCAGCAGAAA 3960  
 AGAGAAAACG TCAACCCCTG ACACCCCTGC TTGGGTCCCA GAGAGAAGGC TGGACAGACA 4020

5	CCCCAGGACT	CCAATGTCTG	CTCCCCAGGG	GCGCCGGCTG	CTCAGCCAGA	GGGCCAGCCT	4080
	CCCCCAGAGC	CAGAGTGCCC	AGGCCCGCAG	CTCAACACGG	GGACACAGCT	GGTCCTCCAG	4140
	CATGTGACAG	CGCTGCTGGT	CAAGAGATTG	CAACACACCA	TCCGCAGCCA	CAAGGACTTC	4200
	CTGGCGCAGA	TGCTGCTCCC	GGCTACCTTT	GTGTTTTTGG	CTCTGATGCT	TTCTATTGTT	4260
	ATCCTTCCCT	TTGGCGAATA	CCCCGCTTTG	ACCCTTCACC	CCTGAGATATA	TGGGCAGCAG	4320
	TACACCTTCT	TCAGCATGGA	TGAACCAGGC	AGTGAGCAGT	TCACGGTACT	TGCAGACGTC	4380
	CTCCTGAATA	AGCCAGGCTT	TGGCAACCGC	TGCTTGAAGG	AAGGGTGGCT	TCCGGAGTAC	4440
10	CCCTGTGGCA	ACTCAACACC	CTGGAAGACT	CCTTCTGTGT	CCCCAAACAT	CACCCAGCTG	4500
	TTCCAGAAGC	AGAAATGGAC	ACAGGTCAAC	CCTTCACCAT	CCTGCAGGTG	CAGCACCAGG	4560
	GAGAAGCTCA	CCATGCTGCC	AGAGTGCCCC	GAGGGTGGCG	GGGGCCTCCC	GCCCCCCCAG	4620
	AGAACACAGC	GCAGCAGCGA	AATTCTACAA	GACCTGACGG	ACAGGAACAT	CTCCGACTTC	4680
	TTGGTAAAAA	CGTATCCTGC	TCTTATAAGA	AGCAGCTTAA	AGAGCAAAT	CTGGGTCAAT	4740
	GAACAGAGGT	ATGGAGGAAT	TTCCATTGGA	GAAAGCTCC	CAGTCGTCCC	CATCACGGGG	4800
15	GAAGCACTTG	TTGGGTTTTT	AAGCGACCTT	GGCCGGATCA	TGAATGTGAG	CGGGGGCCCT	4860
	ATCACTAGAG	AGGCCCTCTAA	AGAAATACCT	GATTTCCCTA	AACATCTAGA	AACTGAAGAC	4920
	AACATTAAGG	TGTGTTTAA	TAACAAAGGC	TGGCATGCCC	TGGTCAGCTT	TCTCAATGTG	4980
	GCCCAACAGC	CCATCTTACG	GGCCAGCCTG	CCTAAGGACA	GGAGCCCCGA	GGAGTATGGA	5040
	ATCACCGTCA	TTAGCCAACC	CCTGAACCTG	ACCAAGGAGC	AGCTCTCAGA	GATTACAGTG	5100
20	CTGACCACIT	CAGTGGATGC	TGTGGTTGCC	ATCTGCGTGA	TTTTCTCCAT	GTCCTTCGTC	5160
	CCAGCCAGCT	TTGTCTTTTA	TTTGATCCAG	GAGCGGGTGA	ACAAATCCAA	GCACCTCCAG	5220
	TTTATCAGTG	GAGTGAGCCC	CACCACCTAC	TGGGTGACCA	ACTTCTCTG	GGACATCATG	5280
	AATTATTCG	TGAGTGCTGG	GCTGGTGGTG	GGCATCTTCA	TCGGGTTTCA	GAAGAAAGCC	5340
	TACACTTCTC	CAGAAAACCT	TCCTGCCCTT	GTGGCACTGC	TCCTGCTGTA	TGGATGGGCG	5400
25	GTCAATCCCA	TGATGTACCC	AGCATCCTTC	CTGTTTGATG	TCCCCAGCAC	AGCCTATGTG	5460
	GCTTTATCTT	GTGCTAATCT	GTTTCATCGC	ATCAACAGCA	GTGCTATTAC	CTTCATCTTG	5520
	GAATTATTTG	ATAATAACCG	GACGCTGCTC	AGGTTCAACG	CCGTGCTGAG	GAAGCTGCTC	5580
	ATTGTCTTCC	CCCACCTCTG	CCTGGGCCGG	GGCCTCATTG	ACCTTGCACT	GAGCCAGGCT	5640
	GTGACAGATG	TCTATTCCCG	GTTTGGTGAG	GAGCACTCTG	CAAAATCCGT	CCACTGGGAC	5700
30	CTGATTGGGA	AGAACTGTT	TGCCATGGTG	GTGGAAGGGG	TGGTGACTTT	CCTCTGACC	5760
	CTGCTGGTCC	AGCGCCACTT	CTTCTCTCC	CAATGGATTG	CCGAGCCCCA	TAAGGAGCCC	5820
	ATTGTTGATG	AAGATGATGA	TGTGGCTGAA	GAAAGACAAA	GAATTATTAC	TGGTGAAAT	5880
	AAAAGTGACA	TCTTAAGGCT	ACATGAACCTA	ACCAAGATT	ATCTGGGCAC	CTCCAGCCCA	5940
	GCAGTGGACA	GGCTGTGTGT	CGGAGTTGCG	CCTGGAGAGT	GCTTTGGCCT	CCTGGGAGTG	6000
35	AATGGTCCCG	GCAAACAAAC	CACATTCAAG	ATGCTCACTG	GGGACACCAC	AGTGACCTCA	6060
	GGGGATGCCA	CCGTAGCAGG	CAAGAGTATT	TAAACCAATA	TTTCTGAAGT	CCATCAAAAT	6120
	ATGGGCTACT	GTCTCTCAGT	TGATGCAATC	GATGAGCTGC	TCACAGGACG	AGAACATCTT	6180
	TACCTTTATG	CCCGGCTTCG	AGGTGTACCA	GCAGAAGAAA	TCGAAAAGGT	TGCAAACTGG	6240
	AGTATTAAAG	GCCTGGGCCT	GACTGTCTAC	GCCGACTGCC	TGGCTGGCAC	GTACAGTGGG	6300
40	GGCAACAAGC	GGAAACTCTC	CACAGCCATC	GCACCTATTG	GCTGCCACCC	GCTGGTGCTG	6360
	CTGGATGAGC	CCACCACAGG	GATGGAGCCC	CAGGCACGCC	GCATGCTGTG	GAAAGTATGC	6420
	GTGAGCATCA	TCAGAAAAGG	GAGGGCTGTG	GTCTTCACAT	CCACAGCAT	GGAAGAATGT	6480
	GAGGCACTGT	GTACCCCGCT	GGCCATCATG	GTAAGGGCG	CCTTTCGATG	TATGGGCACC	6540
	ATTACGCATC	TCAAGTCCAA	ATTTGGAGAT	GGCTATATCG	TCACAAATGAA	GATCAAAATCC	6600
45	CCGAAGGACG	ACCTGCTTCC	TGACCTGAAC	CCTGTGGAGC	AGTTCTTCCA	GGGGAAGTTC	6660
	CCAGGCAGTG	TGCAGAGGGA	GAGGCATAC	AACATGCTCC	AGTTCCAGGT	CTCTCTCTCC	6720
	TCCTTGGCGA	GGATCTTCCA	GCTCTCTCTC	TCCCACAAGG	ACAGCCTGCT	CATCGAGGAG	6780
	TACTCAGTCA	CACAGACCAC	ACTGGACCAG	GTGTTTGTA	ATTTTGCTAA	ACAGCAGACT	6840
50	GAAAGTCAATG	ACCTCCCTCT	GCACCTCGA	GCTGCTGGAG	CCAGTCGACA	AGCCCAAGGAC	6900
	TGATCTTTCA	CACCGCTCGT	TCCTGCAGCC	AGAAAGGAAC	TCTGGGCAGC	TGGAGGCGCA	6960
	GGAGCCTGTG	CCCATATGGT	CATCCAAATG	GACTGGCCCA	GCGTAAATGA	CCCCACTGCA	7020
	GCAGAAAACA	AACACACGAG	GAGCATGCAG	CGAATTGAGA	AAGAGGTCTT	TCAGAAGGAA	7080
	ACCGAAACTG	ACTTGCTCAC	CTGGAACACC	TGATGGTGAA	ACCAAAACAA	TACAAAATCC	7140
	TTCTCCAGAC	CCCAGAACTA	GAAACCCCGG	GCCATCCCA	TAGCAGCTTT	GGCCTCCATA	7200
55	TTGCTCTCAT	TTCAAGCAGA	TCTGCTTTTC	TGCATGTTTG	TCTGTGTGTC	TGCGTTGTGT	7260
	GTGATTTTCA	TGAAAAATA	AAATGCAAA	GCACTCATCA	CAAAAAA	AAAAA	7318

Seq ID NO: C117 DNA Sequence  
Nucleic Acid Accession #: NM\_006671.2  
Coding sequence: 138..1820

60	1	11	21	31	41	51	
	GGCAGGAGGC	TGGTGTTTAG	CAACTCCGAC	CACCTGCCTG	CTGAGGGGCT	AGAGCCCTCA	60
65	GCCCAGACCC	TGTGCCCCCG	GCCGGGCTCT	CATGCGTGGA	ATGGTGTGCT	GCCCCCTGCC	120
	AGCAGGCCAG	GCTCACCATG	GTGCCGCGATG	CCATCTTGGC	ACGGGGGAGG	GACGTGTGCA	180
	GGCGGAATGG	ACTCCTCATC	CTGTCTGTGC	TGTCTGTGAT	CGTGGGCTGC	CTCCTCGGCT	240
	TCTTCTTGAG	GACCCGCGCG	CTCTCACCAC	AGGAAATTAG	TTACTTCCAG	TTCCCTGGAG	300
	AGCTCCTGAT	GAGGATGCTG	AAGATGATGA	TCCTGCCACT	GGTGGTCTCC	AGCTTGATGT	360
70	CCGGACTTGC	CTCCCTGGAT	GCCAAGACCT	CTAGCCGCTT	GGGCGTCTCT	ACCGTGGCGT	420
	ACTACCTGTG	GACCACTTTC	ATGGCTGTCA	TCGTGGGCAT	CTTCATGGTC	TCCATCATCC	480
	ACCCAGGCAG	CGCGGCCCGG	AAGGAGACCA	CGGAGCAGAG	TGGGAAGCCC	ATCATGAGCT	540
	CAGCCGATGC	CCTGTTGGAC	CTCATCCGGA	ACATGTTCCC	AGCCAACCTA	GTAGAAGCCA	600
	CATTCAAACA	GTACCGCACC	AAGACCACCC	CAGTTGTCAA	GTCCCCCAAG	GTGGCACCAG	660
75	AGGAGGCCCC	TCTCTGGCGG	ATCCTCATCT	ACGGGGTCCA	GGAGGAGAAT	GGCTCCCATG	720
	TGCAGAACTT	CGCCCTGGAC	CTGACCCCGC	CGCCCGAGGT	CGTTTACAAG	TCAGAGCCGG	780
	GCACCAAGCA	TGGCATGAAT	GTGCTGGGCA	TCGTCTTCTT	CTCTGCCACC	ATGGGGCATCA	840
	TGCTGGGCGG	CATGGGTGAT	AGCGGGGCCC	CCCTGGTTCAG	CTTCTGCCAG	TGCCTCAATG	900
	AGTCGGTCAT	GAAGATCGTG	GCGGTGGCTG	TGTGGTATTT	CCCTTTCGGC	ATTGTGTTCC	960
80	TCATTGCGGG	TAAGATCCCTG	GAGATGGACG	ACCCAGGGCG	CGTCGGCAAG	AAGCTGGGCT	1020
	TCTACTCAGT	CACCGTGGTG	TGCGGGCTGG	TGCTCCACGG	GCTCTTTATC	CTGCCCTTGC	1080
	TCTACTTCTT	CATCACCAAG	AAGAATCCCA	TCGTCTTCAT	CCGCGGCATC	CTGCAGGCTC	1140
	TGCTCATCGC	GCTGGGCACC	TCTTCCAGCT	CAGCCACACT	GCCCCATCAC	TTCAAGTGCC	1200
	TGCTGGAGAA	CAACCAATC	GACCGGCGCA	TCGCTCGCTT	CGTGCTGCCC	GTGGGTGCCA	1260
	CCATCAACAT	GGACGGCACT	GCGCTCTACG	AGGCTGTGGC	CGCCATCTTC	ATCGCCCAAG	1320

5 TCAACAACTA CGAGCTGGAC TTTGGCCAGA TCATCACCAT CAGTATCACA GCCACTGCAG 1380  
 CCAGCATTTGG GGCAGCTGGC ATCCCCCAGG CCGGCCTCGT CACCATGGTC ATCGTGCTCA 1440  
 CCTCCGTGGG ACTGCCACC GATGACATCA CCTCATCAT TGCCGTGAC TGGGCTCTGG 1500  
 ACCGTTTCCG CACCATGATT AACGTGCTGG GTGATGCGCT GGCAGCGGGG ATCATGGCCC 1560  
 ATATATGTCG GAAGGATTTT GCCCGGGACA CAGGCACCGA GAAACTGCTG CCCTGCGAGA 1620  
 CCAAGCCAGT GAGCCTCCAG GAGATCGTGG CAGCCACGCA GAATGGCTGT GTGAAGAGTG 1680  
 TAGCCGAGGC CTCCGAGCTC ACCCTGGGCC CCACCTGCCC CCACCACGTC CCCGTCAAG 1740  
 TGGAGCGGGA TGAGGAGCTG CCCGCTGCGA GTCTGAACCA CTGCACCATC CAGATCAGCG 1800  
 10 AGCTGGAGAC CAATGTCTGA GCCTGCGGAG CTGCAGGGGC AGGCGAGGCC TCCAGGGGCA 1860  
 GGGTCTTGAG GCAGGAACCT GACTCTCCAA CCCTCTGAG CAGCCGGCAG GGGCCAGGAT 1920  
 CACACATTCT TCTCACCCTT GAGAGGCTGG AATTAACCCC GCTTGACGGA AAATGTATCT 1980  
 CAGAGAAGGG AAAGGCTGCA TGGGGGAGCC CCATCCAGGG AGTGATGGGC CCGGCATTGC 2040  
 CTGAGGCCCC GCTGTGACAG TTCCCCGGT GTGAGCCCGG TGAGGGCGGC AGGCAGGGGT 2100  
 TATCCGGCCC CACTTCTCTG ATGACAGACT TGAGGCTCTG AGAGCTGAAA ACACTTGTCT 2160  
 15 AAGGTCTCAC GTTAAGGTCA AGACACTAAC TCAATCTTT CAAGCCCCG CTCTCTCTT 2220  
 GGAGGACAGG GCAGCTGCA GCTGTGTCCA GGGCCAGGCC CCACCCATA ACAGGTGGCC 2280  
 TCAGCCACAC AGTTCTCCCC AAGGGGAGCA GCCCAGGGCC AAGCCCCGCT GCCTTCCCCA 2340  
 GGCCACAGTG CGTCCAGTCT CTTGTCTTGC CACGTGTCTT TTGCAAGCT CTTTGGATGT 2400  
 20 GGAGACAGAT GTCTTTACTA GAGCTGAAAG GCCCCCTTGA CACATCCAGG CCAACTCCC 2460  
 ATGGAATAGG TAGGCAAGCC AGGACTCCGG GAAGGAGGTG CAGCCAGGAT GCTCTGGTGG 2520  
 AGCTGCCGAT GGGGCCCTGG TGTCAAGACT CCCCAGGC CTGTGCTGCC AAGTGGAGTG 2580  
 AGGTTTTCTA TTCTTTCTG TGTTCGCAA TTCTAGTTTA ACTAATAAAA GGTATTTTGT 2640  
 TTTTCAAAAA AAAAAAAAAA AAA 2663

25 Seq ID NO: C118 DNA Sequence  
 Nucleic Acid Accession #: NM\_005689  
 Coding sequence: 278..2806

30 1 11 21 31 41 51  
 | | | | |  
 GGGCTGCAG TTGGCAGAAG GTCCCCGGGC CCAGAGCCAG CGGGGCCGTG CTGAGACGGC 60  
 GTACGTGCCC TGCGTGAGTG CGTGGCGGCG CGCGTGCGC TAGGGGAGTG GCGGTGAGG 120  
 CCTGGTCCAC GTGCGTCCCT TCCCGGGACC CCCGAGCTT GCGCCGAGC GGCTACGTGA 180  
 35 GCCAAGGCAC CCGGATGTCC GCGCCCTCT CCGAGTGACA AGTCCCGGCC TCCGGTCCCG 240  
 CAGTGCCCGC AGCTCGGCC GCGTCCACG CATTGCCATG GTGACTGTGG GCAACTACTG 300  
 CGAGGCCGAA GGGCCCGTGG GTCCGGCCTG GATGACGAT GGCCTGAGTC CTTGCTCTT 360  
 CTTACAGCTC GTGCCCTCGA CGCGGATGGC TCTAGGACT CTGGCCTTGG TGCTGGCTCT 420  
 TCCTTCGAGA CGCCGGGAGC GGGCCGCTGG TGCTGATTCG CTGTCTTGGG GGGCCGGCCC 480  
 40 TCGCATCTCT CCTACGTGC TGCACTGCT TCTGGCCACA CTTAGGCGG CGCTGCCCT 540  
 GGGCCGCTG GCTGGCCGGG TGGCACTGC CCGGGGGGCC CACTGCCAA GCTATCTACT 600  
 TCTGGCTTCC GTGCTGGAGA GTCTGGCCGG CGCTGTGGC CTGTGGCTGC TTGTCTGGA 660  
 GCGGAGCCAG GCACGGCAGC GTCTGGCAAT GGGCATCTGG ATCAAGTTCA GGCACAGCCC 720  
 TGGTCTCTTG CTCTCTGGA CTGTGGCGTT TGCACTGAG AACTTGGCCC TGGTGTCTTG 780  
 45 GAACAGCCCA CAGTGGTGGT GGGCAAGGGC AGACTTGGGC CAACAGGTTT AGTTTACGCT 840  
 GTGGGTGCTG CGGTATGTGG TCTCTGGAGG GTGTTTGTG CTGGGTCTCT GGGCCCTGG 900  
 ACTTCGTCCC CAGTCCCTATA CATTGCAGGT TCATGAAGAG GACCAAGATG TGGAAAGGAG 960  
 CCAGGTTCCG TCAGCAGCCC AACAGTCTAC CTGGCGAGAT TTTGGCAGGA AGCTCCGCT 1020  
 CCTGAGTGGC TACCTGTGGC CTCGAGGGAG TCCAGCTCTG CAGCTGTGGT TGCTCATCTG 1080  
 50 CCTGGGGCTC ATGGGTTTGG AACGGGCACT CAATGTGTTG GTGCCTATAT TCTATAGGAA 1140  
 CATTGTGAAC TTGCTGACTG AGAAGGCACC TTGGAACCTC CTGGCTTGGG CTGTACCAG 1200  
 TTACGTCTTC CTCAGTTTCC TCCAGGGGGG TGGCACTGGC AGTACAGGCT TCGTGAGCAA 1260  
 CCTGCGCAC TTCTGTGGA TCCGGGTGCA GCAGTTTACG TCTCGCGGG TGGAGCTGCT 1320  
 CATCTTCTCC CACCTGCACG AGCTCTCACT GCGCTGGCAC CTGGGGCGCC GCACAGGGGA 1380  
 55 GGTGCTGCGG ATCGCGGATC GGGGCACATC CAGTGTGACA GGGCTGTCTA GCTACCTGGT 1440  
 GTTCAATGTC ATCCCCACGC TGGCCGACAT CATCATTTGG ATCATCTACT TCAGCATGTT 1500  
 CTTCAACGCC TGGTTTGGCC TCATTGTGTT CCTGTGCATG AGTCTTTACC TCACCCTGAC 1560  
 CATTGTGGTC ACTGAGTGGG GAACCAAGTT TCGTCTGTCT ATGAACACAC AGGAGAACGC 1620  
 TACCOCGGCA CGAGCAGTGG ACTCTCTGCT AAACCTTCGAG ACGGTGAAGT ATTACAACGC 1680  
 CGAGAGTTAC GAAGTGGAAC GCTATCGAGA GGCCATCATC AAATATCAGG GTTTGGAGTG 1740  
 60 GAGTTCGAGC GATTCACTGG TTTTACTAAA TCAGACCCAG AACCTGGTGA TTGGGCTCGG 1800  
 GCTCCTCGCC GGCTCCCTGC TTTGCGCATA CTTTGTCACT GAGCAGAAGC TACAGGTTGG 1860  
 GGACTATGTG CTCCTTGGCA CCTACATTAT CCAGCTGTAC ATGCCCTTCA ATTGGTTTGG 1920  
 CACCTACTAC AGGATGATCC AGACCAACTT CATTGACATG GAGAACATGT TTGACTTGCT 1980  
 65 GAAAGAGGAG ACAGAAGTGA AGGACCTTCC TGGAGCAGGG CCCCTTCGCT TTCAGAAGGG 2040  
 CCGTATTGAG TTTGAGAACG TGCATTTCAG CTATGCCGAT GGGCGGGAGA CTCTGCAGGA 2100  
 CGTGCTTTTC ACTGTGATGC CTGGACAGAC ACTTGCCCTG GTGGGCCCAT CTGGGGCAGG 2160  
 GAAGAGCACA ATTTTGGCGC TGCTGTTTCG CTTCTACGAC ATCAGCTCTG GCTGCATCCG 2220  
 AATAGATGGG CAGGACATTT CACAGGTGAC CCAGGCCTCT CTCCGGTCTC ACATTGGAGT 2280  
 70 TGTGCCCCAA GACACTGTCC TCTTTAATGA CACCATCGCC GACAATATCC GTTACGGCCG 2340  
 TGTACAGCT GGGAAATGAT AGGTGGAGGC TGCTGCTCAG GCTGCAGGCA TCCATGATGC 2400  
 CATTATGGCT TTCTCTGAAG GGTACAGGAC ACAGGTGGGC GAGCGGGGAC TGAAGCTGAG 2460  
 CGGCGGGGAG AAGCAGCGCG TCGCCATTGC CCGCACCATC CTCAGGCTC CGGGCATCAT 2520  
 TCTGCTGGAT GAGGCAACGT CAGCGCTGGA TACATCTAAT GAGAGGGCCA TCCAGGCTTC 2580  
 75 TCTGGCCAAA GTCTGTGCCA ACCGCACCA CACGTAGTGT GCACACAGGC TCTCAACTGT 2640  
 GGTCAATGCT GACCAGATCC TCGTCATCAA GGATGGCTGC ATCGTGGAGA GGGGACGACA 2700  
 CGAGGCTCTG TTGTCCCGAG GTGGGGTGTA TGCTGACATG TGGCAGCTGC AGCAGGGACA 2760  
 GGAAGAAACC TCTGAAGACA CTAAGCCTCA GACCATGGAA CGGTGACAAA AGTTTGGCCA 2820  
 CTTCCCTCTC AAAGACTAAC CCAGAAGGGA ATAAGATGTG TCTCTTTCC CTGGCTTATT 2880  
 80 TCATCTGGT CTTGGGGTAT GGTGCTAGCT ATGGTAAGGG AAAGGAGCTT TTCCGAAAAA 2940  
 CATCTTTTGG GGAATAAAAA ATGTGGACTG TGAAAAAAA AAAAAAAA AAA 2993

Seq ID NO: C119 DNA Sequence  
 Nucleic Acid Accession #: NM\_000676  
 Coding sequence: 333..1331

```

1      11      21      31      41      51
|      |      |      |      |      |
5  GGGCAATTG TTAGTTATCC GCCGCCACCA AGACGCGGCA CGGCGCCTGG ACCGGAGGGG 60
   CCCC GCGCGG GCGCGAACTT TGGGCTCGGG CGAGTGGGTG GTGCTCCGCC CAGCCCGAGA 120
   CGGGCGGGCG CCGCGGGCCAA TGGGTGCGCG CTCTTGGCCG CGGGGGGGCC CGACCCGTGG 180
   GTCCCGGCCA CCAGCGCCCC AGCCCCGAGG CTCAGAAGCG GCAGGCGGAG GCGCGGTCCG 240
   GGCCTATG CCAATGCCCG CGGGTCTCAC GCGGCTGCCC CTCGCCCGGC GCGCCTTCGG 300
10  TAGGGGGCGC CCGGGGCCCA GCTGGCCCCG CCATGCTGCT GGAGACACAG GACGCGCTGT 360
   ACGTGGCGCT GGAGCTGGTC ATCGCCGCGC TTTCGGTGCG GGGCAACGTG CTGGTGTGCG 420
   CGCGGTGGG CACGGCGAAC ACTCTGCAGA CGCCACCAA CTACTTCTCG GTGTCCCTGG 480
   CTGCGGCCGA CGTGGCCGTG GGGCTCTTCG CCATCCCTT TGCCATCACC ATCAGCCTGG 540
   GCTTCTGCAC TGACTTCTAC GGTGCTCTCT TCCTCGCCTG CTTCGTGCTG GTGCTCACGC 600
   AGAGCTCCAT CTTTCAGCCTT CTGGCCGTGG CAGTCGACAG ATACCTGGCC ATCTGTGTCC 660
15  CGCTCAGGTA TAAAAGTTTG GTACCGGGA CCCGAGCAAG AGGGGTCAAT GCTGTCTCT 720
   GGGTCTTGC CTTTGGCATC GGATTGACTC CATTCCTGGG GTGGAACAGT AAAGACAGTG 780
   CCACCAACAA CTCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCCTTGTGA 840
   AGTGTCTCTT TGAGAAATGT GTCCCATGA GCTACATGGT ATATTCAAT TTCTTTGGGT 900
   GTGTTCTGCC CCCACTGCTT ATAATGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT 960
20  GCAGGCAGCT TCAGCGCACT GAGCTGATGG ACCACTCGAG GACCACCTC CAGCGGGAGA 1020
   TCCATGCAGC CAAGTCACTG GCCATGATTG TGGGGATTTT TGCCCTGTGC TGGTTACCTG 1080
   TGATGCTGT TAACTGTGTC ACTCTTTTCC AGCCAGCTCA GGGTAAAAAT AAGCCCAAGT 1140
   GGGCAATGAA TATGGCCATT CTTCTGTAC ATGCCAATTC AGTTGTCAAT CCCATTGTCT 1200
   ATGCTTACCG GAACCGAGAC TTCCGCTACA CTTTTCACAA AATTATCTCC AGGTATCTTC 1260
25  TCTGCCAAGC AGATGTCAAG AGTGGGAATG GTCAGGCTGG GGTACAGCCT GCTCTCGGTG 1320
   TGGGCTATG ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAATCCA CAAGAAACAA 1380
   AGAGGACACG GCTGGTTTTT ATTGTGAAAG ATAGCTACAC CTCACAAGGA AATGGAAGTGC 1440
   CTCTCTTGAG CACTTCCCTG GAGCTACCAC GTATCTAGCT AATATGTATG TGTCAAGTAGT 1500
   AGGCTCCAAG GATTGACAAA TATATTTATG ATCTATTGAG CTGCTTTTAC TGTGTGGATT 1560
30  ATGCCAACAG CTGTAATGGA TTCTAACAGA CTCTTTTGT TTTAAAGTGC TGCCCTTGT 1620
   ATGGTGAAA ATTACTGAAA CTATTTTACT GTGAAACAGT GTGAACATAT ATAATGCAA 1680
   TACTTTTAA CTAGAGGCA ATGAAAAAT AAAAGTTGAC TGTACTAAAA ATG 1733

```

Seq ID NO: C120 DNA Sequence  
Nucleic Acid Accession #: NM\_052932  
Coding sequence: 217..786

```

1      11      21      31      41      51
|      |      |      |      |      |
40  CCCAGCCCCG CCCC GCGGCC CCGGCTGCGC ACGCGAGCGC CCTCCAGGC CCGGCTCCTG 60
   CGCCCTATTG GGTCAATTCGG GGGCAAGCG GCGGAGGGG AAACGTGCGC GGCCGAAGGG 120
   GAAGCGGAGC CCGCGCCGGC TGGCGAGAGG AGCCGCTCTC GCGCGGCCA CCTCGGCTGG 180
   GAGCCACAGA GGTGCGCGCA TCCTGCCCTC GGAACAATGG GACTCGGCGC GCGAGGTGCT 240
   TGGGCGCGCG TGCTCTGGG GACGCTCGAG GTGCTAGCGC TGCTGGGGG CGCCCATGAA 300
45  AGCGCAGCCA TGGCGGAGAC TCTCCAACAT GTGCCCTCTG ACCATACAAA TGAACCTTCC 360
   AACAGTACTG TGAACACCAC AACTTCAGTT GCCTCAGACT CCAGTAATAC AACGGTCACC 420
   ACCATGAAAC CTCACGCGGC ATCTAATAA ACAACACCAG GGATGGTCTC AACAAATATG 480
   ACTTCTACCA CCTTAAAGTC TACACCCAAA ACAACAAGTG TTTCACAGAA CACATCTCAG 540
   ATATCAACAT CCACAATGAC CGTAACCCAC AATAGTTCAG TGACATCTGC TGCTTCATCA 600
50  GTAACAATCA CAACAATAT GCATTCTGAA GCAAGAAAG GATCAAAAT TGATACTGGG 660
   AGCTTTGTTG GTGGTATTGT ATTAACGCTG GGAGTTTAT CTATTCTTTA CATTTGGATGC 720
   AAAATGTATT ACTCAAGAA AGGCATTGCG TATCGAACCA TAGATGAACA TGATGCCATC 780
   ATTTAAGGAA ATCCATGGAC CAAGGATGGA ATACAGATTG ATGCTGCCCT ATCAATTAAT 840
   TTTGGTTTAT TAATAGTTTA AAACAATATT CTCTTTTGA AAATAGTATA AACAGGCCAT 900
55  GCATATAAATG TACAGTGTAT TACGTAAATA TGTAAGATT CTTCAGGTA ACAAGGGTTT 960
   GGGTTTGA AATAACATCT GGATCTTATA GACCGTTTAT ACAATGGTTT TAGCAAGTTC 1020
   ATAGTAAGAC AAACAAGTCC TATCTTTTTT TTTTGGCTG GGGTGGGGG ATTGGTCACA 1080
   TATGACCACT AATTGAAAGA CGTCATCACT GAAAGACAGA ATGCCATCTG GGCATACAAA 1140
   TAAGAAGTTT GTCACAGCAC TCAGGATTTT GGGTATCTTT TGATGCTCAC ATAAAGAACT 1200
60  TCAGTGCTTT TCAGAGCTGG ATATATCTTA ATTACTAATG CCACACAGAA ATTATACAA 1260
   CAAACTAGAT CTGAAGCATA ATTTAAGAAA AACATCAACA TTTTGTGTC TTAAACTGT 1320
   AGTAGTTGGT CTAGAAACAA AATACTCAA GAAAAAGAAA ATTTTCAAAT AAACCCAAA 1380
   ATAATAGCTT TGCTTAGCCC TGTTAGGGAT CCATTGGAGC ATTAAGGAGC ACATATTTT 1440
   ATTAACCTCT TTTGAGCTTT CAATGTTGAT GTAATTTTGT TTCTCTGTGT AATTTAGGTA 1500
65  AACTGCAGTG TTTAACAATA TAATGTTTAA AAGACTTAGT TGTCAGTATT AAATAATCCT 1560
   GGCATTATAG GAAAAAACC TCCTAGAAGT TAGATTATTT GCTACTGTGA GAATATTGTC 1620
   ACCACTGGAA GTTACTTTAG TTCATTTAAT TTTAATTTTA TATTTTGTGA ATATTTAAG 1680
   AACCTGATAG CTGCTTTCAA TATCTAGAAA TTTTAAATTG AGTGTAACA CACCTAAGT 1740
70  TAAGAAAAAG AACCGCTGTG ATGATTTTCA AAAGAACATT TAGAATCTTA TAGAGTCAA 1800
   ACTATAGCGT AATGCTGTGT TTATTAAGCC AGGATTTGTC GGACTTCCCC CAGGCAACTA 1860
   AACCTGCAGG ATGAAATGTC TATATTTTCT TTCATGCACT GTCGATATTA CTCAGATTTG 1920
   GGGAAATGAC ATTTTATATC TAAACAAAC ACCAAATAT TTTAGAAATA ATTCTTAGAA 1980
   AGTTTTGAGA GGAATTTTAA TTTCTCCTTC CTGATTGGGA TATTCCTCA 2040
75  AATCCCTCCT CTTACTCCAT GCTGAAGGAG AAGTACTCTC AGATGCATTA TGTTAATGGA 2100
   GAGAAAAAGC ACAGTATTGT AGAGACACCA ATATTAGCTA ATGATTTTGT GAGTGTTTT 2160
   CATTTTACAG TTTATATTCC AGCACTCAA ACTCAGGGTC AAGTTTAAAC AAAAGAGGTA 2220
   TGTAAGTACA GTAATACTA AGATGGCATT TCTATCTCAG AGGGCCAAAG TGAATCACAC 2280
   CAGTTTCTGA AGGTCTTAAA AATAGCTCAG ATGTCTTAAT GAACATGCAC CTACATTTAA 2340
80  TAGGAGTACA ATAAACTGTG TGTCAAGCTT TGTTTTACAG AGAACGCTAG ATATTAAAGAA 2400
   TTTTGAATG GATCATTTCT ACTTGCTGTG CATTTTAAAC AATAATCTGA TGAATATAGA 2460
   AAAAAATGAT CCAAAATATG GATATGATTG GATGTATGTA ACACATACAT GGAGTATGGA 2520
   GGAATTTTTC TGAATAATAC ATTTAGATTA GTTTAGTTTG AAGGAGAGGT GGGCTGATGG 2580
   CTGAGTTGTA TGTACTAAC TTGGCCCTGA CTGGTTGTGC AACCATTGCT TCATTCTTT 2640
   GCAAAATGTA GTTAAGATAT ACTTTATTCT AATGAAGGCC TTTTAAATT GTCCACTGCA 2700

```

TTCTTGGTAT TTCACTACTT CAAGTCAGTC AGAACTTCGT AGACCGACCT GAAGTTTCTT 2760  
 TTTGAATACT TGTTCCTTTA GCACTTTGAA GATAGAAAAA CCACTTTTTA AGTACTAAGT 2820  
 CATCATTTGC CTTGAAAGTT TCCTCTGCAT TGGGTTTGAA GTAGTTTAGT TATGCTTTTT 2880  
 TCTCTGTATG TAAGTAGTAT AATTTGTTAC TTTCAAATAC CCGTACTTTG AATGTAGGTT 2940  
 TTTTGTGTGT TGTATCTAT AAAAAATTGAG GGAAATGGTT ATGCAAAAAA ATATTTTGCT 3000  
 TTGGACCATA TTTCTTAAGC ATAAAAAAT GCTCAGTTTT GCTTGCAATC CTGAGAAATG 3060  
 TATTTATCTG AAGATCAAAA CAAACAATCC AGATGTATAA GTACTAGGCA GAAGCCAATT 3120  
 TTAATAATTC CTGAATAAT CCATGAAAGG AATAATTCAT ATACAGATAA ACAGAGTTGG 3180  
 CAGTATATTA TAGTGATAAT TTTGTATTTT CAAMAAAAAA AAAGTTAAAC TCTTCTTTTC 3240  
 TTTTATTAT AATGACCAGC TTTTGGTATT TCATTGTAC CAAGTTCTAT TTTTAGATAA 3300  
 AATTGTTCTC CTCTAAAAA AAAAAAATA AAAAAA 3338

Seq ID NO: C121 DNA Sequence  
 Nucleic Acid Accession #: NM\_004195  
 Coding sequence: 1..726

1 11 21 31 41 51  
 | | | | |  
 ATGGCACAGC ACGGGGCGAT GGGCGCGTTT CGGGCCCTGT GCGGCCCTGG GCTGCTGTGC 60  
 GCGCTCAGCC TGGGTGAGCG CCCACCGGG GGTCCCGGGT GCGGCCCTGG GCGCCCTCTG 120  
 CTTGGGACGG GAACGGACGC GCGCTGCTGC CGGTTTACAC CGACCGCGAT CTGCCCGCAT 180  
 TACCCGGGCG AGGAGTGCTG TTCGAGTGG GACTGCATGT GTGTCCAGCC TGAATTCAC 240  
 TCGGAGAGCC CTTGCTGCAC GACCTGCCGG CACCACCTT GTCCCCAGG CCAGGGGGTA 300  
 CAGTCCCAGG GGAATTCAG TTTGGCTTC CAGTGTATCG ACTGTGCTC GGGGACCTTC 360  
 TCCGGGGGCG ACGAAGGCCA CTGCAACCT TGGACAGACT GCACCCAGTT CGGGTTTCTC 420  
 ACTGTGTTCC TGGGAAACA GACCCACAAC GCTGTGTGCG TCCAGGGTC CCGCGGGCA 480  
 GAGCCGCTTG GGTGGCTGAC CGTCGTCTC CTGGCGTGG CCGCTGCGT CCTCTCTCTG 540  
 ACCTCGGCC AGCTTGGACT GCACATCTGG CAGCTGAGGA GTCAGTGCAT GTGGCCCCGA 600  
 GAGACCCAGC TGTGCTGTTG GGTGCGCGG TCGACCGAAG ACGCCAGAAG CTGCCAGTTC 660  
 CCGAGGAAG AGCGGGGCGA GCGATCGGCA GAGGAGAAG GCGGCTGGG AGACCTGTGG 720  
 GTGTGA 726

Seq ID NO: C122 DNA Sequence  
 Nucleic Acid Accession #: AK091896.1  
 Coding sequence: 28..1572

1 11 21 31 41 51  
 | | | | |  
 AGATCCGCGA GCCCGTCAGC CTGCGCCATG GGCTGCGACG GCCGCGTGTC GGGGCTGCTC 60  
 CGCCGCAACC TGACGCCAC GCTCACCTAC TGGAGCGTCT TCTTCAGCTT CGGCCGTGTC 120  
 ATCGCTTCTC TGGGGCCCCA GCTGCTGGAC CTGCGCTGTC AGACGCACAG CTGCTGCCC 180  
 CAGATCTCCT GGGTCTTCTT CTGCGACAG CTCTGCTCTC TGCTGGGCA GCGCCCTCGG 240  
 GGGCTCTTCA AAAGGACCTT GGGCCAGTCA CTATGGGCCC TGTTCACCTC CTCTCTGGCC 300  
 ATCTCCCTGG TGTGTGCCGT CATCCCTTC TGCCGCGACG TGAAGTGCT GGCCTCAGT 360  
 ATGGCGCTGG CGGGCTTGGC CATGGGCTGC ATCGACACCG TGGCCAACAT GCAGCTGGTA 420  
 AGGATGTACC AGAAGGACTT GGCCGTCTTC CTCCAGGTGC TCCATTCTT CTGTTGGCTT 480  
 GGTGCTCTGC TGAGCCCTCT TATGTCTGAC CCTTCTGTGT CTGAGGCCAA CTGCTTGCCT 540  
 GCCAATAGCA CGGCCAACAC CACCTCCCGA GGCCACCTGT TCCATGTCTC CAGGGTGCTG 600  
 GGCCAGCACC ACGTAGATCG CAAGCCTTGG TCCAACCAGA CGTTCCAGG GCTGACTCCA 660  
 AAGGACGGGG CAGGACCCCG AGTGTCTAT GCCTTCTGGA TCATGGCCCT CATCGATCTT 720  
 CCAGTGCCCA TGGCTGTGCT GATGCTGCTG TCCAAGGAGC GGCTGTGAC CTGCTGTCCC 780  
 CAGAGGAGG CCGTGTCTGT GTCTGCTGAT GAGCTTGCTT TGGAGACACA GCCTCCTGAG 840  
 AAGGAAGATG CCTCTCTACT GCCCCCAAAG TTTCACTCAC ACCTAGGGCA TGAGGACCTG 900  
 TTAGCTGTCT GCCAAAGGAA GAACCTCAGA GGAGCCCTT ATTCCTTCTT TGCCATCCAC 960  
 ATCACGGGCG CCTTGGTACT GTTCATGACG GATGGGTGA CGGGTGCCTA TTCCGCTTTC 1020  
 GTGTACAGCT ATGCTGTGGA GAAGCCCTCT TCTGTGGGAC ACAAGGTGGC TGGCTACTCT 1080  
 CCCAGCTCT TCTGGGGCTT CATCACTATG GGGCGGCTCC TCTCCATTCC CATATCTCTA 1140  
 AGAATGAAGC CGGCCACCAT GGTTTTCATC AACGTGGTTG GCGTGGTGGT GACGTTCTCT 1200  
 GTGCTGCTTA TTTTCTCTTA CAACGTGCTC TTCCTGTTCG TGGGGACGGC AAGCCTGGGC 1260  
 CTGTTTCTCA GCAGCACCTT CCCAGCATG CTGGCCTACA CGGAGGACTC GCTGCAGTAC 1320  
 AAAGGCTGTG CAACACAGT GCTGGTGACA GGGCAGGAG TTGGCGAGAT GGTGCTGCAG 1380  
 ATGCTGGTTG GTTCGATATT CCAGGCTCAG GGCAGCTATA GTTTCTTGGT CTGTGGCGTG 1440  
 ATCTTTGGTT GTCTGGCTTT TACCTTCTAT ATCTTGCTCC TGTTTTCCA CAGGATGCAC 1500  
 CCTGGACTCC CATCAGTTCC TACCAGAGC AGATCAATTG GAATGGAATA CTCTGAGTGC 1560  
 TACCAGAGGT AAACTGGGT GAAGAAGGCA AGAGAAGACT TTCAGCTCTT TGATCACCAG 1620  
 CACGACCATA CTGTTTCAGA AAGCTGGGTG GTGGTGGAGG CGCTCTCTCA ATGGCTATTC 1680  
 AAGTCTTCTC CACTAAACTT TGGTTGGGTA GAGGAAATTA AATTGAGTCC TGGTACCTGG 1740  
 TCAAAATCAT TAGAAGTTTA CTTGGCTTCT CAAGTTATCT TCTTCCCTGG TTCAGACTGT 1800  
 TGGTAAGAGC TGTCAGATA CCCAGATGGG AAGGAAGGAG ACAGCCGCGC GCTTCACTCC 1860  
 ATTTGTCACT TCATGCATGG ACCATACTCT GGGTTTGAGA TCATTCTTCA TTGAAGTTTG 1920  
 TAAAAATAGG TTGAAATTGT AAAGCTCCAT GATCACTGCT ATATGTAGAT ATATTTCAAT 1980  
 TTAAGCAAAA CAAGCTGCAA GTTATTCCTT GGCATGCTCA AAGGATTTTC GTGCTTTTCA 2040  
 CTTAATAGTC CAAAGTCTCT TAAATCTCTG CTGCAGATAT CAATAGCTTA TCTATATTCT 2100  
 CAAACACCAA AAGGAAAAGT TGAATCTTGC TCTCTTTGGT ATACTAATGT AGTGGTATGC 2160  
 TAAGCTGGCT CATACCACT TAGAAAAGCT GATTGTAAAA TTTTCATTTT GACAGCTGGT 2220  
 TATTAAATGC AGCCATTATT AAAATCAAAA TCATACAAAC TTATAATTAA ATCAATTACA 2280  
 TTTAAACAA AGGTAATAAA TATTCAAAGC ATATCACTTC CT 2322

Seq ID NO: C123 DNA Sequence  
 Nucleic Acid Accession #: NM\_002203.2  
 Coding sequence: 43..3588

1 11 21 31 41 51  
 | | | | |

	CTGCAAAACCC	AGCGCAACTA	CGGTCCCCCG	GTCAGACCCA	GGATGGGGCC	AGAACGGACA	60
	GGGGCCGCGC	CGCTGCCGCT	GCTGCTGGTG	TAGCGCTCA	GTCAGGGCAT	TTTAAATTGT	120
	TGTTTGGGCT	ACAAATGTTGG	TCTCCAGAA	GCAAAAATAT	TTTCCGGTCC	TTCAGTGAA	180
5	CAGTTTGGGT	ATGCAGTGCA	GCAGTTTATA	AATCCAAAAG	GCAACTGGTT	ACTGGTTGGT	240
	TCACCCCTGGA	GTGGCTTTCC	TGAGAACCGA	ATGGGAGATG	TGTATAAATG	TCCTGTTGAC	300
	CTATCCACTG	CCACATGTGA	AAAACTAAAT	TGCAAACTT	CAACAAGCAT	TCCAAATGTT	360
	ACTGAGATGA	AAACCAACAT	GAGCCTCGGC	TTGATCCTCA	CCAGGAACAT	GGGAACCTGA	420
	GGTTTTCTCA	CATGTGGTCC	TCTGTGGGCA	CAGCAATGTG	GGAAATCAGTA	TTACACAACG	480
10	GGTGTGTGTT	CTGACATCAG	TCCCTGATTTT	CAGCTCTCAG	CCAGCTTCTC	ACCTGCAACT	540
	CAGCCCTGCC	CTTCCTCAT	AGATGTTGTG	GTTGTGTGTG	ATGAATCAAA	TAGTATTTAT	600
	CCTTGGGATG	CAGTAAAGAA	TTTTTTGGAA	AAATTGTGAT	AAGGCCTTGA	TATAGGCCCC	660
	ACAAAGACAC	AGGTGGGGTT	AATTCAGTAT	GCCAATAATC	CAAGAGTTGT	GTTTAACTTG	720
	AACACATATA	AAACCAAGA	AGAAATGATT	GTAGCAACAT	CCCAGACATC	CCAATATGGT	780
15	GGGGACCTCA	CAAAACACAT	CGGAGCAATT	CAATATGCAA	GAAAATATGC	CTATTGACGA	840
	GCTTCTGGTG	CGGCACGAAG	TGCTACGAAA	GTAATGGTAG	TGTAACTGA	CGGTGAATCA	900
	CATGATGGTT	CAATGTTGAA	AGCTGTGATT	GATCAATGCA	ACCATGACAA	TATACTGAGG	960
	TTTGGCATAG	CAGTTCCTGG	GTACTTAAAC	AGAAAACGCC	TTGATACTAA	AAATTTAATA	1020
	AAAGAAATAA	AAGCGATCGC	TAGTATTTCA	ACAGAAAGAT	ACTTTTTCAA	TGTGTCTGAT	1080
20	GAAGCAGCTC	TACTAGAAAA	GGCTGGGACA	TTAGGAGAAC	AAATTTTCAG	CATTGAAGGT	1140
	ACTGTTCAAG	GAGGAGACAA	CTTTCAGATG	GAAATGTCAC	AAGTGGGATT	CAGTGCAGAT	1200
	TACTCTTCTC	AAAATGATAT	TCTGATGCTG	GGTGAGTGG	GAGCTTTTGG	CTGGAGTGGG	1260
	ACCATTTGTC	AGAAAGACAT	TCAATGGCCAT	TTGATCTTTC	CTAAACAAGC	CTTTGACCAA	1320
	ATTCTGACGG	ACAGAAATCA	CAGTTTCATAT	TTAGGTTACT	CTGTGGCTGC	AATTTCTACT	1380
25	GGAGAAAGCA	CTCACTTTGT	TGCTGGTGCT	CCTCGGGCAA	ATTATACCGG	CCAGATAGTG	1440
	CTATATAGTG	TGAATGAGAA	TGGCAATATC	ACGGTTATTC	AGGCTCACCG	AGGTGACCAG	1500
	ATTGGCTCCT	ATTTTGGTAG	TGTGCTGTGT	TCAGTTGATG	TGGATAAAGA	CACCATTAAC	1560
	GACGTGCTCT	TGGTAGGTGC	ACCAATGTAC	ATGAGTGACC	TAAAGAAAGA	GGAAGGAAGA	1620
	GTCACCTGT	TTACTATCAA	AAAGGGCATT	TTGGGTCAGC	ACCAATTTCT	TGAAGGCCCC	1680
30	GAGGGCATTG	AAAACACTCG	ATTTGGTTCA	GCAATTGCAG	CTCTTTCAGA	CATCAACATG	1740
	GATGGCTTTA	ATGATGTGAT	TGTTGGTTCA	CCACTAGAAA	ATCAGAATTC	TGGAGCTGTA	1800
	TACATTTTACA	ATGGCTCATCA	GGGCACTATC	CGCACAAAGT	ATTCCCAGAA	AATCTTGGGA	1860
	TCCGATGGAG	CCTTTAGGAG	CCATCTCCAG	TACTTTGGGA	GGTCCCTGGA	TGGCTATGGA	1920
	GATTTAAATG	GGGATTCAT	CACCGATGTG	TCTATTGGTG	CCTTTGGACA	AGTGGTTCAA	1980
35	CTCTGGTCAC	AAAGTATTGC	TGATGTAGCT	ATAGAAGCTT	CATTCAACCC	AGAAAAATC	2040
	ACTTTGGTCA	ACAAGAATGC	TCAGATAAAT	CTCAAACTCT	GCTTCAGTGC	AAAGTTTACA	2100
	CCTACTAAGC	AAAACAATCA	AGTGGCCATT	GTATATAACA	TCACACTTGA	TGCAGATGGA	2160
	TTTTCATCCA	GAGTAACCTC	CAGGGGGTTA	TTTAAAGAAA	ACAATGAAAG	GTGCCTGCAG	2220
	AAAGATATGG	TAGTAAATCA	AGCACAGAGT	TGCCCCGAGC	ACATCATTTA	TATACAGGAG	2280
40	CCCTCTGATG	TTGTCAACTC	TTTGGATTG	CGTGTGGACA	TCAGTCTGGA	AAACCTGGGC	2340
	ACTAGCCCTG	CCCTTGAAGC	CTATTCTGAG	ACTGCCAAGG	TCTTCAGTAT	TCCTTTCAC	2400
	AAAGACTGTG	GTGAGGATGG	ACTTTGCATT	TCTGATCTAG	TCCTAGATGT	CCGACAAATA	2460
	CCAGCTGCTC	AAGAACAACC	CTTTATTGTC	AGCAACCAAA	ACAAAAGGTT	AACATTTTCA	2520
	GTAACACTGA	AAAAATAAAG	GGAAAGTGCA	TACAACACTG	GAATTTGTTG	TGATTTTTC	2580
45	GAAAACCTGT	TTTTTGCATC	ATTCTCCCTA	CCGGTTGATG	GGACAGAAAG	AACATGCCAG	2640
	GTGGCTGCAT	CTCAGAAGTC	TGTTGCCCTG	GATGTAGGCT	ACCCTGCTTT	AAAGAGAGAA	2700
	CAACAGGTGA	CTTTTACTAT	TAACTTTGAC	TTCAATCTTC	AAAACTTCA	GAATCAGGCG	2760
	TCTCTCAGTT	TCCAAGCTT	AAGTGAAAGC	CAAGAAGAAA	ACAAAGCTGA	TAATTTGGTC	2820
	AACCTCAAAA	TTCCTCTCCT	GTATGATGCT	GAAATTCATC	TAAACAAGATC	TACCAACATA	2880
50	AATTTTATG	AAATCTCTTC	GGATGGGAAT	GTTCCCTCAA	TCGTGCACAG	TTTTGAAGAT	2940
	GTTGGTCCAA	AATTCATCTT	CTCCCTGAAG	GTAACAACAG	GAAGTGTTC	AGTAAGCATG	3000
	GCAACTGTAA	TCATCCACAT	CCCTCAGTAT	ACCAAGAAAA	AGAACCCACT	GATGTACCTA	3060
	ACTGGGGTGC	AAACAGACAA	GGCTGGTGAC	ATCAGTTGTA	ATGCAGATAT	CAATCCACTG	3120
	AAAATAGGAC	AAACATCTTC	TTCTGTATCT	TTCAAAAGTG	AAAATTTTCA	GCACACCCAA	3180
55	GAATTGAAC	GCAGAAGTGC	TTCTGTAGT	AATGTTACCT	GCTGGTTGAA	AGACGTTTCA	3240
	ATGAAGAGAG	AATACTTTGT	TAATGTGACT	ACCAGAATTT	GGAAACGGGAC	TTTCGCATCA	3300
	TCACAGTTCC	AGACAGTACA	GCTAACGGCA	GCTGCAGAAA	TCAACACCTA	TAAACCTGAG	3360
	ATATATGTGA	TTGAAGATAA	CACCTGTTACG	ATTCCTCTGA	TGATAATGAA	ACCTGATGAG	3420
	AAAGCCGAAG	TACCAACAGG	AGTTATAATA	GGAAGTATAA	TTGCTGGAAT	CCTTTTGCTG	3480
60	TTAGCTCTGG	TTGCAATTTT	ATGGAAGCTC	GGCTTCTTCA	AAAGAAAATA	TGAAAAGATG	3540
	ACCAAAAACT	CAGATGAGAT	TGATGAGACC	ACAGAGCTCA	GTAGCTGAAC	CAGCAGACCT	3600
	ACCTGCAGTG	GGAAACCGCA	GCATCCAGC	CAGGGTTTGC	TGTTTTCGCTG	CATGGATTTT	3660
	TTTTTAAATC	CATATTTTTT	TTTATCATGT	CGTAGGTAAA	CTAACCTGGT	ATTTTAAAGAT	3720
	AAAACCTGAC	GTCAGTTTGG	ATGAAGAAAT	TGTGGGGGGT	GGGGGAGGTG	CGGGGGGCAG	3780
65	GTAGGGAAAT	AATAGGAAAA	ATACCTATTT	TATATGATGG	GGGAAAAAAA	GTAATCTTTA	3840
	AACTGGCTGG	CCCAGAGTTT	ACATTCTAAT	TTGCATTGTG	TCAGAAACAT	GAAATGCTTC	3900
	CAAGCATGAC	AACTTTTAAA	GAAAAATATG	ATACTCTCAG	ATTTTAAAGG	GGAAAACTGT	3960
	TCTCTTTAAA	ATATTGTGCT	TTAAACAGCA	ACTACAGAAG	TGGAAGTGCT	TGATATGTAA	4020
	GTACTTCCAC	TTGTGTATAT	TTTAATGAAT	ATTGATGTTA	ACAAGAGGGG	AAAACAAAAC	4080
70	ACAGGTTTTT	TCAATTTATG	CTGCTCATCC	AAAGTTGCCA	CAGATGATAC	TTCCAAGTGA	4140
	TAATTTTATT	TATAAATCTAG	GTAATAATTT	TGTTTGGTTC	CTTTTATACC	ACGGCTGCC	4200
	CTTCCACACC	CCATCTTGCT	CTAATGATCA	AAACATGCTT	GAATAACTGA	GCTTAGAGTA	4260
	TACCTCCTAT	ATGTCCATT	AAGTTAGGAG	AGGGGGCGAT	ATAGAGACTA	AGGCACAAAA	4320
	TTTTGTTTAA	AACCTCAGAA	ATAACATTTA	TGTAATAATCC	CATCTGCTAG	AAGCCCATCC	4380
75	TGTGCCAGAG	GAAGGAAAAG	GAGGAAATTT	CCTTTCTCTT	TTAGGAGGCA	CAACAGTTCT	4440
	CTTCTAGGAT	TTGTTTGGCT	GACTGGCAGT	AACCTAGTGA	ATTTTGTGAA	GATGAGTAAT	4500
	TTCTTTGGCA	ACCTTCTCTC	TCCCTTACTG	AACCACTCTC	GCACCTCTCT	GTTGGTACCAT	4560
	TATTATAGAA	GCCTCTTACA	GCCTGACTTT	CTCTCCAGCG	GTCCAAAGTT	ATCCCTCTCT	4620
	TTACCCCTCA	TCCAAAGTTT	CACTCTCTTC	AGGACAGCTG	CTGTGCATTA	GATATTAGGG	4680
80	GGGAAAGTCA	TCGTGTTAAT	TTACACACTT	GCATGAATTA	CTGTATATAA	ACTCCTTAAC	4740
	TTACAGGGAGC	TATTTTCATT	TAGTGCTAAA	CAAGTAAGAA	AAATAAGCTA	GAGTGAATTT	4800
	CTAAATGTTG	GAATGTTATG	GGATGTAAAC	AATGTAAAGT	AAAACACTCT	CAGGATTTCA	4860
	CCAGAAAGTTA	CAGATGAGGC	ACTGGAAACC	ACCACCAAAT	TAGCAGGTGC	ACCTTCTGTG	4920
	GCTGTCTTGT	TTCTGAAGTA	CTTTTCTTTC	CACAAGAGTG	AATTTGACCT	AGGCAAGTTT	4980
	GTTCAAAAGG	TAGATCTTGA	GATGATTTGG	TCAGATTGGG	ATAAGGCCCA	GCAATCTGCA	5040

TTTTAAACAG CACCCAGTC ACTAGGATGC AGATGGACCA CACTTTGAGA AACACCACCC 5100  
 ATTTCTACTT TTTGCACCTT ATTTTCTCTG TTCCTGAGCC CCCACATTCT CTAGGAGAAA 5160  
 CTTAGATTAA AATTACAGAG CACTACATAT CTAAAGCTTT GACAAGTCCT TGACCTCTAT 5220  
 AAACCTCAGA GTCCCTCATTA TAAATGGGA AGACTGAGCT GGAGTTCAGC AGTGATGCTT 5280  
 TTTAGTTTAA AAAGTCTATG ATCTGATCTG GACTTCCTAT AATACAAATA CACAATCCTC 5340  
 CAAGAATTGG ACTTGAAAA G 5361

Seq ID NO: C124 DNA Sequence  
 Nucleic Acid Accession #: NM\_031460  
 Coding sequence: 103..1101

1 11 21 31 41 51  
 AGCAGGCGTT TGCAGAGAGGA GATACGAGCT GGACGCCTGG CCCTTCCCTC CCACCGGGTC 60  
 CTAGTCCACC GCTCCCGCGG CCGGCTCCCC GCCTCTCCCG CTATGTACCG ACCGCGAGCC 120  
 CGGGCGGCTC CCGAGGGCAG GGTCCGGGGC TGCGCGGTGC CCAGCACCGT GCTCCTGCTG 180  
 CTCGCTTACC TGGCTTACCT GCGCTGGGGC ACCGCGGTGT TCTGGACGCT GGAGGGCCGC 240  
 GCGGCGCAGG ACTCCAGCCG CAGCTTCCAG CCGACAAAGT GGGAGCTGTT GCAGAACTTC 300  
 ACGTGTCTGG ACCGCGCGGC GCTGGACTCG CTGATCCGGG ATGTCTGTCCA AGCATAACAA 360  
 AACGGAGCCA GCCTCCTCAG CAACACCACC AGCATGGGGC GCTGGGAGCT CGTGGGCTCC 420  
 TTCTTCTTTT TGTGTGCCAC CATCACCACC ATTGGCTATG GCAACCTGAG CCCCAACACG 480  
 ATGGCTGCCC GCCTCTCTCT CATCTCTTTT GCCCTTGTGG GGATCCCACT CAACCTCGTG 540  
 GTGCTCAACC GACTGGGGCA TCTCATGCAG CAGGGAGTAA ACCACTGGGC CAGCAGGCTG 600  
 GGGGGCACCT GGCAGGATCC TGACAAGGCG CGGTGGCTGG CGGGCTCTGG CGCCCTCCTC 660  
 TCGGGCTCTC TGCTCTTCTT GCTGCTGCCA CCGCTGCTCT TCTCCACAT GGAGGGCTGG 720  
 AGCTACACAG AGGGCTTCTA CTTCGCTTC ATCACCTCA GCACCGTGGG CTTGCGGCAC 780  
 TACGTGATGG GAATGAACCC CTCCAGAGG TACCACTGT GGTACAAGAA CATGTTGTCC 840  
 CTGTGGATCC TCTTTGGGAT GGCATGGCTG GCCTTGATCA TCAAACCTCAT CCTCTCCAG 900  
 CTGGAGACCG CAGGGAGGGT ATGTTCTCTG TGCCACCACA GCTCTAAGGA AGACTTCAAG 960  
 TCCCAAAGCT GGAGACAGGG ACCTGACCGG GAGCCAGAGT CCCACTCCCC ACAGCAAGGA 1020  
 TGCTATCCAG AGGGACCCAT GGGAAATCATA CAGCATCTGG AACCTTCTGC TCACGTGCA 1080  
 GGCTGTGGCA AGGACAGCTA GTTATACTCC ATTCTTTGGT CGTCTGCTC GGTAGCAAGA 1140  
 CCCTGATTT TAAGCTTTGC ACATGTCCAC CCAAATAAA GACTACATTT TCCATCCACC 1200  
 CTAGAGGCTG GTGTCAGCTA TATGATTAAT TCTGCCAAT AGGGTATACA GAGACATGTC 1260  
 CTGGGTGACA TGGGATGTGA CTTTCGGGTG TCGGGGCAGC ATGCCCTTCT CCCCACCTTC 1320  
 CTTACTTTAG CGGGCTGCAA TGCCGCGGAT ATGATGGCTG GGAGCTCTGG CAGCCATACG 1380  
 GCACCATGAA GTAGCGGACA TGTTTGAGCG GCACAATTAG ATAGGAAGAG TCTGGATCTC 1440  
 TGATGATCAC AGAGCCATCC TAACAAACGG AATATCACCG ACCCTCCTTT ATGTGAGAGA 1500  
 GAAATAACA TCTATGAAA 1519

Seq ID NO: C125 DNA Sequence  
 Nucleic Acid Accession #: NM\_004154  
 Coding sequence: 309..1295

1 11 21 31 41 51  
 AAGGACAGAG GAGGGGCCCT TCCTGTACAG TGGCTGGGAG CAGAGGTGGC TTTGTCTTTT 60  
 CGGAAGAACT GGTCTGTGGG AATTTGTGCT TATTTCCCAT CAAGGATCAA GGACCTGCTC 120  
 TGGGGCTACC TCAGGGCCCC ACAGGATGAG GGGCTGGTTT TCAGATGAGT TTTCTGCTTG 180  
 CCTGTCACTT GGATAGTGTG TAAAAATTTG CAAACTGCCT TCTTGTCACT GTCTTGCTCA 240  
 TTCTTCATGA CACTCTGTAT ATGTCTCTCA GTTTCCTCAT CTGCTGCCTC TCCAGACTTC 300  
 TGCCAGAACCA TTGCACGCGA CAGTTTCAGG CACAGAAGTG ACTGGCAGCA GGGGCTGCTC 360  
 CACGAGTGGG AATTTGCTCC AGCACTTCAC GGACTGCAAG CGAGGCATTG GCTAACTCTT 420  
 GGATAACAAG ACCTCTGCCA GAAGAACCAT GGCTTTGGAA GGCGGAGTTC AGGCTGAGGA 480  
 GATGGGTGCG TGCTCTAGTG AGCCCTGCCC TCCTGAACA TAGGAAACCC ACCTGGGCAG 540  
 CCATGGAATG GGACAATGGC ACAGGCCAGG CTCTGGGCTT GCCACCCACC ACCTGTGTCT 600  
 ACCCGAGAAA CTTCAGCAA CTGCTGCTGC CACCTGTGTA TTCGGCGGTG CTGGCGGCTG 660  
 GCCTGCGGCT GAACATCTGT GTCAATTACC AGATCTGCAC GTCCCGCCGG GCCCTGACCC 720  
 GCACGGCCGT GTACACCCCTA AACCTTGCTC TGGCTGACCT GCTATATGCC TGCTCCCTGC 780  
 CCCTGCTCAT CTACAATAT GCCCAAGGTG ATCACTGGCC CTTTGGCGAC TTGCTGCTGC 840  
 GCCTGGTCCG CTCTCTCTTC TATGCCAACC TGCACGGCAG CATCTCTTTC CTCACCTGCA 900  
 TCAGCTTCCA GCGCTACCTG GGCATCTGCC ACCCGCTGGC CCCCTGGCAC AAACGTGGGG 960  
 GCGCGCGGGC TGCTTGCTTA GTGTGTAG CCGTGTGGCT GGCCGTGACA ACCAGTGCC 1020  
 TGCCACAGC CATCTTCTGT GCCACAGGCA TCCAGCGTAA CCGCACTGTC TGCTATGACC 1080  
 TCAGCCCGCC TGCCCTGGCC ACCCACTATA TGCCCTATGG CATGGCTCTC ACTGTCTATG 1140  
 GCTTCTGCTG GCCCTTTGCT GCCCTGCTGG CTTGCTACTG TCTCTTGGCC TGCCGCTGT 1200  
 GCGCCAGGGA TGGCCCGGCA GAGCCTGTGG CCCAGGAGCG GCGTGGCAAG GCGGCCGCGA 1260  
 TGGCCGTGGT GGTGGCTGCT GCCTTTGCCA TCAGCTTCTT GCCTTTTAC ATCAACCAAGA 1320  
 CAGCTACCTT GGCAGTGGC TCGACGCGG GCGTCCCCTG CACTGTATTG GAGGCCTTTG 1380  
 CAGCGGCTTA CAAAGGCAGC CGGCCGTTTG CAGTGCCAA CAGCGTGTG GACCCCATCC 1440  
 TCTTCTACTT CACCCAGAAG AAGTTCGCC GCGGACCACTA TGAGCTCCTA CAGAACTCA 1500  
 CAGCCAAATG GCAGAGGAGC GGTGCTGAG TCCTCCAGGT CCTGGGCAGC CTTCTATTTT 1560  
 GCCATTGTGT CCGGGGCACC AGGAGCCCA CCAACCCCA ACCATGCGGA GAATTAGAGT 1620  
 TCAGCTCAGC TGGGCATGGA GTTAAGATCC CTCACAGGAC CCAGAAGCTC ACCAAAAACT 1680  
 ATTTCTTCA CCCCCTCTCT GCGCCAGACC CTGTGGGCAT GGAGATGGAC AGACCTGGGC 1740  
 CTGGCTCTTG AGAGGTCCCA GTCAAGCATG GAGAGCTGGG GAAACCACAT TAAGGTGCTC 1800  
 ACAAATAATC AGTGTGACGT GTACTGTCAA AA 1832

Seq ID NO: C126 DNA Sequence  
 Nucleic Acid Accession #: NM\_007197  
 Coding sequence: 18..1763

1 11 21 31 41 51  
 | | | | |

	ACACGTCCAA	CGCCAGCATG	CAGCGCCCGG	GCCCCCGCCT	GTGGCTGGTC	CTGCAGGTGA	60
	TGGGCTCGTG	CGCCGCCATC	AGCTCCATGG	ACATGGAGCG	CCCGGGCGAC	GGCAAAATGCC	120
	AGCCCATCGA	GATCCCGATG	TGCAAGGACA	TCCGCTACAA	CATGACTCGT	ATGCCCAAACC	180
5	TGATGGGCCA	CGAGAACCAG	CGCGAGGCAG	CCATCCAGTT	GCACGAGTTC	GCGCCGCTGG	240
	TGGAGTACGG	CTGCCACGGC	CACCTCCGCT	TCTTCCTGTG	CTCGCTGTAC	GCGCCGATGT	300
	GCACCGAGCA	GGTCTCTACC	CCCATCCCCG	CCTGCCGGGT	CATGTGCGAG	CAGGCCCGGC	360
	TCAAGTGCTC	CCCATTATG	GAGCAGTCA	ACTTCAAGTG	GCCCGACTCC	CTGGAATGCC	420
	GGAAACTCCC	CAACAAGAAC	GACCCCAACT	ACCTGTGCAT	GGAGGCGCCC	AACAACGGCT	480
10	CGGACGAGCC	CACCCGGGGC	TCGGGCGCTG	TCCCGCCGCT	GTTCCGGCCG	CAGCGGCCCC	540
	ACAGCGCGCA	GGAGCACCCG	CTGAAGGACG	GGGGCCCCGG	GCGCGGCGGC	TGCGACAACC	600
	CGGGCAAGTT	CCACCACGTG	GAGAAGAGCG	CGTCGTGCGC	GCCGCTCTGC	ACGCCCGGCG	660
	TGGACGTGTA	CTGGAGCCGC	GAGGACAAGC	GCTTCGCACT	GGTCTGGCTG	GCCATCTGGG	720
	CGGTGCTGTG	CTTCTTCTCC	AGCGCCTTCA	CCGTGCTCAC	CTTCCTCATC	GACCCGGCCC	780
15	GCTTCCGCTA	CCCCGAGCGC	CCCATCATCT	TCCTCTCCAT	GTGCTACTGC	GTCTACTCCG	840
	TGGGTACTCT	CATCGCCTC	TTCGCCGGCG	CCGAGAGCAT	CGCCTGCGAC	CGGGACAGCG	900
	GCCAGCTCTA	TGTCATCCAG	GAGGGACTGG	AGAGCACCGG	CTGCACGCTG	GTCTTCTCTG	960
	TCCTCTACTA	CTTCGGCATG	GCCAGCTCGC	TGTGGTGGGT	GGTCTCTACG	CTCACCTGGT	1020
20	TCCTGGCCGC	CGGCAAGAAC	TGGGGCCACG	AGGCCATCGA	AGCCAAACAG	AGCTACTTCC	1080
	ACCTGGCAGC	CTGGGCCATC	CCGGCGGTGA	AGACCATCCT	GATCCTGGTC	ATGCGCAGGG	1140
	TGGCGGGGGA	CGAGCTCACC	GGGGTCTGCT	ACGTGGGCAG	CATGGACGTC	AACGCGCTCA	1200
	CGGCTTCTGT	GCTCATTTCC	CTGGCCTGCT	ACCTGGTCAT	CGGCACGTCC	TTCATCCTCT	1260
	CGGGCTTCTG	GGCCCTGTTC	CACATCCGGA	GGGTGATGAA	GACGGGCGGC	GAGAACACGG	1320
25	ACAAGCTGGA	GAAGCTCATG	GTGCGTATCG	GGCTCTTCTC	TGTGCTGTAC	ACCGTGCCGG	1380
	CCACCTGTGT	GATCGCCTGC	TACTTTTACG	AACGCCCTCA	CATGGATTAC	TGGAAGATCC	1440
	TGGCGGCGCA	GCACAAGTGC	AAAATGAACA	ACCAGACTAA	AACGCTGGAC	TGCCCTGATG	1500
	CCGCTCCAT	CCCCGCCGTG	GAGATCTTCA	TGGTGAAGAT	CTTTATGCTG	CTGGTGGTGG	1560
	GGATCACCAG	CGGGATGTGG	ATTTGGACCT	CCAAGACTCT	GCAGTCTTGG	CAGCAGGTGT	1620
	GCAGCCGTAG	GTTAAAGAAC	AAGAGCCGGA	GAAACCCGGC	CAGCGTGATC	ACCAGCGGTG	1680
30	GGATTACAA	AAAAGCCAG	CATCCCCAGA	AAACTCACCA	CGGAAATAT	GAGATCCCTG	1740
	CCCAGTCGCC	CACCTGCGTG	TGAACAGGGC	TGGAGGGAAG	GGCACAGGGG	CGCCCGGAGC	1800
	TAAAGTGGG	TGCTTTCTTT	GGTGTGTGTT	TCTTTCTTTC	TCTCTCTTTT	TTTTTTTTTT	1860
	ATAAAGCAA	AAGAGAAATA	CATAAAAG	TGTTTACCTT	GAAATTCAGG	ATGCTGTGAT	1920
	ACACTGAAAG	GAAAAATGTA	CTTAAAGGGT	TTTGTTTTGT	TTTGGTTTTC	CAGCGAAGGG	1980
35	AAGCTCCTCC	AGTGAAGTAG	CCTCTTGTGT	AACTAATTGG	TGGTAAAGTA	GTTGATTCAG	2040
	CCCTCAGAA	AAAACCTTTG	TTTAGAGCCC	TCCGTAAATA	TACATCTGTG	TATTTAGATT	2100
	GGCTTTGCTA	CCCATTTTCA	AATAAGAGGA	CAGATAACTG	CTTTGCAAA	TCAAGAGCCT	2160
	CCCCTGGGTT	AACAAATGAG	CCATCCCCAG	GGCCACCCCC	CAGGAAGGCC	ACAGTGCTGG	2220
	GCGGCATCCC	TGCAGAGGAA	AGACAGGACC	CGGGGCCCGC	CTCACACCCC	AGTGGATTGG	2280
40	GAGTTGCTTA	AAATAGACTG	TGGCCTTCAC	CAATAGTCTC	TCTGCAAGAC	AGAAACCTCC	2340
	ATCAAACCTC	ACATTGTGTA	ACTCAAACGA	TGTGCAATAC	ATTTTCTTCT	CTTTCCTTGA	2400
	AAATAAAAG	AGAAACAAGT	ATTTTGCTAT	ATATAAGAG	AACAAAAGAA	ATCTCCTAAC	2460
	AAAAGAACTA	AGAGCAAGAA	CCCTCAGAAA	CCCTTCAGTG	CTACATTTTG	TGGCTTTTAA	2520
	ATGGAACCA	AGCCAATGTT	ATAGACGTTT	GGACTGATTT	GTGAAAGGGA	GGGGGGAAGA	2580
45	GGGAGAAGGA	TCAATTCAAA	GTTACCCAAA	GGGCTTATG	ACTCTTTCTA	TGTTAAACA	2640
	AATGATTTCC	ACAAACAGAT	CAGGAAGCAC	TAGGTTGGCA	GAGACACTTT	GTCTAGTGTA	2700
	TTCTCTTAC	AGTGCCAGGA	AAGAGTGGTT	TCTGCGTGTG	TATATTTGTA	ATATATGATA	2760
	TTTTTCATGC	TCCACTATTT	TATTAATAAT	AAAATATGTT	CTTTAAAAAA	A	2811

Seq ID NO: C127 DNA Sequence

Nucleic Acid Accession #: NM\_005761.1

Coding sequence: 250..4956

	1	11	21	31	41	51	
55	GCGAGGAGGA	AACGCTGCCG	GAGCGCGCAG	GGCTTGCTGC	CGCCACCGCC	GCTGCACAGG	60
	CTGCCGGAGC	GAGCCTGCCG	CGCGCCGCCG	TCCCCGCTCT	CCTTCCTGGG	CGAGCTGCCG	120
	GGATGGGGCG	GCCGCGGGAG	CCCGAGCGCG	CGCAGGAACC	GCCGCCGCCG	CCGCCCGCCT	180
	CTCCGTTGCC	GCGCGCCTGA	GCCGCGCTCG	CGGCCGCGCG	CCCTGCCCGG	GGGCGGCCCT	240
60	CCCAGCCCCA	TGGAGTCTTC	CCGAGGGAAG	GCGCCGCGCG	GCCCCCGCGC	CCCOCGACGC	300
	CCACTGCCCC	TGCTCGCTTC	CTGCTGGCA	CTGGCGGCTC	CGGCGCGGGG	CGCGGACGAG	360
	CCCGTGTGGC	GGTCGGAGCA	AGCCATCGGA	GCCATCGCGG	CGAGCCAGGA	GGACGCGCTG	420
	TTTGTGGCGA	GCGGCAGCTG	CCTGGACCAG	CTGGACTACA	GCCTGGAGCA	CAGCCTCTCG	480
	CGCCTGTACC	GGGACCAAGC	GGGCAACTGC	ACAGAGCCGG	TCTCGCTGGC	GCCCCCGCGC	540
65	CGGCCCGGCG	CCGGGAGCAG	CTTCAGCAAG	CTGCTGCTGC	CCTACCGCGA	GGGGGCGGCC	600
	GGCCTCGGGG	GGCTGCTGCT	CACCGGCTGG	ACCTTCGACC	GGGGCGCCTG	CGAGGTGCGG	660
	CCCCTGGGCA	ACCTGAGCCG	CAACTCCCTG	CGCAACGGCA	CCGAGGTGGT	GTCTGTCCAC	720
	CCGCAGGGCT	CGACGGCCGG	CGTGGTGTAC	CGCGCGGGCC	GGAAACAACG	CTGGTACCTG	780
	GCGGTGGCCG	CCACCTACGT	GCTGCCTGAG	CCGAGACCGG	CGAGCCGCTG	CAACCCCGCG	840
70	GCATCCGAGC	ACGACACGGC	CATCGCGCTC	AAGGACACGG	AGGGGCGCAG	CCTGGCCACG	900
	CAGGAGCTGG	GGCGCCTCAA	GCTGTGCGAG	GGCGCGGGCA	GCCTGCACCT	CGTGGACGCC	960
	TTTCTCTGGA	ACGGCAGCAT	CTACTTCCCC	TACTACCCCT	ACAACTATAC	GAGCGGCGCT	1020
	GCCACCGGCT	GGCCACGATC	GGCGCGCATC	GCGCAGAGCA	CCGAGGTGCT	GTTCCAGGGC	1080
	CAGGCATCCC	TGCACTGCGG	CCACGGCCAC	CCGACGCGCC	GCGCGCTGCT	CCTCTCTCC	1140
75	AGCCTAGTGG	AGGCCCTGGA	CGTCTGGGCG	GGAGTGTTC	GCGCGGCCCG	TGGAGAGGGC	1200
	CAGGAGCGGC	GCTCCCCCAC	CACCAAGGCG	CTCTGCCTCT	TCAGAATGAG	TGAGATCCAG	1260
	GCGCGCGCCA	AGAGGGTTCG	CTGGGACTTC	AAGACGGCCG	AGAGCCACTG	CAAGAAGAGG	1320
	GATCAACCTG	AAAGAGTCCA	ACCAATCGCA	TCATCTACCT	TGATCCATTC	CGACCTGACA	1380
	TCGCTTTATG	GCACCGTGGT	AATGAACAGG	ACTGTTTAT	TCTTGGGGAC	TGGAGATGGC	1440
80	CAGTTACTTA	AGGTTATTCT	TGGTGAGAA	TTGACTTCAA	ATTGTCCAGA	GTTTATCTAT	1500
	GAAATTAAG	AAGAGACACC	TGTTTCTTAC	AAACTCGTTC	CTGATCCTGT	GAAGAATATC	1560
	TACATTTATC	TACAGCTGGG	GAAAGAGGTG	AGGAGAATTC	GTGTTGCAAA	CTGCAATAAA	1620
	CATAAATCCT	GTTCCGAGTG	TTTAACAGCC	ACAGACCCCT	ACTGCGGTTG	GTGCCATTCC	1680
	CTACAAGGTT	GCACTTTTCA	AGGAGATTGT	GTACATTCAG	AGAACTTAGA	AAACTGGCTG	1740
	GATATTTCTG	CTGGAGCAAA	AAAGTGCCCT	AAAATTCAGA	TAATTCGAAG	CAGTAAAGAA	1800



5	AAGACTACAG	TGACTATGGT	GGGAAGCTTC	TCTCCAAGAC	ACTCAAAGTG	CATGGTGAAG	1860
	AATGTGGACT	CTAGCAGGGA	GCTCTGCCAG	AATAAAAGTC	AGCCCAACCG	GACCTGCACC	1920
	TGTAGCATCC	CAACCAGAGC	AACCTACAAA	GATGTTTCAG	TTGTCAACGT	GATGTTCTCC	1980
	TTCGGTTCTT	GGAAATTTATC	AGACAGATTTC	AACTTTACCA	ACTGCTCATC	ATTAAAAGAA	2040
	TGCCCAGCAT	CGGTAGAAAAC	TGGCTGCGCG	TGGTGTAAAA	GTGCAAGAAG	GTGTATCCAC	2100
	CCCTTCACAG	CTTGCAGACC	TTCTGATTAT	GAGAGAAACC	AGGAACAGTG	TCCAGTGGCT	2160
	GTGAGAGAAG	CATCAGGAGG	AGGAAGACCC	AAGGAGAACA	AGGGGAACAG	AACCAACCAG	2220
	GCTTTACAGG	TCTTCTACAT	TAAGTCCATT	GAGCCACAGA	AAGTATCGAC	ATTAGGGAAA	2280
10	AGCAACGTGA	TAGTAACGGG	AGCAAACTTT	ACCCGGGCAT	CGAACATCAC	AATGATCCTG	2340
	AAAGGAACCA	GTACCTGTGA	TAAGGATGTG	ATACAGGTTA	GCCATGTGCT	AAATGACACC	2400
	CACATGAAAT	TCTCTCTTCC	ATCAAGCCGG	AAAGAAATGA	AGGATGTGTG	TATCCAGTTT	2460
	GATGGTGGGA	ACTGCTCTTC	TGTGGGATCC	TTATCTTACA	TTGCTCTGCC	ACATTGTTCC	2520
	CTTATATTTT	CTGCTACCAC	CTGGATCAGT	GGTGGTCAAA	ATATAACCAT	GATGGGCAGA	2580
15	AATTTTGATG	TAATTGACAA	CTTAATCATT	TCACATGAAT	TAAAAGGAAA	CATAAATGTC	2640
	TCTGAATATT	GTGTGGCGAC	TTACTGCGGG	TTTTTAGCCC	CCAGTTTAAA	GAGTTCAAAA	2700
	GTGCGCACGA	ATGTCACTGT	GAAGCTGAGA	GTACAAAGAC	CCTACTTGGA	TTGTGGAAAC	2760
	CTGCGATATC	GGGAGGACCC	CAGATTTCAG	GGGTATCGGG	TGGAATCCGA	GGTGGACACA	2820
	GAACTGGAAG	TGAAAATTTCA	AAAAGAAAAT	GACAACCTTC	ATATTTCCTA	AAAAGACATT	2880
20	GAAATTACTC	TCTTCCATGG	GGAAAATGGG	CAATTAAATT	GCAGTTTGA	AAATATTACT	2940
	AGAAATCAAG	ATCTTACCAC	CATCCTTTGC	AAAATTAAAG	GCATCAAGAC	TGCAAGCACC	3000
	ATTGCCAACT	CTTCTAAGAA	AGTTCTGGTC	AAGCTGGGAA	ACCTGGAGCT	CTACGTCCAG	3060
	CAGGAGTCAG	TTCTTCCAC	ATGGTATTTT	CTGATTGTGC	TCCCTGCTCT	GCTAGTGATT	3120
	GTCAATTTTTG	CGGCCGTGGG	GGTGACCAGG	CACAAATCGA	AGGAGCTGAG	TGCGAAACAG	3180
25	AGTCAACAAC	TAGAATTGCT	GGAAAAGCGAG	CTCCGGAAG	AGATACGTGA	CGGCTTGTCT	3240
	GAGCTCGAGA	TGGATAAAT	GGATGTGGTT	GATAGTTTTG	GAACTGTTCC	CTTCTTTGAC	3300
	TACAAACATT	TTGCTCTGAG	AACCTTCTTC	CCTGAGTCAG	GTGGCTTCAC	CCACATCTTC	3360
	ACTGAAGATA	TGCATAACAG	AGACGCCAAC	GACAAGAATG	AAAGTCTCAC	AGCTTTGGAT	3420
	GCCTTAATCT	GTAATAAAAG	CTTCTTGTGT	ACTGTCTATC	ACACCTTTGA	AAAGCAGAAG	3480
30	AACCTTTCTG	TGAAGGACAG	GTGTCTGTTT	GCCTCTCTTC	TAACCATTCG	ACTGCAAAAC	3540
	AAGCTGGTCT	ACCTGACCAG	CATCCTAGAG	GTGCTGACCA	GGGACTTGAT	GGAACAGTGT	3600
	AGTAACATCG	AGCCGAAACT	CATGCTGAGA	CGCACGGAGT	CCGTCTGCGA	AAAACCTCCT	3660
	ACAAACCTGGA	GTGCTCTGCT	CCTTCTGGA	TTTCTCCGGG	AGACTGTCGG	AGAGCCCTTC	3720
	TATTTGCTGG	TGACGACTCT	GAACCAAGAA	ATTAACAAGG	GTCCCGTGGG	TGTAATCACT	3780
35	TGCAAAAGCCC	TGTACACACT	TAATGAAGAC	TGGCTGTTGT	GGCAGGTTC	GGAATTCAGT	3840
	ACTGTGGCAT	TAAACGTCGT	CTTTGAAAAA	ATCCCGGAAA	ACGAGAGTGC	AGATGTCTGT	3900
	CGGAATATTT	CAGTCAATGT	TCTCGACTGT	GACACCATTG	GCCAAAGCCAA	AGAAAAGATT	3960
	TTCCAAGCAT	TCTTAAGCAA	AAATGGCTCT	CCTTATGGAC	TTGAGCTTAA	TGAAATTTGGT	4020
	CTTGAGCTTC	AAATGGGCGA	ACGACAGAAA	GAACTTCTGG	ACATCGACAG	TTCTCTCGTG	4080
40	ATTCTTGAAG	ATGGAATCAC	CAAGCTAAAC	ACCATTGGCC	ACTATGAGAT	ATCAAATGGA	4140
	TCCACTATAA	AAGTCTTTAA	GAAGATAGCA	AATTTTACTT	CAGATGTGGA	GTACTCGGAT	4200
	GACCACTGCC	ATTGTATTTT	ACCAGATTCT	GAAGCATTC	AAGATGTGCA	AGGAAAGAGA	4260
	CATCGAGGGA	AGCACAGATT	CAAGTAAAAA	GAAATGTATC	TGACAAAGCT	GCTGTGACAC	4320
	AAGGTGGCAA	TTCATTCTGT	GCTTGAAAAA	CTTTTGTAGG	GCATTGTGGG	TTTACCCAAC	4380
45	AGCAGAGCTC	CATTGTCTAT	AAAATACTTT	TTTGACTTTT	TGGACGCCCA	GGCTGAAAAA	4440
	AAAAAAATCA	CAGATCCCTGA	CGTCGTACAT	ATTTGGAAAA	CAAAACAGCT	TCCTCTTCGC	4500
	TTCTGGGTAA	ACATCCTGAA	GAACCCCTCAG	TTTGTCTTTG	ACATTAGAGG	GACACACAT	4560
	ATAGACGGCT	GTTFGTCTAGT	GATTGCCAG	GCATTCTATG	ATGCATTTTC	TCTCACAGAG	4620
	CAGCAACTAG	GGAAGGAAGC	ACCAACTAAT	AAGCTTCTCT	ATGCCAAGGA	TATCCCAACC	4680
50	TACAAAGAA	AAGTAAATAT	TTATTACAAA	GCAATCAGGG	ATTGCTCTCC	ATTGTCTATC	4740
	TCGAAAGTGG	AAAGTAAATTT	AACTCAGGAA	TCTAAGAAAC	ATGAAATGGA	ATTAAATGAA	4800
	GAAGTGGCCT	TGACAGAAAT	TTACAAATAC	ATCGTAAAT	ATTTTGATGA	GATTCTTAAT	4860
	AAACTAGAAA	GAGAACGAGG	GCTGGAAGAA	GCTCAGAAAC	AACTCTTGCA	TGTAAAAGTC	4920
	TTATTGTGAT	AAAGAAAGAA	ATGCAAGTGG	ATGTAAGCAC	TCTGGGCGCT	GGCTTAATCT	4980
55	GGCAAGTTTC	TTACAGACGAC	TTGGGAGCAA	AATGGCTGCT	TGAGCTACTC	TGTGTCGTTA	5040
	ATTTGTTGTT	TGCACATAGG	TTCCACTTTG	GGCACTGTCT	TTTTAAGAGA	CCAAGGCACA	5100
	TGCACAGCTT	TTAGAAAGCA	A				5121

Seq ID NO: C128 DNA Sequence  
Nucleic Acid Accession #: NM\_002185.1  
Coding sequence: 23..1402

60	1	11	21	31	41	51	
	CTCTCTCTCT	ATCTCTCTCA	GAATGACAAT	TCTAGGTACA	ACTTTTGGCA	TGGTTTTTTC	60
65	TTTACTTCAA	GTCTTTCTG	GAGAAAGTGG	CTATGCTCAA	AATGGAGACT	TGGAAGATGC	120
	AGAACTGGAT	GACTACTCAT	TCTCATGCTA	TAGCCAGTTG	GAAGTGAATG	GATCGCAGCA	180
	TTCACTGACC	TGTGCTTTTG	AGGACCCAGA	TGTCAACACC	ACCAATCTGG	AATTTGAAAT	240
	ATGTGGGGCC	CTCGTGGAG	TAAAGTGCCT	GAATTTACAG	AACTACAAAG	AGATATATTT	300
70	CATCGAGACA	AAGAAATCT	TACTGATTGG	AAAGAGCAAT	ATATGTGTGA	AGGTTGGAGA	360
	AAAGAGTCTA	ACTGCAAAAA	AAATAGACCT	AACCACTATA	GTTAAACCTG	AGGCTCCTTT	420
	TGACCTGAGT	GTCATCTATC	GGGAAGGAGC	CAATGACTTT	GTGGTGACAT	TTAATACATC	480
	ACACTTGCAA	AAGAGTATG	TAAAAGTTT	AATGCATGAT	GTAGCTTACC	GCCAGGAAAA	540
	GGATGAAAA	AAATGGACGC	ATGTGAATTT	ATCCAGCACA	AAGCTGACAC	TCCTGCAGAG	600
75	AAAGCTCCAA	CCGGCAGCAA	TGTATGAGAT	TAAAGTTTGA	TCCATCCCTG	ATCACTATTT	660
	TAAAGGCTTC	TGGAGTGAAT	GGAGTCCAA	TTATTACTTC	AGAACTCCAG	AGATCAATAA	720
	TAGCTCAGGG	GAGATGGATC	CTATCTTACT	AACCATCAGC	ATTTTGAGTT	TTTTCTCTGT	780
	CGCTCTGTTG	GTCATCTTGG	CCTGTGTGTT	ATGGAAAAAA	AGGATTAAGC	CTATCGTATG	840
	GCCAGTCTCT	CCCGATCAT	AGAAGACTCT	GGAACATCTT	TGTAAAGAA	CAAGAAAAAA	900
80	TTTAAATGTG	AGTTTCAATC	CTGAAAGTTT	CCTGGACTGC	CAGATTTCAT	GGGTGGATGA	960
	CATTCAAGCT	AGAGATGAAG	TGGAAGGTTT	TCTGCAAGAT	ACGTTTCCCT	AGCAACTAGA	1020
	AGAATCTGAG	AAGCAGAGGC	TTGGAGGGGA	TGTGCAGAGC	CCCAACTGCC	CATCTGAGGA	1080
	TGTAGTCGTG	ACTCAGAAA	GCTTTGGGAG	AGATTCAATC	CTCACATGCC	TGGCTGGGAA	1140
	TGTCAAGTGA	TGTGACGCCC	CTATTCTCTC	CTCTTCCAGG	TCCCTAGACT	CGAGGGAGAG	1200
	TGGCAAGAAT	GGGCTCATG	TGTACCAGGA	CCTCTGCTTT	AGCCTTGGGA	CTACAAACAG	1260

CACGCTGCCC CCTCCATTTT CTCTCCAATC TGAATCCTG ACATTGAACC CAGTTGCTCA 1320  
 GGGTCAGCCC ATTCTTACTT CCCTGGGATC AAATCAAGAA GAAGCATATG TCACCATGTC 1380  
 CAGCTTCTAC CAAAACCACT GAAGTGTAAG AAACCCAGAC TGAACCTACC GTGAGCGACA 1440  
 AAGATGATTT AAAAGGGGAG TCTAGAGTTC CTAGTCTCCC TCACAGCACA GAGAAGACAA 1500  
 AATTAGCAAA ACCCCACTAC ACAGTCTGCA AGATTCTGAA ACATTGCTTT GACCACTCTT 1560  
 CCTGAGTTCA GTGGCACTCA ACATGAGTCA AGAGCATCCT GCTTCTACCA TGTGGATTGT 1620  
 GTCACAAGGT TTAAGGTGAC CCAATGATTC AGCTATTT 1658

Seq ID NO: C129 DNA Sequence  
 Nucleic Acid Accession #: NM\_002722.1  
 Coding sequence: 15..302

1 11 21 31 41 51  
 ACTCTGGACT CCGGATGGCT GCCGCACGCC TCTGCCTCTC CCTGCTGCTC CTGTCCACCT 60  
 GCGTGGCTCT GTTACTACAG CCCTGCTGG GTGCCCAGGG AGCCCCACTG GAGCCAGTGT 120  
 ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCCACTA TGCAGCTGAT CTCCGTAGAT 180  
 ACATCAACAT GCTGACCAGG CCTAGGTATG GGAAAAGACA CAAAGAGGAC ACGCTGGCCT 240  
 TCTCGGAGTG GGGGTCCCCG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGGACTTAT 300  
 AATGCCACCT TCTGTCTCCT ACGACTCCAT GAGCAGCGCC AGCCCCAGCTC TCCCCTCTGC 360  
 ACCCTTGGCT CTGGCCAAAG CTGTCTCCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420  
 AAGCC 425

Seq ID NO: C130 DNA Sequence  
 Nucleic Acid Accession #: NM\_032545.1  
 Coding sequence: 47..718

1 11 21 31 41 51  
 AAATGATCT TCAATGCACT AAGAGAAGGA GACTCTCAAA CCAAAAATGA CCTGGAGGCA 60  
 CCATGTCAGG CTTCGTGTTA CGGTCAAGTT GGCATTACAG ATCATCAATT TGGGAACACAG 120  
 CTATCAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGGTTG CCACTCAGAA 180  
 GCACCGACAG TCACCGCTCA ACTGGACCTC CAGTCAATTC GGAGAGGTGA CTGGGAGCGC 240  
 CGAGGGCTGG GGGCCGAGG AGCCGCTCCC TACTCCCGG GCTTTCGGAG AGGGTGCGTC 300  
 CGCGCGGCCG CGCTGCTGCA GGAACGCGCG TACCTGCGTG CTGGGCAGCT TCTGCGTGTG 360  
 CCCGGCCAC TTCACGGGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGGCG 420  
 CCTGGAGCAC GGAGCCTGGA CCCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGGC 480  
 CTGCACTGCT CTCCTCTCC AGACGCTGTA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC 540  
 CCACGCTCAC GGGCCGAGCG CCGGGGCGC GCCAGCCTG CTACTCTTG TGCCCTGCGC 600  
 ACTCTGTCAC CGCTCTCTGC GCCCGGATGC GCCCGCGCAC CTCTGGTCCC TGGTCCCTTC 660  
 CGTCTCCAG CGGGAGCGGC GCCCTGCGG AAGGCCGGA CTGGGCATC GCCTTTAATT 720  
 TTCTATGTTG TAAATAATAG ATGTGTTTAG TTACCGTAA GCTGAAGCAC TGGGTGAATA 780  
 TTTTATTGTA GTAATAAATA TTTTCATGAA AGGCCCAAAA AAAAAAATA AAAAAAATA 840  
 AAAAA 846

Seq ID NO: C131 DNA Sequence  
 Nucleic Acid Accession #: NM\_006533.1  
 Coding sequence: 72..467

1 11 21 31 41 51  
 AGGGAGAGAG GGAGGGGAGG AATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT 60  
 CACAGTCCAC GATGGCCCGG TCCTTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGCCT 120  
 TCTCCGGACC TGTGTGTCAG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180  
 CGGACAGGTA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240  
 CCGACTGCCG ATTCTGTACC ATTACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300  
 AGGGCCGTGG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360  
 CTGCTCGCTT GGGCTATTTT CCGAGTAGCA TTGTCCGAGA GGACCGAGCC CTGAAACCTG 420  
 GCAAGTCTGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG 480  
 CTGGCCCTGC CGTTCCCTCT CCTTGGGTTT ATGCAATAC AATCAGCCCA GTGCAAAAC 538

Seq ID NO: C132 DNA Sequence  
 Nucleic Acid Accession #: AB064272  
 Coding sequence: 1..708

1 11 21 31 41 51  
 ATGACACAAG TCACAGAAAA GTCCACAGAA CACCCAGAAA AGACCAGTC AACCACAGAG 60  
 AAAACCACAA GAACCCACAG AAAGCCTACG CTATACTCAG AGAAGACCAT ATGCACCAAA 120  
 GGGAAAAACA CACAGTCCC AGAAAAGCCT ACAGAAAACC TGGGGAACAC CACACTGACC 180  
 ACTGAGACCA TAAAGGCCCC AGTAAAGTCC ACAGAAAACC CAGAAAAAAC AGCAGCAGTC 240  
 ACAAGAGCTA TAAACCTTTC AGTCAAGTTC ACAGGAGACA AATCTCTCAC TACTACCTCT 300  
 TCTCATCTAA ATAAACTTGA AGTTACTCAT CAGGTGCCCA CTGGTTCTTT CACCCTCAT 360  
 ACATCTAGAA CGAAGCTGAG TTCTATCACA TCAGAAGCCA CAGGAAACGA GAGCCATCCA 420  
 TACCTCAATA AAGATGGCTC ACAGAAAGGT ATCCACGCTG GACAGATGGG AGAGAATGAT 480  
 TCAATCCCTG CATGGCCCAT AGTTATTGTG GTCCCTGGTG CTGTGATTCT CCTCTGGTG 540  
 TTCCTTGGCC TGATCTTCTT GGTCTCTTAT ATGATGCGGA CACGCCGCAC ACTAACCAG 600  
 AACACCCAGT ACAATGATGC AGAGGATGAG GGTGGCCCCA ATTCCTACCC GGTCTACCTG 660  
 ATGGAGCAGC AGAATCTTGG CATGGGCCAG ATCCCTTCCC CACGTTGA 708

Seq ID NO: C133 DNA Sequence  
 Nucleic Acid Accession #: NM\_080870.1  
 Coding sequence: 3..710

	1	11	21	31	41	51	
5	AGATGACACA	AGTCACAGAA	AAGTCCACAG	AACACCCAGA	AAAGACCACG	TCAACCCACAG	60
	AGAAAACCCAC	AAGAACCCCA	GAAAAGCCCTA	CGCTATACTC	AGAGAAGACC	ATATGCACCA	120
	AAGGGAAAAA	CACACCAGTC	CCAGAAAAGC	CTACAGAAAA	CCTGGGGAAC	ACCACACTGA	180
	CCACTGAGAC	CATAAAGCC	CCAGTAAAGT	CCACAGAAAA	CCCAGAAAAA	ACAGCAGCAG	240
	TCACAAAGAC	TATAAAACCT	TCAGTCAAGG	TCACAGGAGA	CAAACTCTCTC	ACTACTACCT	300
10	CTTCTCATCT	AAATAAAACT	GAAGTTACTC	ATCAGGTGCC	CAGTGGTTCT	TTCACCCCTA	360
	TTACATCTAG	AACGAAGCTG	AGTTCTATCA	CATCAGAAGC	CACAGGAAAC	GAGAGCCATC	420
	CATACCTCAA	TAAAGATGGC	TCACAGAAAG	GTATCCACGC	TGGACAGATG	GGAGAGAATG	480
	ATTCAATCCC	TGCATGGGCC	ATAGTTATTG	TGGTCTCGGT	GGCTGTGATT	CTCCTCCTGG	540
	TGTTCCCTGG	CCTGATCTTC	TTGGTCTCCT	ATATGATGCG	GACACGCCGC	ACACTAACCC	600
	AGAACACCCA	GTACAAATGAT	GCAGAGGATG	AGGGTGGCCC	CAATTCCCTAC	CCGGTCTACC	660
15	TGATGGAGCA	GCAGAATCTT	GGCATGGGCC	AGATCCCTTC	CCCACGGTGA	TCTTGGAGTA	720
	GGCGCCGAGC	CCTGGCTCTT	CCATGCTCTG	CCCCTTTCCT	GGATGAGGAA	CCGGACTCAC	780
	AAATTTCTATT	TCCGGGACTA	CAGGAAGGGC	AGAGAATACT	GACGGTTACC	AGTATTAAAC	840
	CTTCATCTGT	TCTTGAACCT	GGTTGGGGAA	TGAGGTGATA	AGCAAGGAGG	GTGTAAGTTT	900
20	AGGGGACAAA	GAAGAAAGAA	TGAATAATAC	GAGCAGACAT	TCTCTGTAGA	AGGTAATGGT	960
	CTGAGAATGA	AAAGGTGTTT	GATGGACATG	TTGTGGGGGC	ACCAATGCAG	AACACTGCAC	1020
	TGAGTCCATA	AGGAAGGACA	GGAGCCTTAT	AGGCAATGCC	CCAGACTGAC	TTGTGAGTGG	1080
	GGTTTATGGG	GAAAGGGAGG	GACTGAGGGC	AGAGTCTCTG	GGTTTCAGGA	CAGCATTATG	1140
	TTATTTCCAT	TCACTATTAC	TTAAGAGTTT	GTGTGTAAC	AGGCTCATCT	CTGAGTTCTC	1200
25	AGGACCCTTG	CCCCACCCC	CATTTTTTTA	ATGAAAAAAA	AAAACAAAAA	AAACGGATCC	1260
	AGAAAGAAAA	GAGAAATTAT	TTCTTCTCTC	ACTCTCTCCA	TGCCCTGGAG	AAAAAAAAGT	1320
	CCAGAAGAAA	TCATAAATAT	CTCTCATCTA	CATGGTTGCT	TCCTCTTCCT	CCCAAATCCC	1380
	TTAGTTTCC	TAAATGTCTA	CAGTGGACGC	CCTGTTGGTT	TGGCTTGCTG	GGTTGTGGGT	1440
	GGACACGCAA	GGAGGGGATT	TTTATTGGC	CAGCAGTCTC	ACCCACTGAT	CTCCACCCCA	1500
30	GACCTTCCCT	TGTTGGTGTC	TCAGCATTTA	TTTTCCTGTC	TCTTCCACCA	AAAGCCAGCT	1560
	GTAGCTTTAT	CTCGTAAAG	TTACCCATCT	TCTCTACTGT	CCCCATTCTC	TCTCCTCCCA	1620
	CCTTCACCCC	AGATTCAAGT	TTTCTCCTT	GTAGGCATT	CATCTGTGTG	TGTTTCTCGG	1680
	ATTTCTCTCT	TCTCTCTTA	TGGCCATTTC	ACCTTATTAC	TGATTGGGTA	GAGGGGGAAA	1740
	AGGAGAATGA	TGATGATAGT	TTCTTCTGT	CTATTGACCT	TTTTTATAAT	AAAGTATAAC	1800
35	ATGTT						1805

Seq ID NO: C134 DNA Sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..10674

40	1	11	21	31	41	51	
	ATGTGGCCTC	GCCTGGCCTT	TTGTTGCTGG	GGTCTGGCGC	TCGTTTCGGG	CTGGGCGACC	60
45	TTTCAGCAGA	TGTCCTCCGT	GCGCAATTC	AGCTTCGCC	TCTTCCCGA	GACCGCGCCC	120
	GGGGCCCCCG	GGAGTATCCC	CGCGCCGCC	GCTCCTGGCG	ACGAAGCGGC	GGGGAGCAGA	180
	GTGGAGCGGC	TGGGCCAGGC	GTTCGGCGCA	CGCGTGCGGC	TGCTGCGGGA	GCTCAGCGAG	240
	CGCTGGAGC	TTGTCTTCCT	GGTGGATGAT	TCGTCAGCG	TGGGCGAAGT	CAACTTCCGC	300
	AGCGAGCTCA	TGTTCTGTCG	CAAGCTGCTG	TCCGACTTCC	CCGTGGTGCC	CACGGCCACG	360
50	CGCGTGGCCA	TCGTGACCTT	CTCGTCCAAG	AACTACGTGG	TGCCGCGCGT	CGATTACATC	420
	TCACCCCGCC	GCGCGCGCCA	GCACAAGTGC	GCGCTGCTCC	TCCAAGAGAT	CCCTGCCATC	480
	TCCTACCGAG	GTGGCGGCAC	CTACACCAAG	GGCGCCTTCC	AGCAAGCCGC	GCAAAATCTT	540
	CTTCATGCTA	GAGAAAATCT	AACAAAAGTT	GTATTTCTCA	TCACTGATGG	ATATTCCAAT	600
	GGGGGAGACC	CTAGACCAAT	TGCAGCGTCA	CTGCGAGATT	CAGGAGTGA	GATCTTCACT	660
55	TTTGGCATAT	GGCAAGGGAA	CATTCGAGAG	CTGAATGACA	TGGCTTCCAC	CCCAAAGGAG	720
	GAGCACTGTT	ACCTGCTACA	CAGTTTTGAA	GAATTTGAGG	CTTTAGCTCG	CCGGGCATTG	780
	CATGAAGATC	TACCTCTGCG	GAGTTTTATT	CAAGATGATA	TGGTCCACTG	CTCATATCTT	840
	TGTGATGAAG	GCAAGACTGG	CTGTGACCSA	ATGGGAAGCT	GCAAAATGTG	GACACACACA	900
	GGCCATTTTG	AGTGCATCTG	TGAAAAGGGG	TATTACGGGA	AAAGGCTGCA	GTATGAATGC	960
60	ACAGCTTGCC	CATCGGGGAC	ATACAAACCT	GAAGGCTCAC	CAGGAGGAAT	CAGCAGTTGC	1020
	ATTCCATGTC	CTGATGAAAA	TCACACCTCT	CCACCTGGAA	GCACATCCCC	TGAAGACTGT	1080
	GTCTGCAGAG	AGGGATACAG	GGCATCTGGC	CAGACCTGTG	AACCTTGCCA	CTGCCCTGCC	1140
	CTGAAGCCTC	CCGAAAATGG	TTACTTTATC	CAAAACACTT	GCAACRACCA	CTTCAATGCA	1200
	GCCTGTGGGG	TCCGATGTCA	CCCTGGATTT	GATCTTGTGG	GAAGCAGCAT	CATCTTATGT	1260
65	CTACCCAAATG	TCGTTGTGGT	CGGTTCAAG	AGCTACTGCA	GAGTAAGAAC	ATGTCTCAT	1320
	CTCCGCCAGC	GGAACATGTC	CCACATCAGC	TGTTCTACAA	GGGAATGTGT	ATATAAGACA	1380
	ACATGTTTGG	TTGCCTGTGA	TGAAGGGTAC	AGACTAGAAG	GCAGTGATAA	GCTTACTTGT	1440
	CAAGGAAACA	GCCAGTGGGA	TGGGCCAGAA	CCCCGGTGTG	TGGAGCGCCA	CTGTTCCACC	1500
	TTTCAGATGC	CCAAAGATGT	CATCATATCC	CCCCACAAC	GTGGCAAGCA	GCCAGCCAAA	1560
70	TTTGGGACGA	TCTGCTATGT	AAGTTGCCGC	CAAGGGTCA	TTTATCTGG	AGTCAAAGAA	1620
	ATGCTGAGAT	GTACCACTTC	TGGAATAATG	AATGTCGGAG	TTCAGGCAGC	TGTGTGTAAA	1680
	GACGTGGAGG	CTCCTCAAA	CAACTGTCC	AAGGACATAG	AGGCTAAGAC	TCTGGAAACG	1740
	CAAGATTCTG	CCAATGTTAC	CTGGCAGATT	CCAACAGCTA	AAGACAACCT	TGGTGAAGAA	1800
	GTGTCAGTCC	AGTTTCATCC	AGCTTTCACC	CCACCTTACC	TTTTCCTAAT	TGGAGATGTT	1860
75	GCTATCGTAT	ACACGGCAAC	TGACCTATCC	GGCAACCAGG	CCAGCTGCAT	TTTCCATATC	1920
	AAGGTTATTG	ATGCAGAAC	ACCTGTGATA	GACTGGTGCA	GATCTCCACC	TCCCGTCCAG	1980
	GTCTCGGAGA	AGGTACATGC	CGCAAGCTGG	GATGAGCCTC	AGTTCCTAGA	CAACTCAGGG	2040
	GCTGAATTGG	TCAATACCA	AAGTCATACA	CAAGGAGACC	TTTTCCTTCA	AGGGGAGACT	2100
	ATAGTACAGT	ATACAGCCAC	TGACCCCTCA	GGCAATAACA	GGACATGTGA	TATCCATATT	2160
80	GTCTATAAAG	GTTCCTCCCTG	TGAAATTCCT	TTTCAACCTG	TAAATGGGGA	TTTTATATGC	2220
	ACTCCAGATA	ATACTGGAGT	CAACTGTACA	TTAACTTGCT	TGGAGGGGCTA	TGATTTTACA	2280
	GAAGGGTCTA	CTGACAAGTA	TTATTTGCT	TATGAAGATG	GCGTCTGGAA	ACCAACATAT	2340
	ACCACTGAAT	GGCCAGACTG	TGCCAAAAAA	CGTTTTGCAA	ACCACGGGTT	CAAGTCTCTT	2400
	GAGATGTTCT	ACAAAGCAGC	TCGTTGTGAT	GACACAGATC	TGATGAAGAA	GTTCCTTGAA	2460
	GCATTTGAGA	CCAGCCTGGG	AAAAATGGTC	CCATCATTTT	GTAGTGATGC	AGAGGACATT	2520

	GACTGCAGAC	TGGAGGAGAA	CCTGACCAAA	AAATATTGCC	TAGAATATAA	TTATGACTAT	2580
	GAAATGGCT	TTGCAATTGG	ACCAGGTGGC	TGGGGTGAGC	CTAATAGGCT	GGATTACTCT	2640
	TACGATGACT	TCCTGGACAC	TGTGCAAGAA	ACAGCCACAA	GCATCGGCAG	TGCCAAGTCC	2700
5	TCACGGATTA	AAAGAAATGC	CCCATTATCT	GACTATAAAA	TTAAGTTAAT	TTTAAACATC	2760
	ACAGCTAGTG	TGCATTATCC	CGATGAAAGA	AATGATACCC	TTGAATGGGA	AAATCAGCAA	2820
	CGACTCCTTC	AGACATTGGA	AACTATCACA	AATAAATCTA	AAAGGACTCT	CAACAAAGAC	2880
	CCCATGTATT	CCCTTCAGCT	TGCATCAGAA	ATACTTATAG	CCGACAGCAA	TTTATTAGAA	2940
	ACAAAAAAGG	CTTCCCCCTT	CTGCAGACCA	GGCTCAGTGC	TGAGAGGGCG	TATGTGTGTC	3000
10	AATTGCCCTT	TGGGAACCTA	TTATAATCTG	GAACATTTC	CCTGTGAAAG	CTGCCGGATC	3060
	GGATCCTATC	AAGATGAAGA	AGGGCAACTT	GAGTGCAAGC	TTTGCCCTCT	TGGGATGTAC	3120
	ACGGAATATA	TCCATTCAAG	AAACATCTCT	GATTGTAAAG	CTCAGTGTAA	ACAAGGCACC	3180
	TACTCATACA	GTGGACTTGA	GACTTGTGAA	TCGTGTCCAC	TGGGCACCTA	TCAGCCAAAA	3240
	TTTGGTTCCC	GGAGCTGCCT	CTCGTGTCCA	GAAAACACCT	CAACTGTGAA	AAGAGGAGCC	3300
15	GTGAACATT	CTGCATGTGG	AGTTCCCTGT	CCAGAAGGAA	AATTCTCGCG	TTCTGGGTTA	3360
	ATGCCCTGTC	ACCCATGTCC	TCGTGACTAT	TACCAACCTA	ATGCAGGGAA	GGCCTTCTGC	3420
	CTGGCCTGTC	CTTTTATGG	AACTACCCCA	TTCTGTGGTT	CCAGATCCAT	CACAGAATGT	3480
	TCAACTTCAG	TTCTGAATAT	TACTATTTTC	GGTGGATTGG	GGCATCTGGA	GTTGTATAAT	3540
	TGTCCTCTCG	AGGTTTCCCA	TGAATGCTTC	TTTAAACCTT	GCCACAATAG	TGGAACCTGC	3600
20	CAGCAACTTG	GGCGTGGTTA	TGTTTGTCTC	TGTCCACTTG	GATATACAGG	CTTAAAGTGT	3660
	GAAACAGACA	TCGATGAGTG	CAGCCCACTG	CCTTGCCTCA	ACAATGGAGT	TTGTAAAGAC	3720
	CTAGTTGGGG	AATTCAATTG	TGAGTGCCCA	TCAGGTTACA	CAGGTCAGCG	GTGTGAAGAA	3780
	AATATAAATG	AGTGTAGCTC	CAGTCCTTGT	TTAATAAAG	GAATCTGTGT	TGATGGTGTG	3840
	GCTGGCTATC	GTTCACATC	TGTGAAAGGA	TTTGTAGGCC	TGCATTGTGA	AACAGAAGTC	3900
25	AATGAATGCC	AGTCAAAACC	ATGCTTAAAT	AATGCAGTCT	GTGAAGACCA	GGTTGGGGGA	3960
	TTCTTGTGCA	AATGCCCACT	TGGATTTTTC	GGTACCCGAT	GTGGAAAGAA	CGTCGATGAG	4020
	TGCTCTAGTC	AGCCATGCAA	AAATGGAGCT	ACCTGTAAAG	ACGGTGCCAA	TAGCTTCAGA	4080
	TGCCCTGTGT	CAGCTGGCTT	CACAGGATCA	CACTGTGAAT	TGAACATCAA	TGAATGTCTG	4140
	TCTAATCCAT	GTAGAAATCA	GGCCACCTGT	GTGGATGAAT	TAAATTCATA	CAGTTGTAAA	4200
30	TGTCAGCCAG	GATTTTCAAG	CAAAAGGTGT	GAAACAGAAC	AGTCTACAGG	CTTTAACTGT	4260
	GATTTTGAAG	TTTCTGGCAT	CTATGGATAT	GTCTAGCTAG	ATGGCATGCT	CCCCTCTCTC	4320
	CATGCTCTAA	CTGTACCTT	CTGGATGAAA	TCCTCTGACG	ACATGAACTA	TGGAACACCA	4380
	ATCTCTATG	CAGTTGATAA	CGGCAGCGAC	AATACCTTGC	TCCTGACTGA	TTATAACGGC	4440
	TGGGTTCTTT	ATGTGAATGG	CAGGGAAAAG	ATAACAAACT	GTCCCTCGGT	GAATGATGGC	4500
35	AGATGGCATC	ATATTGCAAT	CACCTTGGACA	AGTGCCAAATG	GCATCTGGAA	AGTCTATATC	4560
	GATGGGAAAT	TATCTGACGG	TGGTGTCTGG	CTCTCTGTTG	GTTCGCCCAT	ACCTGGTGGT	4620
	GGTGGCTTAG	TTCTGGGGCA	AGAGCAGAC	AAAAAAGGAG	AGGGATTGAG	CCCAGCTGAG	4680
	TCCTTTGTGG	GCTCCATAAG	CCAGCTCAAC	CTCTGGGACT	ATGTCTCTGC	TCCACAGCAG	4740
	GTGAAGTCAC	TGGCTACCTC	CTGCCCAGAG	GAACCTCAGT	AAGGAAACGT	GTTAGCATGG	4800
40	CCTGATTTCT	TGTACGAAAT	TGTGGGGAAG	GTGAAGATCG	ATTCTAAGAG	CATATTTTGT	4860
	TCTGATTGCC	CACGCTTAGG	AGGGTCAGTG	CCTCATCTGA	GAACCTGCATC	TGAAGATTTA	4920
	AAGCCAGGTT	CCAAAGTCAA	TCTGTCTGT	GATCCAGGCT	TCCAGCTGGT	CGGGAAACCT	4980
	GTGCACTACT	GTCTGAATCA	AGGACAGTGG	ACACAACCA	TTCCCTCACTG	TGAACGCAAT	5040
	AGCTGTGGGG	TGCCACCTCC	TTTGGAGAAAT	GGCTTCCATT	CAGCCGATGA	CTTCTATGCT	5100
45	GGCAGCACAG	TAACTACCA	GTGCAACAAT	GGCTACTATC	TATTGGGTGA	CTCAAGGATG	5160
	TTCTGTACAG	TAATAGGGAG	CTGGAAACGG	GTTCACCAT	CCTGCCTTGA	TGTCGATGAG	5220
	TGTGCACTTG	GATCAGATTG	TAGTGAGCAT	GCTTCTTGCC	TGAACGTAGA	TGGATCCTAC	5280
	ATATGTTTAT	TGTCTCCACC	GTACACAGGA	GATGGGAAAA	ACTGTGCAGA	ACCTATAAAA	5340
	TGTAAGGCTC	CAGGAAATCC	GGAAAATGGC	CACCTCTCAG	GTGAGATTTA	TACAGTAGGT	5400
50	GCCGGAGTCA	CATTTTCTGT	TCAGGAAGGA	TACCAGTTGA	TGGGAGTAAC	CAAAATCACA	5460
	TGTTTGGAGT	TCGGGAATG	GAATCATCTA	ATACCATATT	GTAAAGCTGT	TTCATGTGGT	5520
	AAACCCGCTA	TTCCAGAAAA	TGGTTGCATT	GAGGAGTTAG	CATTTACTTT	TGGCAGCAAA	5580
	GTGACATATA	GGTGTAAATA	AGGATATACT	CTGGCCGGTG	ATAAAGAATC	ATCCTGTCTT	5640
	GCTAACAGTT	CTTGGAGTCA	TTCCCTCTCT	GTGTGTGAAC	CAGTGAAGTG	TTCTAGTCCG	5700
55	GAAATATATA	ATAATGGAAA	ATATATTTTG	AGTGGGCTTA	CCTACCTTTC	TACTGCATCA	5760
	TATTCATGCG	ATACAGGATA	CAGCTTACAG	GGCCCTTCCA	TTATTGAATG	CACGGCTTCT	5820
	GGCATCTGGG	ACAGAGCGCC	ACCTGCCTGT	CACCTCGTCT	TCTGTGGAGA	ACCACCTGCC	5880
	ATCAAGAGAT	CTGTCTTATC	GGGGAATAAC	TTCACTTTCA	GGAAACCCGT	CACCTACACT	5940
	TGCAAGAAGG	GCTATACTCT	TGCTGGTCTT	GACACCATTG	AATGCCTGGC	CGACGGCAAG	6000
60	TGGAGTAGAA	GTGACCAAGC	GTGCTCTGGT	GTCTCTCTGT	ATGAGCCACC	CATTGTGGAC	6060
	CACGCCCTCT	CAGAGACTGC	CCATCGGCTC	TTTGGAGACA	TTGCATTCTA	CTACTGCTCT	6120
	GATGGTTACA	GCCTAGCAGA	CAATTCACAG	CTTCTCTGCA	ATGCCAGGG	CAAGTGGGTA	6180
	CCCCCAGAA	GTCAAGACAT	GGCCCGTGT	ATAGCTCATT	TCTGTGAAAA	ACCTCCATCG	6240
	GTTTCTTATA	GCATCTTGA	ATCTGTGAGC	AAAGCAAAAT	TTGCAGCTGG	CTCAGTTGTG	6300
65	AGCTTTAAAT	GCATGGAAGG	CTTGTACTG	AACACCTCAG	CAAAGATTGA	ATGTATGAGA	6360
	GGTGGGCACT	GGAAACCTTC	CCCCATGTCC	ATCCAGTGCA	TCCCTGTGCG	GTGTGGAGAG	6420
	CCACCAAGCA	TCATGAATGG	CTATGCAAGT	GGATCAAACT	ACAGTTTGGG	AGCCATGGTG	6480
	GCTTACAGCT	GCAACAAGGG	GTTCTACATC	AAAGGGGAAA	AGAAGAGCAC	CTGCGAAGCC	6540
	ACAGGGCAGT	GGAGTAGTCC	TATACCGACG	TGCCACCCGG	TATCTTGTGG	TGAACCACT	6600
70	AAGTTGAGA	ATGGCTTTCT	GGAGCATACA	ACTGGCAGGA	TCTTTGAGAG	TGAAGTGAGG	6660
	TATCAGTGTA	ACCCGGGCTA	TAAGTCAGTC	GGAAAGTCTG	TATTTGTCTG	CCAAGCCAAT	6720
	CGCCACTGGC	ACAGTGAATC	CCCTCTGATG	TGTGTTCTCT	TCGACTGTGG	AAAACTTCCC	6780
	CCGATCCAGA	ATGCTTTCAT	GAAAGGAGAA	AACTTTGAAG	TAGGGTCCAA	GGTTCAAGTT	6840
	TTCTGTAAAT	AGGGTTATGA	GCTTGTGGT	GACAGTTCTT	GGACATGTCA	GAATCTGGC	6900
75	AAATGGAATA	AGAGTCAAAA	TCCAAGTGC	ATGCCCTGCC	AGTGCCGAGA	CCGCCCTCTC	6960
	TTGGAAGAAC	AGCTAGTAT	AAAGGAGTTG	ACCACCGAGG	TAGGAGTTGT	GACATTTTCC	7020
	TGTAAGAGAG	GGCATGTCTT	GCAAGGCCCC	TCTGTCTGTA	AATGCTTGCC	ATCCAGCAA	7080
	TGGAATGACT	CTTTCCCTGT	TTGTAAGATT	GTTCTTTGTA	CCCCACCTCC	CCTAATTTCC	7140
	TTTGGTGTCC	CCATTCTCTT	TTCTGTCTCT	CAITTTGGAA	GTACTGTCAA	GTATCTTGT	7200
80	GTAGGTGGGT	TTTTCCCTAAG	AGGAAATCT	ACCACCTCT	GCCAACTGA	TGGCACCTGG	7260
	AGCTCTCCAC	TGCCAGATAG	TGTTCCAGTA	GAATGTCCCC	AACTGTAGGA	AATCCCAAT	7320
	GGAAATCATG	ATGTGCAAGG	CCTTGCCTAT	CTCAGCACAG	CTCTCTATAC	CTGCAAGCCA	7380
	GGCTTTGAAT	TGGTGGGAAA	TACTACCACC	CTTTGTGGAG	AAAATGGTCA	CTGGCTTGGG	7440
	GGAAACCAAA	CATGTAAAGC	CATTGAGTGC	CTGAAACCCA	AGGAGATTTT	GAATGGCAAA	7500
	TTCTCTTACA	CGGACCTACA	CTATGGACAG	ACCGTTACCT	ACTCTGCAA	CCGAGGCTTT	7560

	CGGCTCGAAG	GTCCCACTGC	CTTGACCTGT	TTAGAGACAG	GTGATTGGGA	TGTAGATGCC	7620
	CCATCTTGCA	ATGCCATCCA	CTGTGATTCC	CCACAACCCA	TTGAAAATGG	TTTTGTAGAA	7680
	GGTGCAGATT	ACAGCTATGG	TGCCATAATC	ATCTACAGTT	GCTTCCCTGG	TTTTCAGGTG	7740
5	GCTGTGATG	CCATGCAGAC	CTGTGAAGAG	TCAGGATGGT	CAAGTTCCAT	CCCAACATGT	7800
	ATGCCAATAG	ACTGTGGCCT	CCCTCCTCAT	ATAGATTTTG	GAGACTGTAC	TAAACTCAAA	7860
	GATGACCAGG	GATATTTTGA	GCAAGAAGAC	GACATGATGG	AAGTTCCATA	TGTGACTCCT	7920
	CACCCCTCCT	ATCATTTGGG	AGCAGTGGCT	AAAACCTGGG	AAAATACAAA	GGAGTCTCCT	7980
	GCTACACATT	CATCAAACTT	TCTGTATGGT	ACCATGGTTT	CATACACCTG	TAATCCAGGA	8040
10	TATGAACCTC	TGGGGAACCC	TGTGCTGATC	TGCCAGGAAG	ATGGAACTTG	GAATGGCAGT	8100
	GCACATCCT	GCATTTCAT	TGAATGTGAC	TTGCCTACTG	CTCCTGAAAA	TGGCTTTTTG	8160
	CGTTTTACAG	AGACTAGCAT	GGGAAGTGCT	GTGCAGTATA	GCTGTAAACC	TGGACACATT	8220
	CTAGCAGGCT	CTGACTTAAG	GCTTTGTCTA	GAGAATAGAA	AGTGGAGTGG	TGCCCTCCCA	8280
	CGCTGTGAAG	CCATTTCATG	CAAAAAGCCA	AATCCAGTCA	TGAATGGATC	CATCAAAAGGA	8340
15	AGCAACTACA	CATACCTGAG	CACGTTGTAC	TATGAGTGTG	ACCCCGGATA	TGTGCTGAAT	8400
	GGCACTGAGA	GGAGAACATG	CCAGGATGAC	AAAACTGGG	ATGAGGATGA	GCCCATTTCG	8460
	ATTCCTGTGG	ACTGCAGTTT	ACCCCCAGTC	TCAGCCAATG	GCCAGGTGAG	AGGAGACGAG	8520
	TACACATTCC	AAAAAGAGAT	TGAATACACT	TGCAATGAAG	GGTTCTTGCT	TGAGGGAGCC	8580
	AGGAGTCGGG	TTTGTCTTGC	CAATGGAAAT	TGGAGTGGAG	CCACTCCCGA	CTGTGTGCCT	8640
20	GTCAGATGTG	CCACCCCGCC	ACAACCTGGC	AATGGGGTGA	CGGAAGGCCT	GGACTATGGC	8700
	TTTATGAAGG	AAGTAACATT	CCACTGTGAC	GAGGGCTACA	TCTTGCACGG	TGCTCCAAAA	8760
	CTACCTGTGC	AGTCAGATGC	CAACTGGGAT	GCAGAGATTC	CTCTCTGTAA	ACCACTCAAC	8820
	TGTGGACCTC	CTGAAGATCT	TGCCCATGGT	TTCCCTAATG	GTTTTCTCCT	TATTCTATGG	8880
	GGCCATATAC	AGTATCAGTG	CTTTCCTGGT	TATAAGCTCC	ATGGAATTC	ATCAAGAAGG	8940
25	TGCCCTCTCA	ATGGCTCCTG	GAGTGGCAGC	TCACCTTCCT	GCCTGCCTTG	CAGATGTTCC	9000
	ACACCAAGTA	TTGAATATGG	AAGTGTCAAT	GGGACAGATT	TTGACTGTGG	AAAGGCAGCC	9060
	CGGATTTCAG	GCTTCAAGAG	CTTCAAGCTC	CTAGGACTTT	CTGAATACAC	CTGTGAAGCC	9120
	GATGGCCAGT	GGAGCTCTGG	GTTCCCCCAC	TGTGAACACA	CTTCTTGTGG	TCTCTTCCA	9180
	ATGATACCAA	ATGCGTTTAT	CAGTGAGACC	AGCTCTTGGA	AGGAAAATGT	GATAACTTAC	9240
	AGCTGCAGGT	CTGGATATGT	CATACAAGGC	AGTTCAGATC	TGATTTGTAC	AGAGAAAGGG	9300
30	GTATGGAGCC	AGCCTTATCC	AGTCTGTGAG	CCCTTGTCCCT	GTGGGTCCCC	ACCGTCTGTC	9360
	GCCAAATGCAG	TGGCAACTGG	AGAGGCACAC	ACCTATGAAA	GTGAAGTGAA	ACTCAGATGT	9420
	CTGGAAGGTT	ATACGATGGA	TACAGATACA	GATACATTCA	CCTGTGAGAA	AGATGGTCGC	9480
	TGCTTCCCTG	AGAGAATCTC	CTGCAGTCCT	AAAAAATGTC	CTCTCCCGGA	AAACATAACA	9540
	CATATACTTG	TACATGGGGA	CGATTTTCACT	GTGAATAGGC	AAGTTTCTGT	GTCATGTGCA	9600
35	GAAGGGTATA	CCTTTGAGGG	AGTTAACATA	TCAGTATGTC	AGCTTGATGG	AACCTGGGAG	9660
	CCACCATTCT	CCGATGAATC	TTGCAGTCCA	GTTTCTTGTG	GGAAACCTGA	AAGTCCAGAA	9720
	CATGGATTTG	TGTTTGGCAG	TAAATACACC	TTTGAAGACA	CAATTATTTA	TCAGTGTGAG	9780
	CCTGGCTATG	AAGTAGAGGG	GAACAGGGAA	CGTGTCTGCC	AGGAGAACAG	ACAGTGGAGT	9840
	GGAGGGGTGG	CAATATGCAA	AGAGACCAGG	TGTGAACTC	CACCTGAAAT	TCTCAATGGG	9900
40	AAAGCTGACA	TTGAAAACAG	GACGACTGGA	CCCAACGTGG	TATATTCTCT	CAACAGAGGC	9960
	TACAGCTCTG	AAGGGCCATC	TGAGGCACAC	TGCACAGAAA	ATGGAACCTG	GAGCCACCCA	10020
	GTCCCTCTCT	GCAAAACCAA	TCCATGCCCT	GTTCCCTTTG	TGATTCCCGA	GAATGCTCTG	10080
	CTGTCTGAAA	AGGAGTTTAA	TGTTGATCAG	AATGTGTCCA	TCAATGTAG	GGAAGGTTTT	10140
	CTGCTGCAGG	GCCACGGCAT	CATTACCTGC	AACCCCGACG	AGACGTGGAC	ACAGACAAGC	10200
45	GCCAAATGTG	AAAAAATCTC	ATGTGGTCCA	CCAGCTCAGC	TAGAAAATGC	AATTGCTCGA	10260
	GGCGTACATT	ATCAATATGG	AGACATGATC	ACCTACTCAT	GTTACAGTGG	ATACATGTTG	10320
	GAGGGTTTCC	TGAGGAGTGT	TTGTTTAGAA	AATGGAACAT	GGACATCACC	TCTTATTTCG	10380
	AGAGCTGTCT	GTCGATTTCC	ATGTCAGAAT	GGGGGCATCT	GCCAACGCCC	AAATGCTTGT	10440
	TCCTGTCCAG	AGGGCTGGAT	GGGGCGCCTC	TGTGAAGAAC	CAATCTGCAT	TCTTCCCTGT	10500
50	CTGAACGGAG	GTGCTGTGTG	GGCCCTTATC	CAGTGTGACT	CCCGCCCTGG	CTGGACGGGG	10560
	TCTCGCTGTC	ATACAGCTGT	TTGCCAGTCT	CCCTGCTTAA	ATGGTGGAAA	ATGTGTGAAG	10620
	CCAAACCGAT	GTCACGTGCT	TTCTTCTTGG	ACGGGACATA	ACTGTTCCAG	GTAA	10674

Seq ID NO: C135 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..390

	1	11	21	31	41	51	
60	ATGAGGTTC	GTGCTCAGG	CATGAGGACC	GACTACCCCA	GGAGTGTGCT	GGCTCTGCT	60
	TATGTGTGAG	TCTGTCTCCT	CCTCTTGTGT	CCAAGGGGAG	TCATCGCTCC	CGCTGGCTCA	120
	GAACCATGGC	TGTGCCAGCC	GGCACCCAGG	TGTGGAGACA	AGATCTACAA	CCCCTTGGAG	180
	CAGTGTCTGT	ACAATGACGC	CATCGTGTCC	CTGAGCGAGA	CCCGCCAATG	TGGTCCCCCC	240
65	TGCACCTTCT	GGCCCTGCTT	TGAGCTCTGC	TGTCTTGATT	CCTTGGCCT	CACAAACGAT	300
	TTTGTGTGTA	AGCTGAAGGT	TCAGGGTGTG	AATTCCCAGT	GCCACTCATC	TCCCATCTCC	360
	AGTAAATGTG	AAAGAGGCCG	GATATGTTAG				390

Seq ID NO: C136 DNA Sequence  
Nucleic Acid Accession #: BC035671.1  
Coding sequence: 126..1745

	1	11	21	31	41	51	
75	GGCAGCGACT	GCGCCCCGTC	CCGGCGCCGC	GCTCGTCCGC	AGAGGAGGCG	GCCCGGCCCG	60
	GGCAGCTGCG	GCTCGGGATC	CGTCGAGGGG	AGGCGGAGCT	TGCCAAGCTG	GCGCCAGCG	120
	GGGTGATGGT	GCCCGCGGCC	CGCGCGCGCG	GCGCACTGGC	GCGGGCTGCC	GGGCGGGGCC	180
	TCCTGGCTTT	GCTGCTCGCG	GTCTCCGCCC	CGCTCCGGCT	GCAGGCGGAG	GAGCTGGGTG	240
	ATGGCTGTGG	ACACCTAGTG	ACTTATCAGG	ATAGTGGCAC	AATGACATCT	AAGAATTATC	300
80	CCGGGACCTA	CCCCAATCAC	ACTGTTTGCG	AAAAGACAAT	TACAGTACCA	AAGGGGAAAA	360
	GACTGATTCT	GAGGTGCGGA	GATTTGGATA	TCGAATCCCA	GACCTGTGCT	TCTGACTATC	420
	TTCTCTTAC	CAGCTTCTCA	GATCAATATG	GTCCATACTG	TGGAAGTATG	ACTGTTCCCA	480
	AAGAACTCTE	GTTGAACACA	AGTGAAGTAA	CCGTCCGCTT	TGAGAGTGA	TCCCACTTTT	540
	CTGGCCGGGG	TTTTTTGCTG	ACCTATGCGA	GCAGCGACCA	TCCAGATTGA	ATAACATGTT	600

5	TGGAACGAGC TAGCCATTAT TTGAAGACAG AATACAGCAA ATTCTGCCCA GCTGGTTGTA 660
	GAGACGTAGC AGGAGACATT TCTGGGAATA TGGTAGATGG ATATAGAGAT ACCTCTTTAT 720
	TGTGCAAAGC TGCCATCCAT GCAGGAATAA TTGCTGATGA ACTAGGTGGC CAGATCAGTG 780
	TGCTTCAGCG CAAGGGGATC AGTCGATATG AAGGGATTCT GGCCAATGGT GTTCTTTCTGA 840
	GGGATGGTTC CCTGTGACAG AAGCGATTTC TGTTTACCTC CAATGGTTGC AGCAGATCCT 900
	TGAGTTTGA ACCTGACGGG CAAATCAGAG CTTCTTCTC ATGGCAGTCG GTCAATGAGA 960
	GTGGAGACCA AGTTCACCTG TCTCTGGCC AAGCCCGACT TCAGGACCAA GGCCCATCAT 1020
	GGGCTTCGGG CGACAGTAGC AACAAACCACA AACCACGAGA GTGGCTGGAG ATCGATTGG 1080
10	GGGAGAAAAA GAAATAACA GGAATTAGGA CCACAGGATC TACACAGTCG AACTTCAACT 1140
	TTTATGTTAA GAGTTTGTG ATGAACCTCA AAAACAATAA TTCTAAGTGG AAGACCTATA 1200
	AAGGAATTGT GAATAATGAA GAAAAGGTGT TTCAGGGTAA CTCTAACTTT CGGGACCCAG 1260
	TGCAAAACAA TTTTCATCCCT CCCATCGTGG CCAGATATGT GCGGGTTGTC CCCAGACAT 1320
	GGCACCAGAG GATAGCCTTG AAGGTGGAGC TCATTGGTTG CCAGATTACA CAAGGTAATG 1380
15	ATTCATTGGT GTGGCGCAAG ACAAGTCAA GCACCAGTGT TCAACTAAG AAAGAAGATG 1440
	AGACAATCAC AAGGCCATC CCTCGGAAG AAACATCCAC AGGAATAAAC ATTACAACGG 1500
	TGGCTATTCC ATTGGTGCTC CTGTGTGTC TGGTGTGGG ATCTTTGCG 1560
	CTTTTAGAAA GAGAAGAGG AAGGGAAGTC CGTATGGATC AGCAGAGGCT CAGAAAACAG 1620
	ACTGTGGGAA GCAGATTAA TATCCCTTTG CCAGACATCA GTCAGTGGAG TTTACCATCA 1680
20	GCTATGATAA TGAGAAGGAG ATGACACAAA AGTTAGATCT CATCACAGT GATATGGCAG 1740
	GTTAACTCCG TTGACTGCCA AAATAGCATC CCCAACGTGC AGCCCTCCGC ATCTATCAGC 1800
	AGGTGCCCC GGTGCGATC CAGAGATGAG GATCGGAACA CCATGTCTT TCCCACCCTA 1860
	ACAACAACAA AGGCGAGTAA ATTAAGTAC TCTTTGTAAG GTACAGTTAC CGATTATCT 1920
	AGAGATAAAA TATTTTCTTA AAAATATATT TCATTAAACA CCTATGCTGT CTCTATAAAA 1980
25	AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2010

Seq ID NO: C137 DNA Sequence  
Nucleic Acid Accession #: Bos sequence  
Coding sequence: 1..1761

30	1 11 21 31 41 51
	ATGGGATTTC GTGCGGGGCA GCGACTGCGC CCCGTCCCGG CGCCGCGCTC GTCCGCGAGAG 60
	GAGGCGGGCC GGCCCGGGCA GCTGCGGCTC GGGATCCGTC GAGGGGAGGC CGAGCTTGCC 120
	AAGCTGGGCG CCACCGGGGT CATGGTGCCC GCGCGCCGCG GCGCGCGCGC ACTGGCGCGG 180
35	GCTGCGGGGC GGGGCTCCT GGCCTTGCTG CTCGCGGTCT CCGCCCGCT CCGGCTGCAG 240
	GCGGAGGAGC TGGGTGATGG CTGTGGACAC CTAGTGACTT ATCAGGATAG TGGCACAATG 300
	ACATCTAAGA ATTATCCCGG GACCTACCCC AATCACACTG TTTGCGAAAA GACAATTACA 360
	GTACCAAGAG GGAAAGAGT GATTCTGAGG TTGGGAGATT TGGATATCGA ATCCCAGACC 420
	TGTGCTTCTG ACTATCTTCT CTTCAACAGC TCTTCAGATC AATATGGTCC ATACTGTGGA 480
40	AGTATGACTG TTCCCAAAGA ACTCTGTGTG AACACAAGTG AAGTAACCGT CCGCTTTGAG 540
	AGTGGATCCC ACATTTCTGG CCGGGGTTTT TTGCTGACCT ATGCGAGCAG CGACCATCCA 600
	GATTTAATAA CATGTTTGGA ACGAGCTAGC CATTATTTGA AGACAGAATA CAGCAAATTC 660
	TGCCCAGCTG GTTGTAGAGA CGTAGCAGGA GACATTTCTG GGAATATGGT AGATGGATAT 720
	AGAGATACCT CTTTATTGTC CAAAGCTGCC ATCCATGCAG GAATAATTGC TGATGAACATA 780
45	GGTGGCCAGA TCAGTGTGCT TCAGCGCAAA GGGATCAGTC GATATGAAGG GATTCTGGCC 840
	AATGGTGTTC TTTGAGGGA TGGTTCCCTG TCAGACAAGC GATTCTGTGT TACCTCCAAT 900
	GGTTGCAGCA GATCCTTGAG TTTGAACTT GACGGGCAAA TCAGAGCTTC TTTCTCATGG 960
	CAGTCGGTCA ATGAGAGTGG AGACCAAGTT CACTGGTCTC CTGGCCAAGC CCGACTTCAG 1020
	GACCAAGGCC CATCATGGGC TTCGGGGCAG AGTAGCAACA ACCACAACC ACGAGAGTGG 1080
50	CTGGAGATCG ATTTGGGGGA GAAAAAGAAA ATAACAGGAA TTAGGACCAC AGGATCTACA 1140
	CAGTCGAAC TCACTTTTAA TGTAAAGAGT TTTGTGATGA ACTTCAAAAA CAATAATTCT 1200
	AAGTGAAGA CCTATAAAGG AATTGTGAAT AATGAAGAAA AGGTGTTTCA GGGTAACTCT 1260
	AACCTTCGGG ACCCAGTGCA AAACAATTTC ATCCCTCCCA TCGTGGGCCAG ATATGTGCGG 1320
	GTTGTCCCCC AGACATGGCA CCAGAGGATA GCCTTGAAGG TGGAGCTCAT TGGTTGCCAG 1380
55	ATTACACAA GTAATGATTC ATTGGTGTGG CGCAAGACAA GTCAAAGCAC CAGTGTTCAT 1440
	ACTAAGAAAG AAGATGAGAC AATCACAAGG CCCATCCCTT CGGAAGAAAC ATCCACAGGA 1500
	ATAAACATTA CAACGGTGGC TATTCATATG GTGCTCCTTG TTGTCTGGT GTTTGCTGGA 1560
	ATGGGGATCT TTGCGACCTT TAGAAGAAG AAGAAGAAG GAAGTCCGTA TGGATCAGCA 1620
	GAGGCTCAGA AACACAGACT TTGGAAGCAG ATTAATATC CCTTGCCAG ACATCAGTCA 1680
60	GCTGAGTTTA CCATCAGCTA TGATAATGAG AAGGAGATGA CACAAAAGTT AGATCTCATC 1740
	ACAAGTGATA TGGCAGGTTA A 1761

Seq ID NO: C138 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..2310

65	1 11 21 31 41 51
	ATGTTCCAGC GGCAGGAAAG ATTTCTTGAC TTATCTTCAG CTGAAGCAGT GGCAGCTTGG 60
	ATATTACATC AACATCCTGA CATTATTAAC AAAGGTGATG GCTGTGGACA CCTAGTGACT 120
	TATCAGGATA GTGGCACAAT GACATCTAAG AATTATCCCG GGACCTACCC CAATCACACT 180
	GTTTGCAGAA AGACAATTAC AGTACCAAAG GGGAAAGAC TGATTCTGAG GTTGGGAGAT 240
	TTGGATATCG AATCCAGAC CTGTGCTTCT GACTATCTTC TCTTCACCAG CTCTTCAGAT 300
70	CAATATGGAA TGCAGGAAGG GGAGGAGACA GAAGTGCTTT GTCTTTCAGT GGCTGGCGCT 360
	CAGAGAGTGG ACATTCCTGT GCAGCTGTGG CCCAGCTTCC TGGAAAGGTTG GAAGGGTCAT 420
	GCTGATGCAA GAGGTCCATA CTGTGGAAGT ATGACTGTTC CCAAGAAGT CTGTGTGAAC 480
	ACAAGTGAAG TAACGTCCTG CTTTGAGAGT GGATCCACA TTTCTGGCCG GGGTTTTTTG 540
	CTGACCTATG CGAGCAGCGA CCATCCAGAT TTAATAACAT GTTTGGAACG AGCTAGCCAT 600
	TATTTGAAGA CAGAATACAG CAAATTCTGC CCAGCTGGTT GTAGAGACGT AGCAGGAGAC 660
80	ATTTCTGGGA ATATGTGATA TGGATATAGA GATACCTCTT TATTTGTCAA AGCTGCCATC 720
	CATGCAGGAA TAAATTCTGA TGAACAGGT GGCCAGATCA GTGTGCTTCA GCGCAAAGGG 780
	ATCAGTCGAT ATGAAGGGAT TCTGGCCAAT GGTGTTCTTT CGAGGGATGG TTCCCTGTCA 840
	GACAAGCGAT TTCTGTTTAC CTCCAATGGT TGCAGCAGAT CCTTGAGTTT TGAACCTGAC 900
	GGGCAAACTA GAGCTTCTTC CTCATGGCAG TCGGTCAATG AGAGTGGAGA CCAAGTTTCA 960

TGGTCTCTCTG GCCAAGCCCG ACTTCAGGAC CAAGGCCCAT CATGGGCTTC GGGCGACAGT 1020  
 AGCAACAACC ACAAACCACG AGAGTGGCTG GAGATCGATT TGGGGGAGAA AAAGAAAATA 1080  
 ACAGGAATTA GGACCACAGG ATCTACACAG TCGAATTCA ACTTTTATGT TAAGAGTTTT 1140  
 GTGATGAAC TCAAAAACAA TAATTCTAAG TGAAGACCT ATAAAGGAAT TGTGAATAAT 1200  
 GAAGAAAAGG TGTTCAGGG TAACTCTAAC TTTCGGGACC CAGTGCAAAA CAATTTTCATC 1260  
 CCTCCCATCG TGGCCAGATA TGTGCGGTT GTCCCCAGA CATGGCACC AAGGATAGCC 1320  
 TTGAAGGTGG AGCTCATTGG TTGCCAGATT ACACAAGGTA ATGATTCATT GGTGTGGCGC 1380  
 AAGACAAGTC AAAGCACCGG TGTTCAACT AAGAAAGAAG ATGAGACAAT CACAAGGCCG 1440  
 ATCCCCCTCG AAGAAACATC CACAGATGCC ATGCCAGTGC AGATTGTCCG AGACCATAAC 1500  
 CAGATGATCT CACAAAGGGA GAATCTGGGA CCTGATGAGG GCAAAATACC TTTTAAAGGC 1560  
 ACAGCGGAAA GCATGGTTAG AGTAGTGTTC GCTGTGTGG TTAATGACCT TGGCATGCTG 1620  
 TTCTTAGCAC ACACACTGGA GAGGACATT GATCACTACT GTTGGAGCA GATTAAATAT 1680  
 CCCTTTGCCA GACATCAGTC AGCTGAGTTT ACCATCAGCT ATGATAATGA GAAGGAGATG 1740  
 ACACAAAAGT TAGATCTCAT CACAAGTGAT ATGGCAGATT ACCAGCAGCC CCTCATGATT 1800  
 GGCACCGGGA CAGTCACGAG GAAGGGCTCC ACCTTCCGGC CCATGGACAC GGATGCCGAG 1860  
 GAGGCAGGGG TGCCGGCGGC CACTATGACT GCCCGCAGCG GGCCCGGCCG 1920  
 CAGGAGTACG CGCTGCCCTT GGCGCCCGG GAGCCCGAGT ACGCCACGCC CATCGTGGAG 1980  
 CGGCACGTGC TGGCGGCCCA CACGTTCTCT GCGCAGAGCG GCTACCGCGT CCCAGGGCCC 2040  
 CAGCCCGGCC ACAAACTCCT CCTCTCTCG GCGCGTCTT CCCCCGTAGC GGGTGTGGGC 2100  
 GCCCAGGACG GAGACTATCA AAGGCCACAC AGCGCACAGC CTGCGGACAG GGGCTACGAC 2160  
 CGGCCCAAAG CTGTACGCGC CCTCGCCACC GAAAGCGGGC ACCCTGACTC TCAGAAGCCC 2220  
 CCAACGCATC CCGGACGAG TGACAGCTAT TCTGCCCCA GAGACTGCCT CACACCCCTC 2280  
 AACCAGACGG CCATGACTGC CCTTTTGTGA 2310

Seq ID NO: C139 DNA Sequence  
 Nucleic Acid Accession #: NM\_004616.2  
 Coding sequence: 180..893

1 11 21 31 41 51  
 AGTGCCCCAG GAGCTATGAC AAGCAAAGGA ACATACTGCT CTGGAGATAG CCTTTGCGAT 60  
 ATTTAAATGT CCGTGGATAC AGAAATCTCT GCAGGCAAGT TGCTCCAGAG CATATTGCAG 120  
 GACAAGCCTG TAACGAATAG TTAATTCAC GGCATCTGGA TTCTTAATCC TTTCCGAAA 180  
 TGGCAGGTGT GAGTGCCTGT ATAAAATATT CTATGTTTAC CTTCAACTTC TTGTTCTGGC 240  
 TATGTGGTAT CTTGATCCTA GCATTAGCAA TATGGGTACG AGTAAGCAAT GACTCTCAAG 300  
 CAATTTTGG TTCTGAAGAT GTAGGCTCTA GCTCCTACGT TGCTGTGGAC ATATTGATTG 360  
 CTGTAGGTGT CATCATCATG ATTCTGGGCT TCCTGGGATG CTGCGGTGCT ATAAAAGAAA 420  
 GTCGCTGCAT GCTTCTGTTG TTTTTCATAG GCTTGCTTCT GATCCTGCTC CTGCAAGTGG 480  
 CGACAGGTAT CCTAGGAGCT GTTTTCAAAT CTAAGTCTGA TCGCATTGTG AATGAAACTC 540  
 TCTATGAAA CACAAAGCTT TTGAGCGCCA CAGGGGAAAG TGA AAAACAA TTCCAGGAAG 600  
 CCATAATGT GTTTCAAGAA GAGTTTAAAT GCTGCGGTTT GGTCAATGGA GCTGCTGATT 660  
 GGGGAAATAA TTTTCAACAC TATCTGAAT TATGTGCTGT TCTAGATAAG CAGAGACCAT 720  
 GCCAAAGCTA TAATGGAAAA CAAGTTTACA AAGAGACCTG TATTTCTTTC ATAAAAGACT 780  
 TCTTGGCAAA AATTTGATT ATAGTTATTG GAATATCATT TGGACTGGCA GTTATTGAGA 840  
 TACTGGGTTT GGTGTTTTCT ATGGTCTGT ATTGCCAGAT CGGGAACAAA TGAATCTGTG 900  
 GATGCATCAA CCTATCGTCA GTCAAACCCC TTTAAATGT TGCTTTGGCT TTGTAAATTT 960  
 AAATATGTA GTGCTATATA AGTCAGGAGC AGCTGTCTTT TTAATAATGTC TCGGCTAGCT 1020  
 AGACCACAGA TATCTTCTAG ACATATTGAA CACATTTAAG ATTTGAGGGA TATAAGGGAA 1080  
 AATGATATGA ATGTGTAATT TTACTCAAAA TAAAAGTAAC TGTTTACGTT AAAAAAATA 1140  
 AAAAAAATA AAAAAAATA 1159

Seq ID NO: C140 DNA Sequence  
 Nucleic Acid Accession #: NM\_004617.2  
 Coding sequence: 232..840

1 11 21 31 41 51  
 CTTCAAGTCA GGGAGAATGT ATAAATGTCC ATTGCCATCG AGGTTCTGCT ATTTTGGAGA 60  
 AGCTGAAGCA ACTCCAAGGA CACAGTTTCA AGAAATTTGG TTCTCAGCCC CAAAATACTG 120  
 ATTGAATTGG AGACAATTAC AAGGACTCTC TGGCCAAAAA CCCTTGAAGA GGCCCGTGA 180  
 AGGAGGCAGT GAGGAGCTTT TGATGTCTGA CCTGTGTGCT ACCACCCAG AATGTGCACT 240  
 GGGGGCTGTG CCAGATGCCCT GGGGGGGACC CTCATTCCTT TGCTTTTCTT TGGCTTCCTG 300  
 GCTAACATCC TGTATTTTTT TCCTGGAGGA AAAGTGATAG ATGACAAAGA CCACCTTTCC 360  
 CAAGAGATCT GGTTTTTTCG AGGAATATTA GGAAGCGGTG TCTTGATGAT CTTCCCTGCG 420  
 CTGGTGTCTT TGGGCTGAA GAACAATGAC TGCTGTGGGT GCTGCGGCAA CGAGGGCTGT 480  
 GGAAGCGAT TTGCGATGTT CACCTCCACG ATATTGCTG TGGTTGGATT CTTGGGAGCT 540  
 GGATACTCGT TTATCATCTC AGCCATTTCA ATCAACAAGG GTCCTAAATG CCTCATGGCC 600  
 AATAGTACAT GGGGCTACCC CTTCCACGAC GGGGATTATC TCAATGATGA GGCCATTATG 660  
 AACAAAGTGC GAGAGCTCT CAATGTGGTT CCCTGGAATC TGACCCTCTT CTCCATCCTG 720  
 CTGGTGTGAG GAGGAATCCA GATGGTTCTC TGCGCCATCC AGGTGGTCAA TGGCCTCCTG 780  
 GGGACCTCT GTGGGGACTG CCAGTGTGTG GGTGCTGTG GGGGAGATGG ACCCGTTTAA 840  
 ACCTCCGAGA TGAGCTGCTC AGACTCTACA GCATGACGAC TACAATTTCT TTTCAATAAA 900  
 CTTCTTCTCT TCTTGAATT ATTAATTCCT ATCTGCTTCC TAGCTGATAA AGCTTAGAAA 960  
 AGGCAGTTAT TCTCTTTTC CAACAGCTT TGCTCGAGTT AGAATTTTGT TATTTTCAA 1020  
 TAAAAAATAG TTTGGCCACT TAACAAATTT GATTTATAAA TCTTTCAAAT TAGTTCCTTT 1080  
 TTGAATTTA CCAACAGGTT CAAAGCATA TTTTCATGAT TTTTATTA CAAATGTAAA 1140  
 ATGTATAAAG TCACATGTAC TGCCATACTA CTTCTTTGTA TATAAAGATG TTTATATCTT 1200  
 TGAAGTTTT ACATAAATCA AAGGAAGAAA GCACATTTAA AATGAGAAAC TAAGACCAAT 1260  
 TCTGTTTTT AAGAGGAAA AGAATGATTG ATGTATCCTA AGTATTGTTA TTTGTGTCT 1320  
 TTTTGTGCTG CTTGCTTGA GTTGCTGTG ACTGATCTTT TGAGGCTGTC ATCATGGCTA 1380  
 GGGTCTTTTT ATGTATGTTA AATTAAACC TGAATTCAGA GGTAACTG 1428

Seq ID NO: C141 DNA Sequence  
 Nucleic Acid Accession #: NM\_002381.2

Coding sequence: 64..1524

```

1      11      21      31      41      51
5      |      |      |      |      |
AAATCCGAGC CTCGCGTGGG CTCCTGGCCC CCGACGGACA CCACCAGGCC CACGGAGCCC 60
ACCATGCCGC GCCCGGCCCC CGCGCGCCGC CTCCTGGGAC TCCTCTCTGT GCTCTGGCCG 120
CTGCTGCTGC TGCCTCCCGC CGCCCCCGAC CCGCTGGCCC GCCCGGGCTT CCGGAGGCTG 180
GAGACCCGAG GTCCCGGGGG CAGCCCTGGA CGCCGCCCTT CTCCTGCGGC TCCCGACGGC 240
GCGCCCGCTT CCGGGACCAG CGAGCCTGGC CGCGCCCGCG GTGCAGGTGT TTGCAAGAGC 300
AGACCTTGGG ACCTGGTGT TATCATTGAT AGTTCTCGTA GCGTACGGCC CCTGGAATTC 360
ACCAAAGTGA AAACTTTTGT CTCCTGGATA ATCGACACTC TGGACATTGG GCCAGCCGAC 420
ACGCGGGTGG CAGTGGTGAA CTATGCTAGC ACTGTGAAGA TCGAGTTCCA ACTCCAGGCC 480
TACACAGATA AGCAGTCCCT GAAGCAGGCT GTGGGTCGAA TCACACCCTT GTCAACAGGC 540
ACCATGTGAG GCCTAGCCAT CCAGACAGCA ATGGACGAAG CCTTCACAGT GGAGGCAGGG 600
15      GCTCGAGAGC CCTCTTCTAA CATCCCTAAG GTGGCCATCA TTGTTACAGA TGGGAGGCC 660
CAGGACCAAG TGAATGAAGT GGCGGCTCGG GCCCAAGCAT CTGGTATTGA GCTCTATGCT 720
GTGGGCGTGG ACCGGGCAGA CATGGCGTCC CTCGAAGTGA TGGCCAGTGA GCCCTAGAG 780
GAGCATGTTT TCTACGTGGA GACCTATGGG GTCATTGAGA AACTTTCCTC TAGATTCCAG 840
20      GAAACCTTCT GTGCGCTGGA CCCCTGTGTG CTTGGAACAC ACCAGTGCCA GCACGCTCTGC 900
ATCAGTGATG GGGAGGGCAA GCACCACTGT GAGTGTAGCC AAGGATACAC CTTGAATGCC 960
GACAAGAAAA CGTGTTCAGC TCTTGATAGG TGTGCTCTTA ACACCCACGG ATGTGAGCAC 1020
ATCTGTGTGA ATGACAGAAG TGGCTCTTAT CATTGTGAGT GCTATGAAGG TTATACCTTG 1080
AATGAAGACA GGAAAACTTG TTCAGCTCAA GATAAATGTG CTTTGGGTAC CCATGGGTGT 1140
25      CAGCACATTG GTGTGAATGA CAGAACAGGG TCCCATCATT GTGAATGCTA TGAGGGCTAC 1200
ACTCTGAATG CAGATAAAAA AACATGTTCA GTCCGTGACA AGTGTGCCCT AGGCTCTCAT 1260
GGTGTCCAGC ACATTGTGTG GAGTGATGGG GCCGCATCCT ACCACTGTGA TTGCTATCCT 1320
GGCTACACCT TAAATGAGGA CAAGAAAAACA TGTTCAGCCA CTGAGGAAGC ACGAAGACTT 1380
GTTTCCACTG AAGATGCTTG TGGATGTGAA GCTACACTGG CATTCCAGGA CAAGGTCAGC 1440
TCGTATCTTC AAAGACTGAA CACTAAACTT GATGACATTT TGGAGAAAGT GAAAATAAAT 1500
30      GAATATGGAC AAATACATCG TTAATTTGCT CCAATTTCTC ACCTGAAAAA GTGGACAGCT 1560
TGGTGTACTT AATACTCATG CATTCTTTTG CACACCTGTT ATTGCCAATG TTCCTGCTAA 1620
TAATTTGCCA TTATCTGTAT TAATGCTTGA ATATTACTGG ATAAATTGTA TGAAGATCTT 1680
CTGCAGAATC AGCATGATTT TTCCAAGGAA ATACATATGC AGATACTTAT TAAGAGCAAA 1740
CTTTAGTGTG TCTAAGTTAT GACTGTGAAA TGATTGGTAG GAAATAGAAT GAAAAGTTTA 1800
35      GTGTTTCTTT ATCTACTAAT TGAGCCATT TAAATTTTAA TGTTTATATT AGATAACCAT 1860
ATTCACAATG GAAACTTTAG GTCTAGTTTC TTTTGATAGT ATTTATAATA TAAATCAATC 1920
TTATTACTGA GAGTGCAAAT TGTACAAAGT ATTTACACAT ACAACTTCAT ATAACCTAGA 1980
TGAATGTAAT TTTGAACTGT TTAACACTTT TTTGTTTTTG CTATTTTGTG TGGAGTATTA 2040
40      TTGAAGATGT GATCAATAGA TTGTAATACA CATATCTAAA AATAGTTAAC ACAGATCAAG 2100
TGAACATTAC ATTGCCATTT TTAATTCATT CTGGTCTTTG AAAGAAATGT ACTACTAAAG 2160
AGCACTAGTT GTGAATTTAG GGTGTTAAAC TTTTACCATA GTACAAAAAT CCCAATTCA 2220
CTTTATTATT TTGCTTCAGG ATCCAAGTGA CAAAGTTATA TATTTATAAA ATTGCTATAA 2280
ATCGACAAAA TCTAATGTTG TCTTTTAAAT GTTAGTGATC CACCTGCCCT AGCCTCCCAA 2340
45      AGTGTCTGGG TTACAGGCTT GAAAGTCTAA CTTTTTTTAA CTTATATATT TGATACATAT 2400
AATTTCTTTG TTGCAACTTT TGCAACTTTT GAGAAACAAA CAGTCCCTTA AATTTTGAC 2460
TGCTCAATTC TGTTTTTCGT TTGCATTGTC TTTAATATAA TAAAGATTAT TACCTTTACA 2520
TATTATCATG TCTATTTTGT ATGACTCATC AATTTTGTCT ATTAAGATA TTTCTTTAAA 2580
TTAAAAAAA AAAAAAAA 2599

```

Seq ID NO: C142 DNA Sequence  
Nucleic Acid Accession #: NM\_016639.1  
Coding sequence: 40..429

```

1      11      21      31      41      51
55      |      |      |      |      |
GCGGCGGGCG CAGACAGCGG CGGGCGCAGG ACGTGCACTA TGGCTCGGGG CTCGCTGCGC 60
CGGTTGCTGC GGGTCCCTCGT GCTGGGGCTC TGGCTGGCGT TGCTGCGCTC CGTGGCCGGG 120
GAGCAAGCGC CAGCAGCCGC CCCCTGCTCC CGCGGCAGCT CCTGGAGCGC GGACCTGGAC 180
60      AAGTGCATGG ACTGCGCGTC TTGCAGGCGC CGACCGCACA GCGACTTCTG CCTGGGCTGC 240
GCTGCAGCAC CTCCTGCCCC CTTCCGGCTG CTTTGGCCCA TCCTTGGGGG CGCTCTGAGC 300
CTGACCTTCG TGCTGGGGCT GCTTCTGTGC TTTTGTGTCT GGAGACGATG CCGCAGGAGA 360
GAGAAGTTCA CCACCCCAT AGAGGAGACC GCGGAGAGG GCTGCCAGC TGTGGCGCTG 420
65      ATCCAGTGAC AATGTGCCCC CTGCCAGCCG GGGCTCGCCC ACTCATCATT CATTCATCCA 480
TTCTAGAGCC AGTCTCTGCC TCCAGACGC GCGGGGAGCC AAGCTCCTCC AACCACAAGG 540
GGGGTGGGGG GCGGTGAATC ACCTCTGAGG CCTGGGCCCA GGGTTCAGGG GAACCTTCCA 600
AGGTGTCTGG TTGCCCTGCC TCTGGCTCCA GAACAGAAAG GGAGCCTCAC GCTGGCTCAC 660
ACAAAACAGC TGACACTGAC TAAGGAACGT CAGCATTGTC ACAGGGGAGG GGGGTGCCCT 720
70      CCTTCTCTAG GACCTGGGGG CCAGGCTGAC TTGGGGGGCA GACTTGACAC TAGGCCCCAC 780
TCACTCAGAT GTCTGAAAT TCCACCACGG GGGTCACCCT GGGGGGTTAG GGACCTATTT 840
TTAACACTAG GGGCTGGCCC ACTAGGAGGG CTGGCCCTAA GATACAGACC CCCCACCTC 900
CCCAAGCGG GGAGGAGATA TTTATTTTGG GGAGAGTTTG GAGGGGAGGG AGAATTTATT 960
AATAAAGAA TCTTTAAGT TAAAAAATA AAAAAAAA 998

```

Seq ID NO: C143 DNA Sequence  
Nucleic Acid Accession #: NM\_001819  
Coding sequence: 113..2146

```

1      11      21      31      41      51
80      |      |      |      |      |
CCAGGAGGCA CGTGGTTTT CCGGGGCCGC TCCATCGCGC CTCTCTCTG CGCCTCGCTT 60
CTCCGGTCCA GCCGCCATCT TCCTTTCCGC ACAGGGGCGG CCGAGCGGGG CCATGCAGCC 120
AACGCTGCTT CTCAGCCTCC TGGGAGCCGT GGGGCTGGCG GCTGTCAATT CCATGCCAGT 180
GGATAACAGG AACCACCAATG AAGGAATGGT GACTCGCTGC ATCATTGAGG TCCTCTCAAA 240

```



5	TGCCTTGTCG	AAGTCCAGCG	CTCCACCCAT	CACCCCTGAG	TGCCGCCAAG	TCCTGAAGAC	300
	GAGTAGAAAA	GACGTCAAAG	ACAAAGAGAC	AACTGAAAT	GAAAACACAA	AGTTTGAAGT	360
	AAGATTGTTA	AGAGACCCAG	CTGATGCCCTC	GGAAGCCCAC	GAGTCTCTCA	GCAGGGGAGA	420
	GGCAGGAGCC	CCAGGGGAGG	AGGACATCCA	AGGCCCAACA	AAGGCAGACA	CAGAGAAATG	480
	GGCAGAGGGA	GGCGGGCACA	GCCGAGAGCG	AGCGGATGAG	CCCCAGTGGA	GCCTCTATCC	540
	CTCCGACAGC	CAAGTCTCTG	AAGAAGTGAA	GACACGCCAT	TCTGAGAAGA	GCCAGAGAGA	600
	GGATGAGGAG	GAGGAGGAGG	GAGAGAACTA	TCAAAAAGGG	GAGCGAGGGG	AAGATAGCAG	660
	TGAAGAGAAA	CACCTTGAAG	AGCCAGGAGA	GACACAAAAC	GCTTTTCTCA	ATGAAAGAAA	720
	GCAGGCTTCA	GCTATAAAAA	AAGAGGAGTT	AGTGGCCAGA	TCGGAAACAC	ATGCTGCCCG	780
10	GCATTCTCAG	GAGAGACAC	ATAGCCGAGA	GAAGAGTAGC	CAGGAGAGTG	GAGAGGAGGC	840
	AGGGAGCCAG	GAGAATCACC	CCCAGGAGTC	TAAAGGCCAA	CCCCGAAGCC	AGGAAGAATC	900
	TGAGGAAGGT	GAGGAAGATG	CCACCTCTGA	GGTGGACAAA	CGACGCACGA	GGCCCCAGCA	960
	CCACCACGGG	AGGAGCAGGC	CCGACAGGTC	CTCTCAAGGA	GGGAGTCTTC	CCTCTGAGGA	1020
	AAAGGGACAC	CCCCAGGAGG	AATCTGAGGA	GTCAAACGTC	AGCATGGCCA	GTTTAGGGGA	1080
15	AAAGAGGGAC	CACCATTCAA	CCCACTACAG	GGCTTCAGAG	GAAGAACCTG	AATATGGAGA	1140
	AGAAATAAAG	GGTTATCCAG	CGGTCCAGGC	CCCTGAGGAC	CTGGAGTGGG	AGCGCTATAG	1200
	GGGCAGAGGA	AGTGAAGAA	ACAGGGCTCC	AAGACCTCAG	AGTGAGGAGA	GTTGGGATGA	1260
	GGAGGACAAG	AGAACTACCT	CCAGCTTAGA	GCTTGATAAG	ATGGCACATG	GATATGGTGA	1320
	AGAAAGTGAG	GAAGAGAGGG	GCCTTGAGCC	GGGAAAGGGA	CGCCATCACA	GAGGCAGGGG	1380
20	AGGGGAGCCA	CGTGCTTATT	TCATGTCTGA	CACCAGAGAA	GAGAAAAGGT	TCTTGGGTGA	1440
	AGGACACCA	CGTGTCCAAG	AAAACAGAT	GGACAAGGCA	AGGAGGCATC	CACAAGGTGC	1500
	GTGGAAAGAG	CTGGACAGAA	ATTATCTCAA	CTACGGTGAG	GAAGGAGCCC	CAGGGAAGTG	1560
	GCAGCAGCAG	GGAGACCTCG	AGGACACTAA	AGAAAACAGG	GAGGAAGCTA	GTTTCAAGA	1620
25	TAAACAATAT	AGCTCCCATC	ACACAGCTGA	AAAGAGGAAG	AGATTAGGGG	AACTGTTCAA	1680
	CCCATACTAC	GACCCCTCTCC	AGTGGAAAGAG	CAGCCATTTT	GAAAGAAAGAG	ACAACATGAA	1740
	TGACAATTTT	CTCGAGGGTG	AGGAGGAAAA	TGAGCTGACC	TTGAACGAGA	AGAAATTTCT	1800
	CCCAGAATAC	AACATATGACT	GGTGGGAGAA	AAAGCCCTTC	TCTGAGGATG	TGAATGCGG	1860
	GTATGAGAAG	AGAAAACCTCG	CCAGGGTCCC	CAAGCTGGAC	CTGAAAAGGC	AATATGACAG	1920
30	GGTGGCCCAA	CTGGACACAG	TCCTTCACTA	CAGGAAGAAG	TCAGCTGAGT	TTCCAGACTT	1980
	CTATGATTCT	GAGGAGCCCG	TGAGCACCCA	CCAGGAGGCA	GAAAATGAAA	AGGACAGGGC	2040
	TGACCAGACA	GCTCTGACAG	AGGACGAGAA	AAAAGAAGCT	GAAAACCTGG	CTGCAATGGA	2100
	TTTGGAAGCTA	CAGAAGATAG	CTGAGAAATT	CAGCCAAAGG	GGCTGACTGT	CATTGGAGCG	2160
	GTGGGGCATG	TAAAGAAAGCA	GCCATCACAT	GATCTGTTTT	TCACCACTTC	ACTGAAAGAC	2220
35	ACCATTATAT	TACCCAAAGG	CAGAAAGTAG	AACTTACTAT	TCATTAAATG	TTTGACACAA	2280
	TTGGAATTGT	CTTTAATTTT	TGTCAGAAATG	CTATTGAAAA	TGTGAATTGC	ATGACTTGTA	2340
	GCATATTCTT	TTCTGCAAAA	TAGACATATT	AACATGCTTA	TGACAATGAC	TGTGCTACTG	2400
	TCTTTGGAAA	AATGTTTGTC	TCAGTTGGAA	ATAATAAAG	ATTCACCTGA	GACC	2454

Seq ID NO: C144 DNA Sequence  
Nucleic Acid Accession #: XM\_093082.1  
Coding sequence: 93..1988

45	1	11	21	31	41	51	
	CTTCTTGTTG	TAGGGACCTC	TCCTCAGTAT	TTGAAACTAA	CCAGCATCTG	ACAGATTTCTG	60
	AATTTGTAAA	AAATACCCCTC	GAAGATTTCAG	GAATGAAGCT	TCTGTGTGAA	GGATTAATAAC	120
	AGCCCAACTG	TGTATTACAG	ACATTGAGGT	GGTACCGGTG	CCTTATCTCT	TCGTCTTCTT	180
	GTGGGGCTCT	AGCAGCTGTT	CTTAGCACCA	GTCAGTGGCT	CAGTGAAGCTG	GAATTTAGTG	240
50	AGACAAAAT	GGAGGCTTCA	GCTTTGAAAT	TGCTCTATGG	AGGCTTAAAA	GATCCAAATT	300
	GCAAAATTACA	GAGGCTCAAC	TTGCAGTTTT	CTTTATCTGT	AACCGCTGCA	AAACTTCCAG	360
	TTGGAATGGT	TGGAATTTGT	TCTGGTTTCT	CGGGATCATT	GGTGAATCT	CATTTTGGCT	420
	ACTGTCCAGG	CAGTTCTTTC	AAATGTGATC	TTTGTAAGCT	GCTCTGGCCT	TCCACCAGAG	480
	TTGCTGCTGC	AAAGGATTGT	GGGAGTCTTA	AGTCCCTCCT	ATCAGAAGGG	CTGAACTGGG	540
55	CAGGAAGACT	TGAGGCACTG	GAGGAGGTTT	TGGGGTTGGG	GGTGTCTGTA	CAGCCCCGTG	600
	ACCCAGCATC	TCAGGGTGGG	GGGCATTGTG	AAAACATGAG	GTCTTTTAGA	GACTTGGTGG	660
	ACTTAGAAGT	CAAGGCAGAA	CCAAGCCTGA	GAAAAGGTGG	TATGGATCTC	CAGAGACCCA	720
	CCCTACAAGT	TGTCCTCTCT	TGCAAAATCT	TCTCCCTCAA	ACTATTTCTC	TTTATTGCAT	780
	TGCCATAATC	TCCTGGTCAG	GTTAGTGTGG	TGCAAGTGAC	CATCCCAGAC	GGTTTCGTGA	840
60	ACGTGACTGT	TGGATCTAAT	GTCACCTCTA	TCTGCATCTA	CACCACCACT	GTGGCCTCCC	900
	GAGAACAGCT	TTCCATCCAG	TGGTCTTTCT	TCCATAAGAA	GGAGATGGAG	CCAATTTCTT	960
	CTCCTTGGGA	GGAGGGGAAG	TGGCCAGATG	TTGAGGCTGT	GAAGGGCACT	CTTGATGGAC	1020
	AGCAGGCTGA	ACTCCAGATT	TACTTTTCTC	AAGGTGGACA	AGCTGTAGCC	ATCGGGCAAT	1080
	TTAAAGATCG	AATTACAGGG	TCCAACGATC	CAGGTAATGC	ATCTATCACT	ATCTCGCATA	1140
65	TGCAGCCAGC	AGACAGTGGG	ATTACATCT	GCGATGTTAA	CAACCCCCCA	GACTTTCTCG	1200
	GCCAAAACCA	AGGCATCTCT	AACGTCAGTG	TGTTAGTGAA	ACCTTCTAAG	CCCCTTTGTA	1260
	GCGTTCAAGG	AAGACCAGAA	ACTGGCCACA	CTATTTCCCT	TTCTGTCTCT	TCTGCGCTTG	1320
	GAACACCTTC	CCCTGTGTAC	TACTGGCATA	AACTTGAGGG	AAGAGACATC	GTGCCAGTGA	1380
	AAGAAAACCT	CAACCCCAAC	ACCGGGATT	TGGTCAATGG	AAATCTGACA	AATTTTGAAC	1440
70	AAGGTTATTA	CCAGTGTACT	GCCATCAACA	GACTTGGCAA	TAGTTCCTGC	GAAATCGATC	1500
	TCACTTCTTC	ACATCCAGAA	GTTGGAATCA	TTGTTGGGGC	CTTGATTGGT	AGCCTGGTAG	1560
	GTGCCGCCAT	CATCATCTCT	GTTGTGTGCT	TCGCAAGGAA	TAAAGCAAAA	GCAAAAGCAA	1620
	AAGAAAGAAA	TTCTAAGACC	ATCGCGGAAC	TTGAGCCAAT	GACAAAGATA	AACCAAGGG	1680
	GAGAAAGCGA	AGCAATGCCA	AGAGAAGACG	CTACCCAACT	AGAAGTAACT	CTACCATCTT	1740
75	CCATTTCATG	GACTGGGCCCT	GATACCATCC	AAGAACCAGA	CTATGAGCCA	AAGCCTACTC	1800
	AGGAGCCTGC	CCCAAGCCTT	GCCCCAGGAT	CAGAGCCTAT	GGCAGTGCCT	GACCTTGACA	1860
	TCGAGCTGGA	GCTGGAGCCA	GAAACGCACT	CGGAATTGGA	GCCAGAGCCA	GAGCCAGAGC	1920
	CAGAGTCAGA	GCTTGGGGTT	GTAGTTGAGC	CCTTAAGTGA	AGATGAAAAG	GGAGTGGTTA	1980
80	AGGCATAG						1988

Seq ID NO: C145 DNA Sequence  
Nucleic Acid Accession #: FGENESH predicted  
Coding sequence: 1..1242

1	11	21	31	41	51
---	----	----	----	----	----

5	ATGGTGTTCG	CATTTTGGAA	GGTCTTTCTG	ATCCTAAGCT	GCCTTGCAGG	TCAGGTAGT	60
	GTGGTGCAG	TGACCATCCC	AGACGGTTTC	GTGAACGTGA	CTGTTGGATC	TAATGTCAC	120
	CTCATCTGCA	TCTACACCAC	CACCTGTGGC	TCCCGAGAAC	AGCTTTCCAT	CCAGTGGTCT	180
	TTCTTCCATA	AGAAGGAGAT	GGAGCCAATT	TCTTCTCCTT	GGGAGGAGGG	GAAGTGGCCA	240
	GATGTTGAGG	CTGTGAAGGG	CACCTCTGAT	GGACAGCAGG	CTGAACCTCA	GATTTACTTT	300
	TCTCAAGGTG	GACAAGCTGT	AGCCATCGGG	CAATTTAAAG	ATCGAATTAC	AGGGTCCAAC	360
	GATCCAGGTA	ATGCATCTAT	CACATCTCTG	CATATGCAGC	CAGCAGACAG	TGGAATTAC	420
	ATCTGCGATG	TTAACCAACCC	CCCAGACTTT	CTCGGCCAAA	ACCAAGGCAT	CCTCAACGTC	480
10	AGTGTGTTAG	TGAAACCTTC	TAAGCCCCTT	TGTAGCGTTC	AAGGAAGACC	AGAACTGGC	540
	CACACTATTT	CCCTTTCTCTG	TCTCTCTGCG	CTTGGAACAC	CTTCCCCTGT	GTACTACTGG	600
	CATAAACTTG	AGGGAAGAGA	CATCGTGCCA	GTGAAAGAAA	ACTTCAACCC	AACCACCGGG	660
	ATTTTGGTCA	TTGGAATCT	GACAAATTTT	GAACAAGGTT	ATTACCACTG	TACTGCCATC	720
	AACAGACTTG	GCAATAGTTC	CTGCGAAATC	GATCTCACTT	CTTCACATCC	AGAAGTTGGA	780
15	ATCATTGTTG	GGGCCTTGAT	TGGTAGCCTG	GTAGGTGCCG	CCATCATCAT	CTCTGTTGTG	840
	TGCTTCGCAA	GGAATAAGGC	AAAAGCAAAG	GCAAAAGAAA	GAAATTCTAA	GACCATCGCG	900
	GAACCTGAGC	CAATGACAAA	GATAAACCCA	AGGGGAGAAA	GCGAAGCAAT	GCCAAAGAGAA	960
	GACGCTACCC	AACTAGAGT	AACTCTACCA	TCTTCCATTC	ATGAGACTGG	CCCTGATACC	1020
20	ATCCAAGAAC	CAGACTATGA	GCCAAAGCCT	ACTCAGGAGC	CTGCCCCAGA	GCCTGCCCCA	1080
	GGATCAGAGC	CTATGGCAGT	GCCTGACCTT	GACATCGAGC	TGGAGCTGGA	GCCAGAAACG	1140
	CAGTCGGAAT	TGGAGCCAGA	GCCAGAGCCA	GAGCCAGAGT	CAGAGCCTGG	GGTTGTAGTT	1200
	GAGCCCTTAA	GTGAAGATGA	AAAGGGAGTG	GTTAAGGCAT	AG		1242

Seq ID NO: C146 DNA Sequence  
Nucleic Acid Accession #: NM\_003020.1  
Coding sequence: 29..664

30	1	11	21	31	41	51	
	CGCTCCTCGG	GCTGCCCTCG	GGTTGACAAT	GGTCTCCAGG	ATGGTCTCTA	CCATGCTATC	60
	TGGCCTACTG	TTTGTGGCTGG	CATCTGGATG	GACTCCAGCA	TTTGCTTACA	GCCCCCGGAC	120
	CCCTGACCGG	GTCTCAGAA	CAGATATCCA	GAGGCTGCTT	CATGGTGTTA	TGGAGCAATT	180
	GGGCATTGCC	AGGCCCCGAG	TGGAATATCC	AGCTCACCAG	GCCATGAATC	TTGTGGGCCC	240
35	CCAGAGCAT	GAAGGTGGAG	CTCATGAAGG	ACTTCAGCAT	TTGGGTCTCT	TTGGCAACAT	300
	CCCCAACATC	GTGCGAGAGT	TGACTGGAGA	CAACATTCTT	AAGGACTTTA	GTGAGGATCA	360
	GGGGTACCCA	GACCTCCAA	ATCCCTGTCC	TGTTGGAAAA	ACAGATGATG	GATGTCTAGA	420
	AAACACCCCT	GACACTGCAG	AGTTTCAGTCG	AGAGTTCCAG	TTGCACCAGC	ATCTCTTTGA	480
	TCCGGAACAT	GACTATCCAG	GCTTGGGCAA	GTGGAACAAG	AACTTCCTTT	ACGAGAAGAT	540
40	GAAGGGAGGA	GAGAGACGAA	AGCGGAGGAG	TGTCAATCCA	TATCTACAAG	GACAGAGACT	600
	GGATAATGTT	GTTGCAAAGA	AGTCTGTCCC	CCATTTTTCA	GATGAGGATA	AGGATCCAGA	660
	GTAAAGAGAA	GATGCTAGAC	GAAAACCCAC	ATTACCTGTT	AGGCCCTCAGC	ATGGCTTATG	720
	TGCAGTGTA	AATGGAGTCC	CTGTGAATGA	CAGCATGTTT	CTTACATAGA	TAATTATGGA	780
	TACAAAGCAG	CTGTATGTAG	ATAGTGTATT	GTCCTCACAC	CGATGATTCT	GCTTTTGTCT	840
45	AAATTAGAA	AAGAGCTTTT	TTGTTTCTTG	GGTTTTTAAA	ATGTGAATCT	GCAATGATCA	900
	TAAAAATTAA	AATGTGTAAT	TCAACAATAA	AAAGCAAGAG	TATGAAAGGC	TCAGATTCTT	960
	TGCAGTTTAA	AATGTGTCT	GAGGTGTGAC	TATTTTGGCC	AAGTCTGTAG	AAAGCTGTCA	1020
	TTTGATTTTG	ATTATGTAGT	TCATCCAGCC	CTTGGGCATT	GTTATACACC	AGTAAAGAAG	1080
	GCTGTACTCA	AGAGGAGGAG	CTGACACATT	TCACTTGGCT	GCGTCTTAAT	AAACATGAAT	1140
50	GCAAGCATTG	GC					1152

Seq ID NO: C147 DNA Sequence  
Nucleic Acid Accession #: NM\_024021.2  
Coding sequence: 144..806

55	1	11	21	31	41	51	
	AACATTCCCTG	CAATAGGTTT	CAATATATGC	AGATGTCTCG	ATATAGGAAT	GAAATTACGT	60
	CTTTGGAACA	ACTTAAATAA	GTCAATATA	CTTGGAGCTT	TAAAAATTAA	AAGGAGAGAG	120
60	ATTCAGACAC	CTTTTCTGCT	GCCATGACAA	CCATGCAAGG	AATGGAACAG	GCCATGCCAG	180
	GGGCTGGCCC	TGGTGTGCCC	CAGCTGGGAA	ACATGGCTGT	CATACATTCA	CATCTGTGGA	240
	AAGGATTGCA	AGAGAAGTTC	TTGAAGGGAG	AACCCAAAGT	CCTTGGGGTT	GTGCAGATTC	300
	TGACTGCCCT	GATGAGCCCT	AGCATGGGAA	TAACAATGAT	GTGTATGGCA	TCTAATACTT	360
65	ATGGAAGTAA	CCCTATTTC	GTGTATATCG	GGTACACAAT	TTGGGGGTCA	GTAATGTTTA	420
	TTATTTCAGG	ATCCTTGTCA	ATTGCAGCAG	GAATTAGAAC	TACAAAGGC	CTGGTCCGAG	480
	GTAGTCTAGG	AATGAATATC	ACCAGCTCTG	TACTGGCTGC	ATCAGGGATC	TTAATCAACA	540
	CATTTAGCTT	GGCGTTTTAT	TCATTCCATC	ACCCTTACTG	TAACTACTAT	GGCAACTCAA	600
	ATAATTGTCA	TGGGACTATG	TCCATCTTAA	TGGGTCTGGA	TGGCATGGTG	CTCCTCTTAA	660
70	GTGTGCTGGA	ATTCTGCATT	GCTGTGTCCC	TCTCTGCCTT	TGGATGTAAA	GTGCTCTGTT	720
	GTACCCCTGG	TGGGGTTGTG	TTAATTCTGC	CATCACATTC	TCACATGGCA	GAAACAGCAT	780
	CTCCACACAC	ACTTAATGAG	GTTTGGAGCC	ACCAAAAGAT	CAACAGACAA	ATGCTCCAGA	840
	AATCTATGCT	GACTGTGACA	CAAGAGCCTC	ACATGAGAAA	TTACCAAGTAT	CCAACCTCGA	900
	TACTGATAGA	CTTGTGATA	TTATTATTAT	ATGTAATCCA	ATTATGAAC	GTGTGTGTAT	960
75	AGAGAGATAA	TAAATTCAAA	ATTATGTTCT	CATTTTCTTC	CCTGGAACTC	AATAACTCAT	1020
	TTCACTGGCT	CTTTATCGAG	AGTACTAGAA	GTAAATTAAT	TAAATAATGC	ATTTAATGAG	1080
	GCAACAGCAC	TTGAAAGTTT	TTCAATCATC	ATAAGAACTT	TATATAAAGG	CATTACATTG	1140
	GCAAAATAGG	TTTGAAGCAA	GAAGAGCAAA	AAAAAGATAT	TGTTAAATG	AGGCCTCCAT	1200
	GCAAAACACA	TACTTCCCTC	CCATTTTATTT	AACTTTTCTT	TTCTCCTACC	TATGGGGACC	1260
80	AAAGTGCTTT	TPCCTTCAGG	AAAGTGAGAT	GCATGGCCAT	CTCCCTCTCC	CTTTTCTCTT	1320
	CTCTCTGCTT	TCTTCCCTCA	TAGAAAGTAC	CTTGAAGTAG	CACAGTCCGT	CCTTGCTATG	1380
	GCAAGAGCTA	TCATTTGAGT	AAAAGTATAC	ATGGAGTAAA	AATCATATTA	AGCATCAGAT	1440
	TCAACTTATA	TTTTCTATT	CATCTTCTTC	CTTCCCTTCC	TCCCACCTTC	TACTGGGCAT	1500
	AAATTATATCT	TAATCATATA	TGGAAATGTG	CAACATATGG	TATTTGTTAA	ATACGTTTGT	1560
	TTTTATATGCA	GAGCAAAAT	AAATCAAAT	AGAAGCAATA	AAAAAATAAA	AAAAAATAAA	1619

Seq ID NO: C148 DNA Sequence  
Nucleic Acid Accession #: NM\_002091.1  
Coding sequence: 56..502

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60

1	11	21	31	41	51	
AGTCTCTGCT	CTTCCCAGCC	TCCTCCGGCG	GCTCCAAGGG	CTTCCCGTCG	GGACCATGCG	60
CGGCAGTGAG	CTCCCCGCTGG	TCCTGCTGGC	GCTGGTCCTC	TGCCTAGCGC	CCCGGGGGCG	120
AGCGGTCCCG	CTGCCGTGCG	GCGGAGGGAC	CGTGCTGACC	AAGATGTACC	CGCGCGGCAA	180
CCACTGGGCG	GTGGGGCACT	TAATGGGGAA	AAAGAGCACA	GGGGAGTCTT	CTTCTGTTTC	240
TGAGAGAGGG	AGCCTGAAGC	AGCAGCTGAG	AGAGTACATC	AGGTGGGAAG	AAGCTGCAAG	300
GAATTTGCTG	GGTCTCATAG	AAGCAAAGGA	GAACAGAAAC	CACCAGCCAC	CTCAACCCAA	360
GGCCTTGGGC	AATCAGCAGC	CTTCGTGGGA	TTCAGAGGAT	AGCAGCAACT	TCAAAGATGT	420
AGGTTCAAAA	GGCAAAGTTG	GTAAGACTCT	TGCTCCAGGT	TCTCAACGTG	AAGGAAGGAA	480
CCCCCAGCTG	AACCAAGCAAT	GATAATGATG	GCCTCTCTCA	AAAGAGAAAA	ACAAAACCCC	540
TAAGAGACTG	AGTTCTGCAA	GCATCAGTTC	TACGGATCAT	CAACAAGATT	TCCTTGTGCA	600
AAATATTTGA	CTATTCTGTA	TCTTTCATCC	TTGACTAAAT	TCGTGATTTT	CAAGCAGCAT	660
CTTCTGGTTT	AAACTTGTGT	GCTGTGAACA	ATTGTGGAAG	AGAGTCTTCC	AATTAATGCT	720
TTTTTATATC	TAGGCTACCT	GTTGGTTAGA	TTCAAGGCCC	CGAGCTGTGA	CCATTACAAA	780
TAAAGCTTA	AACACAT					797

Seq ID NO: C149 DNA Sequence  
Nucleic Acid Accession #: NM\_012261.1  
Coding sequence: 203..1045

25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

1	11	21	31	41	51	
GATTTGCTCT	GCCAGCAGCT	GTCGGTGCCG	CGCTCGACAC	CGAGTCTTAG	CTAGGCGCTC	60
ACAGAATACG	CGTCCCTCC	CTCCCCCTTC	TCTGTCCCCC	GCCTCTCGCT	CACCCCGGCC	120
CACTCCAGCG	GCGACTTTGA	GGGATTCCCT	CTCTGGCGGC	CTCTGCAGCA	GCACAGCCGG	180
CCTCATTCGG	GGCACTGCGA	GTATGGATCT	CCAAGGAAGA	GGGGTCCCCA	GCATCGACAG	240
ACTTCGAGTT	CTCTGTATGT	TGTTCATATC	AATGGCTCAA	ATCATGGCAG	AACAAGAAAT	300
GGAAAATCTC	TCAGGCTTTT	CCACTAACCC	TGAAAAAGAT	ATATTGTGTG	TGCGGGAAAA	360
TGGGACGACG	TGTCTCATGG	CAGAGTTTGC	AGCCAAATTT	ATTGTACCTT	ATGATGTGTG	420
GGCCAGCAAC	TACGTAGATC	TGATCACAGA	ACAGGCCGAT	ATCGCATTGA	CCCGGGGAGC	480
TGAGGTGAAG	GGCCGCTGTG	GCCACAGCCA	GTCGGAGCTG	CAAGTGTCTT	GGGTGGATCG	540
CGCATATGCA	CTCAAAATGC	TCTTTGTAAA	GGAAAGCCAC	AACATGTCCA	AGGGACCTGA	600
GGCGACTTGG	AGGCTGAGCA	AAGTGCAGTT	TGCTACGAC	TCCTCGGAGA	AAACCCACTT	660
CAAAAGACGA	GTCAGTGTCT	GGAAGCACAC	AGCCAACTCG	CACCACCTCT	CTGCCCTGGT	720
CACCCCGCT	GGGAAGTCTT	ATGAGTGTCA	AGCTCAACAA	ACCATTTCAC	TGGCCTCTAG	780
TGATCCGAG	AAGACGGTCA	CCATGATCCT	GTCTGCGGTC	CACATCCAAC	CTTTTGACAT	840
TATCTCAGAT	TTTGTCTTCA	GTGAAGAGCA	TAAATGCCCA	GTGGATGAGC	GGGAGCAACT	900
GGAAAGAAAC	TTGGCCCTGA	TTTTGGGGCT	CATCTTGGGC	CTCGTCATCA	TGGTAACACT	960
CGCGATTATC	CACGTCCACC	ACAAAATGAC	TGCCAACCCAG	GTGCAGATCC	CTCGGGACAG	1020
ATCCCACTAT	AAGCACATGG	GCTAGAGGCC	GTTAGGCAGG	CACCCCTTAT	TCCTGCTCCC	1080
CCAACCTGGAT	CAGGTAGAAC	AACAAAAGCA	CTTTTCCATC	TTGTACACGA	GATACACCAA	1140
CATAGCTACA	ATCAAAACAGG	CCTGGGTATC	TGAGGCTTGC	TTGGCTTGTG	TCCATGCTTA	1200
AACCCACGGA	AGGGGGAGAC	TCTTTCGGAT	TTGTAGGGTG	AAATGGCAAT	TATCTCTCC	1260
ATGCTGGGGA	GGAGGGGAGG	AGGGTCTCAG	ACAGCTTTCG	TGCTCATGGT	GGCTTGGCTT	1320
TGACTCTCCA	AAGAGCAATA	AATGCCACTT	GGAGCTGTAT	CTGGCCCCAA	AGTTTAGGGA	1380
TTGAAAACAT	GCTTCTTTGA	GGAGGAAACC	CCTTTAGGTT	CAGAAGAATA	TGGGGTGCTT	1440
TGCTCCCTTG	GACACAGCTG	GCTTATCCTA	TACAGTTGTC	AATGCACACA	GAATACAACC	1500
TCATGCTCCC	TGCAGCAAGA	CCCCTGAAAG	TGATTTCATG	TTCTGGCTGG	CATTCTGCAT	1560
GTTTAGTAGT	TGCTTTGGGA	ATGTTTCACT	GCTACCCGCA	TCCAGCGACT	GCAGCACCAG	1620
AAAACGAGTA	ATGTAACAT	GCAGAGTTGT	TTGGACTTCT	TCCTGTGCCA	GGTCCAAGTC	1680
GGGGACCTG	AAGAATCAAT	CTGTGTGAGT	CTGTTTTTCA	AAATGAAATA	AAACACACTA	1740
TTCTCTGGC						1749

Seq ID NO: C150 DNA Sequence  
Nucleic Acid Accession #: NM\_003226.1  
Coding sequence: 2..226

65  
70  
75  
80

1	11	21	31	41	51	
GATGCTGGGG	CTGGTCTTGG	CCTTGCTGTC	CTCCAGCTCT	GCTGAGGAGT	ACGTGGGCCT	60
GTCTGCAAA	CAGTGTCCCG	TGCCGGCCAA	GGACAGGGTG	GACTGCGGCT	ACCCCATGCT	120
CACCCCAAG	GAGTGCAACA	ACCGGGGCTG	CTGCTTTGAC	TCCAGGATCC	CTGGAGTGCC	180
TTGGTGTTC	AAGCCCTTGA	CTAGGAAGAC	AGAATGCACC	TTCTGAGGCA	CCTCCAGCTG	240
CCCCTGGGAT	GCAGGCTGAG	CACCCTTGCC	CGGCTGTGAT	TGCTGCCAGG	CACGTTCAT	300
CTCAGTTTTT	CTGTCCCTTT	GCTCCCGGCA	AGCTTCTGTC	TGAAAGTTCA	TATCTGAGC	360
CTGATGTCTT	AACGAATAAA	GGTCCCATGC	TCCACCCG			398

Seq ID NO: C151 DNA Sequence  
Nucleic Acid Accession #: NM\_002993.1  
Coding sequence: 64..408

75  
80

1	11	21	31	41	51	
GGCACGAGCC	AGTCTCCGCG	CTTCCACCCA	GCTCAGGAAC	CCGCGAACCC	TCTCTTGACC	60
ACTATGAGCC	TCCCGTCCAG	CCGCGCGGCC	CGTGTCCCGG	GTCCCTTCGGG	CTCCTTGTGC	120
GGCTGTCTCG	CGCTGTGCTG	CCTGTGTGAC	CCGCGGGGGC	CCCTCGCCAG	CGCTGGTCTC	180
GTCTCTGCTG	TGCTGACAGA	GCTGCGTTGC	ACTTGTATTAC	GCCTTACGCT	GAGAGTAAAC	240

5	CCCCAAACGA	TTGGTAAACT	GCAGGTGTTC	CCCCGAGGCC	CGCAGTGCTC	CAAGGTGGAA	300
	GTGGTAGCCT	CCCTGAAGAA	CGGGAAGCAA	GTTTGTCTGG	ACCCGGAAGC	CCCTTTTCTA	360
	AAGAAAGTCA	TCCAGAAAAA	TTTGGACAGT	GGAAACAAGA	AAAACGTAGT	AACAAAAAAG	420
	ACCATGCATC	ATAAAATTGC	CCAGTCTTCA	CGCGAGCAGT	TTTCTGGAGA	TCCCTGGACC	480
	CAGTAAGAAT	AAGAAGGAAG	GGTTGGTTTT	TTTCCATTTT	CTACATGGAT	TCCCTACTTT	540
	GAAGAGTGTG	GGGGAAGGCC	TACGCTTCTC	CCTGAAGTTT	ACAGCTCAGC	TAATGAAGTA	600
	CTAATATAGT	ATTTCCACTA	TTTACTGTTA	TTTTACCTGA	TAAGTTATTG	AACCCTTTGG	660
	CAATTGACCA	TATTGTGAGC	AAAGAATCAC	TGGTTATTAG	TCTTTCATG	AATATTGAAT	720
10	TGAAGATAAC	TATTGTATTT	CTATCATACA	TTCCTTAAAG	TCTTACCGAA	AAGGCTGTGG	780
	ATTTCTGTATG	GAAAATAATGT	TTTATTAGTG	TGCTGTTGAG	GGAGGTATCC	TGTTGTTCTT	840
	ACTCACTCTT	CTCATAAAAT	AGGAAATATT	TTAGTTCTGT	TTTCTGGGG	AATATGTTAC	900
	TCTTTACCCCT	AGGATGCTAT	TTAAGTTGTA	CTGTATTAGA	ACACTGGGTG	TGTCATACCG	960
	TTATCTGTGC	AGAATATATT	TCCTTATTCA	GAATTTCTAA	AAATTTAAGT	TCTGTAAGGG	1020
15	CTAATATATT	CTCTTCCTAT	GGTTTTAGAT	GTTTGATGTC	TTCTTAGTAT	GGCATAATGT	1080
	CATGATTTAC	TCATTAAACT	TTGATTTTGT	ATGCTATTTT	TTCACTATAG	GATGACTATA	1140
	ATTTCTGGTCA	CTAAATATAC	ACTTTAGATA	GATGAAGAAG	CCCAAAAACA	GATAAATTCC	1200
	TGATTGCTAA	TTTACATAGA	AATGTATTCT	CTTGTTTTTT	TAAATAAAAG	CAAAATTAAC	1260
	AATGATCTGT	GCTCTGCAAA	GTTTTGAAAA	TATATTGAA	CAATTGGAAT	ATAAATTCAT	1320
20	CATTTAGTCC	TCAAAATATA	TACAGCATTG	CTAAGATTTT	CAGATATCTA	TTGTGGATCT	1380
	TTTAAAGGTT	TTGACCATT	TGTTATGAGG	AATTATACAT	GTATCACATT	CACATATATA	1440
	AAATGCACT	TTTATTTTTT	CCTGTGTGTC	ATGTTGGTTT	TTGGTACTTG	TATTGTCATT	1500
	TGGAGAAACA	ATAAAAGATT	TCTAAACCAA	AAAAAATAAA	AAAAAA		1547

25 Seq ID NO: C152 DNA Sequence  
Nucleic Acid Accession #: NM\_005242.2  
Coding sequence: 148..1341

30	1	11	21	31	41	51	
	CGGCCCGCCC	TGGGGAGGCG	CGCAGCAGAG	GCTCCGATTC	GGGGCAGGTG	AGAGGCTGAC	60
	TTTCTCTCGG	TGCGTCCAGT	GGAGCTCTGA	GTTTCGAATC	GGTGGCGGCG	GATTCCCCGC	120
	GGGCCCGGCG	TGCGGGCTTC	CAGGAGGATG	CGGAGCCCCA	CGCGGCGGTG	GCTGCTGGGG	180
35	CGCGCCATCC	TGCTAGCAGC	CTCTCTCTCC	TGCAGTGGCA	CCATCCAAGG	AACCAATAGA	240
	TCCTCTAAAG	GAAAGAAGCCT	TATTGGTAAG	GTTGATGGCA	CATCCACAGT	CACTGGAAAA	300
	GGAGTTACAG	TTGAAACAGT	CTTTTCTGTG	GATGAGTTTT	CTGCATCTGT	CCTCACTGGA	360
	AAACTGACCA	CGGTCTTCTC	TCCAATTGTC	TACACAATTG	TGTTTGTGGT	GGGTTTGCCA	420
	AGTAACGGCA	TGGCCCTGTG	GGTCTTTCTT	TTCCGAACCTA	AGAAGAAGCA	CCCTGCTGTG	480
40	ATTTACATGG	CCAATCTGGC	CTTGGCTGAC	CTCCTCTCTG	TCATCTGGTT	CCCCTTGAAG	540
	ATTGCCTATC	ACATACATGC	CAACAACCTGG	ATTTATGGGG	AAGCTCTTTG	TAATGTGCTT	600
	ATTGGCTTTT	TCTATGGCAA	CATGTACTGT	TCCATTCTCT	TCATGACCTG	CCTCAGTGTG	660
	CAGAGGTATT	GGGTCTCATG	GAACCCCATG	GGGCACTCCA	GGAAGAAGGC	AAACATTGCC	720
	ATTGGCATCT	CCCTGGCAAT	ATGGCTGCTG	ATTCTGCTGG	TCACCATCCC	TTGTATGTCT	780
45	GTGAAGCAGA	CCATCTTCAT	TCCTGCCCTG	AACATCACGA	CCTGTCATGA	TGTTTTGCCT	840
	GAGCAGCTCT	TGGTGGGAGA	CATGTTCAAT	TACTTCTCTC	CTCTGGCCAT	TGGGGTCTTT	900
	CTGTTCCCGC	CTTTCCTCAC	AGCCTCTGCC	TATGTGCTGA	TGATCAGAAT	GCTGCGATCT	960
	TCCTGCCATGG	AGAAAACTG	AGAGAAGAAA	AGGAAGAGGG	CCATCAAACT	CATTGTCACT	1020
	GTCTGGGCA	TGTACCTGAT	CTGCTTCACT	CCTAGTAACC	TTCTGCTTGT	GGTGCATTAT	1080
50	TTTCTGATTA	AGAGCCAGGG	CCAGAGCCAT	GTCTATGCCC	TGTACATTGT	AGCCCTCTGC	1140
	CTCTCTACCC	TTAACAGCTG	CATCGACCCC	TTTGTCTATT	ACTTTGTTTC	ACATGATTTT	1200
	AGGGATCATG	CAAGAAGCGC	TCTCCTTTGC	CGAAGTGTC	GCACTGTAAA	GCAGATGCAA	1260
	GTATCCCTCA	CCTCAAGAA	ACACTCCAGG	AAATCCAGCT	CTTACTCTTC	AAGTTCAACC	1320
	ACTGTTAAGA	CCTCTTAAGA	AGTTTCCAG	GTCCCTCAGT	GGGAATTGCA	CAGTAGGATG	1380
55	TGGAACCTGT	TTAATGTTAT	GAGGACGTGT	CTGTTATTTT	CTAATCAAAA	AGGTCTCACC	1440
	ACATACCACC	G					1451

Seq ID NO: C153 DNA Sequence  
Nucleic Acid Accession #: NM\_003469.2  
Coding sequence: 92..1945

60	1	11	21	31	41	51	
	GAAACGGCCC	GAGAAGCTCG	CCCGGAGAAC	GGGGAGGAAT	ATGCTGTGGA	GCTCCTCTGC	60
65	CATATAAACA	AAAAGAGGAA	ATCTTTCAAA	CATGGCTGAA	GCAAGACCC	ACTGGCTTGG	120
	AGCAGCCCTG	TCTCTTATCC	CTTTAATTTT	CCTCATCTCT	GGGGCTGAAG	CAGCTTCATT	180
	TCAGAGAAAC	CAGCTGCTTC	AGAAAGAACC	AGACCTCAGG	TTGGAATAATG	TCCAAAAGTT	240
	TCCAGTCTCT	GAAATGATCA	GGGCTTTGGA	GTACATAGAA	AACCTCCGAC	AACAAGCTCA	300
	TAAGGAAGAA	AGCAGCCGAG	ATTATAATCC	CTACCAAGGT	GTCTCTGTCC	CCCTTCAGCA	360
70	AAAAGAAAAT	GGCGATGAAA	GCCACTTGCC	CGAGAGGGAT	TCACTGAGTG	AAGAAGACTG	420
	GATGAGAATA	ATACTCGAAG	CTTTGAGACA	GGCTGAAAAT	GAGCCTCAGT	CTGCACCAAA	480
	AGAAAAATAAG	CCCTATGCCT	TGAATTCAGA	AAAGAAGTTT	CCAATGGACA	TGAGTGATGA	540
	TTATGAGACA	CAGCAGTGGC	CAGAAAGAAA	GCTTAAGCAC	ATGCAATTCC	CTCCTATGTA	600
	TGAAGAGAAT	TCCAGGGATA	ACCCCTTTAA	ACGCACAAAT	GAAATAGTGG	AGGAACAATA	660
75	TACTCTTCAA	AGCCTTGCTA	CATTGGAATC	TGCTTTCCAA	GAGCTGGGGA	AACTGCAGAG	720
	ACCAAACAAC	CAGAAACGTG	AGAGGATGGA	TGAGGAGCAA	AAACTTTATA	CGGATGATGA	780
	AGATGATATC	TACAAGGCTA	ATAACATTGC	CTATGAAGAT	GTGGTCCGGG	GAGAAGACTG	840
	GAACCCAGTA	GAGGAGAAAA	TAGAGAGTCA	AACCCAGGAA	GAGGTGAGAG	ACAGCAAGA	900
	GAATATAGGA	AAAAATGAAC	AAATCAACGA	TGAGATGAAA	CGCTCAGGGC	AGCTTGGCAT	960
80	CCAGGAAGAA	GATCTTCCGA	AAGAGAGTAA	AGACCAACTC	TCAGATGATG	TCTCCAAAGT	1020
	AATTGCCTAT	TTGAAAAGGT	TAGTAAATGC	TGCAGGAAGT	GGGAGGTAC	AGAATGGGCA	1080
	AAATGGGGAA	AGGGCCACCA	GGCTTTTGA	GAAACCTCTT	GATTCTCAGT	CTATTTATCA	1140
	GCTGATTGAA	ATCTCAAGGA	ATTTACAGAT	ACCCCAAGAA	GACTTAATGT	AGATGCTCAA	1200
	AACTGGGGAG	AAGCCGAATG	GATCAGTGGA	ACCGGAGCGG	GAGCTTGACC	TTCTGTTGTA	1260
	CCTAGATGAC	ATCTCAGAGG	CTGACTTAGA	CCATCCAGAC	CTGTTCCAAA	ATAGGATGCT	1320

CTCCAAGAGT GGCTACCCCTA AAACACCTGG TCGTGCTGGG ACTGAGGCC C TACCAGACGG 1380  
 GCTCAGTGTT GAGGATATTT TAAATCTTT AGGGATGGAG AGTGCAGCAA ATCAGAAAAAC 1440  
 GTCGTATTTT CCCAATCCAT ATAACCAGGA GAAAGTTCTG CCAAGGCTCC CTTATGGTGC 1500  
 TGGAGATCT AGATCGAACC AGCTTCCCAA AGCTGCCTGG ATTCCACATG TTGAAAAACAG 1560  
 ACAGATGGCA TATGAAAAAC TGAACGACAA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG 1620  
 GATGCTAGTT AAATACCCCTG AGATCATTAA TTCAAACCAA GTGAAGCGAG TTCCTGGTCA 1680  
 AGGCTCATCT GAAGATGACC TGCAGGAAGA GGAACAAATT GAGCAGGCCA TCAAAGAGCA 1740  
 TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CCGGTGAGCA AAAGGTTCCT 1800  
 TGTGGGGCCC CGAAGAAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860  
 AATGAAAGTG CTGGAATACC TCAATCAAGA AAAGGCAGAA AAGGGAAGGG AGCATATTGC 1920  
 TAAGAGAGCA ATGGAATAA TGTAAAGCTGC TTTTATTAAT TACCCTACTT TCATTCTCTC 1980  
 CACCCCAAGC AAATCCCAAC ATTTCTCTTC AGTGTGTTGA CTTCTATCCT GTTAACACTG 2040  
 TAATATCTTT AAATGATGTA CAGGCAGATG AAACCAGGTC ACTGGGAGT CTGCTTCATT 2100  
 TCCCTGAGC TGTATCTTG TGTATGGATA TGTGTAATG TTATGACTCC TTGATAAAAA 2160  
 ATTTATTATG TCCATTATTG AAGAAAGATA TCTATGACTG TGTTTAATAG TATATCTAAT 2220  
 GGCTGTGGCA TTGTGTATGC TCACATATGA TAAAAAAGTG TCCTATAATT CTATTGAAAG 2280  
 TTTTAAATAT TTATTGAATT ATTTTGTAC TGTCTGTAGC GTTTTGTGGA GTACTGGACC 2340  
 AAAAAATAA AGCATTATAA ATATA 2365

Seq ID NO: C154 DNA Sequence  
 Nucleic Acid Accession #: NM\_030955  
 Coding sequence: 327..5108

1 11 21 31 41 51  
 GAATTCGGGG AGCGGGCGGG CTGCGAGGCC GCGGGGCATG CGGGAGGCGG AGGGGTGGGA 60  
 CCGGGTGGCT GCGCCCATTC CACACCCGCC GAAAGCGGAC ACTGTCAGCT GAATCACTCC 120  
 CCTTTTAGGA GGAAGGAGGG GGAAGAGGTG TCTAGCTAAT TTCTGCTTAA AAAAGCACAG 180  
 GAGATCGCGG GTCAGCTTTG CAGTCGCTGC CTTCTCGCGC CTGACCATGC ACCCTGTCAT 240  
 CTTCTGCTG GGCACAGGCG AGCGCTTTAT TTCTGAGGCT GAGGGCTAAA ACTTTTTTCA 300  
 CTTTCTTCT CCTCAACATC TGAATCATGC CATGTGCCCA GAGGAGCTGG CTGCAAAACC 360  
 TTTCCGTGGT GGCTCAGCTC CTTAACTTTG GGGCGCTTTG CTATGGGAGA CAGCCTCAGC 420  
 CAGGCCCGGT TCCTTCCCG GACAGGAGGC AAGAGCATTT TATCAAGGGC CTGCCAGAAT 480  
 ACCAGCTGGT GGTCCAGTC CGAGTAGATG CCAGTGGGCA TTTTGTGCA TATGGCTTGC 540  
 ACTATCCCAT CAGCAGCAGC AGGAGGAAGA GAGATTGGGA TGGCTCAGAG GACTGGGTGT 600  
 ACTACAGAAT TTCTCACGAG GAGAAGGACC TGTTTTTTAA CTGACGGTC AATCAAGGAT 660  
 TTTCTTCCAA TAGCTACATC ATGGAGAAGA GATATGGGAA CCTCTCCCAT GTTAAGATGA 720  
 TGGCTTCTCT TGCCCCCTC TGCCATCTCA GTGGCACGGT TCTACAGCAG GGCACCAGAG 780  
 TTGGGACGGC AGCCCTCAGT GCCTGCCATG GACTGACTGG ATTTTTCCTAA CTACCCATG 840  
 GAGACTTTTT CATGAAACCC GTGAAGAAGC ATCCACTGGT TGAGGGAGGG TACCACCCGC 900  
 ACATCGTTTA CAGGAGGCAG AAGGTTCCAG AAACCAAGGA GCCAACCTGT GGATTAAAGG 960  
 ACAGTGTTAA CATCTCCAG AAGCAAGAGC TATGGCGGGA GAAGTGGGAG AGGCACAAC 1020  
 TGCCAAGCAG AAGCCTCTCT CGGCGTTCCA TCAGCAAGGA GAGATGGGTG GAGACACTGG 1080  
 TGGTGGCCGA CACAAAGATG ATTGAATACC ATGGGAGTGA GAATGTGGAG TCCTACATCC 1140  
 TCACCATCAT GAACATGGTC ACTGGGTGT TCCATAACCC AAGCATTGGC AATGCAATTC 1200  
 ACATTGTGTG GGTTCGGCTC ATTCTACTCG AAGAAGAAGA GCAAGGACTG AAAATAGTTC 1260  
 ACCATGCAGA AAGACACTG TCTAGCTTCT GCAAGTGGCA GAAGAGTATC AATCCCAAGA 1320  
 GTGACCTCAA TCCTGTTCAT CACGACGTGG CTGTCTTCT CACCAGAAAG GACATCTGTG 1380  
 CTGGTTTCAA TCGCCCTGCG GAGACCTTGG GCCTGTCTCA CCTTTCAGGA ATGTGTCAG 1440  
 CTACCCGCGA CATCTCCAG AATGAAGATT CGGGACTCCC TCTGGCTTTC ACAATTGCC 1500  
 ATGAGCTAGG ACACAGCTTC GGCATCCAGC ATGATGGGAA AGAAATGAC TGTGAGCCTG 1560  
 TGGGCAGACA TCCGTACATC ATGTCCCGCC AGCTCCAGTA CGATCCCACT CCGCTGACAT 1620  
 GGTCCAAGTG CAGCGAGGAG TACATCAACC GCCTTCTGGA CCGAGGCTGG GGGTCTGTG 1680  
 TTGATGACAT ACCTAAAAG AAAGGCTTGA AGTCCAAGGT CATGCCCCC GGAGTGATCT 1740  
 ATGATGTTCA CCACGAGTGC CAGCTACAAT ATGGACCCAA TGCTACCTTC TGCCAGGAAG 1800  
 TAGAAAAAGT CTGCCAGACA CTGTGGTGT CCGTGAAGGG CTTTGTGTCG TCTAAGCTGG 1860  
 ACGTGTCTGC AGATGGAATC CAATGTGGTG AGAAGAAGTG GTGTATGGCA GGCAGGTGCA 1920  
 TCACAGTGGG GAAGAAACCA GAGAGCATTC CTGGAGGCTG GGGCCGCTGG TCACCTGGT 1980  
 CCCACTGTTT CAGGACCTGT GGGGCTGGAG TCCAGAGCGC AGAGAGGCTC TGCAACAACC 2040  
 CCGAGCCCAA GTTTGGAGGG AAATATTGCA CTGGAGAAAG AAAACGCTAT CGCTTGTGCA 2100  
 ACGTCCACCC CTGTGCTCA GAGGCACCAA CATTCGGCA GATGCAGTGC AGTGAATTG 2160  
 ACATGTTTCC CTACAAGAA GAACTCTACC ACTGGTTTCC CATTTTAAAC CCAGCACATC 2220  
 CTTGTGAGCT CTACTGCCGA CCCATAGATG GCCAGTTTTC TGAGAAATG CTGGATGCTG 2280  
 TCATTGATGG TACCCCTTGC TTTGAAGGCG GCAACAGCAG AAATGTCTGT ATTAATGGCA 2340  
 TATGTAAGAT GGTGGCTGT GACTATGAGA TCGATTCCAA TGCCACCAGG GATCGCTGCG 2400  
 GTGTGTGCC TGGGATGGC TCTTCTGCTC AGACTGTGAG AAAGATGTTT AAGCAGAAGG 2460  
 AAGGATCTGG TTATGTTGAC ATTGGGCTCA TTCCAAAAGG AGCAAGGGAC ATAAGAGTGA 2520  
 TGGAAATTGA GGGAGCTGGA AACTTCCTGG CCATCAGGAG TGAAGATCCT GAAAAATATT 2580  
 ACCTGAATGG AGGGTTTATT ATCCAGTGGG ACGGGAACCTA TAAGCTGGCA GGGACTGTCT 2640  
 TTCAGTATGA CAGGAAAAGA GACCTGGAAG AGCTGATGGC CACAGGTCCT ACCAATGAGT 2700  
 CTGTGTGATG CCAGCTTCTA TTCCAGGTGA CTAACCTGG CATCAAGTAT GAGTACACAA 2760  
 TCCAGAAAGA TGGCCTGAC AATGATGTTG AGCAGATGTA CTTCTGGCAG TACGCCACT 2820  
 GGACAGAGTG CAGTGTGACC TGCGGAGCAG GTATCCGCGC CCAAACCTGCC CATTGCAATA 2880  
 AGAAGGGCCG GAGGATGGTG AAAGCTACAT TCTGTGACCC AGAAACACAG CCAATGGGA 2940  
 GACAGAAAGG GTGCCATGAA AAGGCTTGT CACCCAGGTG GTGGGCAGGG GAGTGGGAAG 3000  
 CATGCTCGGC GACATGCGGG CCCCACGGGG AGAAGAAGCG AACCGTGCTG TGCATCCAGA 3060  
 CCATGGTCTC TGACGAGCAG GCTCTCCCGC CCACAGACTG CCAGCACCTG CTGAAGCCCA 3120  
 AGACCTCTCT TTCTGTCAAC AGAGACATCC TGTGCCCCCT GGCATGGACA GTGGGCAACT 3180  
 GGAGTGAGTG TCTGTTTCC TGTGGTGGTG GAGTGGGAT TCGCAGTGTG ACATGTGCCA 3240  
 AGAACCATGA TGAACCTTGC GATGTGACAA GGAAACCCAA CAGCCGAGCT CTGTGTGGCC 3300  
 TCCAGCAATG CCCTTCTAGC CGGAGAGTTC TGAAACCCAA CAAAGGCACCT ATTTCCAATG 3360  
 GAAAAAACCC ACCAACACTA AAGCCCGTCC CTCCACCTAC ATCCAGGCCG AGAATGCTGA 3420  
 CCACACCCAC AGGGCCTGAG TCTATGAGCA CAAGCACTCC AGCAATCAGC AGCCCTAGTC 3480  
 CTACCAACAG CTCCAAAGAA GGAGACCTGG GTGGGAAACA GTGGCAAGAT AGCTCAACCC 3540

AACCTGAGCT GAGCTCTCGC TATCTCATTT CCACTGGAAG CACTTCCCAG CCCATCCTCA 3600  
 CTTCCTCAATC CTTGAGCATT CAGCCAAGTG AGGAAAATGT TTCCAGTTCA GATACTGGTC 3660  
 CTACCTCGGA GGGAGGCTTT GTAGCTACAA CAACAAGTGG TTCTGGCTTG TCATCTTCCC 3720  
 GCACCCCTAT CACTTGGCCT GTGACTCCAT TTTACAATAC CTTGACCAAA GGTCCAGAAA 3780  
 TGGAGATTCA CAGTGGCTCA GGGGAAGAAA GAGAACAGCC TGAGGACAAA GATGAAAGCA 3840  
 ATCTCTGAAT ATGGACCAAG ATCAGAGTAC CTGGAATGA CGCTCCAGTG GAAAGTACAG 3900  
 AAATGCCACT TGCACCTCCA CTAACACCAG ATCTCAGCAG GGAGTCTCTG TGGCCACCCT 3960  
 TCAGCACAGT AATGGAAGGA CTGCTCCCCA GCCAAAGGCC CACTACTTCC GAAACTGGGA 4020  
 CACCACAGT TGAGGGGATG GTTACTGAAA AGCCAGCCAA CACTCTGCTC CCTCTGGGAG 4080  
 GAGACCACCA GCCAGAACC TCAGGAAAGA CGGCAAAACG TAACCACCTG AAACCTCCAA 4140  
 ACAACATGAA CCAACAGAAA AGTTCTGAAC CAGTCTGAC TGAGGAGGAT GCAACAAGTC 4200  
 TGATTACTGA GGGCTTTTGT CTAATGCTT CCAATTACAA GCAGCTCACA AACGGCCACG 4260  
 GCTCTGCACA CTGGATCGTC GGAACCTGGA GCGAGTGTCT CACCACATGT GGCCTGGGGG 4320  
 CCTACTGGAA AAGGGTGGAG TGCACCACCC AGATGGATTG TGAAGTGTGC GCCATCCAGA 4380  
 GACCTGACCC TGCAAAAAGA TGCCACCTCC GTCCCTGTGC TGGCTGGAAA GTGGGAAACT 4440  
 GGAGCAAGTG CTCAGAGAAC TGCAGTGGGG GCTTCAAGAT ACGCGAGATT CAGTGCCTGG 4500  
 ACAGCCGGGA CCACCGGAAC CTGAGGCCAT TTCACTGCCA GTTCCTGGCC GGCATTCTCT 4560  
 CCCCATTGAG CATGAGCTGT AACCCTGAGC CCTGTGAGGC GTGGCAGGTG GAGCCTTGA 4620  
 GCCAGTGTCT CAGTCTCTGT GGAGGTGGAG TTCAGGAGAG AGGAGTGTTC TGTCAGGAG 4680  
 GCCTCTGTGA TTGGACAAAA AGACCACAT CCACCATGTC TTGCAATGAG CACCTGTGCT 4740  
 GTCACCTGGC CTCCAGAAAC TGGGACCTGT GTTCCACTTC CTGTGGAGGT GGCTTTTACA 4800  
 AGAGGATTGT CCAATGTGTG CCCTCAGAGG GCAATAAAAC TGAAGACCAA GACCAATGTC 4860  
 TATGTGATCA CAAACCCAGA CCTCCAGAAT TCAAAAAATG CAACCAGCAG GCCTGCAAGA 4920  
 AAAGTGCCGA TTTACTTTGC ACTAAGGACA AACTGTGAGC CAGTTTCTGC CAGACACTGA 4980  
 AAGCCATGAA GAAATGTTCT GTGCCACCG TGAGGGCTGA GTGTGTCTTC TCGTGTCCCC 5040  
 AGACACACAT CACACACACC CAAAGGCAAA GAAGGCAACG GTTGCTCCAA AAGTCAAAAG 5100  
 AACTCTAAGC CCAAA 5115

Seq ID NO: C155 DNA Sequence  
 Nucleic Acid Accession #: NM\_001062.1  
 Coding sequence: 76..1380

1 11 21 31 41 51  
 GCTCTCATTA CCTTCTGCCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG 60  
 TACACTGTTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTTT 120  
 TCTTTTATTC CAAGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180  
 CTAAACCTTC TGTGAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC 240  
 AATGTTGTGT TGTCCCTCAA ACTTGTGGA ATCCAGATCC AAACCTGAT GCAAAAGATG 300  
 ATCCAAACAA GAAATACAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360  
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACCGTG AGGAAAACTT AATATATGAT 420  
 TACCACCTGA CTGACAAGCT AGAAAATAAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480  
 CACAATGGCA CTCCCTGAC TAACTACTAC CAGCTCAGCC TGGACGTTT GGCCTTGTGT 540  
 CTGTTCAATG GGAACCTACT AACCCTGCGA GTTGTCAACC ACTTCACTCC TGAAAATAAA 600  
 AACTATTATT TTGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CTGGCTCTG 660  
 ACCTGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAAG CAGATGAAGG CAGTTTAAAG 720  
 AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATTG TGTCTGAGAA AAAAGAAAAAT 780  
 GGTCTCATTT GAAACACATT TAGCACAGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840  
 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAACTC TGAATACAGT GCTCACGGAA 900  
 ATTTCTCAAG GAGCATTCAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960  
 GGAAAGACCT TCTTGATAT TAACAAAGAC TCTTCTTGGC TCTCTGCTTC AGGTAACCTC 1020  
 AACATCTCCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC 1080  
 GTCAATTACT CTGTGAGAA CAATGAAACA TATTTACCA ATGTCACTGT GCTAAATGGT 1140  
 TCTGTCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC 1200  
 ACAATGGAGG AGCGCTCATG GGGGCCCTAT ATCACTGTGA TTCAGGGCCT ATGTGCCAAC 1260  
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCCTGAG CCAAGGAGCT 1320  
 GGTAGTTACG TTGTCCGCAA TGGAGAAAAC TTGGAGGTTT GCTGGAGCAA ATACTAATAA 1380  
 GCCCAACTT TCCTCAGCTG CATAAAATCC ATTTGCACTG GAGTTCCATG TTTATTGTCC 1440  
 TTAGCCCTTC TTCTCATTT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCCTTCTC 1500  
 TCTCTACATG TTCAATAAAA GTTGTGAAA GATTAAC 1537

Seq ID NO: C156 DNA Sequence  
 Nucleic Acid Accession #: NM\_004591  
 Coding sequence: 59..349

1 11 21 31 41 51  
 CACTCCCAAA GAAGTGGGTA CTCACACTG AGCAGATCTG TTCTTTGAGC TAAAAACCAT 60  
 GTGCTGTACC AAGAGTTTGC TCCTGGCTGC TTTGATGTCA GTGCTGTAC TCCACCTCTG 120  
 CGGCGAATCA GAAGCAGCAA GCAACTTTGA CTGCTGTCTT GGATACACAG ACCGTATTCT 180  
 TCATCCTAAA TTTATTGTGG GCTTCACACG GCAGCTGGCC AATGAAGGCT GTGACATCAA 240  
 TGCTATCATC TTTACACAAA AGAAAAAGTT GTCTGTGTGC GCAAAATCCAA AACAGACTTG 300  
 GGTGAAATAT ATTTGTGCTC TCCTCAGTAA AAAAGTCAAG AACATGTAAA AACTGTGGCT 360  
 TTTCTGGAAT GGAATTGGAC ATAGCCCAAG AACAGAAAGA ACCTTGCTGG GGTGGAGGT 420  
 TTCACTTGCA CATCATGGAG GGTTTAGTGC TTAATCAATT TGTGCTTAC TGGACTTGTC 480  
 CAATTAATGA AGTTGATGAC TATTGCATCA TAGTTTGCTT TGTTAAGCA TCACATTAAA 540  
 GTTAAACTGT ATTTATGTT ATTTATAGCT GTAGGTTTTC TGTGTTTAGC TATTTAATAC 600  
 TAATTTTCCA TAAGCTATTT TGGTTTAGTG CAAAGTATAA AATATATATT GGGGGGGAAT 660  
 AAGATTATAT GGACTTTCTT GCAAGCAACA AGCTATTTT TAAAAAACT ATTTAATCATT 720  
 CTTTGTGTTA TATGTTTGTG TCTCTAAAT TGTGTGTAAT GCATTATAAA ATAAGAAAAA 780  
 CATTAATAAG ACAATATT 799

Seq ID NO: C157 DNA Sequence  
 Nucleic Acid Accession #: NM\_013271.1

Coding sequence: 27..809

```

1      11      21      31      41      51
5      |      |      |      |      |      |
TCCGGAGCCA GGCTCGCTGG GGCAGCATGG CGGGGTGCGC GCTGCTCTGG GGGCCGCGGG 60
CCGGGGGCGT CGGCCTTTTG GTGCTGCTGC TGCTCGGCCT GTTTCGGCCG CCCCCGCGC 120
TCTGCGCGCG GCCCGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGCTCG 180
AGACTGGCGC TCCTCGCCGC TTCCGGCGGT CAGTGCCCGG AGGTGAGGCG GCGGGGGCGG 240
TGCAGGAGCT GCGCGGGGCG CTGGCGCATC TGCTGGAGGC CGAACGTGAG GAGCGGGCGC 300
10     GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG 360
TCTGGGGCGC CCCCAGCAAC TCTGATCCGG CTCTGGGCCT GGACGACGAC CCGGACGCGC 420
CTGACGCGCA GCTCGCTCGC GCTCTGCTCC GCGCCCGCCT TGACCCCTGCC GCCCTAGCAG 480
CCCAGCTTGT CCCCAGCGCC GTCCCGCGCG CGGCGCTCCG ACCCGGCGCC CCGGTCTACG 540
15     ACGACGGCCC CGCGGGCCCG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660
TGGCAGCCCC GCGCCGCGCT CGCCGTGCCG CCGACCAAGA TGTGGGCTCT GAGCTGCCCC 720
CTGAGGGCGT GCTGGGGGCG CTGCTGCGTG TGAACGCCT AGAGACCCCG GCGCCCCAGG 780
TGCCTGCACG CCGCCTCTTG CCACCTGAG CACTGCCCGG ATCCCGTGCA CCCTGGGACC 840
CAGAAGTGCC CCGGCACATC CGCCACAGG ACTTCTCCCC GCCAGCAGT CCAGAGCAAC 900
20     TTACCCCGGC CAGCCAGCCC TCTACCCGA GGATCCCTAC CCCCCTGGCC ACAATAACAT 960
GATCTGAGC

```

Seq ID NO: C158 DNA Sequence  
Nucleic Acid Accession #: NM\_002245.2  
Coding sequence: 183..1193

```

1      11      21      31      41      51
30     |      |      |      |      |      |
GGGCAGGAAG ACGGCGCTGC CCGGAGGAGC GGGGCGGGCG GGCGCGCGGG GGAGCGGGCG 60
GCGGGCGGGA GCCAGGCCCG GCGCGGGGCG GGGGCGGGCG GGCCAGAAGA GCGGCGGGCG 120
CGCGCTCCGG CCGGTCTGCG GCGTTGGCCT TGGCTTTGGC TTTGGCGGCG GCGGTGGAGA 180
AGATGCTGCA GTCCCTGGCC GGCAGCTCGT GCGTGCGCCT GGTGGAGCGG CACCGCTCGG 240
CCTGGTGCTT CCGCTTCCTG GTGCTGGGCT ACTTGCTCTA CCTGGTCTTC GGGCGAGTGG 300
35     TCTTCTCCTC GGTGGAGCTG CCCTATGAGG ACCTGCTGCG CCAGGAGCTG CGCAAGCTGA 360
AGCGACGCTT CTGAGGAGG CACGAGTGCC TGTCTGAGCA GCAGCTGGAG CAGTTCCTGG 420
GCCGGGTGCT GGAGGCCAGC AACTACGCGG TGTGCGTGCT CAGCAACGCC TCGGGCAACT 480
GGAACCTGGA CTTCACCTCC GCGCTCTTCT TCGCCAGCAC CGTGCTCTCC ACCACAGGTT 540
ATGGCCACAC CGTGCCCTTG TCAGATGGAG GTAAGGCCCT CTGCATCATC TACTCCGTCA 600
40     TTGGCATTCC CTTCACCTC CTGTTCTTGA CGGCTGTGGT CCAGCGCATC ACCGTGCACG 660
TCACCCGCGA GCCCGTCCCT TACTTCCACA TCCGCTGGGG CTCTCCCAAG CAGGTGGTGG 720
CCATCGTCCA TGCCGTGCTC CTGGGTTTGG TCACTGTGTC CTGCTCTCTC TTATCCCCGG 780
CGCGTGTCTT CTCAGTCCCT GAGGATGACT GGAACCTCCT GGAATCCTTT TATTTTGTGT 840
TTATTTCCCT GAGCACCATT GGCCTGGGGG ATTATGTGCC TGGGGAAGGC TACAATCAAA 900
45     AATTGAGAGA GCTCTATAAG ATTGGGATCA CGTGTACCT GCTACTTGGC CTTATTGCCA 960
TGTTGGTAGT TCTGGAACCC TTCTGTGAAC TCCATGAGCT GAAAAAATTC AGAAAAATGT 1020
TCTATGTGAA GAAGGACAAG GACGAGGATC AGGTGCACAT CATAGAGCAT GACCAACTGT 1080
CCTTCTCCTC GATCACAGAC CAGGCAGCTG GCATGAAAGA GGACCAGAAG CAAAATGAGC 1140
CTTTTGGGCG CACCCAGTCA TCTGCCTGCG TGGATGGCCC TGCAAAACCAT TGAGCGTAGG 1200
50     ATTTGTTGCA TTATGCTAGA GCACCAAGGT CAGGGTGCAA GGAAGAGGCT TAAGTATGTT 1260
CATTTTATC AGAATGCAAA AGCAAAAATT ATGTCACTTT AAGAAATAGC TACTGTTTGC 1320
AATGTCTTAT TAAAAACAA CAAAAAAGA CACATGGAAC AAAGAAGCTG TGACCCAGC 1380
AGGATGTCTA ATATGTGAGG AAATGAGATG TCCACCTAAA ATTCTATATG GACAAAATTA 1440
TCTCGACCTT ACATAGGAGG AGAATACTTG AAGCAGTATG CTGCTGTGGT TAGAAGCAGA 1500
55     TTTTATACTT TTAACGTGAA ACTTTGGGGT TTGCATTTAG ATCATTAGC TGATGGCTAA 1560
ATAGCAAAAT TTATATTATG AAGCAAAAAA AAAAAGCATA GAGATGTGTT TTATAAATAG 1620
GTTTATGTGT ATCGTGTGCG ATGTACCCAC CCAAAATGAT TATTTTGGGA GAATCTAAGT 1680
CAAACCTCAT ATTTATAATG CATAGGTAAC CATTAACATG GTACATATAA AGTATAAATA 1740
TGTTTATATT CTGTACATAT GGTTTAGGTC ACCAGATCCT AGTGTAGTTC TGAAACTAAG 1800
60     ACTATAGATA TTTGTGTTCT TTTGATTCT CTTTATACTA AAGAATCCAG AGTTGTCTAC 1860
ATAAAATAAG GGAATAATAA AACTTGAGAG TGAATAACCA T 1901

```

Seq ID NO: C159 DNA Sequence  
Nucleic Acid Accession #: NM\_005472.1  
Coding sequence: 93..404

```

1      11      21      31      41      51
70     |      |      |      |      |      |
AAAGGGACTC CTTGAAACTG ATTGAGAGCC CAGTGGATTG GCCAGCAGTT TGAGCTTCTA 60
CCGAGTCTTC CCCCACCTCA ATCCCTGTTG CTATGGAGAC TACCAATGGA ACGGAGACCT 120
GGTATGAGAG CCTGCATGCC GTGCTGAAGG CTCTAAATGC CACTCTTCAC AGCAATTGTC 180
TCTGCGCGCC AGGGCCAGGG CTGGGGCCAG ACAACCAGAC TGAAGAGAGG CGGGCCAGCC 240
TACCTGGCCG TGATGACAAC TCCTACATGT ACATTCTCTT TGTATGTTT CTATTTGCTG 300
TAACGTGGGG CAGCCTCATC CTGGGATACA CCCGCTCCCG CAAAGTGGAC AAGCGTAGTG 360
75     ACCCTATATC TGTGTATATC AAGAACCCTG TGTCTATGAT CTAACACGAG AGGGCTGGGA 420
CGGTGGAAGA CCAAGACACC TGGGGATTGC GTCTGGGGCC TCCAGAATCT TGCTGTGGAC 480
TGCATCAGGT CT 492

```

Seq ID NO: C160 DNA Sequence  
Nucleic Acid Accession #: NM\_005245.1  
Coding sequence: 187..13959

```

1      11      21      31      41      51
80     |      |      |      |      |      |
CTGGGCGGCC GGGCGCGGGG AGAGGGCGCG GGAGCGGCTC GTGCGGCAGG TACCATGCGG 60

```

	ACGCGCGAGC	CCGCGGAGGC	CCCGGCAGGC	CCGTCCCTGC	TCGGGGGCGC	GCTGAGACGG	120
	CGGGTGAGCT	CCACGAGAGC	GCCGTCGCCA	CTTCGGGCCA	ACTTTGCGAT	TCCCGACAGT	180
	TAAGCAATGG	GGAGACATTT	GGCTTTGCTC	CTGCTTCTGC	TCCTTCTCTT	CCAACATTTT	240
5	GGAGACAGTG	ATGGCAGCCA	ACGACTTGAA	CAGACTCCTC	TGCAGTTTAC	ACACCTCGAG	300
	TACAACGTCA	CCGTGCAGGA	GAACCTCTGA	GCTAAGACTT	ATGTGGGGCA	TCCTGTCAAG	360
	ATGGGTGTTT	ACATTACACA	TCCAGCGTGG	GAACTAAGGT	ACAAAATGTG	TTCCGGAGAC	420
	AGTGA AAAAC	TGTTCAAAGC	TGAAGAGTAC	ATTCCTGGAG	ACTTTTGCTT	TCTAAGAATA	480
	AGGACCAAAG	GAGGAAATAC	AGCTATTCTT	AATAGAGAAG	TGAAGGATCA	CTACACATTG	540
10	ATAGTGAAAG	CAC TTGAAA	AAATACTAAT	GTGGAGGCGC	GAAACAAAGT	CAGGGTGCAG	600
	GTGCTGGATA	CAAAATGACTT	GAGACCGTTA	TTCTCACCCA	CCTCATACAG	CGTTTCTTTA	660
	CCTGAAAAACA	CAGCTATAAG	GACCAATATC	GCAAGAGTCA	GCGCCACGGA	TGCAGACATA	720
	GGAAACCAACG	GGGAATTTTA	CTACAGTTT	AAAGATCGAA	CAGATATGTT	TGCTATTTCAC	780
	CCAACCAAGTG	GTGTGATAGT	GTTAACTGGT	AGACTTGATT	ACCTAGAGAC	CAAGCTCTAT	840
15	GAGATGAAA	TCCTCGCTGC	GGACCGTGGC	ATGAAGTTGT	ATGGGAGCAG	TGGCATCAGC	900
	AGCATGGCCA	AGCTAACCGT	GCACATCGAA	CAGGCCAATG	AATGTGCTCC	GGTGATAACA	960
	CGAGTGACAT	TGTCACCAT	AGAACTGGAC	AGGGACCCAG	CATATGCAAT	TGTGACAGTG	1020
	GATGATCGCG	ATCAGGGTGC	CAATGGTGAC	ATAGCATCTT	TAAGCATCGT	GGCAGGTGAC	1080
	CTTCTCCAGC	AGTTTATGAC	AGTGAGGTCC	TTTCCAGGGA	GTAAGGAGTA	TAAAGTCAAA	1140
20	GCCATCGGTG	ACATTGATTG	GGACAGTCAT	CCTTTCCGGCT	ACAATCTCAC	ACTACAGGCT	1200
	AAAGATAAAG	GAAC TCCGCC	CCAGTTCTCT	TCTGTTAAAG	TCATTACAGT	GACTTCTCCA	1260
	CAGTTCAAAG	CGGGCCAGT	CAAGTTTGAA	AAGGATGTTT	ACAGAGCAGA	AATAAGTGAA	1320
	TTTGCTCCTC	CCAACACACC	TGTGTCATG	GTAAGGCCA	TTCTGCTTTA	TTCCCATTTG	1380
	AGGTATGTTT	TTAAAAGGAC	ACCTGGAAAA	GCTAAATTCA	GTTTAAATTA	CAACACTGGT	1440
25	CTCATTTCTA	TTTTAGAACC	AGTTAAAAGA	CAGCAGGCAG	CCCATTTTGA	ACTTGAAGTA	1500
	ACAACAAGTG	CAGAAAAGC	GTCACCAAG	GTCTTGGTGA	AAGTCTTAGG	TGCAAAATAGC	1560
	AATCCCCCTG	AATTTACCCA	GACAGCGTAC	AAAGCTGCTT	TTGATGAGAA	CGTGCCCAT	1620
	GGTACTACTA	TCATGAGCCT	GAGTGCCGTA	GACCTGATG	AGGGTGAGAA	TGGGTACGTG	1680
	ACATACAGTA	TGCAAAATTT	AAATCATGTG	CCGTTTGCGA	TTGACCATTT	CACTGGTGCC	1740
30	GTGAGTACGT	CAGAAAACCT	GGACTACGAA	CTGATGCCCT	GGGTTTATAC	CTGAGGATT	1800
	CGTGATCAG	ACTGGGGCTT	GCCGTACCGC	CGGGAAGTCG	AAGTCTTTCG	TACAATTACT	1860
	CTCAATAACT	TGAATGACAA	CACACCTTTG	TTTGAGAAAA	TAAATTGTGA	AGGGACAATT	1920
	CCCAGAGATC	TAGGCGTGGG	AGAGCAAATA	ACCCTGTTT	CTGCTATTGA	TGCAGATGAA	1980
	CTTCAAGTTG	TACAGTATGC	GATTGAAGCT	GGAAAATGAA	TGGATTGTTT	TAGTTTAAAC	2040
35	CCCAACTCGG	GGGTATTGTC	ATTAAAGCGA	TCGCTAATGG	ATGGCTTAGG	TGCAAGGGTG	2100
	TCCTTCCACA	GTCTGAGAAT	CACAGCTACA	GATGGAGAAA	ATTTTGCCAC	ACCATTATAT	2160
	ATCAACATAA	CAGTGGCTGC	CAGTCACAAG	CTGGTAAACT	TGCAGTGTGA	AGAGACTGGT	2220
	GTTGCCAAAG	TGCTGGCAGA	GAAGCTCCTG	CAGGCAAATA	AATTACACAA	CCAGGGAGAG	2280
	GTGGAGGATA	TTTTCTTCGA	TTCTCACTCT	GTCAATGCTC	ACATACCGCA	GTTTAGAAGC	2340
40	ACTCTTCCGA	CTGGTATTCA	GGTAAAGGAA	AACCAGCCTG	TGGGTTCCAG	TGTAATTTTC	2400
	ATGAAC TCCA	CTGACCTTGA	CAGTGGCTTC	AATGGAAAAC	TGGTCTATGC	TGTTTCTGGA	2460
	GGAAATGAGG	ATAGTTGCTT	CATGATTGAT	ATGGAAACAG	GAATGCTGAA	AATTTTATCT	2520
	CCCTCTTGACC	GTCAACAACAC	AGACAAATAC	ACCCTGAATA	TTACCGTCTA	TGACCTTGCG	2580
	ATACCCCGAG	AGGCTCGGTG	CGCTCTTCTA	CATGTCGTGG	TTGTCGATGC	CAATGATAAT	2640
45	CCACCCGAGT	TTTTACAGGA	GAGCTATTTT	GTGGAAGTGA	GTGAAGACAA	GGAGGTACAT	2700
	AGTGAAATCA	TCCAGGTTGA	AGCCACAGAT	AAAGACCTGG	GGCCCAACGG	ACACGTGACG	2760
	TACTCAATCT	TTACAGACAC	AGACACATTT	TCAATTGACA	GCGTGACGGG	TGTTGTTAAC	2820
	ATCGCACGCC	CTCTGGATCG	AGAGCTGCAG	CATGAGCACT	CCTTAAAGAT	TGAGGCCAGG	2880
	GACCAAGCCA	GAGAAGAGCC	TCAGCTGTTC	TCCACTGTGC	TTGTGAAAGT	ATCACTAGAA	2940
50	GATGTTAATG	ACAACCCACC	TACATTTATT	CCACCTAATT	ATCGTGTGAA	AGTCCGAGAG	3000
	GATCTTCCAG	ATGGAACCGT	CATCATGTGG	TTAGAAGCCC	ACGATCCTGA	TTTAGGTGAC	3060
	TCTGGTCAGG	TGAGATACAG	CCTTCTGGAC	CACGGAGAAG	GAAACTTCGA	TGTGGATAAA	3120
	CTCAGTGGAG	CAGTTAGGAT	CGTCCAGCAG	TTGGACTTTG	AGAAGAAGCA	AGTGTATAAT	3180
	CTCACTGTGA	GGGCCAAAGA	CAAGGGAAAG	CCAGTTTCTC	TGCTTCTTAC	TTGCTATGTT	3240
55	GAAAGTGAGG	TGTTGATGAT	GAATGAGAAC	CTGCACCCAC	CCGTGTTTTC	CAGCTTTGTG	3300
	GAAAAGGGGA	CAGTGAAGAA	AGATGCACCT	GTTGGTTTAT	TGGTAATGAC	GGTGTCCGCT	3360
	CATGATGAGG	ACGCCGGAAG	AGATGGGGAG	ATCCGATACT	CCATTAGAGA	TGGCTCTGGC	3420
	GTTGGTGTTT	TCAAATATAGG	TGAAGAGACA	GGTGTCTAG	AGACGTGAGA	TCGACTGGAC	3480
	CGTGAATCGA	CTCCCAATTA	TTGGCTAACA	GTCTTTGCAA	CCGATCAGGG	TGCTGTGCTC	3540
60	CTTTTCATCGT	TCATAGAGAT	CTACATAGAG	GTTGAGGATG	TCAATGACAA	TGCACCACAG	3600
	ACATCAGAGC	CTGTTTATTA	CCCAGAAATC	ATGGAAAATT	CTCCTAAAGA	TGTATCTGTG	3660
	GTCCAGATCG	AGGCATTTGA	TCCAGATTCT	AGCTCTAATG	ACAAGCTCAT	GTACAAAATT	3720
	ACAAGTGGAA	ATCCACAAGG	ATTCCTTTTCA	ATACATCCTA	AAACAGGTCT	CATCACAACT	3780
	ACGTCAAGGA	AGCTAGACCG	AGAACAGCAA	GATGAACACA	TATTAGAGGT	TACTGTGACA	3840
65	GACAAATGTA	GTCCCCCACA	ATCAACCAAT	GCAAGAGTCA	TTGTGAAAAT	CCTTGATGAA	3900
	AATGACAACA	AACCTCAGTT	TCTGCAAAAG	TTCTACAAAA	TCAGACTCCC	TGAGCGGGAA	3960
	AAGCCAGACC	GAGAAAGAAA	TGCCAGACGG	GAGCCGCTCT	ATCGCTCAT	AGCCACCCAG	4020
	AAGGATGAGG	GCCCCAATGC	AGAAATCTCC	TACAGCATCG	AAGACGGGAA	TGAGCATGGC	4080
	AAATTTTTC	TGAAACCGAA	AACTGGAGTG	GTTTCGTCCA	AGAGGTTTTC	AGCAGCTGGA	4140
70	GAATATGATA	TTCTTTCAAT	TAAGGCAATT	GACAAATGGT	GCCCCAAAA	GTCACTCAAC	4200
	ACCAGACTCC	ATATTGAATG	GATCTCCAAG	CCCAACAGT	CCCTGGAGCC	CATTTCTATT	4260
	GAAGAATCAT	TTTTTACCTT	TACTGTGATG	GAAAGTGACC	CCGTTGCTCA	CATGATTGGA	4320
	GTAATATCTG	TGGAGCCTCC	TGGCATACCC	CTTTGGTTTG	ACATCACTGG	TGGCAACTAC	4380
	GACAGTCACT	TGATGTGGA	CAAGGGAAC	GGAACCATCA	TTGTTGCCAA	ACCTCTTGAT	4440
75	GCAGAACAGA	AGTCAAACTA	CAACCTCACA	GTCCGAGGCTA	CAGATGGAAC	CACCACTATC	4500
	CTCACTCAGG	TATTATCAAA	AGTAATAGAC	ACAAATGACC	ATCGTCTCTA	GTTTCTTACA	4560
	TCAAAGTATG	AAGTTGTTAT	TCCTGAAGAT	ACAGCGCCAG	AAACAGAAAT	TTTGCAAAAT	4620
	AGTGTCTGTG	ATCAGGATGA	GAAAAACAAA	CTAATCTACA	CTCTGCAGAG	CAGTAGAGAT	4680
	CCACTGAGTC	TCAAGAAAT	TGCTCTTGAT	CCTGCAACCG	GCTCTCTCTA	TACTTCTGAG	4740
80	AAACTGGATC	ATGAAGCTGT	TTCAACAGCA	CACCTCACGG	TCATGGTACG	AGATCAAGAT	4800
	GTGCCGTGTA	AACGCAACTT	TGCAAGGATT	GTGGTCAATG	TCAGCGACAC	GAATGACCAC	4860
	GCCCCGTGGT	TCACCGCTTC	CTCCTACAAA	GGGCGGGTTT	ATGAATCGGC	AGCCGTGTGC	4920
	TCAGTTGTGT	TGCAGGTGAC	GGCTCTGGAC	AAGGACAAAG	GGAAAATATG	TGAAGTGCTG	4980
	TACTCGATCG	AGTCAGGAAA	TATTGGAAAT	ATTGGAAAT	CTTTTATGAT	TGATCCTGTC	5040
	TTGGGCTCTA	TTAAAAGTGC	CAAAGAATTA	GATCGAAGTA	ACCAAGCGGA	GTATGATTTA	5100



	ATGGTAAAAG	CTACAGATAA	GGGCAGTCCA	CCAATGAGTG	AAATAACTTC	TGTGCGTATC	5160
	TTTGTACAAA	TTGCTGACAA	CGCCTCTCCG	AAGTTTACAT	CAAAAGAATA	TTCTGTTGAA	5220
	CTTAGTGAAA	CTGTGAGCAAT	TGGGAGTTTC	GTTGGGATGG	TTACAGCCCA	TAGTCAATCA	5280
5	TCAGTGGTGT	ATGAAATAAA	AGATGGAAT	ACAGGTGATG	CTTTTGATAT	TAATCCACAT	5340
	TCTGGAACATA	TCATCACTCA	GAAAGCCCTG	GACTTTGAAA	CTTTGCCCAT	TTACACATTG	5400
	ATAATACAAG	GAACATAACAT	GGCTGGTTTG	TCCACTAATA	CAACGGTTCT	AGTTCACCTG	5460
	CAGGATGAGA	ATGACAACGC	GCCAGTTTTT	ATGCAGGCAG	AATATACAGG	ACTCATTAGT	5520
	GAATCAGCCT	CAATTAACAG	CGTGGTCCTA	ACAGACAGGA	ATGTCCCCT	GGTGATTGGA	5580
10	GCAGCTGATG	CTGATAAAGA	CTCAATAGCT	TTGCTTGAT	ATCAGATTGT	TGAACCATCT	5640
	GTACACACAT	ATTTTGCTAT	TGATTCTAGC	ACTGGTGCTA	TTCATACAGT	ACTAAGTCTG	5700
	GACTATGAAG	AAACAAGTAT	TTTTCACTTT	ACCGTCCAAG	TGCATGACAT	GGGAACCCCA	5760
	CGTTTATTGG	CTGAGTATGC	AGCGAATGTA	ACAGTACATG	TAATTGACAT	TAATGACTGC	5820
	CCCCCTGTGT	TTGCCAAGCC	ATTATATGAA	GCATCTCTTT	TGTTACCAAC	ATACAAAGGA	5880
15	GTAAAAGTCA	TCACAGTAAA	TGCTACAGAT	GCTGATTCAA	GTGCATTCTC	ACAGTTGATT	5940
	TACTCCATCA	CCGAAGGCCA	CATCGGGGAG	AAGTTTCTA	TGGACTACAA	GACTGGTGCT	6000
	CTCACTGTCC	AAAAACAAC	TCAGTTAAGA	AGCCGCTACG	AGCTAACCGT	TAGAGCTTCC	6060
	GATGGCAGAT	TTGCCGGCCT	TACCTCTGTC	AAAAATTAATG	TGAAAGAAAG	CAAGAAAGAT	6120
	CACCTAAAGT	TTACCCAGGA	TGCTACTCT	CGCGTAGTGA	AAGAGAATTC	CACCGAGGCC	6180
20	GAAACATTAG	CTGTCACTTAC	TGCTATTGGG	AGTCCAATCA	ATGAGCCTTT	GTTTTATCAC	6240
	ATCCTCAACC	CAGATCGCAG	ATTTAAAAATA	AGCCGCACTT	CAGGGGTTCT	GTCAACCACT	6300
	GGCACGCCCT	TGATCGTGA	GCAGCAGGAG	GCCTTTGATG	TGGTTGTAGA	AGTGATAGAG	6360
	GAACATAAGC	CTTCTGCAGT	GGCCACGTT	GTCTGGAAGG	TCATTGTAGA	AGACCAAAAT	6420
	GATAATGCGC	CGGTGTTTGT	CAACCTTCCC	TACTACGCCG	TTGTTAAAGT	GGACACTGAG	6480
25	GTGGGCCATG	TCATTTCGCTA	TGTCAGTCT	GTAGACAGAG	ACAGTGGCAG	AAACGGGGAA	6540
	GTGCATTACT	ACCTCAAGGA	ACATCATGAA	CACCTTCAAA	TTGGAACCTT	GGGTGAAAT	6600
	TCACTGAAA	AGCAATTTGA	GCTTGACACC	TTAAATAAAG	AATATCTTGT	TACAGTGGTT	6660
	GCAAAAGATG	GAGGGAACCC	GGCCTTTTCA	GCGGAAGTTA	TCGTTCCGAT	CACCTGTCATG	6720
	AATAAAGCCA	TGCTCTGTTT	TGAAAAACCT	TTCTACAGTG	CAGAGATTGC	AGAGAGCATC	6780
30	CAGGTGCACA	GGCCTGTGGT	CCACGTGCAG	GCTAACAGCC	CGGAAGGCCCT	GAAAGTGTTC	6840
	TACAGCATCA	CAGACGGAGA	CCCTTTCAGC	CAGTTCACCTA	TTAACTTCAA	TACTGGAGTT	6900
	ATCAATGTCA	TAGCTCTCT	GGACTTTGAG	GGCCACCCGG	CATATAAGCT	GAGCATACGC	6960
	GCAACTGACT	CCTTGACGGG	CGCTCATGCT	GAAGTATTTG	TGGACATCAT	AGTAGACGAC	7020
	ATCAATGATA	AGCCTCTCT	GTTTGCTCAG	CAGTCTTATG	CGGTGACCCT	GTCTGAGGCA	7080
35	TCGTGAATTG	GAACGTCTGT	TGTTCAAGTT	AGAGCCACCG	ATTCTGATT	AGAACCAAAAT	7140
	AGAGGAATCT	CATACCAGAT	GTTTGGGAAT	CACAGCAAGA	GTCTATGATCA	TTTTCATGTA	7200
	GACAGCAGCA	CTGGCCTCAT	CTCACTACTC	AGAACCCTGG	ATTACAGACA	GTCCCGGCAG	7260
	CACACGATTT	TTGTGAGGGC	AGTTGATGGT	GGTATGCCCA	CGCTGAGCAG	TGATGTGATT	7320
	GTACAGGTGG	ACGTTACCGA	CCTCAATGGT	AATCCACCAC	TCTTTGAACA	ACAGATTAT	7380
40	GAAGCCAGAA	TTAGCGAGCA	CGCCCTCAT	GGGCATTTCG	TGACCTGTGT	AAAAGCCTAT	7440
	GATGCAGACA	GTTCAGACAT	AGACAAGTTG	CAGTATTCCA	TTCTGTCTGG	CAATGATCAT	7500
	AAACATTTTG	TCATTGACAG	TGCAACAGGG	ATTATCACCC	TCTCAACCT	GCACCGGCAC	7560
	GCCCTGAAGC	CATTTTACAG	TCTTAACTTG	TCAGTGTCTG	ATGGAGTTTT	TAGAAGTTCC	7620
	ACCCAGGTTT	ATGTAAGTGT	AATTGGAGGC	AATTGTCACA	GTCTGTCTTT	CCTTCAGAAC	7680
45	GAATATGAAG	TGGAACTAGC	TGAAAAACCT	CCCTACATA	CCCTGGTGAT	GGAGGTGAAA	7740
	ACTACGGATG	GGGATTCTGG	TATTATGGT	CAGGTTACTT	ACCATATTGT	AAATGACTTT	7800
	GCCAAAGACA	GATTTTACAT	AAATGAGAGA	GGACAGATAT	TTACTTTGGA	AAAACCTTAT	7860
	CGAGAAACCC	CGGCGAGAAA	AGTGATCTCA	GTCCGTTTAA	TGGCTAAGGA	TGCTGGAGGA	7920
50	AAAGTTGCTT	CTGCAACCGT	GAATGTCATC	CTTACAGATG	ACAATGACAA	TGCACCACAA	7980
	TTTCGAGCAA	CCAAATACGA	AGTGAATATC	GGGTCCAGTG	CTGCTAAAGG	GACTTCAGTC	8040
	GTAAAGTCTG	CGATGATGGC	TCCAATGCCG	ACATCACTTA	TGCCATTGAA		8100
	GCAGACTCTG	AAAGTGTTAA	AGAGAATTTG	GAAATTAACA	AACTGTCCGG	CGTAATCACT	8160
	ACAAAGGAGA	GCCTCATTGG	CTTGGAAAAT	GAATCTTCTA	CTTTCTTTGT	TAGAGCTGTG	8220
55	GATAATGGGT	CTCCATCAAA	AGAACTGTGT	GTTCCTGTCT	ATGTTAAAT	CCTTCCACCG	8280
	GAAATGCAGC	TTCCAAAATT	TTCCAGAACCT	TTCTATACCT	TTACAGTGTG	AGAGGACGTG	8340
	CCTGTTGGAA	CAGAGATAGA	TCTCATCCGA	GCAGAACATA	GTGGGACTGT	TCTTTACAGC	8400
	CTGGTCAAG	GGAATACTCC	AGAAAGCAAT	AGGGATGAGT	CCTTTGTGAT	TGACAGACAG	8460
	AGCGGGAGAG	TGAAGTTGGA	GAAAGAGTCT	GATCATGAGA	CAACTAAGTG	GTATCAGTTT	8520
60	TCCATAGTGG	CCAGGTGCAC	TCAAGATGAC	CATGAGATGG	TGGCTTCTGT	AGATGTTAGT	8580
	ATCCAGTGA	AAGATGCAAA	TGACAAACAGC	CCGGTCTTTG	AATCTAGTCC	ATATGAGGCA	8640
	TTCAATGTTG	AAAACCTGCC	AGGGGGAAGT	AGAGTAATTC	AGATCAGGGC	ATCTGATGCT	8700
	GACTCAGGAA	CCAACGGCCA	AGTTATGTAT	AGCCTGGATC	AGTCACAAAG	TGTGGAAGTC	8760
	ATTGAATCCT	TTGCCATTAA	CATGGAAACA	GGCTGGATTA	CAACTTTAAA	GGAACTTGAC	8820
	CATGAAAAGA	GAGACAAATTA	CCAGATTAAA	GTGGTTGCAT	CAGATCATGG	TGAAAAGATC	8880
65	CAGCTATCCT	CCACAGCCAT	TGTGGATGTT	ACCGTCACCG	ATGTCAACGA	TAGTCCACCA	8940
	CGATTACCGG	CCAGATCTTA	TAAAGGGACT	GTGAGTGAGG	ATGACCCCA	AGGTGGGGTG	9000
	ATTGCCATCT	TAAGTACAC	GGATGCTGAT	TCTGAAGAGA	TCAACAGACA	AGTTACATAT	9060
	TTCATAAACG	GAGGGGATCC	TTTAGGACAG	TTTGCCGTTG	AACTATATCA	GAATGAATGG	9120
	AAGGTATATG	TGAAGAAACC	TCTAGACAGG	GAAAAAAGGG	ACAATTACCT	TCTTACTATC	9180
70	ACGGCAACTG	ATGGCACTTT	CTCATCAAAA	GCGATAGTTG	AAGTGAAAGT	TCTGGATGCA	9240
	AATGACAACA	GTCCAGTTTG	TGAAAAGACT	TTATATTTCAG	ACACTATTCC	TGAAGACGTC	9300
	CTTCTGGGAA	AATTGATCAT	GCAGATCTCT	GCTACAGACG	CAGACATCCG	CTCTAACGCT	9360
	GAAATTAATT	ACACGTTATT	GGGTTTCAAGT	GCAGAAAAAT	TCAAATAAAA	TCCAGACACA	9420
	GGTGAAGTGA	AAACGTCAAC	CCCCCTTGAT	CGTGAGGAGC	AAGCTGTTTA	TCATCTTCTC	9480
75	GTACGGGCA	CAGATGGAGG	AGGAAGATTG	TGCCAAGCCA	GTATTGTGCT	CACGCTAGAA	9540
	GATGTGAACG	ATAAGCCCCC	CGAATTTCTT	GCCGATCCTT	ATGCCATCAC	CGTGTGTTAA	9600
	AAACAGAGC	CGGGAACGCT	GCTGACAGA	GTGCAGGCCA	CAGATGCCGA	CGCAGGATTA	9660
	AATCGGAAGA	TTTTTACTCT	ACTGATTGAC	TCTGCTGATG	GGCAGTTCTC	CATTAAACGAA	9720
	TTATCTGGAA	TTATTTCAGT	AGAAAAACCT	TTGGACAGAG	AACTCCAGGC	AGTATACACC	9780
80	CTCTCTTTGA	AAGCTGTGGA	TCAAGGCTTG	CCAAGGAGGC	TGACTGCCAC	TGGCACTGTG	9840
	ATTGTATCAG	TTCTTGACAT	AAATGACAAC	CCCCCTGTGT	TTGAGTACCG	TGAATATGGT	9900
	GCCACCGTGT	CTGAGGACAT	TCTTGTGGA	ACTGAAGTTC	TTCAAGTGTG	TGCAGCAAGT	9960
	CGGGATATTG	AAGCAATAATG	AGAAATCACCT	TACTCAATAA	TAAGTGGAAA	TGAACATGGG	10020
	AAATTGAGCA	TAGATTCTAA	AACAGGGGCC	GTATTATCA	TTGAGAACTC	GGATTATGAG	10080
	AGCTCTCATG	AGTATTACCT	AACAGTAGAG	GCCACTGATG	GAGGCACGCC	TTCACTGAGC	10140

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

GACGTTGCCA CTGTGAACGT TAATGTAACA GATATCAACG ATAATACCCC TGTGTTACAGC 10200  
CAAGACACCT ACACGACAGT CATCAGTGAA GATGCCGTTT TTGAGCAGTC TGTATCAGC 10260  
GTTATGGCCG ATGATGCCGA TGGACCTTCC AACAGCCACA TCCACTACTC AATTATAGAT 10320  
GGCAACCAGG GAAGCTCGTT CACAATTGAC CCCGTAGGGG GAGAAAGTCAA AGTGACCAAA 10380  
CTTCTCGACC GAGAAAAGAT TTCAAGTTAC ACGCTCACGG TTCAAGCTTC TGATAATGGC 10440  
AGTCCACCCA GAGTCAACAC GACGACCGTG AACATCGATG TGTCCGATGT CAATGACAAC 10500  
GCCGCCGTCT TCTCCAGGGG AAATACAGT GTCAATTATCC AGGAAAATAA GCCAGTGGGC 10560  
TTCAGCGTGC TGCAGCTGGT AGTAACAGAT GAGGATTCTT CCCATAACGG TCCACCCTTC 10620  
TTCTTTACTA TTGTAACGTG AAATGATGAG AAGGCTTTTG AAGTTAACCC GCAAGGAGTC 10680  
CTCCTGACAT CATCTGCCAT CAAGAGGAAG GAGAAAGATC ATTACTTACT GCAGGTGAAG 10740  
GTGGCAGATA ATGGAAGGCC TCAGTTGTCA TCTTTGACAT ACATTGACAT TAGGGTAATT 10800  
GAGGAGAGCA TCTATCCGCC TGCATTTTG CCCCTGGAGA TTTTCATCAC CTCTTCTGGA 10860  
GAAGAATACT CAGGTGGCGT CATTTGGGAAG ATCCATGCCA CAGACCAGGA CGTGTATGAT 10920  
ACTCTAACCT ACAGTCTCGA CCCTCAGATG GACAACCTGT TCTCTGTTTC CAGCACAGGG 10980  
GGCAAGCTGA TAGCACACAA AAAGCTAGAC ATAGGGCAAT ACCTTCTCAA TGTACGCGTA 11040  
ACAGATGGGA AGTTGAGGAT GGTGGCCGAC ATCAGAGTGC ATATCAGACA AGTCACACAG 11100  
GAGATGTTGA ACCACACCAT CGCGATCCGC TTTGCCAACC TCACTCCGGA AGAATTCTGT 11160  
GGTGACTACT GGCACCACTT CCAGCGAGCT TTACGGAACA TCCTGGGTGT GAGGAGGAAC 11220  
GACATACAGA TTGTTAGTTT GCAGTCTCTT GAACCTCACC CACATCTGGA CGTCTTACTT 11280  
TTTGTAGAGA AACCAGGTAG TGCTCAGATC TCAACAAAAC AACTTCTGCA CAAGATTAA 11340  
TCTTCCGTGA CTGACATTGA GGAATCATT GGAGTTAGGA TACTGAATGT ATTCCAGAAA 11400  
CTCTGCGCGG GACTGGACTG CCCCTGGAAG TTCTGCGATG AAAAGGTGTC TGTGGATGAA 11460  
AGTGTGATGT CAACACACAG CACAGCCAGA CTGAGTTTTG TGAATCCCCC CCACCACAG 11520  
GCAGCGGTGT GTCTCTGCAA AGAGGGAAGG TGCCACCTG TCCACCATGG CTGTGAAGAT 11580  
GATCCGTGCC CTGAGGGATC CGAATGTGTG TCTGATCCCT GGGAGGAGAA ACACACCTGT 11640  
GTCTGTCCCA GCGGCAGGTT TGGTCAGTGC CCAGGGAGTT CATCTATGAC ACTGACTGGA 11700  
AACAGTACG TGAAATACCG TCTGACGGAA AATGAAAACA AATTAGAGAT GAAACTGACC 11760  
ATAGGGCTCA GAACATATT CACGCTGCG GTTGTCAATG ATGCTCGAGG AACTGACTAT 11820  
AGCATCTTGG AGATTCTGCA TGGAAAGGCT CAGTACAAGT TTGACTGTGG AAGTGGCCCT 11880  
GGAATTGTCT CTGTTTCAAG CATTGAGTGC AATGATGGGC AGTGGCAGCG AGTGGCCCTG 11940  
GAAGTGAATG GAAACTATGC TCGCTTGGTT CTAGACCAAG TTCATCTGCA ATCGGGCACA 12000  
GCCCCAGGGA CTCTGAAAAC CCTGAACCTG GATAACTATG TGTTTTGGG TGGCCACATC 12060  
CGTCAGCAGG GAACAGAGCA TGGAAAGAGT CCTCAAGTTG GTAATGGTTT CAGGGGTGTG 12120  
ATGGACTCCA TTTATTTGAA TGGGCAGGAG CTCCTTTTAA ACAGCAAACC CAGAAGCTAT 12180  
GCACACATCG AAGAGTCGGT GGATGTATCT CCAGGCTGCT TCCTGACGGC CACGGAAGAC 12240  
TGCGCCAGCA ACCCTTGCCA GAATGGAGGC GTTGTCAATC CGTCACCTGC TGGAGGTAT 12300  
TACTGCAAAAT GCAGTGCCTT GTACATAGGG ACCCACTGTG AGATAAGCGT CAATCCGTGT 12360  
TCCTCAACCC CATGCTCTTA TGGGGGCACG TGTGTGTGTC ACAACGGAGG CTTTGTTTGC 12420  
CAGTGTAGAG GATTATATAC TGGTCAGAGG TGTCAGCTTA GTCCATCTG CAAAGATGAA 12480  
CCCTGTAAGA ATGGCGGAAC ATGCTTTGAC AGTTTGGATG GCGCCGTTTG TCAGTGTGAT 12540  
TCGGGTTTTA GGGGAGAAAG GTGTGAGAGT GATATCGACG AGTGCTCTGG AAACCCCTGC 12600  
CTGCACGGGG CCTCTGTGTA GAACACGCAC GGCTCCTATC ACTGCAACTG CAGCCACGAG 12660  
TACAGGGGAC GTCACTGCGA GGATGCTGCG CCCAACCAAT ATGTGTCCAC GCCGTGGAAC 12720  
ATTGGGTTGG CGGAAGGAAT TGGAAATCGT GTGTTTGTGT CAGGGATATT TTTACTGGTG 12780  
TGGGTGTTTG TTCTCTGCGG TAAGATGATT AGTCGGAAAA AGAAGCATCA GGCTGAACCT 12840  
AAAGACAAGC ACCTGGGACC CGCTACGGCT TTCTTGCAAA GACCGTATT TGAATCCAAG 12900  
CTAAATAAGA ACATTACTC AGACATACCA CCCAGGTGC CTGTCCGGCC TATTTCTTAC 12960  
ACCCCGAGTA TTCCAAGTGA CTCAAGAAAC AATCTGGACC GAAATCTCT CGAAGGATCT 13020  
GCTATCCAGC AGCATCCCGA ATTCAGCACT TTTAAACCCG AGTCTGTGCA CGGGCACCAG 13080  
AAAGCAGTGG CGGTCTGTCG AGTGGCGCCA AACCTGCCTC CCCCACCCCT TCAAACTCC 13140  
CCTTCTGACA GCGACTCCAT CCAGAAGCCT AGCTGGGACT TTGACTATGA CACAAAAGTG 13200  
GTGGATCTTG ATCCCTGTCT TTCCAAGAAG CCTCTAGAGG AAAAGCCTTC CCAGCCATAC 13260  
AGTGCCCGGG AAAGCCTGTC TGAAGTGCAG TCCTTCAGCT CCTTCAGTC CGAATCGTGC 13320  
GATGACAATG GGTATCACTG GGATACATCA GATTGGATGC CAAGCGTTCC TCTGCCGGAC 13380  
ATACAAGAGT TCCCCAATA TGAGGTGATT GATGAGCAGA CACCCTGTGA CTCAGCAGAT 13440  
CCAAAACGCCA TCGATACGGA CTATTACCCT GGAGGCTACG ACATCGAAAG TGATTTTCCT 13500  
CCACCCCCAG AAGACTTCCC CGCAGCTGAT GAGCTACCAC CGTTACCGCC CGAATTTCAG 13560  
AATCAGTTTG AATCCATCCA CCCTCCTAGA GACATGCCTG CCGCGGGTAG CTTGGGTTCT 13620  
TCATCAAGAA ACCGCGAGAG GTTCAACTTG AATCAGTATT TGCCCAATTT TTATCCCTC 13680  
GATATGTCTG AACCTCAAAC AAAAGGCACT GGTGAGAATA GTACTGTGAG AGAACCCAT 13740  
GCCCTTACC CGCCAGGGTA TCAAAGACAC TTCGAGGCGC CCGCTGTGCA GAGCATGCC 13800  
ATGCTGTGT ACGCCCTCCAC CGCCTCCTGC TCTGACGTGT CAGCCTGTCTG CGAAGTGGAG 13860  
TCCGAGGTCA TGATGAGTGA CTATGAGAGC GGGGACGACG GCCACTTCGA AGAGGTGACG 13920  
ATCCCGCCCC TGGATTCCCA GCAGCACACG GAAGTCTGAC TCTCAACTCC CCCCAGAGTG 13980  
CCTGACTTTA GTGAACCTAG AGGTGATGTG AGTAATCCGC GCTGTTCTTT GCAGCAGTGC 14040  
TTCCAAGCTT TTTTGTGTGA GCCGAATGGG CATGGCTGCG CTGGATCCTG CGCCTCTGGA 14100  
CGTGCTAGCC ATTTCAGTG TCCCAACTAC TGTCTATCGT AGGTTTTCAT CGGCTGTGCC 14160  
ATTTCCCAAC GTCTTTTGGG ATTTACATCT GTCTGTGTTA AAATAATCAA ACGAAAATC 14220  
AGTCCTGTGT TGTGAGCATG ATTCATGTAT TTATATAGAT TTGATTATTT TAATTTTCCT 14280  
GTCTCTTTT TTTGTAAATT TTATGTACAG ATTTGATTTT TCATAGTTT AACTAGATT 14340  
CCAAGATATT TTGTGCAATT GTTTCACTG AATTTTGGTG GTGTCAGTGC CATTATCTAG 14400  
CACCCGTGAT TTTTTTTTTT TACTATAACC AGGGTTTCAT TCTGCTCTTT TCCACTGAAG 14460  
TGTGACATTT TGTGATGACA TTTGAGTGA GTCAATTCAT TCTAGCTGTA CATAGGATGA 14520  
AGGAGAGATC AGATACATGA ACATGCTTTA CATGGGTGTC TGTATTTAGA ATTATAACA 14580  
TTTTTCATTA TTGGAAAGTG TAACGGGGAC CTTCTGCATA CCTGTTTGA ACCAAAACCA 14640  
CCATGACACA GTTTTTATAG TGTCTGTATA TTTGTGATGC AATGGTCTTG TAAAGGTTTT 14700  
TAATGAAAAC TACCATTAGC CAGTCTTTCT TACTGACAAT AAATTATTAA TAAAT 14756

Seq ID NO: C161 DNA Sequence  
Nucleic Acid Accession #: NM\_014220.1  
Coding sequence: 102..710

1 11 21 31 41 51  
| | | | | |

	GTGGTGTTTG	CTTCTCCAC	CAGAAAGGCA	CACTTTCATC	TAATTTGGGG	TATCACTGAG	60
	CTGAAGACAA	AGAGAAGGGG	GAGAAAAACCT	AGCAGACCAC	CATGTGCTAT	GGGAAGTGTG	120
	CACGATGCGAT	CGGACATTCT	CTGGTGGGGC	TCGCCCTCCT	GTGCATCGCG	GCTAATATTT	180
5	TGCTTTACTT	TCCCAATGGG	GAAACAAAGT	ATGCCTCCGA	AAACCACCTC	AGCCGCTTCG	240
	TGTGGTCTT	TTCCTGCATC	GTAGGAGGTG	GCCTGCTGAT	GCTCCTGCCA	GCATTTGTCT	300
	TCATTGGGCT	GGAACAGGAT	GACTGCTGTG	GCTGCTGTGG	CCATGAAAAC	TGTGGCAAAC	360
	GATGTGCGAT	GCTTTCTTCT	GTATTGGCTG	CTCTCATTTG	AATTGCAGGA	TCTGGCTACT	420
	GTGTCAATTG	GGCAGCCCTT	GGCTTAGCAG	AAGGACCACT	ATGTCTTGAT	TCCCTCGGCC	480
10	AGTGGAACTA	CACCTTTGCC	AGCACCGAGG	GCCAGTACCT	TCTGGATACC	TCCACATGGT	540
	CCGAGTGCAC	TGAACCCAAG	CACATTGTGG	AATGGAATGT	ATCTCTGTTT	TCTATCCTCT	600
	TGGCTCTTGG	TGGAATTGAA	TTTACTTTGT	GTCTTATTCA	AGTAATAAAT	GGAGTGTCTG	660
	GAGGCATATG	TGGCTTTTGC	TGCTCTCACC	AACAGCAATA	TGACTGCTAA	AAGAACAAC	720
	CCAGGACAGA	GCCACAATCT	TCTCTATTTT	CATTGTAATT	TATATATTTT	ACTTGTATTCT	780
15	ATTTGTAAAA	CTTTGTATTA	GTGTAACATA	CTCCCCACAG	TCTACTTTTA	CAAACGCCTG	840
	TAAAGACTGG	CATCTTCACA	GGATGTCAGT	GTTTAAATTT	AGTAAACTTC	TTTTTTGTTT	900
	GTTTATTGTG	TTTTTAAAGAA	TGAGGAAACA	AACCAACCTC	TGGGGGTAGT		960
	TTACAGACTG	AGTGACAGTA	CTCAGTATAT	CTGAGATAAA	CTCTATAATG	TTTTGGATAA	1020
	AAATAACATT	CCAATCACTA	TGTATATATAT	GTGCATGTAT	TTTTTAAATT	AAAGATGTCT	1080
20	AGTTGCTTTT	TATAAGACCA	AGAAGGAGAA	AATCCGAGAA	CCTGGAAAGA	TTTTTGTGTT	1140
	CACCTGCTGT	ATGATGTTTC	CCATTTCATAC	ACCTATAAAT	CTCTAACCAAG	AGGCCCTTTG	1200
	AACCTGCCTG	TGTTCTGTGA	GAAACAATAA	TTTACTTAGA	GTGGAAGGAC	TGATTGAGAA	1260
	TGTTCCAATC	CAATGAATG	CATCACAACT	TACAATGCTG	CTCATTTGTTG	TGAGTACTAT	1320
	GAGATTCAAA	TTTTTCTAAC	ATATGGAAGG	CCTTTGTGTC	TCCAAAGATG	AGTACTAGGG	1380
25	ATCATGTGTT	TAAAAAAGA	AAGGCTACGA	TGACTGGGCA	AGAAGAAAGA	TGGGAACTG	1440
	AAATAAGCAG	TTGATCAGCA	TCAATTGGAAC	ATGGGGACGA	GTGACGGCAG	GAGGACCACG	1500
	AGGAAATACC	TCAAAACTA	ACTTGTTTAC	AACAAAATAA	AGTATTCACT	ACGAAAAAAA	1560
	AAAAAAAATA	AAAAAAAATA	AAA				1583

Seq ID NO: C162 DNA Sequence  
Nucleic Acid Accession #: NM\_003759.1  
Coding sequence: 150..3257

	1	11	21	31	41	51	
35	GTTCCTTTTG	ACACATCACA	CAGAATTGGA	GTGCTGTCTT	TCTGGAGAGT	GGTGGAGAAC	60
	CAAGATACAG	TTCAGAACCA	AAGGAATAGA	GAAGGGCTTT	GATTTCTTTT	TGGCTTTAGA	120
	TTGGGGATTT	GGGAGGCTTA	GCAGGAAAGA	TGTCCACTGA	AAATGTGGAA	GGGAAGCCCA	180
	GTAACCTTGG	GGAGAGAGGA	AGAGCCCGGA	GCTCCACTTT	CCTCAGGGTT	GTCCAGCCAA	240
40	TGTTTAAACA	CAGTATTTTC	ACTTCTGCAG	TCTCTCTGCG	TGCAGAACGC	ATCCGATTCA	300
	TCTTGGGAGA	GGAGGGATGAC	AGCCCAAGCTC	CCCCTCAGCT	CTTCACGGAA	CTGGATGAGC	360
	TGCTGGCCGT	GGATGGGCGG	GAGATGGAGT	GGAAGGAAAC	AGCCAGGTGG	ATCAAGTTTG	420
	AAGAAAAAGT	GGAACAGGGT	GGGGAAAGAT	GGAGCAAGCC	CCATGTGGCC	ACATTGTCCC	480
	TTCATAGTTT	ATTTGAGCTG	AGGACATGTA	TGGAGAAAGG	ATCCATCATG	CTTGATCGGG	540
45	AGGCTTCTTC	TCTCCACAG	TTGGTGGAGA	TGATTGTTGA	CCATCAGATT	GAGACAGGCC	600
	TATTGAAACC	TGAACCTTAAG	GATAAGGTGA	CCTATACTTT	GCTCCGGAAG	CACCGGCATC	660
	AAACCAAGAA	ATCCAACCTT	CGGTCCCTGG	CTGACATTGG	GAAGACAGTC	TCCAGTGCAA	720
	GTAGGATGTT	TACCAACCTT	GATAATGGTA	GCCCAGCCAT	GACCCATAGG	AATCTGACTT	780
	CCTCCAGTCT	GAATGACATT	TCTGATAAAC	CGGAGAAAGG	CCAGCTGAAG	AATAAGTTCA	840
50	TGAAAAAATT	GCCACGTGAT	GCAGAAAGCT	CCAACGTGCT	TGTTGGGGAG	GTTGACTTTT	900
	TGGATACTCC	TTTCAATTGC	TTTGTAGGCG	TACAGCAGGC	TGTCATGCTG	GGTGCCCTGA	960
	CTGAAGTTCC	TGTGCCACCA	AGGTCTTGTG	TCATTCTCTT	AGGTCTTAAG	GGGAAAGCCA	1020
	AGTCTCTACC	CGAGATTGGC	AGAGCCATTG	CCACCCTGAT	GTCTGATGAG	GTGTTCCATG	1080
	ACATTGCTTA	TAAAGCAAAA	GACAGGACAG	ACCTGATTGC	TGGTATTGAT	GAGTTCCTAG	1140
	ATGAAGTCAT	CGTCTCTCCA	CCTGGGGAAT	GGGATCCAGC	AATTAGGATA	GAGCCTCCTA	1200
55	AGAGTCTTCC	ATCCTCTGAC	AAAAGAAAGA	ATATGTACTC	AGGTGGAGAG	AATGTTTCTA	1260
	TGAATGGGGA	TACGCCCCAT	GATGGAGGTC	ACGGAGGAGG	AGGACATGGG	GATTGTGAAG	1320
	AATTGCAGCG	AACTGGACGG	TTCTGTGGTG	GACTAATTAA	AGACATAAAG	AGGAAAGCGC	1380
	CATTTTTTGC	CAGTGATTTT	TATGATGCTT	TAAATATTCA	AGCTCTTTTC	GCAATTCTCT	1440
	TCATTTATCT	GGCAACTGTA	ACTAATGCTA	TCATTTTGGG	AGGACTGCTT	GGGGATGCCA	1500
60	CTGACAACAT	GCAGGGCGTG	TTGGAGAGTT	TCCTGGGCAC	TGCTGTCTCT	GGAGCCATCT	1560
	TTTGCCTTTT	TGCTGGTCAA	CCACTCACTA	TTCTGAGCAG	CACCGGAACCT	GTCTAGTTT	1620
	TTGAGAGGCT	TCTATTTAAT	TTGAGCAAGG	ACAATAATTT	TGACTATTTC	GAGTTTCGCC	1680
	TTTGGATTGG	CCTGTGGTCC	GCCTTCTCTAT	GTCTCATTTT	GGTAGCCACT	GATGCCAGCT	1740
65	TCTTGGTTCA	ATACTTCACA	CGTTTCACGG	AGGAGGGCTT	TTCTCTCTCT	ATTAGCTTCA	1800
	TCTTTATCTA	TGATGCTTTC	AAGAAGATGA	TCAAGCTTGC	AGATTACTAC	CCCATCAACT	1860
	CCAACTTCAA	AGTGGGCTAC	AACACTCTCT	TTTCTGTGAC	CTGTGTGCCA	CCTGACCCAG	1920
	CTAATATCTC	AATATCTAAT	GACACCACAC	TGGCCCCAGA	GTATTTTGCCA	ACTATGTCTT	1980
	CTACTGACAT	GTACCAATAAT	ACTACCTTTG	ACTGGGCATT	TTTGTGCAAG	AAGGAGTGTG	2040
70	CAAAATACGG	AGGAAACCTT	GTCCGGGAACA	ACTGTAATTT	TGTTCTCTGAT	ATCACACTCA	2100
	TGTCTTTTAT	CCTCTTCTTG	GGAACCTACA	CCTCTTCCAT	GGCTCTGAAA	AAATTTCAAAA	2160
	CTAGTCCTTA	TTTCTCAACC	ACAGCAAGAA	AACATGATCAG	TGATTTTGCC	ATTATCTTGT	2220
	CCATTCTCAT	CTTTTGTGTA	ATAGATGCCC	TAGTAGGCGT	GGACACCCCA	AAACTAATTG	2280
	TGCCAAGTGA	GTTTCAAGCCA	ACAAGTCCAA	ACCGAGGTTG	GTTCTGTCCA	CCGTTTGGAG	2340
75	AAAACCCCTG	GTGGGTGTGC	CTTGCTGCTG	CTATCCCGGC	TTTGTGGTTC	ACTATACTGA	2400
	TTTTCATGGA	CCAACAAATT	ACAGCTGTGA	TTGTAAACAG	GAAAGAACAT	AAACTCAAGA	2460
	AAGGAGCAGG	GTATCACTTG	GATCTCTTTT	GGTGGGCCAT	CCTCATGGTT	ATATGCTCCC	2520
	TCATGGCTCT	TCCGTGGTAT	GTAGCTGCTA	CGGTCACTCT	CATTGTCTAC	ATCGACAGTT	2580
	TGAAGATGGA	GACAGAGACT	TCTGCACCTG	GAGAACCAAC	AAAGTTTCTA	GGAGTGAGGG	2640
	AACAAAGAGT	CACCTGGAAAC	CTTGTGTTTA	TTCTGACTGG	TCTGTCAAGT	TTTATGGCTC	2700
80	CCATCTTGAA	GTTTATACCC	ATGCCTGTAC	TCTATGGTGT	GTTCCTGTAT	ATGGGAGTAG	2760
	CATCCCTTAA	TGGTGTGCAG	TTTATGGATC	GTCTGAAGCT	GCTTCTGATG	CCTCTGAAGC	2820
	ATCAGCCTGA	CTTCACTCAT	CTGCGTCATG	TTCTCTGCGC	CAGAGTCCAC	CTGTTCACTT	2880
	TCTGCAAGGT	GTGTGTCTG	GCCCTGCTTT	GGATCCTCAA	GTCAACGGTG	GCTGCTATCA	2940
	TTTTTCCAGT	AATGATCTTG	GCATTGTGAT	CTGTGAGAAA	AGGCATGGAC	TACCTCTTCT	3000

	CCCAGCATGA	CCTCAGCTTC	CTGGATGATG	TCATTCCAGA	AAAGGACAAG	AAAAAGAAGG	3060
	AGGATGAGAA	GAAAAAGAAA	AAGAAGAAGG	GAAGTCTGGA	CAGTGACAA	GATGATTCTG	3120
	ACTGCCCAT	CTCAGAAAAA	GTTCCAAGTA	TTAAATTTCC	AATGGACATC	ATGGAACAGC	3180
5	AACTTTCTCT	AAGCGATAGC	AAACCTTCTG	ACAGAGAAAA	ATCACCACAA	TTCTTTGAAC	3240
	GCCACACATC	ATGCTGATAA	AATTCCTTTC	CTTCAGTCAC	TCCGTATGCC	AAGTCCTCCT	3300
	AGAACTCCAG	TAAAGTTGCG	CTCAAATTAG	ACTAGAACTT	GAACCTGAAG	ACAATGATTA	3360
	TTTCTGGAGG	AGCAAGGGAA	CAGAAACTAC	ATTGTAACTT	GTTTGTCTTT	CTTAAAACTG	3420
	ACATTTGTGT	TTAATGTCAT	TTGTTTTTGT	TTGGCTGTTT	GTTTATTTT	TAACTTTTAT	3480
10	TTCTGCTCAG	TTTTTGGTCA	CAGGCCAAAT	AATACAGCGC	TCTCTCTGCT	TCTCTCTTGC	3540
	ATAGATACAA	TCAAGACAA	AGTGCACCGT	TCCTTAAAAA	CAGCATCTGA	GGAATCCCCC	3600
	TTTTGTCTCT	AAACTTTTCA	ATGTGTCTCT	TGATAACCAA	ATTCTGTCTC	TCAAGACACA	3660
	GACACCCACA	GACCTGTGCC	TTTGCTCTTA	TTAAGCAGAG	GATGGAAGTA	TTAAGGATTT	3720
	TGTAACACCT	TTTATGAAAA	TGTTGAAGGA	ACTTAAAACT	TTAGCTTTGG	AGCTGTGCTT	3780
15	ACTGGCTTGT	CTTTGTCTGG	TAGAACAAC	CTTGACCTCC	AGACAGAGTC	CCTTCTCACT	3840
	TATAGAGCTC	TCCAGGACTG	GAAAAAGTGC	TGCTATTTTA	ACTTGTCTCT	GCTTGTAAAT	3900
	CCTAATCTTA	GAGTTATCAA	AAGAAGAAAA	AACTGAAGGT	ACTTTACTCC	CTATAGAGAA	3960
	TAACCTGCCA	TCATTTGTAG	AAGTGCTGGA	ATGTCCCTTT	TTTCTATGTC	AACTTTTTTA	4020
	TAACCTCTTA	ATGAACCTAT	CTGTGGAGTA	CATTGAAGAA	TATTTTCTCT	CCTAGATTTT	4080
20	GTTGTTTAAA	TTATGGGGCC	TAACCTGCCA	CTTATTTTTT	GTCAATTTTT	AAAACTTTTT	4140
	TTTAATTAAT	GTAAGAAAAA	TGAATTTTTT	CCTGCAGCAG	GAAACATAGT	TTTCAGTAGT	4200
	TCTACCTCTT	ATTTGTAGCT	GCCAGGCTTT	CTGTAAAAAT	TGTATTGTAT	ATAATGTGAT	4260
	TTTTACACAT	ACATACACAC	ACAATACAC	AATCTCTAGG	GTAAGCCAGA	AGGCAAGATC	4320
	AGATTAAAAA	CACCATGTCT	CTAAGCATCC	ATTTTTCCCT	TTCTTTAAAA	GAACTTTAAC	4380
25	TGTTCTATGA	AGGAGATTGA	GGGAGAAGAG	ACAACTCCT	ATGTCATGAG	AATAACCGAT	4440
	GTTCTGATAA	TAGTAGCATC	TAGGTACAGA	TGCTGGTGT	ATTACCACGT	CAATGTCCCTA	4500
	TGCAATATGT	TAGACATTT	TCTCATTTTG	AAATATTTGT	GTGTTTGTGT	ATGTGCTCTG	4560
	TGCCATGGCT	GGTGTATATA	TGTGCAATGT	TAGAAGGCAA	AAGAGTGATG	GTAGGCAGAG	4620
	GGCAAGTCA	TTGAATCTCT	TATGCCAGTT	TTCAATAAAC	CCAAACCACA	TATGAAAAAA	4680
30	TCCATTAAAG	GTCCAAGAGT	TCTGTCCATA	TGAAATGAG	GGTAAATATA	TTTTATTTC	4740
	CAGGTATCAG	TCATTTATAAT	TGATATAATA	GCTCTAACAT	GCAATATAAA	ATTCATAGGA	4800
	GTATTAAATG	CCCATTTTACA	CATCTATAAA	ATGTAATGGG	ATTGCAGAGC	TGCAGAGTAC	4860
	AGTGTAACAG	TACTCTCATG	CAATTTTTTT	CAGGATGCAA	AGGCAATTAT	TCTTTGTAAG	4920
	CGGGACATTT	AGATATATTT	GTGTACATAT	TATATGTATG	TATATTTCAA	AGTACCACAC	4980
35	TGAAATTTAG	ACATTTATTA	ACCAATTTA	ACGTGGTATT	TAAAGGTAAT	ATTTTAAATA	5040
	TGATACATTA	CATATTGTGA	ATGTATACTA	AAAAACATTT	TTAAATGTTA	AAATATAAAT	5100
	TTCAGATTCA	TATAACCACA	ACTGTGATAT	ATCCTAACCTA	TAACCAAGTTG	TTGAGGGGTA	5160
	TACTAGAAGC	AGAATGAAC	CACATTTTTT	GGTTTGATAA	TATGCACCTA	TTGACTCCCA	5220
	CTCATTTGTT	TGTTAATTTA	GTTATTTATC	TGCTCTCTTG	TAATTTTGAT	TACAAAAATT	5280
40	TTATTATCCT	GAGTTTACCTG	TTACTTTTTAC	AGTACCTGAT	ACTCCTAAAA	CTTTTAACTT	5340
	ATACAAATTA	GTCAATAATG	ACCCCAATTT	TTTCATTAAA	ATAATAGTGG	TGAATTATAT	5400
	GTTATTGTGT	TAAAACTTCA	CTTGCCAAAT	TCTGGCTTCA	CATTTGTATT	TAGGGCTATC	5460
	CTTAAATATG	TGAGTCTATA	TTATCTAGCT	TTCTATTACC	CTAATATAAA	CTGGTATAAG	5520
	AAGACTTTCC	TTTTTCTTTT	ATGCATGGAA	GCATCAATAA	ATTGTTTAAA	AACCATGTAT	5580
45	AGTAAATTC	GCTTAACCCG	TGATCTTCTT	AAGTTAAAGG	TACTTTTGTT	TTATAAAGC	5640
	TCTAGATAAA	ACTTTCTTTT	CTGATCATGA	ATCAAGTATC	TGTGGTTTCA	TGCCCCCTCT	5700
	TATACCTTTC	AAAGAACTCC	TGAAGCAACT	TAACTCATCA	TTTCAGCCTC	TGAGTAGAGG	5760
	TAAACCTTAT	GTGTACTTCT	GTTTATGATC	CATATTGATA	TTTATGACAT	GAACACAGAA	5820
	TAGTACCTTA	CATTTGCTAA	ACAGACAGTT	AATATCAAAT	CCTTTCAATA	TTCTGGGAAC	5880
50	CCAGGGAAGT	TTTTAAAAAT	GTCAATTACT	TCAAAGGAAC	AGAAGTAGTT	AACCAAACTA	5940
	ACAAGCAAAA	TGAGTCTTAT	ACCTAGTGAC	ACCAAAATTA	CGGTATTTTA	ACTGAATTTA	6000
	CCCATTTGACT	AAGAAATGAAC	CGGATTTGGT	GGTGGTTTTG	TTTCTATGCA	AACTGGACAC	6060
	AAATTACAAC	AGTAAATTTT	TTTATAAGTG	CTTCTCCCTT	CTCCATGATG	TGACTTCCGG	6120
55	AGATAAAGGA	TTCAAAGAGT	AAAGACAAAG	TACGCTCAGA	GTGTTTAAAC	AGAAAGTCCT	6180
	GGCTGTGGTT	GCAGAAACAC	TGTTGGAAGA	AAAGAGATGA	CTAAGTCAAG	TGTCTGCCTT	6240
	ATCAAAAGAG	CAAAAATGCC	TCTGGTTTTG	TGTTTGGGAG	AAAAATATCT	TGGACGCACT	6300
	GTTTTCTCTG	ATAAAAGTCA	TCTTCTCTAC	TGTTGTAAAT	GAATACCTGG	AATTCTAATT	6360
	GTTTTGTGTG	CCAGGGGCGAG	TAATGTCCCT	GCCTCTTCTC	CCAATCAAGG	TTGAGGAGTG	6420
	GGGCTGGGGA	GAGGACTTAA	CTGACTTAAG	AAGTAGGAAA	ACAAAAACCT	CTCTCCTCAG	6480
60	CCTTCCACCT	CCAAGAGAGG	AGGAAAAACA	GTTGTCTGCT	GTCTGTAAAT	CAGTTTGCCT	6540
	GTATTTTATG	CTCATGCAAC	AACCCATACA	GAGTAAATCT	TTTATCAACT	ATATCTGGT	6600
	GTTAATAGAG	GAATGATTGT	CTTCCGAGTT	TTTTGGTTCC	TTTTTTAACT	GTGTTAAAGT	6660
	ACTTGAATAT	TATTGACTGC	TGACTATATT	TTAAAAACAA	AATGAAATAA	TTTGAGTTGT	6720
	ATTACAGAGG	TGACATTTGT	TCAGGGATGG	GACAAAGCCT	TCTTCAATCC	TTTTCATACT	6780
65	ACTTAATGAT	TTTGGTGCAG	GAACCTGAGA	TTTTCTGATT	TATATTTCAT	GATATTTCAC	6840
	ATTGTCTCTT	CACAGCATGA	GCATGAAGCC	CAGTGGCACC	AAATGGCTGG	GTACAATCAA	6900
	GTGATATTTT	GTAGCACCTC	ACTATCTGAA	AGGCCATGAG	TTTTTCAGATG	ATTTCAATTGA	6960
	GCTTCAATGC	AGCCTGAAAT	TTTAAAAAAG	TTGTGTAATA	CGCCAACCAG	TCAAGTTGTG	7020
	TTTTGGCCAG	AGTATTTAGT	ATGTCCAATT	TCCTGGCTCA	TTTCATTGTG	CTTATGGGT	7080
70	ACGTATAAAA	AGCAAGAATT	CTGTTTCTTA	GGCAAACATT	GCAACTCAGG	GCTAAAGTCA	7140
	TCCAGTGAAT	CTTTTAGAGC	CAGAAGTAAC	TTTGTCCCGG	TCCTACAATG	TGAAAAGAGT	7200
	GAATAGTTGC	CTCTTTTATG	CCATTTTCAT	GGCTGGTACA	TATTCGTACG	CATTACTTTT	7260
	CAGAATCAAT	ACGCACCTTC	AGATATTCTT	ATTTTTATTC	TCTTAAGTCT	TTATTAACCT	7320
	TGGAGAGAGA	AATGATGCAT	CTTTTTATTT	TAAATGAAGT	AGATCAACAT	GGTGGAACAA	7380
75	AATGATAAAG	AACAGAAAAA	ATTTCAATAT	ATTACTAATA	ACTTTTCCCA	ATATAAATCC	7440
	TAAATTTCTT	ATAACATAGT	ATTTTACAGT	TTTATGAAGC	TTTCTATTGT	GACTTTTATG	7500
	GAATTAAGAG	ATGAAGAAGA	TGAGATATTT	TAGCATTTAT	ATTTTTCCAA	ATTATATGTA	7560
80	TACTTAAAAA	TAAAGTAACT	TTATGTC				7586

Seq ID NO: C163 DNA Sequence  
Nucleic Acid Accession #: NM\_000958  
Coding sequence: 389..1855

1 11 21 31 41 51  
| | | | |

CGGCACAGCC TCACACCTGA AGCTGTCTCT CCCGACAGCG AGACCGGCGG GCACTGCAAA 60  
 GCTGGGACTC GTCTTTGAAG GAAAAAAAT AGCGAGTAAG AAATCCAGCA CCATTCTTCA 120  
 CTGACCCATC CGCTGCACCC TCTTGTTCCT CAAGTTTTGG AAAGCTGGCA ACTCTGACCT 180  
 CGGTGTCCAA AAATCGACAG CCACTGAGAC CGGCTTTAGG AAGCCGAAGA TTTGGCAGTT 240  
 TCCAGACTGA GCAGGACAAG GTGAAAGCAG GTTGGAGGCG GGTCCAGGAC ATCTGAGGGC 300  
 TGACCTCTGG GGCTCGTGAG GCTGCCACCG CTGCTGCCCG TACAGACCCA GCCTTGCACT 360  
 CCAAGGCTGC GCACCGCCAG CCACTATCAT GTCCACTCCC GGGGTCAATT CGTCCGCCTC 420  
 CTTGAGCCCC GACCCGCTGA ACAGCCCACT GACCATCCCG GCGGTGATGT TCATCTTCGG 480  
 GGTGGTGGGC AACCTGGTGG CCATCGTGGT GCTGTGCAAG TCGCGCAAGG AGCAGAAGGA 540  
 GACGACCTTC TACACGCTGG TATGTGGGCT GGCTGTCAAC GACCTGTTGG GCACTTTGTT 600  
 GGTGAGCCCC GTGACCATCG CCACGTACAT GAAGGGCCAA TGGCCCGGGG GCCAGCCGCT 660  
 GTGCGAGTAC AGCACCTTCA TTCTGCTCTT CTTCAGCCTG TCCGGCCTCA GCATCATCTG 720  
 CGCCATGAGT GTGAGCGCT ACCTGGCCAT CAACCATGCC TATTTCTACA GCCACTACGT 780  
 GGACAAGCGA TTGGCGGGCC TCACGCTCTT TGCAGTCTAT GGTCCAACG TGCTCTTTTG 840  
 CGCGCTGCCC AACATGGGTC TCGGTAGCTC GCGGCTGCAG TACCCAGACA CTGGTGCTT 900  
 CATCGACTGG ACCACCAACG TGACCGCGCA CGCCGCTAC TCCTACATGT ACGCGGGCTT 960  
 GAGCTCCTTC CTCACTTCG CCACCGTCTT CTGCAACGTG CTGTGTGTCG GCGCGCTGCT 1020  
 CGCATGACAC CGCCAGTTCA TGGCGCGCAC CTCGCTGGGC ACCGAGCAGC ACCACGCGGC 1080  
 CGCGGCGGCC TCGGTTGCCCT CCGGGGGCCA CCCCCTGCCC TCCCCAGCCT TGCCGCGCCT 1140  
 CAGCGACTTT CGGCGCCGCG GAGGCTTCCG CCGCATCGCG GCGCGCGAGA TCCAGATGGT 1200  
 CATCTTACTC ATTGCCACCT CCCTGGTGGT GCTCATCTGC TCCATCCCGC TCGTGGTGCG 1260  
 AGTATTCTGC AACCAAGTAT ATCAGCCAAG TTTGGAGCGA GAAGTCAGTA AAAATCCAGA 1320  
 TTTGAGGCC ATCCGAATTG CTCTGTGTA CCCCATCCTA GACCCCTGGA TATATATCCT 1380  
 CTTGAGAAAG ACAGTGTCTA GTAAAGCAAT AGAGAAGATC AAATGCCTCT TCTGCCGCAT 1440  
 TGGCGGGTCC CGCAGGGAGC GCTCCGAGCA GCACTGTCTA GACAGTCAA GGACATCTTC 1500  
 TGCCATGTCA GGCACATCTC GCTCCTTCAT CTCCCGGAG CTGAAGGAGA TCAGCAGTAC 1560  
 ATCTCAGACC CTCTGCCAG ACCTCTCACT GCCAGACCTC AGTGAATATG GCCTTGGAGG 1620  
 CAGGAATTTG CTTCCAGGTG TGCTTGGCAT GGGCCTGGCC CAGGAAGACA CCACCTCACT 1680  
 GAGGACTTTG CGAATATCAG AGACCTCAGA CTCTTCACAG GGTCAAGACT CAGAGAGTGT 1740  
 CTCTACTGGT GATGAGGCTG GTGGAGCGG CAGGGCTGGG CCTGCCCTA AGGGGAGCTC 1800  
 CCGTCAAGTC ACATTTCCCA GTGAAACACT GAACCTATCA GAAAAATGTA TATAATAGGC 1860  
 AAGGAAAGAA ATACAGTACT GTTCTGGAC CTTATAAAA TCCTGTGCAA TAGACACATA 1920  
 CATGTCACAT TTAGCTGTGC TCAGAAGGGC TATCATCA 1958

Seq ID NO: C164 DNA Sequence  
 Nucleic Acid Accession #: NM\_002659.1  
 Coding sequence: 427..1434

1 11 21 31 41 51  
 | | | | |  
 CAGTATCCCT CCTGACAAAA CTAACAAAA TCCTGTTAGC CAAATAATCA GCCACATTCA 60  
 TATTACCGT CAAAGTTTTT ATCCTCATTT TACAGCAGTG GAGAGCGATT GCCCGGGGTC 120  
 CCACGTTAGG AAGAGAGAGA ACTGGGATT GCACCCAGGC AATCTGGGGA CAGAGCTGTG 180  
 ATCAACAATC CATGAGTCAG GGCGGAGCCA GCCCCTTCAC CACCAGCCGG CCGCGCCCGG 240  
 GGAAGGAAGT TTGTGGCGGA GGAGGTTCTG ACGGGAGGAG GGGGAGGCGC CCACGCTACT 300  
 GGGGCTGACT CGCTCTTTG CAAAACGCTT GGGAGGAGTC CCTGGGGCCA CAAAACCTGCC 360  
 TCCTTCTGTA GGCCAGAAGG AGAGAAGACG TGCAGGGACC CCGCGCACAG GAGCTGCCCT 420  
 CGCGACATGG GTCACCCGCC GCTGCTGCCG CTGCTGCTGC TGCTCCACAC CTGCGTCCCA 480  
 GCCTCTTGGG GCCTGCGGTG CATGCAGTGT AAGACCAACG GGGATTTCCG TGTGGAAGAG 540  
 TGCGCCCTGG GACAGGACT CTGCAGGACC ACGATCGTGC GCTTGTGGGA AGAAGGAGAA 600  
 GAGCTGGAGC TGGTGGAGAA AAGCTGTACC CACTCAGAGA AGACCAACAG GACCTTGAGC 660  
 TATCGGACTG GCTTGAAGAT CACCAGCCTT ACCGAGGTTG TGTGTGGGTT AGACTTGTGC 720  
 AACAGGGCA ACTCTGGCCG GCTGTCTACC TATTCCCGAA GCCGTACCTT CGAATGCATT 780  
 TCTGTGGCT CATCAGACT GAGCTGTGAG AGGGGCCGCG ACCAGAGCCT GCAGTGCCGC 840  
 AGCCCTGAAG AACAGTGCCT GGATGTGGTG ACCACTTGA TCCAGGAAGG TGAAGAAAGG 900  
 CGTCCAAAGG ATGACCGCCA CCTCCGTGGC TGTGGCTACC TTCCCGGCTG CCGGGCTCC 960  
 AATGTTTCC ACAACAAACA CACCTTCCAC TTCTGAAAT GCTGCAACAC CACCAATGTC 1020  
 AACGAGGGCG CAATCTCGGA GCTTGAATAA CTGCGCGAGA ATGGCCGCCA GTGTTACAGC 1080  
 TGCAAGGGGA ACAGCACCCA TGGATGCTCC TCTGAAGAGA CTTTCTCAT TGAATGCCGA 1140  
 GGCCCCATGA ATCAATGTCT GGTAGCCACC GGCACCTACG AACCAGAAAA CCAAGCTAT 1200  
 ATGGTAAGAG GCTGTGCAAC CGCCTCAATG TGCCAACATG CCCACCTGGG TGACGCCTTC 1260  
 AGCATGAACC ACATTGATGT CTCCGTCTGT ACTAAAAGTG GCTGTAAACA CCCAGACCTG 1320  
 GATGTCCAGT ACGCAGTGG GGCTGCTCT CAGCCTGGCC CTGCCCCTCT CAGCCTCACC 1380  
 ATCACCTGTC TAATGACTGC CAGACTGTGG GGAGGCACTC TCCTCTGAC CTAACCTGA 1440  
 AATCCCCCTC TCTGCCCTGG CTGGATCCGG GGGACCCCTT TGCCCTTCCC TCGGCTCCCA 1500  
 GCCCTACAGA CTTGCTGTGT GACCTCAGGC CAGTGTGCCG ACCTCTCTGG GCCTCAGTTT 1560  
 TCCAGCTAT GAAACAGCT ATCTCACAAA GTTGTGTGAA GCAGAAGAGA AAAGCTGGAG 1620  
 GAAGGCGGTG GGCAATCTGT GAGCTCTTGT TATTATTAAT ATTGTTGCCG CTGTTGTGTT 1680  
 GTTGTATTA TTAATATTC ATATTATTTA TTTTACTCT ACATAAAGAT TTTGTACCAG 1740  
 TGG 1743

Seq ID NO: C165 DNA Sequence  
 Nucleic Acid Accession #: AK027843.1  
 Coding sequence: 193..1731

1 11 21 31 41 51  
 | | | | |  
 TTGCTTGAGT CATCTTCTGA AGCTTTAAAA ACAATTGATG AATTGGCCTT CAAGATAGAC 60  
 CTAATAGCA CATCACATGT GAATATTACA ACTCGGAAC TGGCTCTCAG CGTATCATCC 120  
 CTGTTACCAG GGACAAATGC AATTTCAAAT TTTAGCATTG GTCTTCCAAG CAATAATGAA 180  
 TCGTATTTCC AGATGGATTG TGAGAGTGGG CAAGTGGATC CACTGGCCTC TGAATTTTG 240  
 CCTCCAAACT TACTTGAAG TTTAAGTCCA GAAGATTCTG TATTAGTTAG AAGAGCACAG 300  
 TTTACTTTCT TCAACAAAC TGGACTTTTC CAGGATGTAG GACCCCAAAG AAAAATCTTA 360  
 GTGAGTTATG TGATGGCGTG CAGTATTGGA AACATTACTA TCCAGAATCT GAAGGATCCT 420

5	GTTCAAATAA	AAATCAAACA	TACAAGAAGT	CAGGAAGTGC	ATCATCCCAT	CTGTGCCTTC	480
	TGGGATCTGA	ACAAAAACAA	AAGTTTTGGA	GGATGGAACA	CGTCAGGATG	TGTTGCACAC	540
	AGAGATTTCAG	ATGCAAGTGA	GACAGTCTGC	CTGTGTAACC	ACTTCACACA	CTTTGGAGTT	600
	CTGATGGACC	TTCCAAGAAG	TGCCTCACAG	TTAGATGCAA	GAAACACTAA	AGTCCCTCACT	660
	TTTCATCAGCT	ATATTGGGTG	TGGAATATCT	GCTATTTTTT	CAGCAGCAAC	TCTCCTGACA	720
	TATGTTGCTT	TTGAGAAATT	GCGAAGGGAT	TATCCCTCCA	AAATCTTGAT	GAACCTGAGC	780
	ACAGCCCTGC	TGTTCTCTGAA	TCTCCTCTTC	CTCCTAGATG	GCTGGATCAC	CTCCTTCAAT	840
	GTGGATGGAC	TTTGCAATTG	TGTTGCAGTC	CTGTTGCATT	TCTTCCTTCT	GGCAACCTTT	900
10	ACCTGGATGG	GGCTAGAAGC	AAATTCACATG	TACATTGCTC	TAGTTAAAGT	ATTTAACACT	960
	TACATTCGCC	GATACATTCT	AAAATTCTGC	ATCATTGGCT	GGGGTTTGCC	TGCCTTAGTG	1020
	GTGTCAAGTG	TTCTAGCGAG	CAGAAACAAC	AATGAAGTCT	ATGGAAGA	AAGTTATGGG	1080
	AAAGAAAAAG	GTGATGAATT	CTGTTGGATT	CAAGATCCAG	TCATATTTTA	TGTGACCTGT	1140
	GCTGGGTATT	TTGGAGTCAT	GTTTTTCTG	AACATTGCCA	TGTTTATTGT	GGTAATGGTG	1200
15	CAGATCTGTG	GGAGGAATGG	CAAGAGAAGC	AACCGGACCC	TGAGAGAAGA	AGTGTTAAGG	1260
	AACTGCGCGA	GTGTGGTTAG	CTTGACCTTT	CTGTTGGGCA	TGACATGGGG	TTTTGCATTG	1320
	TTTGCCCTGG	GACCCCTTAA	TATCCCCTTC	ATGTACCTCT	TCTCCATCTT	CAATTCATTA	1380
	CAAGGCTTAT	TTATATTCAT	CTTCCACTGT	GCTATGAAGG	AGAATGTTCA	GAAACAGTGG	1440
	CGCGCGCATC	TCGCTGTGG	TAGATTTCGG	TTAGCAGATA	ACTCAGATTG	GAGTAAGACA	1500
20	GCTACCAATA	TCATCAAGAA	AAGTTCTGAT	AATCTAGGAA	AATCTTTGTC	TTCAAGCTCC	1560
	ATTGGTTCCA	ACTCAACCTA	TCTTACATCC	AAATCTAAAT	CCAGCTCTAC	CACCTATTTT	1620
	AAAGGAATA	GCCACACAGA	TAATGTCTCC	TATGAGCATT	CCTTCAACAA	AAGTGGATCA	1680
	CTCAGACAGT	GCTTCCATGG	ACAAGTCTCT	GTCAAACTG	GCCCATGCTG	ATGGAGATCA	1740
	AAACATCAATC	ATCCCTGTCC	ATCAGGTCAT	TGATAAGGTC	AAGGGTTATT	GCAATGCTCA	1800
25	TTTCAGACAAC	TTCTATAAAA	ATATTATCAT	GTGAGACACC	TTGAGCCACA	GCACAAAGTT	1860
	TTAATGTCTT	TAAGAAAAAG	AAATCAATCT	GCAGAAATGT	GAAGATTGTC	AAGCAGTGTA	1920
	AACTGCAACT	AGTGATGTAA	ATGTGCTATT	ACCTAGGTAA	CTGCATATAT	ATAAGGAATG	1980
	TATTTTGTTA	AGAAGGCTTT	TGTGAAATTC	AGAATTTTTC	TTTTTAATAT	ATTTCTTCCA	2040
	TGGAAGAGTT	GTCTACCTA	AACTTCTCAGT	ACTGAGAGTA	ACATGACTCA	GTAGCCACAG	2100
30	AAGCTATGAT	TTGTAAAAAT	TATAATTGAA	TCAGAGTAAT	CATAATGCAG	GGGAGACATT	2160
	CAAATTAGAG	ACAAGGGAGA	AGCAATGCTG	AGGAAGACCC	TAGATAGAGC	TCATTTTACT	2220
	CCACCTAATC	GTTATATCTG	GATATACCCA	TTTTCTGCAT	CTTCTTTTCT	AACAATAAAC	2280
	TGTCCTTGCT	TTGGAGACTT	TAAGACATTT	CCTAAAAGCAC	AAATAAAAGC	CTCGTATTTT	2340
	CCCATTGAGA	GTGTTGTTC	AAGGAATATG	AAGTGAGACA	TATGGGTGAG	TCATAATAAT	2400
35	CAAAATAAAT	TATGAAGAGC	TGGGTCTGCA	ATAGCTAGTC	TAAAAACTAC	TTGTGTGTCA	2460
	GTCTCTTGGT	TATAGTATAT	AAGAGCCTGA	GGAGGTCTGG	CAAGATAGAT	GGTGTATTAT	2520
	TTATGGATCA	GGCTGTCTGA	TACAAACCTT	GCATACTATT	ATGCAGCTTA	CCTAACTCTC	2580
	AGACTATTCT	GAGTAATGCT	TGCTTGCTAA	TGAATGTATA	GGAGACCACA	TTGTAATTGT	2640
	TCTTAGATGA	TGGAGTCCAT	GCAGTTTCTT	AGAAATCGGT	CTCAGTGATC	GCTGTGCTTT	2700
40	TTACATTGTT	CTCTGGGTTA	TCTGGGAAGT	ATCAGGTTCT	GGGAGGCAAC	AGCATTAAAT	2760
	GATAAGAAAA	GGAGACATTC	TGGCAAAAGC	AATCTGCTTA	AAGGCAAAAT	CCAGAACCTG	2820
	GAACCTAGAG	GCCTTCTCT	CTGCACGAAA	AACAGGTAGT	TTGCAGTCTG	AGATATTGGG	2880
	GAGCTTTTAG	GCTACACAGC	AACCAAGGG	ACCTCTCACC	TTTTGCTGAG	CTTCAATCAG	2940
	GAAGCTATTT	GCCTGGCTCC	AGCAGATGAT	GAGATAATGA	GGTAGTGGGT	TTTTTATTAC	3000
45	TGTTCCATTT	TGCAACATCC	TGCAACACCA	TCCTGGGAGA	CAAGAGCATT	ACCCAGCTTG	3060
	GCTTTCACGG	GGGAGGGTTG	TATTCAGT				3088

Seq ID NO: C166 DNA Sequence  
Nucleic Acid Accession #: NM\_000574.1  
Coding sequence: 66..1211

50	1	11	21	31	41	51	
	CCGCTGGGCG	TAGCTGCGAC	TCGGCGGAGT	CCCGCGCGCG	CGTCCTTGTG	CTAACCCGGC	60
	GCGCCATGAC	CGTGCAGCGG	CCGAGCGTGC	CCGCGGCGCT	GCCCTCTCTC	GGGGAGCTGC	120
55	CCCGGCTGCT	CGTGTCTGGT	CTGTTGTGCC	TGCCGCGCGT	GTGGGGTGAC	TGTGGCCTTC	180
	CCCCAGATGT	ACCTAATGCC	CAGCCAGCTT	TGGAAGGCGG	TACAAGTTTT	CCCAGGATA	240
	CTGTAATAAC	GTACAAATGT	GAAGAAAGCT	TTGTGAAAT	TCCTGGCGAG	AAGGACTCAG	300
	TGATCTGCCT	TAAGGGCAGT	CAATGGTCAG	ATATTGAAGA	GTTCTGCAAT	CGTAGCTGCG	360
	AGGTGCCAAC	AAGGCTAAAT	TCTGCATCCC	TCAAACAGCC	TTATATCACT	CAGAATTATT	420
60	TTCCAGTCGG	TACTGTTGTG	GAATATGAGT	GCCGTCCAGG	TTACAGAAGA	GAACCTTCTC	480
	TATCACCAAA	ACTAATCTGC	CTTCAGAAAT	TAAAATGGTC	CACAGCAGTC	GAATTTTGTA	540
	AAAAGAAATC	ATGCCCTAAT	CCGGGAGAAA	TACGAAATGG	TCAGATTGAT	GTACCAGGTG	600
	GCATATTATT	TGGTGCAACC	ATCTCCTTCT	CATGTAACAC	AGGGTACAAA	TTATTGGGCT	660
	CGACTTCTAG	TTTTTGTCTT	ATTTCAAGCA	GCTCTGTCCA	GTGGAGTGAC	CCGTTGCCAG	720
65	AGTGACAGAG	AATTTATTGT	CCAGCACCAC	CACAAATTGA	CAATGGAATA	ATTCAGGGG	780
	AACGTGACCA	TTATGGATAT	AGACAGTCTG	TAACGTATGC	ATGTAATAAA	GGATTACCA	840
	TGATTGGAGA	GCACTCTATT	TATTGTACTG	TGAATAATGA	TGAAGGAGAG	TGGAGTGGCC	900
	CACCACCTGA	ATGCAGAGGA	AAATCTCTAA	CTTCCAAGGT	CCCACCAACA	GTTTCAGAAAC	960
70	CTACCACAGT	AAATGTTCCA	ACTACAGAAG	TCTCACCAAC	TTCTCAGAAA	ACCACCACAA	1020
	AAACCAACCAC	ACCAAAATGCT	CAAGCAACAC	GGAGTACACC	TGTTTCCAGG	ACAAACCAAGC	1080
	ATTTTTCATGA	ACAACACCCA	AATAAAGGAA	GTGGAACCAAC	TTCAAGTACT	ACCCGTCTTC	1140
	TATCTGGGCA	CAGTGTGTTT	ACGTTGACAG	GTTTGCTTGG	GACGCTAGTA	ACCATGGGCT	1200
	TGCTGACTTA	GCCAAAGAAG	AGTTAAGAAG	AAAATACACA	CAAGTATACA	GACTGTTCTC	1260
75	AGTTTCTTAG	ACTTATCTGC	ATATTGGATA	AAATAAATGC	AATTGTGCTC	TTCAATTAGG	1320
	ATGCTTTTCAT	TGCTTTTAAG	ATGTGTTAGG	AATGTCAACA	GAGCAAGGAG	AAAAAGGCA	1380
	GTCTCGGAAT	CAGATTTCTTA	GCACACCTAC	ACCTCTTGAA	AATAGAACAA	CTTGCAGAAT	1440
	TGAGAGTGAT	TCCTTTTCTTA	AAAGTGTAAG	AAAGCATAGA	GATTTGTTTC	TATTTAGAAAT	1500
	GGGATCACGA	GGAAAAGAGA	AGGAAAGTGA	TTTTTTTCCA	CAAGATCTGT	AATGTTATTT	1560
80	CCACTATATA	GAACAAATAAA	AAATGAAAAA	CATTATTGGA	ATATCAAAAG	CAAAATAAAA	1620
	CCCAATTTCAG	TCCTTCTCAA	GCAAAATGTC	TAAAGAGAGA	TGAACCATAT	TATAAAGTAA	1680
	TCTTTGGCTG	TAAGGCATTT	TCATCTTTCC	TTGCGGTTGG	CAAAATATTT	TAAAGGTAAA	1740
	ACATGCTGGT	GAACCGGGG	TGTTGATGGT	GATAAGGGAG	GAATATAGAA	TGAAAGACTG	1800
	AACTCTTCTT	TGTTGACAAA	ATAGAGTTTG	GAAAAAGCCT	GTGAAAGGTG	TCTTCTTTGA	1860
	CTTAATGTCT	TAAAAAGTAT	CCAGAGATAC	TACAATATTA	ACATAAGAAA	AGATTATATA	1920

TTATTCTGA ATCAGAGTGT CCATAGTCAA ATTTGTAAAT CTTATTCTTT TGTAATATTT 1980  
 ATTTATATTT ATTTATGACA GTGAACATTC TGATTTTACA TGTAACAA GAAAAGTTGA 2040  
 AGAAGATATG TGAAGAAAAA TGTATTTTTC CTAAATAGAA ATAAATGATC CCATTTTGTG 2100  
 GT 2102

Seq ID NO: C167 DNA Sequence  
 Nucleic Acid Accession #: Eos sequence  
 Coding sequence: 1..2651

1 11 21 31 41 51  
 ATGGACACCT CCCGGCTCGG TGTGCTCCTG TCCTTGCCCTG TGCTGCTGCA GCTGGCGACC 60  
 GGGGGCAGCT CTCCCAGGTC TGGTGTGTTG CTGAGGGGCT GCCCACACA CTGTCATTGC 120  
 GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG ACCTGGGGCT CTCGGAGCTG 180  
 CCTTCCAACC TCAGCGTCTT CACCTCTAC CTAGACCTCA GTATGAACAA CATCAGTCAG 240  
 CTGCTCCCGA ATCCCTGCC CAGTCTCCGC TTCCTGGAGG AGTTACGTCT TCGCGGAAAC 300  
 GCTCTGACAT ACATTCCCAA GGGAGCATTC ACTGGCCTTT ACAGTCTTAA AGTTCTTATG 360  
 CTGCAGAATA ATCAGCTAAG ACACGTACCC ACAGAAGCTC TGCAGAAATTT GCGAAGCCTT 420  
 CAATCCCTGC GTCTGGATGC TAACCACATC AGCTATGTGC CCCCAGCTG TTTCACTGGC 480  
 CTGCATTCCC TGAGGCACCT GTGGCTGGAT GACAATGCGT TAACAGAAAT CCCCCTCCAG 540  
 GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG CCTGAACAA AATACACCAC 600  
 ATACGAGACT ATGCTTTTGG AAACCTCTCC AGCTTGGTAG TTCTACATCT CCATAACAA 660  
 AGAATCCACT CCCTGGGAAA GAAATGCTTT GATGGGCTCC ACAGCCTAGA GACTTTAGAT 720  
 TTAAATTACA ATAACTTGA TGAATCCCC ACTGCAATTA GGACACTCTC CAACCTTAAA 780  
 GAACATACAT TCTATGACAA TCCCATCCAA TTTGTTGGGA GATCTGCTTT TCAACATTTA 840  
 CCTGAACATA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACTGAATT TCCTGATTTA 900  
 ACTGGAACCTG CAACCTGGA GAGTCTGACT TTAACCTGGAG CACAGATCTC ATCTCTTCTC 960  
 CAAACCGTCT GCAATCAGTT ACCTAATCTC CAAGTGCTAG ATCTGTCTTA CAACCTATTA 1020  
 GAAGATTTAC CCAGTTTTTC AGTCTGCCAA AAGCTTCAGA AAATTGACCT AAGACATAAT 1080  
 GAAATCTACG AAAATAAAGT TGACACTTTC CAGCAGTTGC TTAGCCTCCG ATCGCTGAAT 1140  
 TTGGCTTGGG ACAAAATTGC TATTATTAC CCAATGCAAT TTTCCACTTT GCCATCCCTA 1200  
 ATAAAGCTGG ACCTATCGTC CAACCTCCTG TCGTCTTTTC CTATAACTGG GTTACATGGT 1260  
 TTAACCTACT TAAAATTAAC AGGAAATCAT GCCTTACAGA GCTTGATATC ATCTGAAAAC 1320  
 TTTCCAGAAC TCAAGGTAT AGAAATGCCT TATGCTTACC AGTGTCTGTC ATTTGGAGTG 1380  
 TGTGAGAAAT CCTATAAGAT TTCTAATCAA TGGAATAAAG GTGACAAACAG CAGTATGGAC 1440  
 GACCTTCATA AGAAAGATGC TGGAAATGTT CAGGCTCAAG ATGAACGTGA CCTTGAAGAT 1500  
 TTCTGCTTGG ACTTTGAGGA AGACCTGAAA GCCCTTCATT CAGTGCAGTG TTCACCTTCC 1560  
 CCAGGCCCCCT TCAAAACCCTG TGAACACCTG CTGTATGGCT GGCTGATCAG AATTGGAGTG 1620  
 TGGACCATAG CAGTCTCTGGC ACTTACTTGT AATGCTTTGG TGAATTCAC AGTTTTCAGA 1680  
 TCCCCTCTGT ACATTTCCCC CATTAACTG TTAATTGGGG TCATCGCAGC AGTGAACATG 1740  
 CTCACGGGAG TCTCCAGTGC CGTGTGGCT GGTGTGGATG CGTTCATT TTGGCAGCTTT 1800  
 GCACGACATG GTGCTGGTG GGAGAATGGG GTTGGTTGCC ATGTCTTGG TTTTGTGTC 1860  
 ATTTTGTCTT CAGAATCATC TGTCTTCTG CTACTCTGG CAGCCCTGGA GCGTGGGTTT 1920  
 TCTGTGAAAT ATTCTGCAAA ATTTGAAACG AAAGCTCCAT TTTCTAGCCT GAAAGTAATC 1980  
 ATTTTGCTCT GTGCCCTGCT GGCCCTGACC ATGGCCGAG TTCCCTGCT GGGTGGCAGC 2040  
 AAGTATGGCG CCTCCCTCT CTGCCCTGCT TTGCCCTTTG GGGAGCCGAG CACCATGGGC 2100  
 TACATGGTGC TCTCATCTT GCTCAATTCC CTTTGTCTCC TCATGATGAC CATTGCTTAC 2160  
 ACCAAGCTCT ACTGCAATTT GGACAAGGGA GACCTGGAGA ATATTGGGA CTGCTCTATG 2220  
 GTAAAACACA TTGCCCTGTT GCTCTTACC AACTGCATCC TAAACTGCC TGTGGCTTTT 2280  
 TTGTCTTCTT CCTCTTTAAT AAACCTTACA TTTATCAGTC CTGAAGTAAT TAAGTTTATC 2340  
 CTCTGGTGG TAGTCCCCTT TCCTGCATGT CTCAATCCCC TTCTCTACAT CTTGTTCAAT 2400  
 CCTCACTTTA AGGAGGATCT GGTGAGCCTG AGAAAGCAAA CCTACGCTG GACAAGATCA 2460  
 AAACACCCAA GCTTGTATGTC AATTAACCTT GATGATGTGC AAAACAGTC CTGTGACTCA 2520  
 ACTCAAGCCT TGGTAACCTT TACCAGCTCC AGCATCACTT ATGACCTGCC TCCAGTTTCC 2580  
 GTGCCATCAC CAGCTTATCC AGTGACTGAG AGTGCCATC TTTCTCTGCT GGCATTTGTC 2640  
 CCATGCTTAA A 2651

Seq ID NO: C168 DNA Sequence  
 Nucleic Acid Accession #: NM\_003667.2  
 Coding sequence: 49..2772

1 11 21 31 41 51  
 TGCTGCTCTC CGCCCGCGTC CGGCTCGTGG CCCCTACTT CGGGCACCAT GGACACCTCC 60  
 CGGCTCGGTG TGCTCCTGTC CTGCTGCTG CTGCTGCAGC TGGCGACCGG GGGCAGCTCT 120  
 CCCAGGTCTG GTGTGTTGCT GAGGGGCTGC CCCACACACT GTCATTGCGA GCCCGACGGC 180  
 AGGATGTTGC TCAGGGTGGG CTGCTCCGAC CTGGGGCTCT CGGAGCTGCC TTCCAACTC 240  
 AGCGTCTTCA CCTCTACCT AGACCTCAGT ATGAACAACA TCAGTCAGCT GCTCCCGAAT 300  
 CCCTGCCCA GTCTCCGCTT CTTGGAGGAG TTACGTCTTG CGGGAACGC TCTGACATAC 360  
 ATTCCCAAGG GAGCATTCAT TGGCCTTTAC AGTCTTAAAG TTCTTATGCT GCAGATAAT 420  
 CAGCTAAGAC ACGTACCCAC AGAAGCTCTG CAGAATTTGC GAAGCCTTCA ATCCCTGCGT 480  
 CTGGATGCTA ACCACATCAG CTATGTGCCC CCAAGCTGTT TCAGTGGCCT GCATTCCCTG 540  
 AGGCACCTGT GGCTGGATGA CAATGCGTTA ACAGAAATCC CCGTCCAGGC TTTTAGAAGT 600  
 TTATCGGCAT TGAAGCCAT GACCTTGGCC CTGAACAAA TACACCACAT ACCAGACTAT 660  
 GCCTTTGGAA ACCTCTCCAG CTGTGGTAGT CTACATCTCC ATAACAATAG AATCCACTCC 720  
 CTGGGAAAGA AATGCTTTGA TGGGCTCCAC AGCCTAGAGA CTTAGATTT AAATTACAAT 780  
 AACCTTGATG AATTCCCCAC TGCAATTAGG ACACTCTCCA ACCTTAAAGA ACTAGGATTT 840  
 CATAGCAACA ATATCAGGTG GATACCTGAG AAAGCATTTG TAGGCAACCC TTCTCTTATT 900  
 ACAATACATT TCTATGACAA TCCCATCCAA TTTGTTGGGA GATCTGCTTT TCAACATTTA 960  
 CCTGAACATA GAACACTGAC TCTGAATGGT GCCTCACAAA TAACTGAAT TCCTGATTTA 1020  
 ACTGGAACCT CAAACCTGGA GAGTCTGACT TTAACCTGGAG CACAGATCTC ATCTCTTCTC 1080  
 CAAACCGTCT GCAATCAGTT ACCTAATCTC CAAGTGCTAG ATCTGTCTTA CAACCTATTA 1140  
 GAAGATTTAC CCAGTTTTTC AGTCTGCCAA AAGCTTCAGA AAATTGACCT AAGACATAAT 1200  
 GAAATCTACG AAATTAAAGT TGACACTTTC CAGCAGTTGC TTAGCCTCCG ATCGCTGAAT 1260

TTGGCTTGGA ACAAAATTGC TATTATTAC CCCAATGCAT TTTCCACTTT GCCATCCCTA 1320  
 ATAAAGCTGG ACCTATCGTC CAACCTCCTG TCGTCTTTTC CTATACTGG GTTACATGGT 1380  
 TTAACCTCACT TAAAATTAAAC AGGAAATCAT GCCTTACAGA GCTTGATATC ATCTGAAAAC 1440  
 TTTCCAGAAC TCAGAGTTAT AGAAATGCCT TATGCTTACC AGTGCTGTGC ATTTGGAGTG 1500  
 TGTGAGAAAT CCTATAAGAT TTCTAATCAA TGGAAATAAG GTGACAACAG CAGTATGGAC 1560  
 GACCTTCATA AGAAAGATGC TGAATGTTT CAGGCTCAA AGAACCTGA CCTTGAAGAT 1620  
 TTCTCTGCTT ACTTTGAGGA AGACCTGAAA GCCCTTCATT CAGTGCAGTG TTCACCTTCC 1680  
 CCAGGCCCTT TCAAACCTCTG TGAACACCTG CTTGATGGCT GGCTGATCAG AATTGGAGTG 1740  
 TGGACCATAG CAGTTCTGGC ACTTACTTGT AATGCTTTGG TGACTTCAAC AGTTTTCAGA 1800  
 TCCCCTCTGT ACATTTCCCC CATTAACTG TTAATTGGGG TCATCGCAGC AGTGAACATG 1860  
 CTCACGGGAG TCTCCAGTGC CGTGCTGGCT GGTGTGGATG CGTTCACTTT TGGCAGCTTT 1920  
 GCACGACATG GTGCCTGGTG GGAGAAATGGG GTTGGTTGCC ATGTCAATGG TTTTGTGTC 1980  
 ATTTTGTGCT CAGAATCATC TGTTTTCTTG CTTACTCTGG CAGCCCTGGA CGGTGGGTTC 2040  
 TCTGTGAAAT ATTTGCAAA ATTTGAAACG AAAGCTCCAT TTTCTAGCCT GAAAGTAATC 2100  
 ATTTTGTCTT GTGCCCTGCT GGCTTGACC ATGGCCGCG TCCCCTGCT GGGTGGCAGC 2160  
 AAGTATGGCG CCTCCCTCTT CTGCTGCTT TGGCTTTTG GGGAGCCAG CACCATGGGC 2220  
 TACATGGTCG CTCTCATCTT GCTCAATTCC CTTTGCTTCC TCATGATGAC CATTCCTAC 2280  
 ACCAAGCTCT ACTGCAATTT GGACAAGGGA GACCTGGAGA ATATTGGGA CTGCTCTATG 2340  
 GTAAACACA TTGCCCTGTT GCTCTTACC AACTGCATCC TAAACTGCC TGTGGCTTTC 2400  
 TTGTCCTTCT CCTCTTTAAT AAACCTTACA TTTATCAGTC CTGAAGTAAT TAAGTTTATC 2460  
 CTTCTGGTGG TAGTCCACTT TCCTGCATGT CTCATCCCC TCTCTACAT CTTGTTCAAT 2520  
 CCTCACTTTA AGGAGGATCT GGTGAGCCTG AGAAAGCAA CCTACGCTG GACAAGATCA 2580  
 AAACACCCAA GCTTGATGTC AATTAACCTT GATGATGTCG AAAACAGTC CTGTGACTCA 2640  
 ACTCAAGCCT TGGTAACCTT TACCAGCTCC AGCATCACTT ATGACCTGCC TCCCAGTTCC 2700  
 GTGCCATCAC CAGCTTATCC AGTGACTGAG AGCTGCCATC TTTCTCTGT GGCATTTGTC 2760  
 CCATGTCTCT AATTAAATAG TGAAGGAAA TGTTTTCAA GGTGAGAAC CTGAAAATGT 2820  
 GAGATTGAGT ATATCAGAGC AGTAATTAAT AAGAAGAGCT GAGGTGAAC TCGGTTTAAA 2880

Seq ID NO: C169 DNA Sequence  
 Nucleic Acid Accession #: NM\_003506.1  
 Coding sequence: 259..2379

1 11 21 31 41 51  
 GCAGCTCCAG TCCCGGACGC AACCCCGGAG CCGTCTCAGG TCCCTGGGGG GAACGGTGGG 60  
 TTAGACGGGG ACGGGAAGGG ACACGGGCCT TCGACCGCCC CCCGAGTAAT TGACCCAGGA 120  
 CTCATTTTCA GGAAAGCCTG AAAATGAGTA AAATAGTGAA ATGAGGAATT TGAACATTTT 180  
 ATCTTTGGAT GGGGATCTTC TGAGGATGCA AAGAGTGAT CATCCAAGCC ATGTGGTAAA 240  
 ATCAGGAATT TGAAGAAAT GGAGATGTTT ACATTTTGTG TGACGTGTAT TTTCTACCC 300  
 CTCCTAAGAG GGCACAGTCT CTTACCTGTG GAACCAATTA CTGTTCCTCAG ATGTATGAAA 360  
 ATGGCTTACA ACATGACGTT TTTCCCTAAT CTGATGGGTC ATTATGACCA GAGTATTGCC 420  
 GCGGTGGAAA TGGAGCATTT TCTTCTCTC GCAAATCTGG AATGTTTACC AAACATTGAA 480  
 ACTTTCTCTC GCAAAGCATT TGTACCAACC TGATAGAAC AAATTCATGT GGTTCACCT 540  
 TGTCTGTAAC TTGTGAGAA AGTATATTCT GATTGCAAAA AATTAATTGA CACTTTTGGG 600  
 ATCCGATGGC CTGAGGAGCT TGAATGTGAC AGATTACAAT ACTGTGATGA GACTGTTCT 660  
 GTAACCTTTG ATCCACACAC AGAATTTCTT GGTCTCTAGA AGAAAACAGA ACAAGTCCAA 720  
 AGAGACATGG GATTTTGGTG TCCAAGGCAT CTTAAGACTT CTGGGGGACA AGGATATAAG 780  
 TTTCTGGGAA TTGACCAAGT TGCCTCTCCA TGCCCCAACA TGTATTTTAA AAGTGATGAG 840  
 CTAGAGTTTG CAAAAGTTTT TATTGGAACA GTTTCAATAT TTTGTCTTTG TGCAACTCTG 900  
 TTCACTTCC TTACTTTTTT AATTGATGTT AGAAGATTCA GATACCCAGA GAGACCAATT 960  
 ATATATTACT CTGTCTGTTA CAGCATTTGA TCTCTTATGT ACTTCATTGG ATTTTGTCTG 1020  
 GCGCATAGCA CAGCTGCAA TAAGGCAGAT GAGAAGCTAG AACTTGGTGA CACTGTTGTC 1080  
 TAGGCTCTCT AAAATAAGGC TTGCACCGTT TTGTGATTT TTTTCAATG TTTTCAATG 1140  
 GCTGGCACTG TGTGTTGGGT GATTCTTACC ATTACTTGGT TCTTAGCTGC AGGAAGAAAA 1200  
 TGGAGTTGTG AAGCCATCGA GCAAAAAGCA GTGTGGTTTC ATGCTGTTGC ATGGGGGAACA 1260  
 CCAGGTTTCC TGACTGTTAT GCTTCTTGCT CTGAACAAAG TTGAAGGAGA CAACATTAGT 1320  
 GGAGTTTGCT TTGTGGCCTT TTAGACCTG GATGCTTCTC GCTACTTTGT ACTCTTGCCA 1380  
 CTGTGCTTTT GTGTGTTTGT TGGCTCTCT CTTCTTTTAG CTGGCATTAT TTCCCTAAAT 1440  
 CATGTTTCGAC AAGTCATACA ACATGATGGC CGGAACCAAG AAAAATAAA GAAATTTATG 1500  
 ATTGCAATTG GAGTCTTCAG CGGCTTGTAT CTTGTGCCAT TAGTGACACT TCTCGGATGT 1560  
 TACGCTCTATG AGCAAGTGAA CAGGATTACC TGGGAGATAA CTTGGGTCTC TGATCATTGT 1620  
 CGTCAGTACC ATATCCCATG TCCTTATCAG GCAAAAGCAA AAGCTCGACC AGAATTGGCT 1680  
 TTATTTATGA TAAATACCTT GATGACATTA ATTGTTGGCA TCTCTGCTGT CTTCTGGGTT 1740  
 GGAAGCAAAA AGACATGCAC AGAATGGGCT GGGTTTTTTA AACGAAATCG CAAGAGAGAT 1800  
 CCAATCAGTG AAAGTCGAAG AGTACTACAG GAATCATGTG AGTTTTTCTT AAAGCACAAT 1860  
 TCTAAAGTTA AACACAAAAA GAAGCACTAT AAACCAAGTT CACACAAGCT GAAGGTCATT 1920  
 TCCAAATCCA TGGGAACCGC CACAGGAGCT ACAGCAAATC ATGGCACTTC TGCAAGTAGA 1980  
 ATTTACTAGC ATGATTACCT AGGACAAGAA ACTTTGACAG AAATCCAAC CTCAACGAA 2040  
 ACATCAATGA GAGAGTGAA AGCGGACGGA GCTAGCACCC CCAGGTTAAG AGAACAGGAC 2100  
 TGTGGTGAAC CTGCCCTGCC AGCAGCATCC ATCTCCAGAC TCTCTGGGGA ACAGGTCGAC 2160  
 GGGAAAGGCC AGGCAGGCGA TGTATCTGAA AGTGCGCGGA GTGAAGGAAG GATTAGTCCA 2220  
 AAGAGTGATA TTTACTGACAC TGGCCTGGCA CAGAGCAACA ATTTGCAGGT CCCAGTTCT 2280  
 TCAGAACCAA GCAGCTCAA AGGTTCCACA TCTCTGCTTG TTCACCCAGT TCCAGGAGTG 2340  
 AGAAAAGAGC AGGGAGGTGG TTGTCTTCA GATACTTGA GAACATTTTC TCTCGTTACT 2400  
 CAGAAGCAAA TTTGTGTTAT ACTGGAAGTG ACCTATGCAC TGTTTGTGAA GAATCACTGT 2460  
 TACGTTCTTC TTTTGCCTT AAAGTTGCAT TGCCTACTGT TATACTGGAA AAAATAGAGT 2520  
 TCAAGAATAA TATGACTCAT TTCACACAAA GGTAAATGAC AACAATATAC CTGAAAACAG 2580  
 AAATGTGACG GTTAATAATA TTTTTTTAA AGTGTGGGAG GACAGAGTTA GAGGAATCTT 2640  
 CCTTTTCTAT TTATGAAGAT TCTACTCTTG GTAAGAGTAT TTTAAGATGT ACTATGCTAT 2700  
 TTTACCTTTT TGATATAAAA TCAAGATATT TCTTTGCTGA AGTATTTAAA TCTTATCTTT 2760  
 GTATCTTTT ATACATATT GAAAATAAGC TTATATGTAT TTGAACTTT TTTGAAATCCT 2820  
 ATTCAAGTAT TTTTATCATG CTATTGTGAT ATTTTAGCAC TTTGGTAGCT TTTTACTGTA 2880  
 ATTTCTAAGA AAATGTGAAA ATAGTCTTCT TTTTACTGTG AAAAAAAGAT ATACCAAAAA 2940  
 GTCCTATAAT AGGAATTATA CTTTAAAAAC CCATTATTTG ATACCTTACC ATCTAAAAATG 3000



TGTGATTTT ATAGTCTCGT TTTAGGAATT TCACAGATCT AAATTATGTA ACTGAAATAA 3060  
 GGTGCTTACT CAAGAGTGT CCACTATTGA TTGTATTATG CTGCTCACTG ATCCTTCTGC 3120  
 ATATTTAAAA TAAATGTCC TAAAGGGTTA GTAGACAAAA TGTAGTCTT TTGTATATTA 3180  
 5 GGCCAAGTGC AATTGACTTC CCTTTTAA TGTTCATGA CCACCCATTG ATTGTATTAT 3240  
 AACCACTTAC AGTTGCTTAT ATTTTGT TTAACTTTG TTTCTTAACT TTTAGAAATAT 3300  
 TACATTTTGT ATTATACAGT ACCTTTCTCA GACATTTTGT AG 3342

Seq ID NO: C170 DNA Sequence  
 Nucleic Acid Accession #: NM\_000582  
 Coding sequence: 88...990

1 11 21 31 41 51  
 GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60  
 15 AACGCCGACC AAGGAAAAC CACTACCATG AGAATTGCAG TGATTGCTT TTGCCTCCTA 120  
 GGCACTACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAAAGCAG 180  
 CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240  
 CAGAATCTCC TAGCCCCACA GACCCCTCCA AGTAAGTCCA ACGAAAAGCCA TGACCATATG 300  
 20 GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360  
 AACGACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420  
 TCTGATGAAT CTGATGAAC TGTCACTGAT TTTCCACCGG ACCTGCCAGC AACCGAAGTT 480  
 TTCACTCCAG TTGTCCCAAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540  
 GGACTGAGGT CAAAATCTAA GAAGTTTCGC AGACCTGACA TCCAGTACCC TGATGCTACA 600  
 25 GACGAGGACA TCACCTCACA CATGGAAAAG GAGGAGTGA ATGGTGCATA CAAGGCCATC 660  
 CCGGTTGCC AGGACCTGAA CGCGCCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT 720  
 GAAACGAGTC AGCTGGATCA CCGAGTGTCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780  
 TATAAGCGGA AAGCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATGA TAGTCAGGAA 840  
 30 CTTTCCAAAG TCAGCCGTGA ATTCACAGC CATGAATTC ACAGCCATGA AGATATGCTG 900  
 GTTGTAGACC CCAAAAAGTA GGAAGAAGAT AAACACCTGA AATTTCGTAT TTCTCATGAA 960  
 TTAGATAGTG CATCTTCTGA GGTCAATTA AAGGAGAAAA AATACAATTT CTCACITTTG 1020  
 ATTTAGTCAA AAGAAAAAAT GCCTTATAGC AAAATGAAAG AGAACATGAA ATGCTCTTTT 1080  
 CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA 1140  
 ATTAGTTTAG TTTGTGGCTT CATGGAAACT CCCTGTAAAC TAAAAGCTTC AGGGTTATGT 1200  
 35 CTATGTTTAT TCTATAGAAG AAATGCRAAC TATCACTGTA TTTTAATATT TGTATTCTC 1260  
 TCATGAATAG AAATTTATGT AGAAGCAAA AAAATACTTT TACCACCTTA AAAAGAGAAT 1320  
 ATAACATTTT ATGTCATFAT AATCTTTTGT TTTTAAAGTT AGTGTATATT TTGTTGTGAT 1380  
 TATCTTTTGG TGGGTGGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGGTGTC 1440  
 AATTGCTTAT TTGTTTCCG ACGGTTGTCC AGCAATTAAT AAAACATAAC CTTTTTACT 1500  
 40 GCCTAAAAAA AAAAAA AAAA 1524

Seq ID NO: C171 DNA Sequence  
 Nucleic Acid Accession #: NM\_002821  
 Coding sequence: 150...3362

1 11 21 31 41 51  
 AACTCCCGCC TCGGGAGGCC TCGGGGTCGG GCTCCGGCTG CGGCTGCTGC TGCGGCGCCC 60  
 45 GCGCTCCGGT GCGTCCGCTT CCTGTGCCCG CCGCGGAGCA GTCTGCGGCC GCGCTGCGC 120  
 CCTCAGCTCC TTTTCTGAG CCCGCCGCGA TGGGAGCTGC GCGGGGATCC CCGGCCAGAC 180  
 50 CCGCGCGGTT GCCTCTGCTC AGCGTCCCTG TGTCTGCCGT GCTGGGCGGT ACCCAGACAG 240  
 CCATTGTCTT CATCAAGCAG CCGTCTCCCG AGGATGCACT GCAGGGGCGC CGGGCGCTGC 300  
 TTCGCTGTGA GGTGAGGCTT CCGGGCCCGG TACATGTGTA CTGGCTGCTC GATGGGGCCC 360  
 CTGTCAGGA CACGAGCGCG CGTTTCGCCG AGGGCAGCAG CCTGAGCTTT GCAGCTGTGG 420  
 55 ACCGGCTGCA GGACTCTGGC ACCTTCCAGT GTGTGGCTCG GGATGATGTC ACTGGAGAAG 480  
 AAGCCCGCAG TGCCAAACGCC TCCTTCAACA TCAATGGAT TGAGGCAGGT CCTGTGGTCC 540  
 TGAAGCATCC AGCCTCGGAA GCTGAGATCC AGCCACAGAC CCAGGTCACA CTTCGTTGCC 600  
 ACATTGATGG GCACCTCTCG CCCACCTACC AATGTTCCG AGATGGGACC CCCCTTCTG 660  
 ATGGTCAGAG CAACACACA GTACAGCAGCA AGGAGCGGAA CCTGACGCTC CGGCCAGCTG 720  
 60 GTCTGAGCA TAGTGGCTG TATTCTGCTT GCGCCACAG TGCTTTTGGC CAGGCTTGCA 780  
 GCAGCCAGAA CTTCACCTTG AGCATTGCTG ATGAAGCTT TGCCAGGGTG GTGCTGGCAC 840  
 CCCAGGACGT GGTATGAGG AGGTATGAGG AGGCCATGTT CCATTGCCAG TTCTCAGCCC 900  
 AGCCACCCCG GAGCCTGCGT TGGCTCTTTG AGGATGAGAC TCCCATCACT AACCGCAGTC 960  
 65 GCGCCCGACA CCTCCGAGA GCCACAGTGT TTGCCAACGG GTCTCTGCTG CTGACCCAGG 1020  
 TCCGGCCACG CAATGCAGGG ATCTACCGCT GCATTGGCCA GGGGCAGAGG GGCCACCCA 1080  
 TCATCTGGA AGCCACACTT CACCTAGCAG AGATTGAAGA CATGCCGCTA TTTAGCCAC 1140  
 GGGTGTTCAC AGCTGGCAGC GAGGAGCGTG TGACCTGCCT TCCCCCAAG GGTCTGCCAG 1200  
 AGCCAGCGT GTGGTGGGAG CACGCGGGAG TCCGGCTGCC CACCCATGGC AGGGTCTACC 1260  
 70 AGAAGGGCCA CGAGCTGGTG TTGGCCAATA TTGCTGAAAG TGATGCTGGT GTCTACACCT 1320  
 GGCACGCGCG CAACCTGGCT GGTCAAGCGA GACAGGATGT CAACATCACT GTGGCCACTG 1380  
 TGCCCTCCTG GCTGAAGAAG CCCCAAGACA GCCAGCTGGA GGAGGGCAAA CCGGCTACT 1440  
 TGGATTGCCT GACCCAGGCC ACACCAAAAC CTACAGTTGT CTGGTACAGA AACAGATGC 1500  
 75 TCATCTCAGA GGACTCACGG TTCGAGTCTT TCAAGAATGG GACCTTGCAG ATCAACAGCG 1560  
 TGGAGGTGTA TGATGGGACA TGGTACCGTT GTATGAGCAG CACCCAGGCC GGCAGCATCG 1620  
 AGGCGCAAGC CCGTGTCCAA GTGCTGGAAA AGCTCAAGTT CACACCAACA CCCCAGCCAC 1680  
 AGCAGTGCAT GGAAGTTTGA AAGGAGGCCA CCGTGCCTTG TTCAGCCACA GGCCGAGAGA 1740  
 AGCCCACTAT TAAGTGGGAA CGGGCAGATG GGAGCAGCCT CCCAGAGTGG GTGACAGACA 1800  
 80 ACCTGGGAC CCTGCATTTT GCCCGGTGA CTCGAGATGA CCGTGGCAAC TACACTTGCA 1860  
 TTGCTCCAA CGGGCCGCGG GGCAGATTC GTGCCATGT CCAGCTCACT GTGGCAGTTT 1920  
 TTATCACCTT CAAAGTGGAA CCAGAGCGTA CGACTGTGTA CCAGGGCCAC ACAGCCCTAC 1980  
 TGCACTGCGA GGCCTCAGGG GACCCCAAGC CGCTGATTCA GTGGAAAGGC AAGGACCGCA 2040  
 TCCTGGACCC CACCAAGCTG GGACCCAGGA TGACATCTT CCAGAATGGC TCCTGTGTGA 2100  
 TCCATGACGT GACCCCTGAG GACTCAGGCC GCTACACTG CATGTCAGG CACAGCTGCA 2160  
 ACATCAAGCA CACGGAGGCC CCCCTCTATG TCGTGGACAA GCCTGTGCCG GAGGAGTCGG 2220  
 AGGCGCCTGG CAGCCCTCCC CCCTACAAGA TGATCCAGAC CATTGGGTTG TCGGTGGGTG 2280  
 CCGCTGTGGC CTACATCATT GCCGTGCTGG GCCTCATGTT CTACTGCAAG AAGCGCTGCA 2340

AAGCCAAGCG GCTGCAGAAG CAGCCCCAGG GCGAGGAGCC AGAGATGGAA TGCCTCAACG 2400  
 GAGGGCCTTT GCAGAACGGG CAGCCCTCAG CAGAGATCCA AGAAGAAGTG GCCTTGACCA 2460  
 GCTTGGGCTC CGGCCCCGGG GCCACCAACA AACGCCACAG CACAAGTGAT AAGATGCACT 2520  
 TCCACCGTTC TAGCCTGCAG CCCATCACCA CGCTGGGGAA GAGTGAAGTT GGGGAGGTGT 2580  
 TCCTGGCAAA GGCTCAGGCG TTGGAGGAGG GAGTGGCAGA GACCTGGTA CTTGTGAAGA 2640  
 GCCTGCAGAC GAAGGATGAG CAGCAGCAGC TGGACTTCCG GAGGGAGTTG GAGATGTTTG 2700  
 GGAAGCTGAA CCACGCCAAC GTGGTCCGGC TCCTGGGGCT GTGCCGGGAG GCTGAGCCCC 2760  
 ACTACATGGT GCTGGAATAT GTGGATCTGG GAGACCTCAA GCAGTTCCTG AGGATTTCCA 2820  
 AGAGCAAGGA TGAAAAATTG AAGTCACAGC CCCTCAGCAC CAAGCAGAAG GTGGCCCTAT 2880  
 GCACCCAGGT AGCCCTGGGC ATGGAGCACC TGTCCAACAA CCGCTTTGTG CATAAGGACT 2940  
 TGGCTGCGCG TAACTGCCTG GTCAGTGCCC AGAGACAAGT GAAGGTGTCT GCCCTGGGCC 3000  
 TCAGCAAGGA TGTGTACAAC AGTGAGTACT ACCACTTCCG CCAGGCCTGG GTGCCCTGTC 3060  
 GCTGGATGTC CCCCAGGGCC ATCCTGGAGG GTGACTTCTC TACCAAGTCT GATGTCTGGG 3120  
 CCTTCGGTGT GCTGATGTGG GAAGTGTTTA CACATGGAGA GATGCCCAT GGTGGGCAGG 3180  
 CAGATGATGA AGTACTGGCA GATTTGCAGG CTGGGAAGGC TAGACTTCCT CAGCCCGAGG 3240  
 GCTGCCCTTC CAAACTCTAT CGGCTGATGC AGCGCTGCTG GCCTCTCAGC CCCAAGGACC 3300  
 GGCCCTCCTT CAGTGAGATT GCCAGCGCCC TGGGAGACAG CACCGTGGAG AGCAAGCCGT 3360  
 GAGGAGGGAG CCGCTCAGG ATGGCCTGGG CAGGGGAGGA CATCTCTAGA GGGAGCTCA 3420  
 CAGCATGATG GGCAGATACC CTGTCTCTCT GGGCCTGAG GTGCCCTAGT GCAACAGGCA 3480  
 20 TGCTGAGGT CTGAGCAGGG CCTGGCCTTT CCTCTCTTC CTCACCTCA TCCTTTGGGA 3540  
 GGCTGACTTG GACCCAACT GGGCGACTAG GGCTTTGAGC TGGGCAGTTT CCCCTGCCAC 3600  
 CTCTTCTCT ATCAGGGACA GTGTGGGTGC CACAGGTAAC CCCAATTTCT GGCCTTCAAC 3660  
 TTCTCCCTCT AACTCTGGCA AACTCTGCCA CTCATCTGCC AACTTTGCCT GGGGAGGGCT 3720  
 25 AGGCTTGGGA TGAGCTGGGT TTGTGGGAG TTCTTAATA TTCTCAAGT CTGGGCACAC 3780  
 AGGGTTAATG AGTCTCTTGC CCACTGGTCC ACTTGGGGGT CTAGACCAGG ATTATAGAGG 3840  
 ACACAGCAG TGAGTCTCTC CCACTCTGGG CTGTGACACA CTGACCCAGA CCCACGTCTT 3900  
 CCCCACCTCT CTCTCTCTTC CTCATCTTAA GTGCCCTGAG GATGAAGGAG TTTTCAGGAG 3960  
 CTTTGTGACAT TATATAAAC GCCCTTTTGT TATGCACCAC GGGCGGCTTT TATATGTAAT 4020  
 30 TGCAGCGTGG GGTGGGTGGG CATGGGAGGT AGGGGTGGGC CCTGGAGATG AGGAGGGTGG 4080  
 GCCATCCTTA CCCCACACTT TTATTGTTGT CGTTTTTTGT TTGTTTGTGT TTTTGTGTTT 4140  
 TGTTTTGTGT TTTACACTCG CTGCTCTCAA TAAATAAGCC TTTTTTA 4187

Seq ID NO: C172 DNA Sequence

Nucleic Acid Accession #: NM\_002309.2

Coding sequence: 65..673

1 11 21 31 41 51  
 40 ATGAACCTCT GAAAACTGCC GGCATCTGAG GTTTCCTCCA AGGCCCTCTG AAGTGCAGCC 60  
 CATAATGAAG GTCTTGGCGG CAGGAGTTGT GCCCCTGCTG TTGGTTCTGC ACTGGAACAA 120  
 TGGGGCGGGG AGCCCTCTCC CCATCACCCC TGTCACGCC ACCTGTGCCA TACGCCACCC 180  
 ATGTACAAAC AACCTCATGA ACCAGATCAG GAGCCAACTG GCACAGCTCA ATGGCAGTGC 240  
 CAATGCCCTC TTATTCTCT ATTACACAGC CCAGGGGGAG CCGTTCCCA ACAACCTGGA 300  
 45 CAAGCTATGT GGCCTCAACG TGACGGACTT CCGCCCTTTC CACGCCAACG GCACGGAGAA 360  
 GGCCAAGCTG GTGGAGCTGT ACCGCATAGT CGTGTACCTT GGCACCTCCC TGGGCAACAT 420  
 CACCCGGGAC CAGAAGATCC TCAACCCAG TGCCCTCAGC CTCACAGCA AGCTCAACGC 480  
 CACCCCGCAG ATCTGTGAGG GCCTCTTAG CAACGTGCTG TGCCCGCTGT GCAGCAAGTA 540  
 CCACGTGGGC CATGTGGACG TGACCTACGG CCTGACACC TCGGGTAAGG ATGTCTTCCA 600  
 50 GAAGAAGGAG CTGGGCTGTC AACTCTGGG GAAGTATAAG CAGATCATCG CCGTGTGTCG 660  
 CCAGCCCTTC TAGCAGGAGG TCTTGAAGTG TGCTGTGAAC CGAGGGATCT CAGGAGTTGG 720  
 GTCCAGATGT GGGGGCTGT CCAAGGGTGG CTGGGGCCCA GGGCATCGCT AAACCCAAAT 780  
 GGGGGCTGCT GGCAGACCCC GAGGGTGCCT GGCCAGTCCA CTCCACTCTG GGTGGGCTG 840  
 TGATGAAGCT GAGCAGAGTG GAAACTTCCA TAGGGAGGGA GCTAGAAGAA GGTGCCCTT 900  
 55 CCTCTGGGAG ATTGTGGACT GGGGAGCGTG GGCTGGACTT CTGCCCTTAC TTGTCCCTTT 960  
 GGGCCCTTGC TCACCTTTGT CAGTGAACAA ACTACACAAG TCATCTACAA GAGCCCTGAC 1020  
 CACAGGGTGA GACAGCAGGG CCCAGGGGAG TGGACCAAGC CCCAGCAAAT TATCACCATC 1080  
 TGTGCTTTTG TGTCCCTTAA GGTGGGACT TAGGTGGGCC AGAGGGGCTA GGATCCCAAA 1140  
 GGACTCCTTG TCCCCTAGAA GTTTGATGAG TGGAGATAG AGAGGGGCCT CTGGGATGGA 1200  
 60 AGGCTGTCTT CTTTTGAAGA TGATCAGAGA ACTTGGGCAT AGGAACAATC TGGCAGAAAT 1260  
 TTCCAGAAGG AGGCTCACTG GCATTGAGG TCTTGGGGAG GCAGAGAAGC CACCTTCAGG 1320  
 CCTGGGAAGG AAGACACTGG GAGGAGGAGA GGCCTGGAAA GCTTTGTTAG GTTCTTCGTT 1380  
 CTCTTCCCCG TGATCTTCCC TGCAGCCTGG GATGGCCAGG GTCTGATGGC TGGACCTGCA 1440  
 GCAGGGGTTT GTGGAGGTGG GTAGGGCAGG GGCAGGTTGC TAAGTCAGGT GCAGAGGTTT 1500  
 65 TGAGGGACCC AGGCTCTTCC TCTGGGTAAA GGTCTGTAAG AAGGGGCTGG GGTAGCTCAG 1560  
 AGTAGCAGCT CACATCTGAG GCCCTGGGAG GTCTGTGAG GTACACAGA GGTACTTGAG 1620  
 GGGGACTGGA GGCCTCTCT GGTCCCCAGG GCAAGGGAAC AGCAGAACTT AGGGTCAGGG 1680  
 TCTCAGGGAA CCCTGAGCTC CAAGCGTGCT GTGCGTCTGA CCTGGCATGA TTTCTATTTA 1740  
 70 TTATGATATC CTATTATAT TAACTTATTG GTGCTTTCAG TGGCCAAGTT AATTCCCTTT 1800  
 TCCCTGTTCC CTACTCAACA AAATATGATG ATGGCTCCCG ACACAAGCGC CAGGGCCAGG 1860  
 GCTTAGCAGG CTACTGGTCT GAAGTCGACA ATGTTACAAG TGAATAAGC TTACGGGTGA 1920  
 AGCTCAGAGA AGGTGCGGAT CTGAGAGAAT GGGGAGGCCT GAGTGGGAGT GGGGGGCTTT 1980  
 GCTCCACCCC CATCCCTTAC TGTGACTTGC TTTAGCGTGT CAGGGTCCAG GCTGCAGGGG 2040  
 CTGGGCCAAT TTGTGGAGAG GCCGGGTGCC TTTCTGTCTT GCTTCCAGGG GGCTGGTTCA 2100  
 75 CACTGTTCTT GGGCGCCCCA GCATTGTGTT GTGAGGCGCA CTGTTCTCTG CAGATATTGT 2160  
 GCCCCCTGGA GCAGTGGGCA AGACAGTCTT TGTGGCCAC CCTGTCTCTG TTTCTGTGTC 2220  
 CCCATGCTGC CTCTGAAATA GCGCCCTGGA ACAACCTGTC CCTGCAACC AGCATGCTCC 2280  
 GACACAGCAG GGAAGCTCCT CCTGTGGCCC GGACACCCAT AGACGGTTCG GGGGGCCTGG 2340  
 CTGGGCCAGA CCCCAGGAAG GTGGGGTAGA CTGGGGGAT CAGCTGCCCA TTGCTCCCAA 2400  
 80 GAGGAGGAGA GGGAGGCTGC AGACGCTTGG GACTCAGACC AGGAAGCTGT GGGCCCTCT 2460  
 GCTCCACCCC CATCCCACTG CCACCATGTT CTGGGCTCCC AGGCAGGGAA CCCGATCTCT 2520  
 TCCTTTGTGC TGGGGCCAGG CGAGTGGAGA AACGCCCTCC AGTCTGAGAG CAGGGGAGGG 2580  
 AAGGAGGCAG CAGAGTTGGG GCAGCTGCTC AGAGCAGTGT TCTGGCTTCT TCTCAAACCC 2640  
 TGAGCGGGCT GCCGGCCTCC AAGTTCCTCC GACAAGATGA TGGTACTAAT TATGGTACTT 2700  
 TTCACCTACT TTGCACCTTT CCCTGCTGCT CTCTAAGCAC TTTACCTGGA TGGCGCGTGG 2760

GCAGTGTGCA GGCAGGTCTT GAGGCTCTGG GTTGGGGTGG AGGGTGCGGC CCGAGTGTGT 2820  
 CCATCTGTCC ATCCCAACAG CAAGACGAGG ATGTGGCTGT TGAGATGTGG GCCACACTCA 2880  
 CCCTTGTCCA GGATGCAAGG ACTGCTCTCT CTTCTCTGCT TCATCCGGCT TAGCTTGGGG 2940  
 5 CTGGCTGCAT TCCCCAGGA TGGGCTTCGA GAAAGACAAA CTTGTCTGGA AACCAGAGTT 3000  
 GTGATTCCA CCGGGGGGGC CCGGCTGACT CGCCCATCAC CTCATCTCCC TGTGGACTTG 3060  
 GGAGCTCTGT GCCAGGCCCA CCTTGCGGCC CTGGCTCTGA GTGCTCTCC CACCAGCCT 3120  
 GGACTTGGCC CCATGGGACC CATCTCAGT GCTCCCTCCA GATCCCGTCC GGCAGCTTGG 3180  
 CGTCCACCTT GCACAGCATC ACTGAATCAC AGAGCCTTTG CGTGAACAG CTCTGCCAGG 3240  
 10 CCGGGAGCTG GGTTCCTCTT CCCTTTTAT CTGCTGGTGT GGACCACACC TGGGCTGGC 3300  
 CCGAGGAAGA GAGAGTTTAC CAAGAGAGAT GTCTCCGGGC CCTTATTAT TATTAAACA 3360  
 TTTTAAATA AAGCACTGCT AGTTTACTTG TCTCTCTCC CCATCGTCCC CATCGTCTC 3420  
 CTTGTCCCTG ACTTGGGGCA CTTCCACCTT GACCCAGCCA GTCCAGCTCT GCCTTGGCCG 3480  
 CTCTCCAGAG TAGACATAGT GTGTGGGGTT GGAGCTCTGG CACCCGGGGA GGTAGCATTT 3540  
 15 CCCTGCAGAT GGTACAGATG TTCTTGCCTT AGAGTCATCT CTAGTTCCTC ACCTCAATCC 3600  
 CGGCATCCAG CCTTCAGTCC CGCCACGTG CTAGCTCCGT GGGCCACCG TGCGGCCCTA 3660  
 GAGGTTTCCC TCCTTCCTTT CCACTGAAAA GCACATGGCC TTGGGTGACA AATTCCTCTT 3720  
 TGATGAATGT ACCCTGTGGG GATGTTTCAT ACTGACAGAT TATTTTATT TATTCATGT 3780  
 CATATTTAAA ATATTTATTT TTTATACCAA ATGAATCACT TTTTATTTTA AGAAAAAAA 3840  
 20 GAGAAATGAA TAAAGAACTT ACTCTTCG 3868

Seq ID NO: C173 DNA Sequence  
 Nucleic Acid Accession #: XM\_097508  
 Coding sequence: 44..2788

25 1 11 21 31 41 51  
 | | | | |  
 TGAAAGGCGG TTGTGGTGA AAGGAAAACC CACAGGCCAA GGAATGGGAA GACCAAGGTT 60  
 GACACTTGTG TGTACAGTGT CAATAATCAT CTCTGCCCGG GACCTCAGCA TGAACAACCT 120  
 30 CACAGAGCTT CAGCCTGGCC TCTTCCACCA CCTGCGCTTC TTGGAGGAGC TGCGTCTCTC 180  
 TGGGAACCAT CTCTCACACA TCCCAGGACA AGCATCTCTT GGTCTCTACA GCCTGAAAAA 240  
 CCTGATGCTG CAGAACATCT AGCTGGGAGG AATCCCCGCA GAGGCGCTGT GGGAGCTGCC 300  
 GAGCCTCGAG TCGCTGCGCC TAGATGCCAA CCTCATCTCC CTGTCCCGG AGAGGAGCTT 360  
 TGAGGGGCTG TCCTCCCTCC GCCACCTCTG GCTGGACGAC AATGCATCA CGGAGATCCC 420  
 35 TGTACGGGCC CTCACAAACC TCCCTGCCCT GCAGGCCATG ACCCTGGCCC TCAACCGCAT 480  
 CAGGCACATC CCGGACTAGC CGTTCAGAA TCTCACCAGC CTTGTGGTGC TGCATTGCA 540  
 TAACAACGCG ATCCAGATC TGGGGACCCA CAGCTTCGAG GGGCTGCACA ATCTGGAGAC 600  
 ACTAGACCTG AATTATAACA AGCTGCAGGA GTTCCCTGTG GCCATCCGGA CCCTGGGCAG 660  
 ACTGCAGGAA CTGGGGTTCC ATAACAACAA CATCAAGGCC ATCCCAGAAA AGGCCTTCAT 720  
 40 GGGGAACCCCT CTGCTACAGA CGATACACTT TTATGATAAC CCAATCCAGT TTGTGGGAAG 780  
 ATCGGCATTG CAGTACCTGC CTAACCTCCA CACACTATCT CTGAATGGTG CCATGGACAT 840  
 CCAGGAGTTT CCAGATCTCA AAGGCACCAC CAGCCTGGAG ATCTGACCC TGACCCGCGC 900  
 AGGCATCCGG CTGCTCCCAT CGGGGATGTG CCAACAGCTG CCCAGGCTCC GAGTCTGGA 960  
 ACTGTCTCAC AATCAAAATG AGGAGCTGCC CAGCCTGCAC AGGTGTGAGA AATTGGAGGA 1020  
 45 AATCGGCCTC CAACACAACC GCATCTGGGA AATTGGAGCT GACACCTTCA GCCAGCTGAG 1080  
 CTCCCTGCAA GCCCTGGATC TTAGCTGGAA CGCCATCCGG TCCATCCACC CCGAGGCTTT 1140  
 CTCCACCTTG CACTCCCTGG TCAAGCTGGA CCTGACAGAC AACCAGCTGA CCACACTGCC 1200  
 CTTGGCTGGA CTTGGGGGCT TGATGCATCT GAAGCTCAAA GGGAACTCTG CTCTCTCCCA 1260  
 GGCTTCTCTC AAGGACAGTT TCCCAAACT GAGGATCTCT GAGGTGCTTT ATGCTTACCA 1320  
 50 GTGCTGTCCC TATGGGATGT GTGCCAGCTT CTTCAAGGCC TCTGGGCACT GGGAGCTGA 1380  
 AGACCTTACG TTGATGATG AGGAGTCTTC AAAAAGGCCC CTGGGCTCTC TTGGCAGACA 1440  
 AGCAGAGAAG CACTATGACC AGGACCTGGA TGAGCTCCAG CTGGAGATGG AGGACTCAAA 1500  
 GCCACACCCC AGTGTCCAGT GTAGCCCTAC TCCAGGCCCC TTCAAGCCCT GTGAGTACCT 1560  
 CTTTGAAGC TGGGGCATCC GCCTGGCCGT GTGGGCCATC GTGTGCTCT CCGTGTCTG 1620  
 55 CAATGGACTG GTGCTGCTGA CGGTGTTGCG TGGCGGGCCT GTCCCCCTGC CCCCCTGCA 1680  
 GTTTGTGGTA GGTGCGATTG CAGGCGCCAA CACCTTGACT GGCATTCTCT GTGGCCTTCT 1740  
 AGCCTCAGT GATGCCCTGA CCTTTGGTCA GTTCTCIGAG TACGGAGCCC GCTGGGAGAC 1800  
 GGGCTTAGGC TGCGGGGCCA CTGGCTTCCT GGCAGTACTT GGGTCGGAGG CATCGGTGCT 1860  
 GCTGCTCACT CTGGCGCGAG TGCAGTGCAG CGTCTCCGTC TCCTGTGTCC GGGCCTATGG 1920  
 60 GAAGTCCCCC TCCTTGGGCA GCGTTGAGC AGGGGTCTTA GGCTGCCTGG CACTGGCAGG 1980  
 GCTGGCGGCC GCGCTGCCCC TGGCCTCAGT GGGAGAATAC GGGGCTCCC CACTCTGCT 2040  
 GCCTACGCG CCACCTGAGG GTCAGCCAGC AGCCTTGGGC TTCACCGTGG CCTGTGTAT 2100  
 GATGAACCTC TTCTGTTTCC TGGTCGTGGC CGGTGCCTAC ATCAAACTGT ACTGTGACCT 2160  
 65 GCCGCGGGG GACTTTGAGG CCGTGTGGGA CTGCGCATG GTGAGGCAG TGGCCTGGCT 2220  
 CATCTTCGCA GACGGGCTCC TCTACTGTCC CGTGGCCTTC CTCAGCTTTG CCTCATGCT 2280  
 GGGCTCTTC CCGTTCAGC CGAGGCCGT CAAGTCTGTC CTGCTGGTGG TGCTGCCCT 2340  
 GCCTGCCTGC CTCACCCAC TGCTGTACCT GCTCTTCAAC CCCCCTTCC GGGATGACCT 2400  
 TCGGCGGCTT CGGCCCGCG CAGGGGACTC AGGGCCCTTA GCCTATGTG CGGCCGGGGA 2460  
 70 GCTGGAGAAG AGCTCCTGTG ATTCTACCCA GGCCTTGGTA GCCTTCTCTG ATGTGGATCT 2520  
 CATTTGGAAG GCTTCTGAAG CTGGGCGGCC CCCTGGGCTG GAGACCTATG GCTTCCCTC 2580  
 AGTGACCTTC ATCTCTGTG AGCAGCCAGG GGGCCCCAGG CTGGAGGGCA GCCATTGTGT 2640  
 AGAGCCAGAG GGAACCACT TTGGGAACCC CCAACCTTCC ATGGATGGAG AACTGCTGCT 2700  
 GAGGGCAGAG GGAATACGCG CAGCAGGTGG AGGCTTGTCA GGGGGTGGCG GCTTTAGGCC 2760  
 75 CTCTGGCTTG GCCTTTGCTT CACACGTGTA AATATCCCTC CCAATCTTCT TCTTCCCTC 2820  
 TCTTCCCTTT CTTCTCTCCC CTTGGGTGAA TGATGGCTGC TTTTAAACA AATACAACCA 2880  
 AAATCAGCA GTGTGATCTA TAGCAGGATG GCCCAGTCCC TGGCTCCACT GATCACCTCT 2940  
 CTCTGTGAC CATCACCAAC GGGTGCCTCT TGGCCTGGCT TTTCCCTTGG CTTCCCTCAGC 3000  
 TTTACCTTGA TACTGGGCTT CTTCTTGTG ATGTCTGAAG CTGTGGACCA GAGACCTGGA 3060  
 CTTTGTCTG CTTAAGGGAAG ATGAGGGAAG TAAAGACAGT GAAGGGGTGG AGGTTGATC 3120  
 80 AGGGCACAGT GGAACGGGAG ACCTCACAGA GAAAGGCTG GAAGGTGATT TCCCGTGTGA 3180  
 CTCATGGATA GGATACAAAA TGTGTTCCAT GTACCATTA TCTTGACATA TGCCATGCAT 3240  
 AAAGACTTCC TATTAAAAA AGCTTTGGA GAG 3273

Seq ID NO: C174 DNA Sequence  
 Nucleic Acid Accession #: NM\_130849

Coding sequence: 101..2044

```

1      11      21      31      41      51
|      |      |      |      |      |
5  AGTCTGGCCC TGGACAACCC CAGCAAAGCC GCCCTCAGCC AGCCCAGAAG CACTGGGCCT 60
   TGGCCACAGC AACACCCACT GAGCACGCTG GGAGCTGAGT ATGGCGTCCC TGGTCTCGCT 120
   GGAGCTGGGG CTGCTTCTGG CTGTGCTGGT GGTGACGGCG ACGGCGTCCC CGCTGCTGG 180
   TCTGCTGAGC CTGCTCACCT CTGGCCAGGG CGCTCTGGAT CAAGAGGCTC TGGGCGGCCT 240
10 GTTAAATACG CTGGCGGACC GTGTGCACTG CACCAACGGG CCGTGTGGAA AGTGCTGTCT 300
   TGTGGAGGAC GCCCTGGGCC TGGGCGAGCC TGAGGGGTCA GGGCTGCCCC CGGGCCCGGT 360
   CCTGGAGGCC AGGTACGTCG CCCGCCTCAG TGGCGCCGCC GTCTGTATCC TCAGCAACCC 420
   CGAGGGCACC TGTGAGGACA CTCGGGCTGG CCTCTGGGCC TCTCATGCAG ACCACCTCCT 480
   GGCCCTGCTC GAGAGCCCCA AGGCCCTGAC CCCGGGCTG AGCTGGCTGC TGCAGAGGAT 540
   GCAGGCCCGG GCTGCCGGCC AGACCCCAA GACGGCTGTC GTAGATATCC CTCAGCTGCT 600
15 GGAGGAGGCG GTGGGGGCGG GGGCTCCGGG CAGTGTGGC GGCCTCCTGG CTGCCCTGCT 660
   GGACCATGTC AGGAGCGGGT CTTGCTTCCA CGCCTTGCCG AGCCCTCAGT ACTTCGTGGA 720
   CTTTGTGTTT CAGCAGCACA GCAGCGAGGT CCTATGACG CTGGCCGAGC TGTGAGCCTT 780
   GATGCAGCGC CTGGTGGGCG GCAGGGAGGC CCACAGTGAC CACAGTCATC GGCACAGGGG 840
   AGCCAGCAGC CGGACCCCTG TGCCCTCAT CAGCTCCAGC AACAGCTCCA GTGTGTGGGA 900
20 CACGGTATGC CTGAGTGCCA GGGACGTGAT GGCTGCATAT GGACTGTCGG AACAGGCTGG 960
   GGTGACCCCG GAGGCCCTGG CCCAACTGAG CCTTGCCTG CTCCAACAGC AGCTGAGTGG 1020
   AGCCTGCACC TCCAGTCCA GGGCCCCCGT CCAGGACCAG CTCAGCCAGT CAGAGAGGTA 1080
   TCTGTAGCGC TCCTTGGCCA CGCTGCTCAT CTGCCCTGCG GCGGTCTTTG GCCTCCTGCT 1140
   GCTGACCTGC ACTGGCTGCA GGGGGGTGCG CCACTACATC CTGCAGACCT TCTGAGCCT 1200
25 GGCAGTGGGT GCACTCACTG GGGACGCTGT CCTGCATCTG ACGCCCAAGG TGCTGGGGCT 1260
   GCATACACAC AGCGAAGAGG GCCTCAGCCC ACAGCCCAAC TGGCGCTTCC TGGCTATGCT 1320
   GGGCGGGCTC TAGCCCTTCT TCCTGTTTGA GAACCTCTTC AATCTCCTGC TGCCACGGGA 1380
   CCCGGAGGAC CTGGAGGACG GGCCTGCGG CCACAGCAGC CATAGCCACG GGGGCCACAG 1440
   CCACGGTGTG TCCTTGCAGC TGGCACCCAG CGAGCTCCGG CAGCCCAAGC CCCCCACGA 1500
   GGGCTCCCGC GCAGACCTGG TGGCGGAGGA GAGCCCGGAG CTGCTGAACC CTGAGCCGCT 1560
30 GAGACTGAGC CCGAGATTGA GGCTACTGCC CTATATGATC ACTCTGGGCG ACGCGTGCA 1620
   CAACTTCGCC GACGGGCTGG CCGTGGGCGC CGCCTTCGCG TCCTCCTGGA AGACCGGGCT 1680
   GGCCACCTCG CTGGCCGTGT TCTGCCACGA GTTGCCACAC GAGCTGGGGG ACTTCGCCGC 1740
   CTTGCTGCAC GCGGGGCTGT CCGTGCGCCA AGCACTGTCT CTGAACCTGG CCTCCGCTG 1800
   CACGGCCTTC GCTGGTCTCT ACGTGGCACT CGCGGTTGGA GTCAGCGAGG AGAGCGAGGC 1860
35 CTGGATCCTG GAGTGGGCA CCGGCTGTT CCTCTACGTA GCACTCTGCG ACATGCTCCC 1920
   GGCATGTTG AAAGTACGGG ACCCGCGGCC CTGGCTCCTC TTCCTGCTGC ACAACGTGGG 1980
   CCTGCTGGGC GGTGGAACCG TCCTGCTGCT GCTGTCCCTG TACGAGGATG ACATCACCTT 2040
   CTGATACCTT GCCCTAGTCC CCCACCTTTG ACTTAAGATC CCACACCTCA CAAACCTACA 2100
40 GCCAGAAAC CAGAAGCCCC TATAGAGGCC CCAGTCCCAA CTCAGTAAA GACACTCTTG 2160
   TCCTTGGAAA AAAAAAAAAA AAAAAAAAAA AA 2192

```

Seq ID NO: C175 DNA Sequence  
Nucleic Acid Accession #: NM\_018971  
Coding sequence: 1..1128

```

1      11      21      31      41      51
|      |      |      |      |      |
50 ATGGCGAAGC CGAGCGAGCC GGGTGGCAGC GCGGCGGCGG AGGCGGCCGC CCTGGGCCTC 60
   AAGCTGGCCA CGCTCAGCCT GCTGCTGTGC GTGAGCCTAG CGGGCAACGT GCTGTTGCGG 120
   CTGCTGATCG TCGGGGAGCG CAGCCTGCAC CGCGCCCCGT ACTACCTGCT GCTCGACCTG 180
   TGCCTGGCCG ACGGGCTGCG CGCGCTCGCC TGCCCTCCCG CCGTCATGCT GCGCGCGCGG 240
   CGTGGCGCGG CCGCGGCGGG GCGCGCGCGG GCGCGCTGG GCTGCAAGCT GCTCGCCTTC 300
55 CTGGCGCGCG TCTTCTGCTT CCACGCCGCC TTCCTGCTGC TGGGCGTGGG CGTCACCCGC 360
   TACCTGGCCA TCGCGCACCA CCGCTTCTAT GCAGAGCGCC TGGCGGCTG GCGGTGCGCC 420
   GCCATGCTGG TGTGCGCCCG CTGGGCGCTG GCGCTGGCGG CGGCCTTCCC GCCAGTGTG 480
   GACGGCGGTG GCGACGACGA GACGCGCGCG TCGCCCTGG AGCAGCGGCC CGACGGCGCC 540
   CCCGCGCGCG TGGGCTTCTT GCTGCTGCTG GCGGTGGTGG TGGGCGCCAC GCACCTCGTC 600
   TACCTCCGCC TGCTCTTCTT CATCCACGAC CGCCGCAAGA TCGCGCCCGC GCGCCTGGTG 660
60 CCGCGCTTCA CGCACGACTG GACCTTCCAC GCGCCGGGCG CCACCGGCCA GCGCGCGGCC 720
   AACTGGACGG CCGGCTTCGG CCGCGGGCCC ACGCCGCCCG CGCTTGTGGG CATCCGGCCC 780
   GCAGGGCCCG GCCGCGGCGC GCGCCGCCTC CTCGTGCTGG AAGAATTCAA GACGAGAAAG 840
   AGGCTGTGCA AGATGTTCTA CGCCGTCACG CTGCTCTTCC TGCTCCTCTG GGGGCCCTAC 900
   GTCGTGGCCA GCTACCTGCG GGTCTGCTGG CCGCCCGCGG CCGTCCCCCA GGCCTACCTG 960
65 ACGGCTCCG TGTGGCTGAC CTTGCGCAG GCGGCGATCA ACCCGTCTGT GTGCTTCTCT 1020
   TTCAACAGGG AGCTGAGGGA CTGCTTCAGG GCCCAGTTCC CTTGCTGCCA GAGCCCCCGG 1080
   ACCACCCAGG CGACCCATCC CTGCGACCTG AAAGGCATTG GTTTATGA 1128

```

Seq ID NO: C176 DNA Sequence  
Nucleic Acid Accession #: NM\_005631  
Coding sequence: 290..2653

```

1      11      21      31      41      51
|      |      |      |      |      |
75 GGCACGAGGG GGCTGAAGAC AACTTGGATT GCGAGGCTAG GGCTTGGGGA GTCGTGCATC 60
   CCTTCCCGG CCTCCGACG CCAACATGGG CCCCAGGTTT CAAAGTTTGC GAAAGTTGGG 120
   CGCGAGGGGG CCGGGCGCGC GGAGCGTCCG GGGGGGCCCC GGCCTGGATT CTCTGGGCGC 180
   ACAGTTCGCG TGAGCGCCT CCGCGGCCCG CAGGTCGTG CTTGTGGCCG GGGGGTCCG 240
80 AGGAGCAGGC GGGGGCGCGG GGGCTTTTGC TGAGTTGGCG GGGTTGGCCA TGGCCGCTGC 300
   CGGCCACGCG CCGGGGCGCG AGCTCCCGCT CTTGGGGCTG CTGCTGCTGC TGCTGCTGGG 360
   GGAACCGGGC CCGGGGCGCG CCTCGAGCGG GAACGCGACC GGGCCTGGGC CTCGAGAGCG 420
   GGGCGGGAGC GCGAGGAGGA GCGCGGCGGT GACTGGCCCT CCGCCGCCCG TGAGCCACTG 480
   CGGCCGGGCT GCCCCTGCG AGCCGCTGCG CTACAACGTC TGCCCTGGGT CCGTGTGCTG 540
   CTACGGGGCC ACCTCCACAC TGCTGGCCCG AGACTCGAC TCCAGGAGG AAGCGCACCG 600

```

5	CAAGCTCGTG	CTCTGGTCGG	GCCTCCGGAA	TGCCCCCGC	TGCTGGGCAG	TGATCCAGCC	660
	CCTGCTGTGT	GCCGTATACA	TGCCCCAAGT	TGAGAAATGAC	CGGGTGGAGC	TGCCCCAGCCG	720
	TACCTCTGCG	CAGGCCACCC	GAGGCCCTTG	TGCCATCGTG	GAGAGGGAGC	GGGGCTGGCC	780
	TGACTTCCTG	CGCTGCACTC	CTGACCGCTT	CCCTGAAGGC	TGCACGAATG	AGGTGCAGAA	840
	CATCAAGTTC	AACAGTTTCA	GCCAGTGCAG	AGTGCCCTTG	GTTCGGACAG	ACAACCCCAA	900
	GAGCTGGTAC	GAGGACGTGG	AGGGCTGCGG	CATCCAGTGC	CAGAACCCGC	TCTTCACAGA	960
	GGCTGAGCAC	CAGGACATGC	ACAGCTACAT	CGCGGCCTTC	GGGGCCGTCA	CGGGCCTCTG	1020
	CACGCTCTTC	ACCTTGCCCA	CATTCTGGGC	TGACTGGCGG	AACCTCGAATC	GCTACCCCTGC	1080
10	TGTTATTCTC	TTCTACGTCA	ATGCGTGCTT	CTTTGTGGGC	AGCATTGGCT	GGCTGGCCCA	1140
	GTTTCATGGAT	GGTGCCCGCC	GAGAGATCGT	CTGCCGTGCA	GATGGCACCA	TGAGGCTTGG	1200
	GGAGCCCAAC	TTCAATGAGA	CTCTGTCTGT	CGTCATCATC	TTTGTATCG	TGTACTACGC	1260
	CCTGATGGCT	GGTGTGGTTT	GGTTTGTGGT	CCTCACCTAT	GCCTGGCACA	CTTCCTTCAA	1320
	AGCCCTGGGC	ACCACCTACC	AGCCTCTCTC	GGGCAAGACC	TCCTACTTCC	ACCTGCTCAC	1380
15	CTGGTCACTC	CCCTTTGTCC	TCACTGTGGC	AATCCTTGCT	GTGGCGCAGG	TGGATGGGGA	1440
	CTCTGTAGT	GGCATTGTGT	TTGTGGGCTA	CAAGAACTAC	CGATACCGTG	CGGGCTTCGT	1500
	GCTGGCCCCA	ATCGGCCTGG	TGCTCATCGT	GGGAGGCTAC	TTCTCTATCC	GAGGAGTCAT	1560
	GACTCTGTTC	TCCATCAAGA	GCAACCAACC	CGGGCTGCTG	AGTGAGAAGG	CTGCCAGCAA	1620
	GATCAACGAG	ACCATGTCTG	GCCTGGGCAT	TTTTGGCTTC	CTGGCCCTTG	GCTTTGTGCT	1680
20	CATTACCTTC	AGCTGCCACT	TCTACGACTT	CTTCAACCAG	GCTGAGTGGG	AGCGCAGCTT	1740
	CCGGGACTAT	GTGCTATGTC	AGGCCAATGT	GACCATCGGG	CTGCCACCA	AGCAGCCCAT	1800
	CCCTGACTGT	GAGATCAAGA	ATCGCCCGAG	CCTTCTGGTG	GAGAAGATCA	ACCTGTTTGC	1860
	CATGTTTGGG	ACTGGCATCG	CCATGAGCAC	CTGGGTCTGG	ACCAAGGCCA	CGCTGCTCAT	1920
	CTGGAGGCGT	ACCTGGGTGA	GGTTGACTGG	GCAGAGTGAC	GATGAGCCAA	AGCGGATCAA	1980
25	GAAGAGCAAG	ATGATTGCCA	AGGCCTTCTC	TAAGCGGCAC	GAGCTCTCTG	AGAACCCAGG	2040
	CCAGGAGCTG	TCCTTTCAGCA	TGCACACTGT	GTCCCACGAC	GGGCCCGTGG	CGGGCTTGGC	2100
	CTTTGACCTC	AATGACCTC	CAGCTGATGT	CTCCTCTGCC	TGGGCCCAGC	ATGTCAACAA	2160
	GATGGTGGCT	CGGAGAGGAG	CCATACTGCC	CCAGGATATT	TCTGTACACC	CTGTGGCAAC	2220
	TCCAGTGCCC	CCAGAGGAAC	AAGCCAACCT	GTGGCTGGTT	GAGGCAGAGA	TCTCCCCAGA	2280
30	GCTGCAGAAG	CGCCTGGGCC	GGAGAAGAA	GAGGAGGAAG	AGGAAGAAGG	AGGTGTGCCC	2340
	GCTGGCGCCG	CCCCCTGAGC	TTACCCCCCC	TGCCCTTGCC	CCCAAGTACC	TTCTCTGACT	2400
	GCCTCAGCTG	CCCCGGCAGA	AATGCCTGGT	GGCTGCAGGT	GCCTGGGGAG	CTGGGGACTC	2460
	TTGCCGACAG	GGAGCGTGGA	CCCTGGTCTC	CAACCCATTG	TGCCCAGAGC	CCAGTCCCCC	2520
	TCAGGATCCA	TTTCTGCCCA	GTGCACCGGC	CCCCGTGGCA	TGGGCTCATG	GCCGCCGACA	2580
35	GGGCTTGGGG	CCTATTCACT	CCCCCACCAC	CCTGATGGAC	ACAGAACTCA	TGGATGCAGA	2640
	CTCGGACTTC	TGAGCCTGCA	GAGCAGGACC	TGGGACAGGA	AAGAGAGGAA	CCAATACCTT	2700
	CAAGGCTCTT	CTTCTCTACC	GAGCATGCTT	CCCTAGGATC	CCGTCTTCCA	GAGAACCTGT	2760
	GGGCTGACTG	CCCTCCGAAG	AGAGTTCTGG	ATGCTCTGGT	CAAAGCAGCA	GGACTGTGGG	2820
	AAAGAGCCTA	ACATCTCCAT	GGGGAGGGCT	CACCCAGGGG	ACAGGGCCCT	GGAGCTCAGG	2880
40	GTCTCTTGT	CTGCTCTGCC	AGCTGCAGCC	TGGTTGGCAG	CATCTGTCTC	ATCGGGGCAG	2940
	GGGGTATGCA	GAGCTTGTGG	TGGGGCAGGA	ACGGTGGAGG	CAGAGGTGAC	AGTTCCCAAG	3000
	GTGGGCTTTG	GTGGCCAGGG	AGGCAGCCTA	GCCTATGTCT	GGCAGATGAG	GGCTGGCTGC	3060
	CGTTTTCTGG	GCTGATGGGT	GCCCTTTCCCT	GGCAGTCTCA	GTCCAAAGT	GTTGACTGTG	3120
	TCATTAGTCC	TTTGTCTAAG	TAGGGCCAGG	GCACCGTATT	CCTCTCCAG	GTGTTTGTGG	3180
45	GGCTGGAAGG	ACCTGCTCCC	ACAGGGGCCA	TGTCCTCTCT	TAATAGTGG	CACCTACCCCA	3240
	AACCCATCTT	TGTTTCTCCT	ATATCCTCCT	TCTCCTGTTC	CATTTCAGTT	CAGTTTCAGC	3300
	GGTGCCAAAC	TCTTTGCGTT	TCCTTTTGTG	TGATGAGGAC	CCAGAGCTGC	TGCACACACT	3360
	CACCTCTAAC	CCCCCTCCCT	CGCTGCTGGG	CCCCATCTCC	ACAGGAGAGA	CTGGTTCCGG	3420
	TCTAGGGCCT	CAGTCTGGAG	TGGGATAGGA	GCAGTGAGTG	ACAAAGCCTC	TGAAAGATGC	3480
50	ATCATCTCTT	CCTCACACCC	ATTTAGTGGG	GGATGGGTCC	TCTAGACTTG	AGGGGCTACC	3540
	CTGGGAAGCT	GCCCTGCTGT	CAGCCAGGCA	AGAAAGCTTC	CTTCAACCTG	CATAGCCGGT	3600
	GGGTGAGGAG	ATTCCCACTT	TCCATAGCCT	CCAAACATGT	TCCCAAGGCC	CCACTTTCAA	3660
	GAATCAGACA	GCAGGAAGCC	ATAGATGCTG	GCTGGGTTCC	AGGTTATGGG	GAGAAGAAAT	3720
55	ACAGTCAATA	AAAGGTTTTT	GTATAAAAAA	AAAAAATAAA	AAAAAATAAA	AAAAAATAAA	3780
	A						3781

Seq ID NO: C177 DNA Sequence  
 Nucleic Acid Accession #: AK094595  
 Coding sequence: 1..2853

60	1	11	21	31	41	51	
	ATGGGGGCCC	GGAGCGGAGC	TGGGGGCGCG	CTGCTGCTGG	CAGTCTGCTG	CTGCTGGGAC	60
	CCGAGGCTGA	GCCAAAGCAG	TAGGAAGCGA	TCGGGTGAGG	TGCTCCCTGA	CTCCTTCCCG	120
65	TCAGCGCCAC	CAGAGCCGCT	GCCCTACTTC	CTGCAGGAGC	CACAGGACGC	CTACATTGTG	180
	AAGAACAAGC	CTGTGGAGCT	CGCTGCGCG	GCCTTCCCG	CCACACAGAT	CTACTTCAAG	240
	TGCAACGGCG	AGTGGGTCAG	CCAGAACGAC	CACGTACAC	AGGAAGGCCT	GGATGAGGCC	300
	ACCCTGGGGG	CGCGGGGCGG	CCTGCGGGTG	CGCGAGGTGC	AGATCGAGGT	GTGCGGGCAG	360
	CAGGTGGAGG	AGCTCTTTGG	GCTGGAGGAT	TACTGGTGCC	AGTGCCTGGC	CTGGAGCTCC	420
70	GCGGGCACCA	CCAAGAGTCG	CCGAGCCTAC	GTCCGTCATG	CCTACCTGCG	CAAGAACTTC	480
	GATCAGGAGC	CTCTGGGCAA	GGAGGTGCCC	CTGGACCATG	AGGTTCTCCT	GCAGTGCCGC	540
	CGCGCGGAGG	GGGTGCTCTG	GGCCGAGGTG	GAATGGCTCA	AGAATGAGGA	TGTCTATCGA	600
	CCACCCAGG	ACACCAACTT	CCTGCTCACC	ATCGACCACA	ACCTCATCAT	CCGCCAGGCC	660
	CGCCTGTCCG	ACACTGCCAA	CTATACCTGC	GTGGCCAAGA	ACATCGTGGC	CAACGCCCGG	720
75	AGCACCACCTG	CCACCGTCAT	CGTCTACGTG	AATGGCGGCT	GGTCCAGCTG	GGCAGAGTGG	780
	TCAACCTGCT	CCAACCGCTG	TGGCCGAGGC	TGGCAGAAGC	GCACCCGAGC	CTGCACCAAC	840
	CCGCTTCCAC	TCAACCGAGG	GGCCTTCTGC	GAGGGCCAGG	CATTCCAGAA	GACCCGCTCG	900
	ACCACCATCT	GCCCAATCGA	TGGGGCGTGG	ACGGAGTGGA	GCAAGTGGTC	AGCCTGCAGC	960
	ACTGAGTGTG	CCCACTGGCG	TAGCCGCGAG	TGCATGGCGC	CCCCACCCCA	GAACGGAGGC	1020
80	CGTGACTGCA	CGGGGACGCT	GCTCGACTCT	AAGAACTGCA	CAGATGGGCT	GTGCATGCAA	1080
	AATAAGAAAA	CTCTAAGCGA	CCCCAACAGC	CACCTGCTGG	AGGCCTCAGG	GGATGCGGCG	1140
	CTGTATGCGG	GGCTCGTGGT	GGCCATCTTC	GTGGTCGTGG	CAATCTCTAT	GGCGGTGGGG	1200
	GTGGTGGTGT	ACCGCCGCAA	CTGCCGTGAC	TTGCACACAG	ACATCACTGA	CTCATCTGCT	1260
	GCCTGACTG	GTGGTTTCCA	CCCCGTCAAC	TTTAAGACGG	CAAGGCCAGG	CAACCCGACG	1320
	CTCTACACAC	CCTCTGTGGT	TCTGTACCTG	ACAGCCAGCG	CGGCATCTA	CCGCGGACCC	1380

5 GTGTATGCCCC TGCAGGACTC CACCGACAAA ATCCCCATGA CCAACTCTCC TCTGCTGGAC 1440  
 CCCTTACCCA GCCTTAAGGT CAAGGTCTAC AGCTCCAGCA CCACGGGCTC TGGGCCAGGC 1500  
 CTGGCAGATG GGGCTGACCT GCTGGGGGTC TTGCCGCTG GCACATACCC TAGCGATTTC 1560  
 GCGCGGGACA CCCACTTCCT GCACCTGCGC AGCGCCAGCC TCGGTTCCCA GCAGCTCTTG 1620  
 GGCCTGCCCC GAGACCCAGG GAGCAGCGTC AGCGGCACCT TTGGCTGCCT GGGTGGGAGG 1680  
 CTCAGCATCC CCGGCACAGG GGTGAGCTTG CTGGTGCCCA ATGGAGCCAT TCCCAGGGGC 1740  
 AAGTTCTACG AGATGTATCT ACTCATCAAC AAGGCAGAAA GTACCCTCCC GCTTTCAGAA 1800  
 GGGACCCAGA CAGTATTGAG CCCCTCGGTG ACCTGTGGAC CCACAGGCTC CTGTCTGTGC 1860  
 10 CGCCCCGTCA TCCTCACCAT GCCCCTCTGT GCCGAAGTCA GTGCCCGTGA CTGGATCTTT 1920  
 CAGCTCAAGA CCCAGGCCCA CCAGGGCCAC TGGGAGGAGG TGGTGACCTT GGATGAGGAG 1980  
 ACCCTGAACA CACCTGTGTA CTGCCAGCTG GAGCCCGAGG CCTGTACATC CTGTCTGGAC 2040  
 CAGCTGGGCA CTTACGTGTT CACGGGCGAG TCCTATTCCC GCTCAGCAGT CAAGCGGCTC 2100  
 CAGCTGGCCG TCTTCGCCCC CGCCCTCTGC ACCTCCCTGG AGTACAGCCT CCGGGTCTAC 2160  
 TGCTTGGAGG ACACGCTGTG AGCACTGAAG GAGGTGCTGG AGCTGGAGCG GACTCTGGGC 2220  
 15 GATACCTTGG TGGAGGAGCC GAAACCGCTA ATGTTCAAGG ACAGTTACCA CAACCTGCGC 2280  
 CTCTCCCTCC ATGACCTCCC CATATGCCAT TGGAGGAGCA AGCTGTCTGG CAAATACCAG 2340  
 GAGATCCCCT TCTATCAGT TTGGAGTGGC AGCCAGAAGG CCCTCCACTG CACTTTCACC 2400  
 CTGGAGAGGC ACAGCTTGGC CTCACCTGCA AGATCTGCGT GCGGCAAGTG 2460  
 20 GAAGGGGAGG GCGAGATATT CCAGCTGCAT ACCACTCTGG CAGAGACACC TGCTGGCTCC 2520  
 CTGGCACTC TTGCTCTGTC CCCTGGCAGC ACTGTACCA CCCAGCTGGG ACCTTATGCC 2580  
 TTCAAGATCC CACTGTCCAT CCGCCAGAAG ATATGCAACA GCCTAGATGC CCCCACCTCA 2640  
 CGGGGCAATG ACTGGCGGAT GTTAGCACAG AAGCTCTCTA TGGACCGGTA CCTGAATTAC 2700  
 TTTGCCACCA AAGCGAGCCC CACGGGTGTG ATCCTGGACC TCTGGGAAGC TCTGCAGCAG 2760  
 25 GACGATGGGG ACCTCAACAG CTTGGCGAGT GCCTTGGAGG AGATGGGCAA GAGTGAGATG 2820  
 CTGGTGGCTG TGGCCACCGA CCGGGACTGC TGAGCTCTCT GGGACAGCGG GCTGGCAGGG 2880  
 ACTGGCAGGA GGCAGGTGCA GGGAGGCCTG GGGCAGCCTC CTGATGGGGA TGTTTGGCCT 2940  
 CTGCTTCTCT CCAGTTTACA GCCAGAGTTG CCTCTCTCTC TCCTCTTCCC CAACCCCCAG 3000  
 30 ACCATGACCA GCCTTAGAAA ATCCATGTAC TCTGTTGTTA GAGGGCCCGG AGTTCTCTCT 3060  
 CCACCCCGCG TCTCTCTCTC TTGCCCTGAG ATCTCTGTGC AGGAACCAAG ATGGGGCTGA 3120  
 AGCCTCTGGA GGCAGTTGGT TGGGGGCGGG CAGGCAGGAG GCCCTCCCTC CACCCCCCA 3180  
 CCTCAGCCC GGCACACTTCT GGGTTCCATG GGTTTAGTTT CCGTTCTCGT TTTCTTCTCT 3240  
 CGTTATGTAT TTTCTCTTTC TCCTTAAGCC CCTTCTGTCT TCACAGCCCTT TTTCTCTTCT 3300  
 35 GAAAGATCAA GTACAATTCA GACAACTGC TTTCTCTCTG CCAAAAGCAA AAAGGCAAAG 3360  
 GAAAGAAAGA AAGCTTCAGA CCGCTAGTAA GGCTCAAAGA AGAAGAAAAA CACCAAAACC 3420  
 ACAAGGGAAA AGAAAAACCC AGTTTCTTAG GAAACGCAAA CGATTATTAT TCCAGATTAT 3480  
 TTGGATAAGT CCTTTTAA A 3501

Seq ID NO: C178 DNA Sequence  
 Nucleic Acid Accession #: NM\_004625  
 Coding sequence: 310..1359

40 1 11 21 31 41 51  
 | | | | | |  
 45 GAGGGAGGGG CGGGGGCTGG AGGCAGCAGC GCCCCCGCAC TCCCCGCGTC TCGCACACTT 60  
 GCACCGGTCTG CTCGCGCGCA GCCCGGCGTC GCCCCAGGCC GCGCTCGCTC CTCCCTCCCT 120  
 CCTCCCCTCTC CGTGGCTCCC GTGCTCTCTG CGAGGCTCAG GCGCGGAGCG CGCGGACGGG 180  
 CGCACCGACA GACGGGCCCG GGGACGCTC GGTCTCGCGC TCCCGGGCGG GCTATGTTGA 240  
 TTGCCCCGCC GGGGCGCGCC CGCGGGATCA GCACAGCCCG GCCCGCGGCC CCGGCGGCCA 300  
 50 ATCGGGACTA TGAACCGGAA AGCGCGCGC TGCCCTGGGCC ACCTCTTTCT CAGCCTGGGC 360  
 ATGGTCTACC TCCGATCGG TGGCTTCTCC TCAGTGGTAG CTCTGGGCGC AAGCATCATC 420  
 TGTAAACAGA TCCAGGGCTT GGTCTCCAGA CAGCGGGCGA TCTGCCAGAG CCGGCCCGAC 480  
 GCCATCATCG TCATAGGAGA AGGCTCACAA ATGGGCTGG ACCAGTGTCA GTTTCAGTTC 540  
 CGCAATGGCC GCTGGAATG CTCTGCACTG GGAGAGCGCA CCGTCTTCGG GAAGGAGCTC 600  
 55 AAAGTGGGGA GCGGGAGGCT TGCGTTTACC TACGCCATCA TTGCCGCGCG CGTGGCCCCA 660  
 GCCATCAGAG CTCCTGTATC CCAGGGCAAC CTGAGCGACT GTGGCTCGCA CAAAGAGAAG 720  
 CAAGGCCATG ACCACCGGGA CGAGGGCTGG AAGTGGGGTG GCTGCTCTGC CGACATCCGC 780  
 TACGGCATCG GCTTCGCCAA GGTCTTTGTG GATGCCCGGG AGATCAAGCA GAATGCCCGG 840  
 ACTCTCATGA ACTTGACAA CACGAGGCA GGCCGAAAGA TCCTGGAGGA GAACATGAAG 900  
 60 CTGGAATGTA AGTGCCACGG CGTGTACGGC TCGTGACCCA CCAAGACGTG CTGGACCA 960  
 CTGCCACAGT TTCGGGAGCT GGGCTACGTG CTCAAGGACA AGTACAACGA GGCCGTTTAC 1020  
 GTGGAGCCTG TGCCTGCCAG CCGCAACAAG CGGCCACCTT TCCTGAAGAT CAAGAAGCCA 1080  
 CTGTGCTACC GCAAGCCCAT GGACACGGAC CTGGTGTA TCGAGAAGTC GCCCAACTAC 1140  
 TGCGAGGAGG ACCCGGTGAC CGGCAGTGTG GGCACCCAGG GCCGCGCTG CAACAAGACG 1200  
 GCTCCCCAGG CCAGCGGCTG TGACCTCATG TGCTGTGGGC GTGGCTACAA CACCCACCAG 1260  
 65 TACGCGCCCG TGTGGCAGTG CAACTGTAAG TTCCACTGGT GCTGCTATGT CAAGTGCAAC 1320  
 ACGTGCAGCG AGCGCACGGA GATGTACAGC TGCAAGTGAG CCCCGTGTGC ACACCACCTT 1380  
 CCCGCTGCAA GTGAGATTGC TGGGAGGACT GGACCGTTTC CAAGCTGCGG GCTCCCTGGC 1440  
 AGGATGCTGA GCTTGTCTTT TCTGTGAGG AGGGTACTTT TCCTGGGTTT CCTGCAGGCA 1500  
 70 TCCGTGGGGG AAAAAAATC TCTCAGAGCC CTCACTATT CTGTTCCACA CCCAATGCTG 1560  
 CTCCACCCCT CCCACAGAC AGCCCAAGTC CCTCCGCGGC TGGAGCGAAG CCTTCTGCAG 1620  
 CAGGAAGTCT GGACCCCTGG GCCTCATCAC AGCAATATTT AACAAATTTAT TCTGATAAAA 1680  
 ATAAATATTAA TTTATTTAAT TAAAAAGAA TCTTCCACAA AAAAAA 1736

Seq ID NO: C179 DNA Sequence OBR3  
 Nucleic Acid Accession #: NM\_003786  
 Coding sequence: 71..4654

75 1 11 21 31 41 51  
 | | | | | |  
 80 CTCCGGCGCC CGCTCTGCCC GCCGCTGGGT CCGACCGCGC TCGCCTTCCT TGCAGCCGCG 60  
 CCTCGGCCCC ATGGACGCCCT TGTGCGGTTT CCGGGAGCTC GGCTCCAAGT TCTGGGACTC 120  
 CAACCTGTCT GTGCACACAG AAAACCCGGA CCTCACTCCC TGCTTCCAGA ACTCCCTGCT 180  
 GGCTTGGGTG CCTGTGATCT ACCTGTGGGT CGCCCTGCCC TGCTACTTGC TCTACCTGCG 240  
 GCACCATTTG CTGTGGCTACA TCATCTCTCT CCACCTGTCC AAGCTCAAGA TGGTCTGGG 300

	TGTCCTGCTG	TGGTGCCTCT	CCTGGGCGGA	CCTTTTTTAC	TCCTTCCATG	GCCTGGTCCA	360
	TGGCCGGGCC	CCTGCCCTTG	TTTTCTTTGT	CACCCCTTG	GTGGTGGGGG	TCACCATGCT	420
	GCTGGCCACC	CTGCTGATAC	AGTATGAGCG	GCTGCAGGGC	GTACAGTCTT	CGGGGGTCTT	480
5	CATTATCTTC	TGGTTCCTGT	GTGTGGTCTG	CGCCATCGTC	CCATTCCGCT	CCAAGATCCT	540
	TTTAGCCAAAG	GCAGAGGGTG	AGATCTCAGA	CCCTTCCGCG	TTCAACCACT	TCTACATCCA	600
	CTTTTGCCCTG	GTACTCTCTG	CCCTCATCTT	GGCCTGCTTC	AGGGAGAAAC	CTCCATTTTT	660
	CTCCGCAAAAG	AATGTCGACC	CTAACCCCTA	CCCTGAGACC	AGCGCTGGCT	TTCTCTCCCG	720
	CCTGTTTTTC	TGGTGGTTCA	CAAAGATGGC	CATCTATGGC	TACCGGCATC	CCCTGGAGGA	780
10	GAAGGACCTC	TGGTCCCTAA	AGGAAGAGGA	CAGATCCAG	ATGGTGGTGC	AGCAGCTGCT	840
	GGAGGCATGG	AGGAAGCAGG	AAAAGCAGAC	GGCACGACAC	AAGGCTTCAG	CAGCACCTGG	900
	GAAAAATGCC	TCCGGCGAGG	ACGAGGTGCT	GCTGGGTGCC	CGGCCGAGGC	CCCGGAAGCC	960
	CTCCTTCCTG	AAGGCCCTGC	TGGCCACCTT	CGGCTCCAGC	TTCTCTATCA	GTGCCTGCTT	1020
	CAAGCTTATC	CAGGACCTGC	TCTCCTTCAT	CAATCCACAG	CTGCTCAGCA	TCCTGATCAG	1080
	GTCTTATCTCC	AACCCCATGG	CCCCCTCCTG	GTGGGGCTTC	CTGGTGGCTG	GGCTGATGTT	1140
15	CCTGTGCTCC	ATGATGCGAT	CGCTGATCTT	ACAACACTAT	TACCACTACA	TCTTGTGAC	1200
	TGGGGTGAAG	TTTCGTACTG	GGATCATGGG	TGTCATCTAC	AGGAAGGCTC	TGGTTATCAC	1260
	CAACTCAGTC	AAACGTGCGT	CCACTGTGGG	GGAAATTGTC	AACCTCATGT	CAGTGGATGC	1320
	CCAGCGCTTC	ATGGACCTTG	CCCCCTTCCT	CAATCTGCTG	TGGTCAGCAC	CCCTGCAGAT	1380
20	CATCCTGGCG	ATCTACTTCC	TCTGGCAGAA	CCTAGGTCCC	TCTGTCTTGG	CTGGAGTCGC	1440
	TTTCATGGTC	TTGCTGATTC	CACCTCAACG	AGCTGTGGCC	GTGAAGATGC	GCGCCTTCCA	1500
	GGTAAAGCAA	ATGAATTTGA	AGGACTCGCG	CATCAAGCTG	ATGAGTGAGA	TCCTGAACGG	1560
	CATCAAGGTG	CTGAAGCTGT	ACGCCCTGGG	GCCACAGCTT	CTGAAGCAGG	TGGAGGGCAT	1620
	CAGGCAGGTG	GAGCTCCAGC	TGCTGCGCAC	GGCGGCCTAC	CTCCACACCA	CAACCACTT	1680
25	CACCTGGATG	TGCAGCCCTT	TCCTGGTGAC	CCTGATCACC	CTCTGGGTGT	ACGTGTACGT	1740
	GGACCCAAAC	AATGTGCTGG	ACGCCGAGAA	GGCCTTTGTG	TCTGTGTCTT	TGTTTAATAT	1800
	CTTAAAGACTT	CCCTCAACCA	TGCTGCCCCA	GTTAATCAGC	AACCTGACTC	AGGCCAGTGT	1860
	GTCTCTGAAA	CGGATCCAGC	AATTCCTGAG	CCAAGAGGAA	CTTGACCCCC	AGAGTGTGGA	1920
	AAGAAAGACC	ATCTCCCCAG	GCTATGCCAT	CACCATACAC	AGTGGCACCT	TCACCTGGGC	1980
30	CCAGGACCTG	CCGCCCACTC	TGCACAGCCT	AGACATCCAG	GTCCCGAAAG	GGGCACCTGT	2040
	GGCCGTGGTG	GGGCCCTGTG	GCTGTGGGAA	GTCCCTCCCTG	GTGTCTGCCC	TGCTGGGAGA	2100
	GATGGAGAAAG	CTAGAAGGCA	AAGTGCACAT	GAAGGGCTCC	GTGGCCTATG	TGCCCCAGCA	2160
	GGCATGGATC	CAGAACTGCA	CTCTTCAGGA	AAACGTGCTT	TTCCGCAAAAG	CCCTGAACCC	2220
	CAAGCGCTAC	CAGCAGACTC	TGGAGGCTTG	TGCCTTGCTA	GCTGACCTGG	AGATGCTGCC	2280
35	TGGTGGGGAT	CAGACAGAGA	TTGGAGAGAA	GGGCATTAAAC	CTGTCTGGGG	GCCAGCGGCA	2340
	GCGGGTCAGT	CTGGCTCGAG	CTGTTTACAG	TGATGCCGAT	ATTTTCTTGC	TGGATGACCC	2400
	ACTGTCCCGG	GTGGACTCTC	ATGTGGCCAA	GCACATCTTT	GACCACGTCA	TCCGGCCAGA	2460
	AGGCGTGCTG	GCAGGCAAGA	CGCGAGTGCT	GGTGACGCAC	GGCATTAGCT	TCCTGCCCCA	2520
	GACAGACTTC	ATCATTTGTG	TAGCTGATGG	ACAGGTGTCT	GAGATGGGCC	CGTACCCAGC	2580
40	CCTGCTGCGG	CGCAACGGCT	CCTTTGCCAA	CTTTCTCTGC	AACTATGGCC	CCGATGAGGA	2640
	CCAAGGGCAC	CTGGAGGACA	GCTGGACCGC	GTTGGAAGGT	GCAGAGGATA	AGGAGGCAT	2700
	GCTGATTGAA	GACACACTCA	GCAACCAAC	GGATCTGACA	GACAATGATC	CAGTCACCTA	2760
	TGTGGTCCAG	AAGCAGTTTA	TGAGACAGCT	GAGTGCCCTG	TCCTCAGATG	GGGAGGGACA	2820
	GGGTGCGCCT	GTACCCCGGA	GGCACCTGGG	TCCATCAGAG	AAGGTGCAGG	TGACAGAGGC	2880
45	GAGGACAGAT	GGGGCACTCA	CCCAAGAGGA	GAAAGCAGCC	ATTGGCAGTG	TGGAGCTCAG	2940
	TGTGTTCTGG	GATTATGCCA	AGGCCGTGGG	GCTCTGTACC	ACGCTGGCCA	TCTGTCTCCT	3000
	GTATGTGGGT	CAAAGTGCGG	CTGCCATTGG	AGCCAATGTG	TGGCTCAGTG	CCTGGACAAA	3060
	TGATGCCATG	GCAGACAGTA	GACAGAACAA	CACCTCCCTG	AGGCTGGGCG	TCTATGCTGC	3120
	TTTAGGAATT	CTGCAAGGGT	TCTTGGTGAT	GCTGGCAGCC	ATGGCCATGG	CAGCGGGTGG	3180
50	CATCCAGGCT	GGCCGTGTGT	TGCACCAGGC	ACTGCTGCAC	AACAAGATAC	GCTCGCCACA	3240
	GTCTTCTTTT	GACACCAAC	CATCAGGCCG	CATCCTGAAC	TGCTTCTCCA	AGGACATCTA	3300
	TGTGCTGTAT	GAGGTTCTGT	CCCTGTCTAT	CCTCATGCTG	CTCAATTCTT	TCTTCAACGC	3360
	CATCTCCACT	CTGTGCTGCA	TCATGGCCAG	CACGCCGCTC	TTCACTGTGG	TCATCTGTCC	3420
	CCTGGCTGTG	CTCTACACCT	TAGTGACGCG	CTTCTATGCA	GCCACATCAC	GGCAACTGAA	3480
55	GCGGCTGGAA	TCAGTCAAGC	GCTCACCTAT	CTACTCCCAC	TTTTCGGAGA	CAGTGACTGG	3540
	TGCCAGTGTG	ATCCGGGCGT	ACAACCGCAG	CCGGGATTTT	GAGATCATCA	GTGATACTAA	3600
	GGTGGATGCC	AACCAGAGAA	GCTGCTACCC	CTACATCATC	TCCAACCGGT	GGCTGAGCAT	3660
	CGGAGTGGAG	TTCTGTGGGG	ACTGCGTGGT	GCTCTTTGCT	GCACTATTTG	CCGTCACTCG	3720
	GAGGAGCAGC	CTGAACCCGG	GGCTGGTGGG	CCTTTCTGTG	TCCTACTCCT	TGCAGGTGAC	3780
60	ATTGCTCTCT	AATCTGATGA	TACGAATGAT	GTGAGATTG	GAATCTAACA	TCGTGGCTGT	3840
	GGAGAGGGTG	AAGGAGTACT	CCAAGACAGA	GACAGAGGCG	CCCTGGGTGG	TGGAAGGCAG	3900
	CCGCCCTCCC	GAAGGTTGGC	CCCCACGTGG	GGAGGTGGAG	TTCCGGAATT	ATTCTGTGCG	3960
	CTACCGGCGG	GGCCTAGACC	TGGTGCTGAG	AGACCTGAGT	CTGCATGTGC	ACGGTGGCGA	4020
	GAAGGTGGGG	ATCGTGGGCG	GCACCTGGGG	TGGCAAGTCT	TCCATGACCC	TTTGCTCTGT	4080
65	CCGCATCCTG	GAGGCGGCAA	AGGGTGAAAT	CCGCATGTAT	GGCCTCAATG	TGGCAGACAT	4140
	CGGCTCCCAT	GAGCTGCGCT	CTCAGCTGAC	CATCATCCCG	CAGGACCCCA	TCCTGTTCTC	4200
	GGGGACCCCTG	CGCATGAACC	TGGACCCCTT	CGGCAGCTAC	TCAGAGGAGG	ACATTTGGTG	4260
	GGCTTTGGAG	CTGTCCCACT	TGCACACGTT	TGTGAGCTCC	CAGCCGGCAG	GCCTGGACTT	4320
70	CCAGTGCTCA	GAGGGCGGGG	AGAATCTCAG	CGTGGGCCAG	AGGCAGCTCG	TGTGCCCTGGC	4380
	CCGAGCCCTG	CTCCGCAAGA	GCCGCATCCT	GGTTTTAGAC	GAGGCCACAG	CTGCCATCGA	4440
	CCTGGAGACT	GACAACCTCA	TCCAGGCTAC	CATCCGCACC	CAGTTTGATA	CCTGCACTGT	4500
	CCTGACCATC	GCACACCGCG	TTAACAATAT	CATGGACTAC	ACCAGGGTCC	TGGTCTTGGA	4560
	CAAGAGGAGTA	GTAGCTGAAT	TTGATTCTCC	AGCCAACTTC	ATTGCAGCTA	GAGGCATCTT	4620
	CTACGGGATG	GCCAGAGATG	CTGGAATTGC	CTAAAAATATA	TTCTGTAGAT	TTCTCTCTGG	4680
75	CCTTTCTCTG	TTTTCATCAG	GAAGGAAATG	ACACCAAATA	TGTCCGCAGA	ATGGACTTGA	4740
	TAGCAAAACAC	TGGGGGCAC	TTAAGATTTT	GCACCTGTAA	AGTGCCTTAC	AGGGTAACTG	4800
	TGTGAAATGC	TTGATATGAG	GAAATGATCC	CCAAGTGGTG	AATGACACGC	CTAAGGTAC	4860
	AGCTAGTTTG	AGCCAGTTAG	ACTAGTCCCC	CGGTCTCCCG	ATTCCCAACT	GAGTGTATT	4920
	TGCACACTGC	ACTGTTTTCA	AATAACGATT	TTATGAAATG	ACCTCTGTCC	TCCCTCTGAT	4980
80	TTTTCATATT	TTCTTAAAGT	TTCTTTCTG	TTTTTAATA	AAAAGCTTTT	TCCTCTGGA	5040
	ACAGAAGACA	GCTGCTGGGT	CAGGCCACCC	CTAGGAACCTC	AGTCTGTAC	TCTGGGGTGC	5100
	TGCTGAAATC	CATTAAAAAT	GGGAGTACTG	ATGAAATAAA	ACTACATGGT	CAACAGTAAA	5160
	AAAAAAAAAA	AAAAAA					5176

Seq ID NO: C180 DNA Sequence

Nucleic Acid Accession #: NM\_004626  
Coding sequence: 124..1188

```

5      1      11      21      31      41      51
|      |      |      |      |      |
TAACCCGCGG CCTCCGCTCT CCCCGGCTGC AGGCGGCGTG CAGGACCAGC GGCGGCCGTG 60
CAGGCGGAGG ACTTCGGCGC GGCTCCTCCT GGGTGTGACC CCGGGCGCGC CCGCCGCGCG 120
ACGATGAGGG CGCGGCCGCA GGTCTGCGAG GCGCTGCTCT TCGCCCTGGC GCTCCAGACC 180
GGCGTGTGCT ATGGCATCAA GTGGCTGGCG CTGTCCAAGA CACCATCGGC CCTGGCACTG 240
10    AACCAGACGC AACACTGCAA GCAGCTGGAG GGTCTGGTGT CTGCACAGGT GCAGCTGTGC 300
CGCAGCAACC TGGAGCTCAT GCACACGGTG GTGCACGCGG CCCGCGAGGT CATGAAGGCC 360
TGTCGCGGGG CCTTTGCCGA CATGCGCTGG AACTGCTCCT CCATTGAGCT CGCCCCAAC 420
TATTTGCTTG ACCTGGAGAG AGGGACCCGG GAGTCGGCCT TCGTGTATGC GCTGTGCGGC 480
15    GCGGCCATCA GCCACGCCAT CGCCCGGGCC TGCACCTCCG GCGACCTGCC CGGCTGCTCC 540
TGCGGCCCGG TCCAGGTGA GCCACCGGGG CCGGGGAACC GCTGGGGAGG ATGTGCGGAC 600
AACTCAGCT ACGGGCTCCT CATGGGGGCC AAGTTTTCG ATGCTCCTAT GAAGTGAAA 660
AAAACAGGAT CCCAAGCCAA TAAACTGATG CGTCTACACA ACAGTGAAGT GGGGAGACAG 720
GCTCTGCGCG CCTCTCTGGA AATGAAGTGT AAGTGCCATG GGGTGTCTGG CTCCTGCTCC 780
ATCCGCACTT GCTGGAAGGG GCTGCAGGAG CTGCAGGATG TGGCTGCTGA CCTCAAGACC 840
20    CGATACCTGT CGGCCACCAA GGTAGTGCAC GCACCCATGG GCACCCGCAA GCACCTGGTG 900
CCCAAGGACC TGGATATCCG GCCTGTGAAG GACTCGGAAC TCGTCTATCT GCAGAGCTCA 960
CCTGACTTCT GCATGAAGAA TGAGAAGGTG GGCTCCACG GCACACAAGA CAGGCAGTGC 1020
AACAAAGACAT CCAACGGAAG CGACAGCTGC GACCTTATGT GCTGCGGGCG TGGCTACAAC 1080
CCTTACACAG ACCGCTGGT CGAGCGGTGC CACTGTAAAT ACCACTGGTG CTGCTACGTC 1140
25    ACCTGCCGCA GGTGTGAGCG TACCGTGGAG CGCTATGTCT GCAAGTGAGG CCCTGCCCTC 1200
CGCCCCACGC AGGAGCGAGG ACTCTGCTCA AGGACCCCTCA GCAACTGGGG CCAGGGGCGT 1260
GGAGACACTC CATGGAGCTC TGCTTGTGAA TTCAGATGTC CAGGCATGGG AGCGCGCTTG 1320
TGCTTTGCCCT TCACTTGGAA GCCACCAGGA ACAGAAGGTC TGGCCACCTT GGAAGGAGGG 1380
CAGGACATCA AAGGAAACCG ACAAGATTAA AATAACTTGG GCAGCCTGAG GCTCTGGAGT 1440
30    GCGCCACAGG TGGTGTAAAG AGCGGGGCTT GGGATCGGTG AGACTGATAC AGACTTGACC 1500
TTTCAGGGCC ACAGAGACCA GCCTCCGGGA AGGGGTCTGC CGCCTTCTT CAGAATGTTT 1560
TGCGGGACCC CCTGGCCCAT CCTGGGGTCT GAGCCTGCTG GGCCCAACCAC ATGGAATCAC 1620
TAGCTTGGGT TGTAAATGTT TTTCTTTGTT TTTTGTCTTT TCTTCTTTG GGATGTGGAA 1680
35    GCTACAGAAA TATTTATAAA ACATAGCTTT TTTCTTTGGG TGGCACTTCT CAATTCTCTT 1740
TTATATATTT TATATATATA AATATATATG TATATATATA ATGATCTCTA TTTTAAAACT 1800
AGCTTTTAA GCAGCTGAT GAAATAAATG CTGAGTGAGC CCCAGCCCGC CCCTGCAGTT 1860
CCCGGCCCTC TCAAGTGAAC TCGGCAGACC CTGGGGCTGG CAGAGGGAGC TCTCCAGTTT 1920
CCAGGCA 1927

```

40 Seq ID NO: C181 DNA Sequence  
Nucleic Acid Accession #: NM\_031866  
Coding sequence: 6..2090

```

45      1      11      21      31      41      51
|      |      |      |      |      |
ACAGCATGGA GTGGGGTTAC CTGTTGGAAG TGACCTCGCT GCTGGCCGCC TTGGCGCTGC 60
TGACAGCGCTC TAGCGGCGCT GCGGCCGCTT CCGCCAAGGA GCTGGCATGC CAAGAGATCA 120
CCGTGCGGCT GTGTAAAGGG ATCGGCTACA ACTACACCTA CATGCCCAAT CAGTTCAACC 180
50    ACGACACGCA AGACGAGGCG GCGCTGGAGG TGCACCAATT CTGGCCGTG GTGGAGATCC 240
AGTGCTCGCC CGATCTCAAG TTCTTCTGTG GCAGCATGTA CACGCCCATC TGCCTAGAGG 300
ACTACAAGAA GCGGCTGCGC CCCTGCCGCT CGGTGTGCGA GCGCGCCAAG GCGGCTGCG 360
CGCGCTCAT GCGCGAGTAC GGCTTGCCTT GCGCCGACCG CATGCGCTGC GACCGGCTGC 420
CCGAGCAAGG CAACCCCTGAC ACGCTGTGCA TGGACTACAA CCGCACCGAC CTAACCACCG 480
55    CCGGCGCCAG CCCGCCGCGC CGCCTGCCGC CCGCGCCGCC CCGCGAGCAG CCCTCTCGG 540
GCAGCGGCCA CGGCGGCCCG CCGGGGGCCA GCGCCCGCCA CCGCGAGGCG GGCAGGGGCG 600
GTGGCGGCGG GAGCGCGCGC GCGCCCCCAG CTCGCGCGCG CCGCGGTGGC GGAAGGCGC 660
GGCCCCCTGG CGGCGGCGCG GCTCCCTGCG AGCCCGGGTG CCAGTGCCGC GCGCCTATGG 720
TGAGCGTGTG CAGCGAGCGC CACCCGCTCT ACAACCGCGT CAAGACAGGC CAGATCGCTA 780
60    ACTGCGCGCT GCCCTGCCAT AACCCCTTTT TCAGCCAGGA CGAGCGCGCC TTCACCGTCT 840
TCTGGATCGG CCTGTGTTGC GTGCTCTGCT TCGTGTCCAC CTTGCGCACG GTCTCCACCT 900
TCCTTATCGA CATGGAGCGC TTCAGTACC CGGAGCGGCC CATTATCTTC CTCTCGGCCT 960
GCTACCTCTT CGTGTGCTG GGTACCTTAG TGCGCCTGGT GCGCGGCCAC GAGAAGGTGG 1020
CGTGCAGCGG TGGCGCGCGC GCGCGGGGGG GCGCTGGGGG CCGCGGCGGC GCGGCGCGCG 1080
65    GCGCGGGCGC GCGGCGCGCG GCGCGGGGCG GCGCGGGCGG CCGCGGCGAG TACGAGGAGC 1140
TGGGCGCGGT GGAGCAGCAC GTGCGCTACG AGACCACCGG CCGCGCGCTG TGCACCGTGG 1200
TCTTCTTGCT GGTCTACTTC TTCCGCATGG CCAGCTCCAT CTGGTGGGTG ATCTTGTGCG 1260
TCACATGGTT CCTGGCGGCC GGTATGAAGT GGGGCAACGA AGCCATCGCC GGCTACTGCG 1320
AGTACTTCCA CCTGGCCGCG TGGCTTGTGC CCAGCGTCAA GTCCATCGCG GTGCTGGCGC 1380
TCAGCTCGGT GGACGGCGAG CCGGTGGCGG GCATCTGCTA CGTGGGCAAC CAGAGCCTGG 1440
70    ACAACTCGCG CGGCTTCTGT CTGGCGCGCG TGGTCTATCT CCTCTTCTC GGCACCATGT 1500
TCCTGCTGGC CGGCTTCTGT TCCCTGTGCC GCATCCGCTC GGTCTATCAAG CAACAGGAGC 1560
GCCCCACCAA GACGACAAAG CTGGAGAAGC TGATGATCCG CCTGGGCTGT TTCACCGTGC 1620
TCTACACCGT GCGCGCGCGG GTGGTGGTCT CCGCTCTCTT CTACGAGCAG CACAACCGCC 1680
CGCGCTGGGA GGCCACGCAC AACTGCCCGT GCCTGCGGGA CCTGCAGCCC GACCAGGCAC 1740
75    GCAGGCCCCG CTACGCCGTC TTCTATGCTCA AGTACTTCTG GTGCTTAGTG GTGGGCATCA 1800
CCTCGGGCGT GTGGGTCTGG TCCGGCAAGA CGCTGGAGTC CTGGGCTCTC CTGTGCACCC 1860
GCTGTGCTGG GGCCAGCAAG GCGCGCGCGG TGGGCGGGGG CCGCGGCGCC ACGGCGCGCG 1920
GGGGTGGCGG CGGCGCGGGG GCGCGCGGCG GCGGGGACCC CCGCGGCGGC GGGGGGCGCG 1980
80    GCGGCGGCGG GGGCTCCCTC TACAGCGAGC TCAGCACTGG CCTGAGCTGG CCGTGGGCA 2040
CGGCGAGCTC CGTGTCTTAT CCAAGCAGAG TGCCATTGTC CCAGTCTGA GCGGAGGGGA 2100
GGGGCGCGCC AGGAGGGGTG GGGAGGGGGG CGAGGAGACC CAAGTGACAG GAAGGGACAC 2160
TTGATGGGCT GAGGTTCACA CCCTTCACA GTGTTGATTG CTATTAGCAT GATAATGAAC 2220
TCTTAATGGT ATCCATTAGC TGGGACTTAA ATGACTCACT TAGAACAAAG TACCTGGCAT 2280
TGAAGCTCC CAGACCCAGC CCCTTTCTCT CCATTGATGT GCGGGGAGCT CCTCCGCCA 2340

```



5 CGCGTTAATT TCTGTGGCT GAGGAGGGTG GACTCTGCGG CGTTTCCAGA ACCCGAGATT 2400  
 TGGAGCCCTC CCTGGCTGCA CTTGGCTGGG TTTGCAGTCA GATACACAGA TTTCACCTGG 2460  
 GAGAACCCTT TTTTCTCCCT CGACTCTTCC TACGTAAACT CCCACCCCTG ACTTACCCCTG 2520  
 GAGGAGGGGT GACCGCCACC TGATGGGATT GCACGGTTTG GGTATTCTTA ATGACCAGGC 2580  
 AAATGCCTTA AGTAAACAAA CAAGAAATGT CTTAATTATA CACCCACCTG AAATACGGGT 2640  
 TTCTTACATT AGAGGATGTA TTTATATAAT TATTTGTTAA ATTGTAAAAA AAAAAAGTGT 2700  
 AAAATATGTA TATATCCAAA GATATAGTGT GTACATTTT TTGTAAAAAG TTTAGAGGCT 2760  
 TACCCCTGTA AGAACAGATA TAAGTATTCT ATTTTGTCAA TAAATGACT TTTGATAAAT 2820  
 10 GATTTAACCA TTGCCCTCT CCCCGCCTCT TCTGAGCTGT CACCTTTAAA GTGCTTGCTA 2880  
 AGGACGCATG GGGAAAATGG ACATTTTCTG GCTTGTCTAT CTGTACACTG ACCTTAGGCA 2940  
 TGGAGAAAAAT TACTTGTATA ACTCTAGTTC TTAAGTTGTT AGCCAAGTAA ATATCATTGT 3000  
 TGAAC TGAAA TCAAAATTGA GTTTTGTGAC CTTCCTCCAA GACGGTGT TTTCATGGAG 3060  
 CTCTTTCTG ATCCATGGAT AACAACCTCT ACTTTAGTGG ATGTAAATGG AACTTCTGCA 3120  
 15 AGGCAGTAAT TCCCTTAGG CTTTGTATT TATCTGTCAT GGTATCACTA AAGGTTTCAA 3180  
 AACCCTGAAA AAAAA 3195

Seq ID NO: C182 DNA Sequence  
 Nucleic Acid Accession #: XM\_050625  
 Coding sequence: 222..1109

20 1 11 21 31 41 51  
 | | | | | |  
 CCGGGTCGGA GCCCCCCGGA GCTGCGCGCG GGCTTGCGAGC GCCTCGCCCG CGCTGTCCTC 60  
 25 CCGGTGTCCC GCTTCTCCGC GCCCCAGCCG CCGGCTGCCA GCTTTTCGGG GCCCCGAGTC 120  
 GCACCCAGCG AAGAGAGCGG GCCCGGACAG AGCTCGAACT CCGGCCGCGT CGCCCTTCCC 180  
 CGGCTCCGCT CCCTCTGCCC CCTCGGGGTC GCGCGCCAC GATGCTGCAG GGCCCTGGCT 240  
 CGCTGCTGCT GCTCTTCTCT GCTCTGCACT GCTGCTGGG CTCGGCGCGC GGGCTCTTCC 300  
 TCTTTGGCCA GCCCGACTTC TCCTACAAGC GCAGCAATTG CAAGCCCATC CCTGCCAACC 360  
 30 TGCAGCTGTG CCACGGCATC GAATACCAGA ACATGCGGCT GCCCAACCTG CTGGGCCACG 420  
 AGACCATGAA GGAGGTGCTG GAGCAGGCCG GCGCTTGGAT CCCGCTGGTC ATGAAGCAGT 480  
 GCCACCCGGA CACCAAGAAG TTCCTGTGCT CGCTCTTCGC CCCGCTGTC CTGATGACC 540  
 TAGACGAGAC CATCCAGCCA TGCCACTCGC TCTGCGTGCA GGTGAAGGAC CGCTGCGCCC 600  
 CGGTATGTC CGCCTCTCGC TTCCCTGGC CCGACATGCT TGAGTGCGAC CGTTTCCCCC 660  
 35 AGGACAACGA CTTTGTGATC CCCCTCGCTA GCGACGACCA CCTCTGCCA GCCACCGAGG 720  
 AAGCTCCAAA GGTATGTGAA GCCTGCAAAA ATAAAAATGA TGATGACAA GACATAATGG 780  
 AAACGCTTTG TAAAAATGAT TTTGCACTGA AAATAAAAGT GAAGGAGATA ACCTACATCA 840  
 ACCGAGATAC CAAAATCATC CTGGAGACCA AGAGCAAGAC CATTACAAAG CTGAACGGTG 900  
 TGTCCGAAAG GGACCTGAAG AAATCGGTGC TGTGGCTCAA AGACAGCTTG CAGTGACCTT 960  
 40 GTGAGGAGAT GAACGACATC AACGCGCCCT ATCTGGTCAT GGGACAGAAA CAGGGTGGGG 1020  
 AGCTGGTGAT CACCTCGGTG AAGCGGTGGC AGAAGGGGCA GAGAGAGTTC AAGCGCATCT 1080  
 CCGCAGCATC CGCAAGCTG CAGTGCTAGT CCGGCATCC TGATGGCTCC GACAGGCCGT 1140  
 CTCCAGAGCA CGGCTGACCA TTTCTGCTCC GGGATCTCAG CTCCTGTTCC CCAAGCACAC 1200  
 TCTAGCTGC TCCAGTCTCA GCCTGGGCAG CTTCCTCCCTG CTTTGTGCAC GTTGTGATCC 1260  
 45 CCAGCATTTT CTGAGTTATA AGGCCACAGG AGTGATAGC TGTTTTACC TAAAGGAAAA 1320  
 GCCACCCGA ATCTTGTAGA AATATTCAAA CTAATAAAAT CATGAATATT TTTATGAAGT 1380  
 TT 1382

Seq ID NO: C183 DNA Sequence  
 Nucleic Acid Accession #: NM\_001306.1  
 Coding sequence: 199..861

50 1 11 21 31 41 51  
 | | | | | |  
 AATTCCGGCAC GAGGGCAGGT GCAGGCGCAC GCGGCGAGAG CGTATGGAGC CGAGCCGTTA 60  
 55 GCGCGCGCCG TCGGTGAGTC AGTCCGTCCG TCCGTCCGTC CGTCCGGGCG CCGCAGCTCC 120  
 CGCCAGGCCG AGCGGCCCCG GCCCTCTGTC TCCCGCACCC CGGAGCCACC CGGTGGAGCG 180  
 GGCTTTGGCG CGCGAGCTTC GTCCATGGGC CTGGAGATCA CGGGCACCCG GCTGGCCGTG 240  
 CTGGGCTGGC TGGGCACCAT CGTGTGCTGC GCGTTGCCCA TGTGGCGCGT GTCGGCCTTC 300  
 60 ATCGGCAGCA ACATCATCAC GTCGCAAGC ATCTGGGAGG GCCTGTGGAT GAACTGCGTG 360  
 GTGCAGAGCA CCGGCCAGAT GCAGTGCAAG GTGTACGACT CGCTGTGTC ACTGCCACAG 420  
 GACCTTCAGG CGGCCCGCGC CCTCATCTGT GTGGCCATCC TGCTGGCCGC CTTGCGGCTG 480  
 CTAGTGGCGC TGCTGGGCGC CCAAGTGCAC AACTGCGTGC AGGACGACAC GGCCAAAGGC 540  
 AAGATCACCA TCGTGGCAGG CGTGCTGTTT CTCTCGCCG CCCTGCTCAC CCTCGTCCG 600  
 65 GTGTCCTGGT CGGCCAACAC CATTATCCGG GACTTCTACA ACCCCGTGGT GCCCGAGGCG 660  
 CAGAAGCGCG AGATGGGCGC GGGCCTGTAC GTGGGCTGGG CGGCCGCGGC GCTGCAGCTG 720  
 CTGGGGGGCG CGCTGCTCTG CTGCTCGTGT CCCCCACGCG AGAAGAAGTA CACGGCCACC 780  
 AAGGTCTGCT ACTCCGCGCC GCGCTCCACC GGCCCGGGAG CCAGCTCTGG CACAGGCTAC 840  
 GACCGCAAGG ACTACGTCTA AGGGACAGAC GCAGGGAGAC CCCACCACCA CCACCACCAC 900  
 70 CAACACCACC ACCACCACCG CGAGCTGGAG CGCGCACCA GGCATCCAGC GTGCAGCCTT 960  
 GCCTCGGAGG CCAGCCCAACC CCCAGAAGCC AGGAAGCCCC CGCGCTGGAC TGGGGCAGCT 1020  
 TCCCCAGCAG CCACGGCTTT GCGGGCGGGG CAGTCGACTT CCGGGCCACG GGACCAACCT 1080  
 GCATGGACTG TGAACCTCA CCCTTCTGGA GCACGGGGCC TGGGTGACCG CCAATACTTG 1140  
 75 ACCACCCCGT CGAGCCCATC CGGCCGCTG CCCCATGTC GCGCTGGGCA GGGACCGGCA 1200  
 GCCTGGAAG GGGCATTGA TATTTTCAA TAAAGCCTC TCGTTTACG 1250

Seq ID NO: C184 DNA Sequence  
 Nucleic Acid Accession #: NM\_012449.1  
 Coding sequence: 66..1085

80 1 11 21 31 41 51  
 | | | | | |  
 CCGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60  
 AATTAATGGA AAGCAGAAAA GACATCACAA ACCAAGAAGA ACTTTGGAAA ATGAAGCCTA 120  
 GGAGAAATTT AGAAGAAGAC GATTATTTGC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180

AAAGACCTGT GCTTTTGCAT TTGCACAAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240  
 CAGAACTTCA GCACACACAG GAACTCTTTC CACAGTGGCA CTGCCCAATT AAAATAGCTG 300  
 CTATTATAGC ATCTCTGACT TTCTTTTACA CTCTTCTGAG GGAAGTAATT CACCCTTTAG 360  
 CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAGTCTTGC 420  
 CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG 480  
 TCCAACCTCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540  
 TAACAAGAAA GCAGTTTGGG CTCTCAGTT TCTTTTTCG TGTACTGCAT GCAATTTATA 600  
 GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAACTGG GCATATCAAC 660  
 AGGTCCAACA AAATAAAGAA GATGCCTGGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT 720  
 ATGTGTCTCT GGAATTTGTG GGATTGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC 780  
 CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACTA TATTCAGAGC AAGCTAGGAA 840  
 TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCCTGSAAT AAGTGGATAG 900  
 ATATAAAACA ATTTGTATGG TATACACCTC CAACTTTTAT GATAGCTGTT TTCTTCCAA 960  
 TTGTTGTCTT GATATTTAAA AGCATACTAT TCCTGCCATG CTGAGGAAG AAGATACTGA 1020  
 AGATTAGACA TGGTTGGGAA GACGTACCA AAATTAACAA AACTGAGATA TGTTCACAGT 1080  
 TGTAAGATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140  
 TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAAAAAA AAAAA 1195

Seq ID NO: C185 DNA Sequence  
 Nucleic Acid Accession #: NM\_001775.1  
 Coding sequence: 70..972

1 11 21 31 41 51  
 CTAAAGCTCT CTGCTGCCT AGCCTCCTGC CGGCCTCATC TTCGCCAGC CAACCCCGCC 60  
 TGGAGCCCTA TGGCCAACTG CGAGTTTCAGC CCGGTGTCCG GGGACAAACC CTGCTGCCGG 120  
 CTCTCTAGGA TGAGCCCACT CTGTCTTGGC GTCACTATCC TGGTCTGAT CCTCGTCGTG 180  
 GTGCTCGCGG TGGTCTGCCC GAGGTGGCGC CAGACGTGGA GCGGTCCGGG CACCACCAAG 240  
 CGCTTTCCCG AGACCGTCTT GGCCTGATGC GTCAAGTACA CTGAAATTCA TCCTGAGATG 300  
 AGACATGTAG ACTGCCAAAG TGTATGGGAT GCTTTCAAGG GTGCATTTAT TTCAAAACAT 360  
 CCTTGCACAA TACTGAAGA AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCCGA 420  
 CCTTGCACAA AGATTCTTCT TTGGAGCAGA ATAAAAGATC TGGCCCATCA GTTCACACAG 480  
 GTCCAGCGGG ACATGTTTAC CCTGGAGGAC ACGCTGCTAG GCTACCTTGC TGATGACCTC 540  
 ACATGGTGTG GTGAATTCAC CACTTCCAAA ATAACTATC AATCTTGCCC AGACTGGAGA 600  
 AAGGACTGCA GCACAAACCC TGTTCAGTA TTCTGGAAAA CCGTTTCCCG CAGGTTTGCA 660  
 GAAGCTGCCT GTGATGTGGT CCAATGTATG CTCAATGGAT CCGCAGTAA AATCTTTGAC 720  
 AAAACAGCA CTTTGGGAG TGTGGAAGTC CATAATTGTC AACCAGAGAA GGTTCAGACA 780  
 CTAGAGGCCT GGTGATACA TGGTGAAGA GAAGATTCCA GAGACTTATG CCAGGATCCC 840  
 ACCATAAAG AGCTGGAATC GATTATAAGC AAAAGGAATA TTCAATTTTC CTGCAAGAAT 900  
 ATCTACAGAC GTGACAAAGT TCTTCAGTGT GTGAAAATC CTGAGGATTC ATCTTGACA 960  
 TCTGAGATCT GAGCCAGTCG CTGTGGTGT TTTAGCTCCT TGACTCCTTG TGGTTTATGT 1020  
 CATCATACAT GACTCAGCAT ACCTGCTGGT GCAGAGCTGA AGATTTTGA GGGTCTCCA 1080  
 CAATAAGGTC AATGCCAGAG ACGGAAGCCT TTTTCCCAA AGTCTTAAAA TAACCTATAT 1140  
 CATCAGCATA CTTTATTGT GATCTATCAA TAGTCAAGAA AAATTATTGT ATAAGATTAG 1200  
 AATGAAAATT GTATGTTAAG TTACTTCCTT TAG 1233

Seq ID NO: C186 DNA Sequence  
 Nucleic Acid Accession #: XM\_120513.2  
 Coding sequence: 1..2208

1 11 21 31 41 51  
 ATGGTGTTCAT GCACGTTCTC GGGGCCCTTA CGGGAAACAA ATGAAAACGT GAAAAAGTTC 60  
 TACGCCCTTG GAGCTTTTAT GTTCCGCATG AGCTCAGAGG CCGCGATGCT CGGGGAAAGC 120  
 AGGACCCCAA AGCTCGGTAA ACACCCGCGC ACCACCCGGG CCAAGATCTT CAAGAGGTTT 180  
 TTTTCAGAA GATCGGAGAG CAATTCCCGA TTGGTAGAAG AACTTGTCTG AATACACACG 240  
 TACTGTAGC ATCCCGCCCC AACGACTAGC CCCTCCTCTG TGCAACCCCG AGAGTTTGGG 300  
 GTCATGCAGG GGGCGCCACG AGCTCGTTTC GGAAGCCGGA CCGCGCCCGC AGCCGAGAA 360  
 GCCTCGAGTC CACATCTGGG CATTTGGCGAG GCAGCTGTG AATCAGGAGC TCGGGCGGCA 420  
 GCCCCCGCGC CGGGGGCTCG CGATGCCAG CCTCAGCGAC AGGCGGCGGC GGGCGGCGCC 480  
 ACGGCACAGA CACACACCTC CCCACACGCG CGCACAGGGG CAGACCCGGC GGGCAGGCGG 540  
 CGGAGGCACC CTCGGAGCCC GCGCGCCGCG GGGGAGGGGA CGTGCTCCGA GGGACCGGCC 600  
 CCGAGGCGCC GGTGAGGAGA AGAGATGCAG CCGGCAGAGG AGGGGCCAG CGTCCCAAA 660  
 ATCTACAAGC AGCGCAGCCC CTACAGCGTC CTCAAGACGT TCCCAGCAA GAGACCGCGC 720  
 CTGGCCAAGC GCTACGAGCG ACCACCCCTG GTGGAGCTGC CGCACGGCCA CTTGAGGACT 780  
 CCGGCGCAGC CGCGCGCCGC GTCCCGCCGC GCCTCCTCGT CGTCTTCTG GTCCGCTGTC 840  
 GTCAGACTCG GGGCTCTTCC GCGTCCGCCA CGCCGTGGAT TTCGGGCGCG GGGAAACCATC 900  
 CCGCCCTCTC TTCTGCCCCC GGGAGTCGCA GGCACCTGTC TCCACCCGCC CACGTCGTG 960  
 TCCCGGCCAT CCCCTCGTCC CCGTCCGTGG CACGCTGCCG CGCCGCGGGG AGGGACCTCA 1020  
 CATACACATA TGTGGAGTTC CCAGTCCACA CTTCCAGGAT CTGACACCAT GGTCTCTGTC 1080  
 TTTGGATTGA TGGCTCAGAG AAGATGGCAG CATAGATCTT TAAAGCAGTT TGAGTGGGGA 1140  
 ATTCTTGGAT CTTGGGGTAC TTGGCCATGT GGCAGGAGT GGTGGAGAA GGGAGGTGAG 1200  
 GTGGCGGTCC TGCTGCCAAG GTCTGAGGCT AATACTGCTC CTAAGAAGAG TCGAATGATC 1260  
 TTGGATGCCT TTGCCAGCA GTGCAGTCA GTTCTTAGCC TCTTAAATTG TGGAGGAAAA 1320  
 CTCCTGGACT CCAACCATTC TCAGTCCATG ATTTCTTGGC TAAAGCAGGA AGGCTCAAGT 1380  
 TACAACGAAA GACAGGAGCA CTGTACATT GGGAAAGGGG TCCACAGTCA GACCTCAGAC 1440  
 AATGTAGACA TAGAGATGCA GTATATGCAA AGGAAACAAC AAACCTTCTGC CTTTGTGAGG 1500  
 GTTTTCACTG TCTCTCACTG AAATTACCTG CTCTCGGGA GCTTCCAAAC TCCAACCCCC 1560  
 TCGTCAGCCA GTGAATATGG CCATCTGGCC GACGTGGATC CTCTGTCAAC CTCTCCTGTG 1620  
 CATACATTAG AAAATATTTT ACTTGATTCC ACAGCTTCCC TGTGTAAATC TAGGCATCTA 1680  
 TCCAGAGAGC CCCCAGTCAA GAGTGATTTT CCAATCCTT TGCAGCAGGC CTTGGCTGGG 1740  
 GGTGCTTCAA GACCATTTTC AGGGGCACAG CAAAGCATCG CTTACAGGGT GAACTCTGAA 1800  
 CTTGAGGATG GCATCCGCGC CCCCCTCCCT TTGAGTTGT AGGCCCTTGA AATGGATTG 1860  
 ACCTCCTTGG GAAGCAAGCA GCTGTTGAAC AACTATCCTG TCTACATAAC GAGCAACAG 1920

TGGGATGAGG CTGTAAATTC TTCAAAGAAA GATGGGAGAC GGCTCCTTCG ATACCTCATC 1980  
 AGATTGTGTT TCACAACCGA TGAGCTTAAG TACTCATGCG GCCTTGGGAA AAGGAAAAGG 2040  
 TCAGTGCAGT CAGGAGAGAC AGGTCCCGAA AGACGCCCTC TGGATCCAGT TAAAGTAACA 2100  
 TGCTCCGAG GTACTGCATC CTTCGCTCA GTGTACCAT CTGTGATCTC ATTTACCCTG 2160  
 ATTGGCTGTG GCTCTCCCGG TACAAGTGTT CAGCCTTCTG TATTTTGA 2208

Seq ID NO: C187 DNA Sequence  
 Nucleic Acid Accession #: AB037745.1  
 Coding sequence: 26..1744

1 11 21 31 41 51  
 | | | | |  
 ATGGTGGAA CCGTGTCCCA CAAACATGGA AACGACCGTT CTCAGTGGGA TCAACTTCGA 60  
 GTACAAGGGC ATGACAGGCT GGGAGGTGGC TGGTGATCAC ATTTACACAG CTGCTGGAGC 120  
 CTCAGACAA GACTTCATGA TTCTCACTCT GGTGTGCGCA GGATTTAGAC CTCCGCAGTC 180  
 GGTGATGGCA GACACAGAGA ATAAAGAGGT GGCCAGAATC ACATTTGTCT TTGAGACCCT 240  
 CTGTTCTGTG AACTGTGAGC TCTACTTTCAT GGTGGGTGTG AATTCTAGGA CCAACACTCC 300  
 TGTGGAGACG TGGAAAGGTT CCAAGGCGAA ACAGTCTTAT ACCTACATCA TTGAGGAGAA 360  
 CACTACCACG AGCTTCACCT GGGCCTTCCA GAGGACCACT TTTTCATGAG CAAGCAGGAA 420  
 GTACACCAAT GACGTTGCCA AGATCTACTC CATCAATGTC ACCAATGTTA TGAATGGCGT 480  
 GGCTCTCTAC TGCCGTCCCT GTGCCCTAGA AGCCTCTGAT GTGGGCTCCT CCTGCACCTC 540  
 TTGTCCTGCT GGTTCATATA TTGACCGAGA TTCAGGAACC TGCCACTCCT GCGCCCTTAA 600  
 CACAATTCGT AAAGCCCAAC AGCCTTATGG TGTCCAGGCC TGTGTGCCCT GTGGTCCAGG 660  
 GACCAAGAAC AACAGATCC ACTCTCTGTG CTACAATGAT TGCACCTTCT CACGCAACAC 720  
 TCCAACACAG ACTTCAACT ACACTTCTC CGCTTGGCA AACACCGTCA CTCTGTCTGG 780  
 AGGGCCAAAG TTCACTTCCA AAGGGTTGAA ATACTTCCAT CACTTTACCC TCAGTCTCTG 840  
 TGGAAACACG GGTAGGAAAA TGTCTGTGTG CACCGACAAT GTCACGTACC TCCGGATTCC 900  
 TGAGGGTGAG TCAGGGTTCT CCAATCTAT CACAGCCTAC GTCGTCCAGG CAGTCATCAT 960  
 CCGCCACAGAG GTGACAGGCT ACAAGGCCGG GGTTCCTCA CAGCCTGTCA GCCTGTCTGA 1020  
 TCGACTTATT GGGGTGACAA CAGATATGAC TCTGGATGGA ATCACTCCC CAGCTGAAC 1080  
 TTTCCACCTG GAGTCTTGG GAATACCGGA CGTGATCTTC TTTTATAGGT CCAATGATGT 1140  
 GACCCAGTCC TGCAGTTCTG GGAGATCAAC CACCATCCGC GTCAGGTGCA GTCCACAGAA 1200  
 AACTGTCCCT GGAAGTTTGC TGCTGCCAGG AACGTGCTCA GATGGGACCT GTGATGGCTG 1260  
 CAACTTCAC TCCCTGTGGG AGAGCGCGGC TGCTTGCCCG CTCTGCTCAG TGGCTGACTA 1320  
 CCATGCTATC GTCAGCAGCT GTGTGGCTGG GATCCAGAAG ACTACTTACG TGTGGCGAGA 1380  
 ACCCAAGCTA TGCTCTGGTG GCATTCTCT GCCTGAGCAG AGAGTCACCA TCTGCAAAAC 1440  
 CATAGATTTC TGGCTGAAAG TGGGCATCTC TGCAGGCACC TGTACTGCCA TCCTGCTCAC 1500  
 CGTCTTGACC TGCTACTTTT GGAAGAAAGAA TCAAAACTA GAGTACAAGT ACTCCAAGCT 1560  
 GGTGATGAAT GCTACTCTCA AGGACTGTGA CCTGCCAGCA GCTGACAGCT GCGCCATCAT 1620  
 GGAAGGCGAG GATGTAGAGG ACGACCTCAT CTTTACCAGC AAGAAGTCAC TCTTTGGGAA 1680  
 GATCAAATCA TTTACTTCCA AGCAGCCAGC TCCTGTCACC ATCTCTCTTT CAGAGGACTC 1740  
 CTGATGGATT TGACTCAGTG CCGCTGAAGA CATCCTCAGG AGGCCAGAC ATGGACCTGT 1800  
 GAGAGGCACT GCCTGCTCA CTGCTCCT CACCTTGCA AGCACCTTTG CAAGCCTGCG 1860  
 GCGATTGGG TGCCAGCATC CTGCAACACC CACTGTGTGA AATCTCTTCA TTGTGCCCTT 1920  
 ATCAGATGTT TGAATTTTCA ATCTTTTTTT ATAGAGTACC CAAACCCTCC TTTCTGCTTG 1980  
 CCTCAAACCT GCCAAATATA CCCACACTTT GTTTGTAAAT TATGCCCTTG CTTGTATCTT 2040  
 GTTTCCAAAT ATGGCCCATC CGCCAGAGCC ATAGCTTCGT CTGCTCATAA TTCTTATAGC 2100  
 TTTGGAATGA AATATTTCT ATCTTCTTAA GTATAGAAAC TATTTCTCT GTCTCTAAC 2160  
 TTAAGGCGAG AAACAGCTGG GAGTTTTCTT CGCATGCCCT CAGCTCATGA TCTCTTCAGG 2220  
 AGAGAGGCTG GGTGAGGAGG GTGTGCGGT TCCCTGGTGG ATAATCTTCA TAGCAGCTG 2280  
 GATCCATTTC CCTGTGATAA CCAGCTCAAA GGGAGTGAAA ATGGTAGTCT GAGGGCAAGG 2340  
 GGAGCAAGGC TGGGGTAAGA AAAGCCTTGA AAAGCATAAA AAGAGGCCGG GCGCGGTGGC 2400  
 TCACGCCTGT AATCCAGCA CTTTGGGAGG CCGAGGCGGG CAGATCATGA GGTGCGGAGA 2460  
 TTGAGACCAT CCTGGCTAAC ACGGTGAAGC CCCGTCTCTA CTGGAATATC AAAAAATTAG 2520  
 CCGGGCGTGG TGGCGGGTGC CTGTGCTCCC AGCTACTCGG GAGGCTGAGG CCGGAGAAAT 2580  
 GCGTGGGCCT GGAAGGCGGA GCTTGCAAGT AGCCGAGATC GCGCCACTGC ACTCCATCCA 2640  
 GCCTGGGTGA CAGAGTGAGA CTCTGCCTCA AAAAAAAGAA AAGCACAAGG 2700  
 AGAGGCAACA AGGAATGTTT TTGTTTTTGA GACAGGCTCT CACTCTGTCA CTAGGCTGG 2760  
 AGTGACAGTG CGTAATCACT GTTCAGTGCA GCCTCAAGCT CTGGGCTCA GGCTATCCTC 2820  
 CCATCTCAGC CTCTCAAGTA GCTGGGACTA CGAGTGTGCA CCACCAGGCT CACTAATTTT 2880  
 TGTGTTTTTT GTAGACACGG GGTTCACCG TGTGCCCAG GCTGTCTCC AACTCCTGGG 2940  
 CTCAGATGAT CTGTCCGCTT CCGCCTCCCA AACTGCTGGG ATTACAGGCA TAAGCCACTG 3000  
 CACTCAGCCT TTTATTTGTT TTTTAAACCA CGTAGCTCAT TGCCTTCTCT TAAGTAAATG 3060  
 ATAGATATTC TCACTGAAGC CAAAGGAATA AGTTTCATCA GAAAATGCCC AAAGCCCTGG 3120  
 TGGATACATC CTCCCTATCT TTTTTTTAAA CCTTCCACTA TCACTCTATG AACTGAAAA 3180  
 GAACCAAGTA AGCCCCAAAC CCAGATGTTT CAGCCTTATC CTCTATTGGG TTTACCCACA 3240  
 GACATAGCAA ACCCTGTGAG TGAGGAAAT TCCCCATCCT TGAGTGCCCC CGTCTTAGAA 3300  
 GTTTGGGCCA TATTATGGAA CAGGGGTCTC TTATTTGAAA AGAGCACAAG GAGGCCAAGA 3360  
 TTTTAATGGG GCACCTTAGG GGATACAGCC CACAATGGCA TGGGCTGAG GTGGCGTGA 3420  
 TGCTGTCTTC TAAGCTTAAC GCATCTGCTC AGGCACAGAA TAAACGTCTA GGCTGGCCAA 3480  
 AAAAGGAAT GAATCCAGG CCCATACGCC AGCACCAGAA TCAACACAGT CTTCAAGGAA 3540  
 GGAAGGCTAG GAGAGTTTAA CAAGATTTTC ACTGGGCCCA GCATGGTGGC TCACACCTGT 3600  
 AATCCCAAG CAGAATGGTG GCTTGAGCTC AGGAGTTCAA GACCAGCCTG GGCAACACAG 3660  
 TGAGACCTTG TCTCTAAAAA ATTTAAAAAT AAACAAGGTG TTCACCAAGC TGGGATACTT 3720  
 CTCACTATTA AGCCCTTATC TTTCTCTTTT TTTTATTCTC AATTGCTTTG TGTGATAAAA 3780  
 AACTAAAGAG ACTTCTGGTC CAATTTCTGG CAACATCCCT TCTGAAAGGT GAGTAGAGTG 3840  
 GGTGTCTTCT ATGCCCATTT TCCCAATTT TACACAACT ATTATCAATG AACTTTTAAG 3900  
 TACCTAGAA GGGTAAAAAC AGAGCAAGAC TTTAAATTAC CTTCTCTTTT CTTCTACTGG 3960  
 CAGTTCTGCC TCCATCACTA TCAGGCTAGG GTGACCTTCC CTTGGTCAAG CCCCATTGTC 4020  
 CCATGATTG TGCTGTGCC CTTTCTCCAG TGACCAATTG GTGACCAAGT GGTAGATATA 4080  
 GAAAGGGGAT GGCATTTGCA AGTGACTAGT CTGCCACAAA ATGCTCATCT GATTAGCCAC 4140  
 TGCTGCCCTG GCAATGGCTT TGTAAGAGTC AATGAGAAGT AGAGCCAGGC TGTGGTCCCT 4200  
 GGCCATCAAC AGTGTGGTG ACGGCAGGGA GTCCCTTTGG TTTAATAAAT CCAATTTTTT 4260  
 TTTGGGTATC CAAATTTCTC CTTCTTTTGG TAGGAGTCAG GCTCTCAGAA CCTGTGCCA 4320

TGTGTGGAAGT TCCCCAGTG TGGATGCAGA TACGCAGCTC CTGAGCTCCA GCCTAAAGTC 4380  
 TTCTGTAGCC TCAGCAATAC TTGGGCACCT GCTGTCTCAC TGAATAGCTT TCTTTTGTGA 4440  
 CAAAGGCCAC AGACAGCCCT TAGACTATTC CGGAAACAGT AGGAAAAATT ACATATGTCT 4500  
 5 TTGACTTCTT TATTCTGACT CCACTGATTT TAGCCATAAT ACTTTAAGGA GCTACTTTTT 4560  
 ACTACCCCTT ACCGTGCTGA CTTCTGCAGG TCTGCCCTGT GACCTGTCAG GAACTCCTGA 4620  
 GTTACGCTAC TGGGGTCACC TGTGTCTCCC CTAGCAAGTT AGGCATGTCA TATATTTTFA 4680  
 ACAGCTTTAT TGAGATATAA TTCACATATT ATACAATTCA CCTTTAAAC ATACGATTCA 4740  
 ATGGTTTTCA GCAAACTCAC AGAGTTGTCC GCCCACTTGA GAGCAAAAC ATGTTCAATT 4800  
 10 TTCTTTTCTT TTTTTTTTTT GAGACAGAGT CAGCTTTGTC GCCCAGGCTG GAGTGCAGTG 4860  
 CCATGATCTT GGTCACTGCG AGCCTCCCCA TCCTGGGTTT AAGTGATCCT TCTGCTTCAG 4920  
 CCTCCCCAGT AGCTGGGATT ACAGGCATGC GCCACCACGC CTAGCTAATT TTTGTGTTTT 4980  
 TAGTAGAGAT GGGGTTTCAC CGTGTGGGCC AGGCTGGTCT CAAACTCCTG GACTCAAGTG 5040  
 ATCCACCCAC CTCGGCCTCC CAAAGTGCTG GGATTGCAGG TGTGAGCCAC CGTGCCTGGC 5100  
 15 CTACGTGTC AATTTTCTAT GAACAAAGGC TTTAGTCCTT GACCCAGGCG TAAAGTGGTC 5160  
 TGTCCAAGCT GTTGTGGTA GAGGGAGTAT GATAAAATGT TTAATCTCA TTTGGTTACC 5220  
 TTGAGTCTCG GAACACGCAG TAACGTGTCAT GCTATAGTCA TCATCTGTAT TTGGCTGGGA 5280  
 ATACAAATGA AGATTGTTGT GTATTCAAGC AGTAGGGTTT TTGCTTTTGT TTTTGTTTTA 5340  
 GTGCCAACAA AACTTTTTTTT TGTCTGACTA CATTAAGAT AAGACTGACT ATATTTATAC 5400  
 AACAGAAACT TTGTAATAGA TTTTTCAGC TTTGTGAAAT CGAATTTTTT TTCATCAGGG 5460  
 20 CTGGTGGAT TTCCTTTTTA CCCTGTAATC CAAGCGTTAA TAGTTTGTGA GAAGATGGGT 5520  
 TATTGCATGT CACTTTTTTT TTTTGTGAAA ATAAAAACAT ACCTTAC 5567

Seq ID NO: C188 DNA Sequence  
 Nucleic Acid Accession #: NM\_014324.1  
 Coding sequence: 89..1237

1 11 21 31 41 51  
 | | | | |  
 30 GGC GCCCGGA TTGGAGGGG TTTCTGCAGG CTGCTGGGCT GGGGCTAAGG GCTGCTCAGT 60  
 TTCTTTCAGC GGGGCACCTG GAAGCGCCAT GGCCTCTCAG GGCATCTCGG TCGTGGAGCT 120  
 GTCCGGCTCG GCCCGGGGCC GTNTCTGTGC TATGGTCTCG GCTGACTTCG GGGCGCTGTG 180  
 GGTACGCGTG GACCGGCCCG GCTCCCGCTA CGACGTGAGC CGCTTGGGCC GGGGCAAGCG 240  
 CTCGCTAGTG CTGACCTTGA AGCAGCCGCG GGAGCCGCGT GCTGCGGCGT CTGTGCAAGC 300  
 35 GGTCCGATGT GCTGCTGGAG CCCTTCCGCC GCGGTGTCTG GGAGAAACTC CAGCTGGGCC 360  
 CAGAGATTCT GCAGCGGGAA AATCCAAGGC TTAATTTATG CAGGCTGAGT GGATTTGGCC 420  
 AGTTTCAGAA AGCTTCTGCC GGTAGCTGG CCACGATATC AACTATTGG CTTTGTGAG 480  
 TGTTCTCTCA AAAATTTGGCA GAAGTGGTGA GAATCCGTAT GCCCGCTGA ATCTCGTGGC 540  
 TGACTTTGCT GGTGTGGGCC TATGTGTGCT ACTGGGCATT ATAATGGCTC TTTTTCAGCG 600  
 40 CACACGCACT GACAAGGGTC AGGTCAATTG TGCAAAATAG GTGGAAGGAA CAGCATATTT 660  
 AAGTTCTTTT CTGTGGAATA CTCAGAAATC GAGTCTGTGG GAAGCACCTC GAGGACAGAA 720  
 CATGTTGGAT GGTGGAGCAC CTTTCTATAC GACTTACAGG ACAGCAGATG GGGAAATTCAT 780  
 GGCTGTTGGA GCAATAGAAC CCCAGTTCTA CGAGCTGCTG ATCAAAGGAC TTGGACTAAA 840  
 GTCTGATGAA CTTCCCAATC AGATGAGCAC GGATGATTGG CCAGAAATGA AGAAGAAGTT 900  
 45 TGCAGATGTA TTTGCAAGA AGACGAAGGC AGAGTGGTGT CAAATCTTGG ACGGCACAGA 960  
 TGCCGTGTG ACTCCGGTTC TGACTTTTGA GGAGGTTGTT CATCATGATC ACAACAAGGA 1020  
 ACGGGGCTCG TTTATCACC A GTGAGGAGCA GGACGTGAGC CCCCCTCTTG CACCTCTGCT 1080  
 GTTAAACACC CAGCCATCC CTTCTTCCAA AGGGGATCCT TCCATAGGAG AACACACTGA 1140  
 GGAGATACCT GAAGAATTTG GATTACGCCG AGAAGAGATT TATCAGCTTA ACTCAGATAA 1200  
 50 AATCATTGAA AGTAATAAGG TAAAGCTAG TCTCTAATT CCAGGCCAC GGTCAAGTG 1260  
 AATTGGAATA CTGCATTTAC AGTGTAGAGT AACACATAAC ATTGTATGCA TGGAAACATG 1320  
 GAGGAACAGT ATTACAGTGT CCTACCACTC TAATCAAGAA AAGAATTACA GACTCTGATT 1380  
 CTACAGTGAT GATTGAATTC TAAAAATGGT TATCATTAGG GCTTTTGATT TATAAAACTT 1440  
 TGGGTACTTA TACTAAATTA TGGTAGTTAT TCTGCCTTCC AGTTTGTCTG ATATATTTGT 1500  
 55 TGATATTAAG ATTCTTGACT TATATTTTGA ATGGGTTCTA GTGAAAAAGG AATGATATAT 1560  
 TCTTGAAGAC ATCGATATAC ATTTATTTAC ACTCTTGATT CTACAATGTA GAAAATGAGG 1620  
 AAATGCCACA AATTGTATGG TGATAAAAGT CACGTGAAAC AGAGTGATTG GTTGCATCCA 1680  
 GGCCTTTTGT CTGGTGTTC ATGATCTCCC TCTAAGCACA TTCCAAACTT TAGCAACAGT 1740  
 TATCACTTCT TGAATTTTGC AAAGAAAAGT TTCACTGTGA TTGAATCAGA ATGCCCTCAA 1800  
 60 CTGAAAAAAA CATATCCAAA ATAATGAGGA AATGTGTTGG CTCACCTACG AGAGTCCAGA 1860  
 GGGACAGTCA GTTTTAGGGT TGCCTGTATC CAGTAACCTG GGGCCTGTTT CCCCCTGGGT 1920  
 CTCTGGGCTG TCAGCTTTCC TTTCTCCATG TGTGTGATTT CTCCTCAGGC TGGTAGCAAG 1980  
 TTTCTGGATCT TATACCCAAC ACACAGCAAC ATCCAGAAAT AAAGATCTCA GGACCCCCCA 2040  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2068

Seq ID NO: C189 DNA Sequence  
 Nucleic Acid Accession #: XM\_091332.1  
 Coding sequence: 1..1401

1 11 21 31 41 51  
 | | | | |  
 70 ATGCAAAAGT GGACACTGTG GGCTGCAGCC TTTCTGACCC TCCACTCTGC ACAGGCCTTT 60  
 CCACAAACAG ACATCAGTAT CAGTCCAGCC CTGCCAGAGC TGCCCTGTGC TTCCCTGTGC 120  
 CCCCTGTTCT GGATGGAGTT CAAAGGCCAC TGCTATCGAT TCTTCCCTCT CAATAAGACC 180  
 75 TGGGCTGAGG CCGACCTCTA CTGTTCTGAG TTTCTGTGG GCAGGAAGTC CGCCAAGCTG 240  
 GCCTCCATCC ACAGCTGGGA GGAGAATGTC TTTGTATATG ACCTCGTGAA CAGCTGTGTT 300  
 CCCGGCATCC CAGCTGACGT CTGGACAGGC CTTCTATGAT ACAGACAGGA AGGGCAGTTT 360  
 GAATGGACTG ATGGCTCATC CTATGACTAC AGCTACTGGG ATGGCAGCCA GCCAGATGAT 420  
 GGCCTCCACG CGGACCCAGA AGAAGAGGAC TGCGTGCAGA TATGGTACAG GCCTACCACT 480  
 80 GAGCAGCTAC AGGCCCCAGA GCCCCAGTTA CCTTATCAA TCTCAGAGGC CACAGATGTC 540  
 TATCTCCCTG AGGATTTCCC AGCTGAGCCC AAGCTCATGG ACCAGTCCCTG GGTGTCCAGG 600  
 AAGAGCCTGA AACCATCCCA GAGTCATCTT ATGGAGCCAC CCACTCCAGT GGCCAAGCAC 660  
 CAAAAGGCCA AGACCCGACA TAGGAGCCTG CGCGGCGTCT GGTGGCCATC AGGTAAGGCT 720  
 GGGTCATGGA AAGAAAGAAAT GAATGCAGAC TACGGGCGAA GAAAGCGATC GGGCCCCAGG 780  
 CAGGAAGGCC GGCTCCGGTG CAGGGAGCGC GCCTGCGGG CTGCTTCGGG CCAGGGTCTGA 840

CCGAGGGGCC AGCGCAAGCA GCGGCAACAG GAGCGCCAGG AGAGAGGCTG GGAAGAACTG 900  
 GGAGGGGTGT CCCCATGCG GGGCGCCCAA GCGTGGCAGC ACGGGCTGGG AGCGGGGAGC 960  
 CAGCGGGGTG CGGCGCCGGA GTGCGGGGAG AACCACCAGG CGCCGGAAAT GGGGAGCAGC 1020  
 TGGAGGGGGC AGCGGCTCCA GCGCCAGACC GCGCGCTCTT GTCACCTTGC ATTAAGAAAG 1080  
 CTTCCGGGGA ATGACACAGG CCTGGCCGCC GCCTTCGTGC AGCCCGCCCT GCAGGTGCAG 1140  
 GAAGAAAAGA ATAATCGCAC CCGTTTCTCA GGTGCTTACT TCACCATGTC CGATCCGACG 1200  
 TGTGACCAAG ATAGCAAGGA GCAGTCTTTA AGGCGACAGC GCAGAGAGGC AGAAAAAGAT 1260  
 GGGCCTTACC GGTAGTTAA GAAAAAAGA GGACCTGTTG CCTGTCCCTC TAGCTTTGAA 1320  
 CTACAAAGTG GAGGGGAAGT TTGTCTGGAT TTCTCTGTAG AACTGAGGGC AGGGACCTGG 1380  
 ATTGCTCGAG AACCTCCATA A 1401

Seq ID NO: C190 DNA Sequence  
 Nucleic Acid Accession #: XM\_054869.2  
 Coding sequence: 26..2902

1 11 21 31 41 51  
 | | | | |  
 TAGACGCGGA GCCCAAGGAG GTAAAAATGCA CACTTGCTGC CCCCAGTAA CTTTGAACA 60  
 GGACCTTCAC AGAAAAATGC ATAGCTGGAT GCTGCAGACT CTAGCGTTTG CTGTAACATC 120  
 TCTCGTCTCT TCGTGTGCAG AAACCATCGA TTATTATGGG GAAATCTGTG ACAATGCATG 180  
 TCCTTGTGAG GAAAAGGACG GCATTTTAAAC TGTGAGCTGT GAAAACCGGG GGATCATCAG 240  
 TCTCTCTGAA ATTAGCCCTC CCGCTTTCCC AATCTACCAC CTCTGTGTGT CCGGAAACCT 300  
 TTTGAACCGT CTCATATCCA ATGAGTTTGT CAATTACACT GGGGCTTCAA TTTTGCATCT 360  
 AGGTAGCAAT GTTATCCAGG ACATTGAGAG CGGGGCTTTC CATGGGCTAC GGGGTTTGA 420  
 GAGATTGCAT CTAACAATA ATAAACTGGA ACTTCTGCGA GATGATACCT TCCTTGGCTT 480  
 GGAGAACCTG GAGTACCTAC AGGTGATTA CAACTACATC AGCGTCATTG AACCCAATGC 540  
 TTTTGGGAAA CTGCAATTGT TGCAGGTGCT TATCTCAAT GACAATCTT TGTCCAGTTT 600  
 ACCCAACAAT CTTTTCCTGT TTGTGCCCTT AACGCACTTG GACCTCCGGG GGAACCGGCT 660  
 GAAACTTCTG CCTACGTTGG GGCTCTTGCA GCACATGGAT AAAAGTTGTG AGCTACAGCT 720  
 GGAGGAAAAA CCTTGGAAAT GTTCTTGTGA GCTGATCTCT CTAAAGGATT GGTGGGACAG 780  
 CATCTCTAT TCAGCCCTGG TGGGGGATGT AGTTTGTGAG ACCCCCTTCC GCTTACACGG 840  
 AAGGGACTTG GACGAGGTAT CCAAGCAGGA ACTTTGCCCA AGGAGACTTA TTTCTGACTA 900  
 CGAGATGAGG CCGCAGACGC CTTTGAGCAC CACGGGGTAT TTACACACCA CCCCGGCGTC 960  
 AGTGAATTC GTGGCCACTT CTTCCTCTGC TGTTTACAAA CCCCCTTTGA AGCCCCCTAA 1020  
 GGGGACTCGC CAACCAACA AGCCCAAGGT GCGCCCCACC TCTCGGCAGC CCTCTAAGGA 1080  
 CTTGGGCTAC AGCAACTATG GCCCAGCAT CGCTATCAG ACCAAATCCC CGTGCCTTT 1140  
 GGAGTGTCCC ACCCGTGTCT CTTGCAACCT GCAGATCTCT GATCTGGGCT TCAACGTAAA 1200  
 CTGCCAGGAG CGAAAGATCG AGAGCATCGC TGAAGTGCAG CCCAAGCCCT ACAATCCCAA 1260  
 GAAAAATGAT CTGACAGAGA ACTACATCGC TGTCTGCGC AGGACAGACT TCCTGGAGGC 1320  
 CACGGGGCTG GACCTCTGTC ACCTGGGGAA TAACCGCATC TCGATGATCC AGGACCGGCG 1380  
 TTTCCGGGAT CTCACCAATC TGAGGGCGCT CTACCTGAAT GGCAACAGGA TCGAGAGGCT 1440  
 GAGCCCGGAG TTATTCTATG GCCTGCAGAG CCGTGCAGTAT CTCTTCTTCC AGTACAATCT 1500  
 CATCCGCGAG ATTCACTCTG GAACCTTTGA CCGGTCCCA AACCTCCAGC TGCTATTCTT 1560  
 GAATAACAAC CTCCTCAGG CCATGCCCTC AGGCGCTTTC TCTGGCTTGA CCCTCTCAG 1620  
 GCTAAACCTG AGGAGTAACC ACTTCACTC CTTGCCAGTG AGTGGAGTTT TGGACCAGCT 1680  
 GAAGTCACTC ATCCAAATCG ACCTGCATGA CAATCCTTGG GATTGTACCT GTGACATTGT 1740  
 GGGCATGAAG CTGTGGGTGG AGCAGCTCAA AGTGGGCGTC CTAGTGGACG AGGTGATCTG 1800  
 TAAGGCGCCC AAAAAATTCG CTGAGACCGA CATGCGCTCC ATTAAGTCGG AGCTGCTGTG 1860  
 CCCTGACTAT TCAGATGTAG TAGTTTCCAC GCCCACACCC TCCTCTATCC AGGTCCCTGC 1920  
 GAGGACGAGC GCGGTGACTC CTGCGGTCCG GTTGAATAGC ACCGGGGCCC CCGCGAGCTT 1980  
 GGGCGCAGCG GAGGGGGCGT CGTCGGTGCC CTTGTCTGTG TTAATTCTCA GCCTCCTGCT 2040  
 GGTTTTCTAT ATGTCGTCTC TCGTGCCGCG CGGGCTCTTC GTGCTGGTCA TGAAGCGCAG 2100  
 GAAGAAGAAC CAGAGCGACC ACACCAGCAC CAACAACCTC GACGTGAGCT CCTTTAATAT 2160  
 GCAGTACAGC GTGTACGGCG GCGGCGGCGG CACGGGCGGC CACCCACAGC CGCAGGTGCA 2220  
 TCACCGCGGG CCGCGCTGTC CCAAGGTGAA GACGCGCGCG GGCCACGTGT ATGAATACAT 2280  
 CCCCCACCCA CTGGGCCACA TGTGCAAAAA CCCCCTCTAC CGCTCCCGAG AGGGCAACTC 2340  
 CGTAGAGGAT TACAAAGACC TGACAGAGCT CAAGGTCAAC TACAGCAGCA ACCACCACT 2400  
 GCAGCAGCAG CAGCAGCCGC CGCGGCCACC GCAGCAGCCA CAGCAGCAGC CCCCAGCGCA 2460  
 GCTGCAGCTG CAGCCCCGGG AGGAGGAGAG GCGGGAAAGC CACCACTTGC GGAGCCCCGC 2520  
 CTACAGCGTC AGCACCATCG AGCCCCGGGA GGACCTGCTG TCGCCGGTGC AGGACGCGCA 2580  
 CCGCTTTTAC AGGGGCATTT TAGAACCAGA CAAACTCTGC TCACCAACCC CCGCCGGCAA 2640  
 TAGCTCCCG GAATATCCCA AATTCCCGTG CAGCCCCGCT GCTTACACTT TCTCCCCCAA 2700  
 CTATGACCTG AGACGCCCCC ATCAGTATTT GCACCCGGGG GCAGGGGACA GCAGGTACG 2760  
 GGAACCGGTG CTCACAGCC CCCCAGGTGC TGTCTTTGTA GAACCAACCC GGAACGAATA 2820  
 TCTGGAGTTA AAGCAAAAC TAAACGTTGA GCCGACTAC CTCGAAGTGC TGGAAAAACA 2880  
 GACCACGTTT AGCCAGTTCT AAAAGCAAAG AAACCTCTCT GGAGCTTTTG CATTTAAAC 2940  
 AAACAAGCAA GCAGACACAC ACAGTGAACA CATTTGATTA ATTGTGTGT TCAACGTTT 3000  
 AGGGTGAAGT GCCTTGGCAC GGGATTTCTC AGCTTCGGTG GAAGATACGA AAAGGGTGTG 3060  
 CAATTTCTCT TAAATTTTAC ACGTGGGAAA CATTTGTGTA AACTGGGCAC ATCACTTTCT 3120  
 CTTCTTGGCT GTGGGGCAGG TGTGGAGAAG GGCCTTAAAG AGGCCAATTT GCTGCGCGGG 3180  
 TGACCTGTGA AAGGTCAACG TCATTTTGT AGTGGTTGGA AGTGCTAAGA ATGGTGGATG 3240  
 ATGGCAGAGC ATAGATTCTA CTCTTCTCT TTTGCTTCT CCCCCTCCCC CGCCCCCTGCC 3300  
 CCACCTCTCT TTCTCCCTT TTAAGCCATG GGTGGGTCTA ACTGGCTTTT GTGGAGAAAT 3360  
 TAGCACACCC CAACCTTAAT AGGAAATTTG TTCCTTTTT CCGCCCCCTCT CTTCTCTCTC 3420  
 TCCCTCTCCC TCCCTTCTCA TTCCTTTTCT TTGTTTTTAA AGGATGTGTT TGTATGCATT 3480  
 CTGGACATTG GAATTAATAA AAAAGTATTG TGATCCTGTA AAGGATCACC ATAGATGTGG 3540  
 ACAATATCAT AAAATTACAG AGCTATATGA TCCATAATTG ATTAGTCAAA ATAACCTATT 3600  
 GATGAATAT ACAATATTT TATTGTAGCA CCTATTTTAA TATGCACATT TAGCATTCCT 3660  
 CTTTCTTCA TATTTAGCC TATGATTTTG CAGAGGTGTC ACACCTGTAT AGGATCTGCA 3720  
 TTTCTAAAC TGACGTGTGA TCAGGAAGGC ATTTTCAATC ATTCAAAATG TGGAGAATTT 3780  
 AATGGCTAAA TCTTTAAAG CCAATGCAAC CCACCCAATT GAATCTGCAT TTTCTTTTAA 3840  
 GAAAACAGAG CTGATTGTAT CCCAATGTAT TTTAAAAAT AGGGCAATTG ATTGGGCCAT 3900  
 TCCGAGAGAA TTGTTTGCAA GTTTTGGGTT TTATTAGAAA ATATTGAAA GTATTTTAT 3960  
 TAATGAACCA AAATGACATG TTCATTTGAC TACTATTGTA GCCGATTTTC GATTGTTTAA 4020

CCAAACCCAG TTGCATTGT ACAGATCCAC GTGTACTGGC ACCTCAGAAG ACCAAATCAT 4080  
 GGACTGTACA AGTCTCTATA CAATGTCTTT ATCCCTGTGG GCAGCAAGCA ATGATGATAA 4140  
 TGACAAACAG GATATCTGTA AGATGGGGCT ACTGTTGTGA CAGTCTCATA TGTATCCAG 4200  
 CATATGTAAT TTTTAAATA GTTCTGTAAT AAACACTTGA TAACTATGTC 4250

Seq ID NO: C191 DNA Sequence  
 Nucleic Acid Accession #: NM\_000793.2  
 Coding sequence: 401..1222

1	11	21	31	41	51	
GCCTGCAGAG	AGAGGCACCTT	TGCACCACAG	ACAGATAGCA	AGAAGGGAAA	GACAGAGAGT	60
GAGAAAAAAG	AGGAGTCAGT	CGCTCCTGGG	GAAGGGAGAG	AGTGAGACTG	GGAGAAAGAG	120
AAGCACAGAA	AGTGTGTGTA	AAACGGAGTA	AAGAAAGAAA	AAAAAAAAC	TACCCCTAAA	180
GCACATTAA	AAAAAATAA	CTCTGGCAAT	TCAAGAAAGA	AACAGGCTAC	GTTTAAAGAG	240
CATAGAGACA	ATGAAAGGCT	AAAGAAAATT	TTAAATCTC	TGCCACAGTC	TCATAGGTGC	300
TTGGAATGA	AAGTAGAACT	GCCTGTCTTT	AACGGACTCT	GACAGAGAGG	GTGAAGGGGA	360
ACCAGAGCGC	ACAAGGGAAC	TGACTCAGGA	GGCAGAGAAG	ATGGGCATCC	TCAGCGTAGA	420
CTTGCTGATC	ACACTGCATA	TTCTGCCAGT	TTTTTCTCC	AACTGCCTCT	TCCTGGCTCT	480
CTATGACTCG	GTCAATTCTGC	TCAAGCACGT	GGTGCTGCTG	TTGAGCCGCT	CCAAGTCCAC	540
TCGCGGAGAG	TGGCGGCGCA	TGCTGACCTC	AGAGGGACTG	CGCTGCGTCT	GGAAAGACTT	600
CCTCCTCGAT	GCCTACAAC	AGGTGAAATT	GGGTGAGGAT	GCCCCCAATT	CCAGTGTGGT	660
GCATGTCTCC	AGTACAGAAG	GAGGTGACAA	CAGTGGCAAT	GGTACCCAGG	AGAAGATAGC	720
TGAGGGAGCC	ACATGCCACC	TTCTTGACTT	TGCCAGCCCT	GAGCGCCAC	TAGTGGTCAA	780
CTTTGGCTCA	GCCACTTGAC	CTCCTTTTCA	GAGCCAGCTG	CCAGCCTTCC	GCAAAGTGGT	840
GGAAAGATT	TCCTCAGTGG	CTGACTTCCT	GCTGGTCTAC	ATTGATGAGG	CTCATCCATC	900
AGATGGCTGG	GCGATACCGG	GGGACTCCTC	TTTGTCTTTT	GAGGTGAAGA	AGCACCAGAA	960
CCAGGAAGAT	CGATGTGACG	CAGCCCAGCA	GCTTCTGGAG	CGTTCCTCCT	TGCCGCCCCA	1020
GTGCCGAGTT	GTGGCTGACC	GCATGGACAA	TAACGCCAAC	ATAGCTTACG	GGGTAGCCTT	1080
CTACAGTGTG	TGCAATTGTC	AGAGACAGAA	AATTGCTTAT	CTGGAGGAGAA	AGGGCCCCCT	1140
TGCTTACAA	CTTCAAGAAG	TCCGGCATTG	GCTGGAGAAG	AATTTACAGC	AGAGATGAAA	1200
GAAACTAGA	TAGCTGTTT	AAAGGTATGA	TTATAAGAGA	GCTTATTGTT	TTAAAAAGTT	1260
ATATAAAGGC	AAGGAAATTA	AGAAGTGAAT	CCATATTTCA	ACAGAGCCCT	ATTGGCTTAC	1320
TGAAAGACAG	GAGTTTATCT	ATCGGAAGAA	CATGAATCTC	TAACAGCTCC	ATACTTCTTT	1380
CACTACTCAA	ATGGCATTGG	GCTGAGTAAG	TAACCATATC	ACCTCTCTTC	TTAGTAAAAA	1440
GCCCTATGTG	AAAAGATCCC	AAGATGGAGA	GGAAGAAACG	CTAATTCAGC	ATGTGTTTAT	1500
TCTGCATTGA	GAAGGAACCT	ATACATCTGA	TGCATGCTTT	GAGACCAGAA	GAAAAGACTT	1560
ACCTGAATAA	TTACTACATT	AGGGAAGCTA	CTGTCTACGT	TAAGATAAAG	GGTATTGCTC	1620
TGGCTCTATT	TGGCATGGAT	GGAGCCAGT	TGGAATAATC	CCAAATATTA	CAACAAGTCC	1680
TTGAACCCAG	GCCATGTGGT	TAGACGTTGG	TGTTAAGGTT	AGACCTTATG	TTAGAGTCAT	1740
TTCTGATGTT	CCAGCTTCTA	GCCATGTAGT	GCTCTCAGTC	TTATACCCCT	AGAAATTATT	1800
GGTATATTTG	TAGATACCGA	GAATGATCCC	TCAGTCTGAG	AGGTTAGAAT	GATCATCTGT	1860
AATCTGAGGG	TAAATTTCTA	GGCAGGTGGA	GAGAGTGGTA	AAAAAGAAAT	GAAATTGACA	1920
AGCTAGGAAA	AGGGAGGACG	AAAGATTGGG	AAAATTACCA	GAGTTTCACC	CTTAAGCTGT	1980
AGAGAGTGGG	TCACATTTGT	TAGCCACGGA	AACATAGAAA	CATACACAAG	GCCAGAAAAA	2040
GAAGAAGGAG	CTCAACTAAA	AGTGGCATAG	AGAATACACA	TATAAAAAA	ATATATTGTT	2100
CATATGCTCC	TAGAGAGGAG	AAAGGGGTGA	TTGAAGAGAA	AAAAAATACT	TAAATATTTG	2160
TAAATGTGAG	GGGTTTCTTT	TGGAATAAAT	TACTTTTGAA	CCATGTATGT	GGTATGTATA	2220
TTTTAGTGG	GTTAATTATA	CCCCATGATA	CCTATTAAAG	GAAAACCACT	GGGTCTGGTG	2280
GTGCTGGTCT	TTTCTCTCCC	ATTCCTACAA	TTTCTATGTG	GCCCAAGTCA	TTCTTAATCT	2340
TGGTCTCTAT	AGCAGTGTTC	TCTCTGAATG	CTGAGCTGAA	GAAATTATAC	GTACATACAC	2400
ACATACATAC	ATACATACAA	ATATATGTAT	ATATATTCTC	AGCTGCTGCG	GGAGGTAGGT	2460
ACCATGGCCA	TTCAAGCACAG	CCTTGATTTT	CTCCCAAGT	AGGTGAGCTA	TAGTGAAGAA	2520
TAGGTGCAAA	CAAAACAGCT	TACTTCCATT	GCAAAATAGA	AGAAGAGGAA	GTTAGAGATA	2580
ATTCTGATCA	ATCATTTTGG	AGGCTTTGTT	ATAAGGCAAC	CCCCGGTATA	TCATGGAAAT	2640
TCCATTGACA	TTTGAATTTG	GACTTGGATC	TTCCCTTGGT	CCCATTAGCT	GAGGTTTATG	2700
AATCTAAAGT	CCCTATAGTA	TATGATTATA	ATGCTATTTT	AAAAAATATA	TATATAAAAT	2760
ATTTTCTTCT	TTTTTAAATA	GACACTATAG	TTTTACCCAT	AAGTAATATT	TAAAGATTAT	2820
AGCTCCCAAA	AGAATGGACC	AACCACTTTC	GTATCATAAT	TTCTTTTGGG	TAAATATGAG	2880
ACTATTATGA	AATCATAGTA	TATGATTGTA	TTTAAAGGTA	CAATCAAGG	ATCTTTTGTC	2940
CATTCCATTA	ATAACTGAAT	AAAAAATAAA	TAAATGGAT	AGAAAAAAC	TAAAGTTGAA	3000
AATACATTCT	TAAACTAGTT	GTCTGAAATG	AGAAAAGAGT	GAGAACTAGG	TGTGCAAGAA	3060
CCAAACGTAT	TTTATTTTAT	TTTTTAAATG	GGAGCAACAT	ATCAGTCGTG	TCACCAGCTG	3120
GTATATTGTG	TAAATATTAA	AGCTCCATTG	GGACTGATTT	TTCATGGCAA	CATCAGCTTT	3180
CTAATGTTCT	AAATTCTATA	AAAACCACTG	ACAAAGAAAC	AAAGCRAATT	TCATTATCTA	3240
ATGAGTTGCT	GGAAAAATCAT	ATTGAGAATA	ATTATTTTCA	ATTCCTCAGT	TGTTAACTTC	3300
TACATTCAAG	GGCTTATCTC	TGCCCCCAT	GATTTTAAAC	CTCAAATG	TGTGAGATTT	3360
ACTGTGGAAC	CCTAAAGCAG	TAAATATAAA	AACCTGGTTG	CAGCACATTC	ACACTGTTGT	3420
CCTTAAATTT	CCCCTTTTTT	CTCTATGTAC	GATAAAGTAA	CAGTATGTCA	GATAAGCCGG	3480
TGGGGGGATG	AGATTAGGCT	GAGGCAGTGC	TAGTCAACTG	GGGGAAAAGG	ATGATGGAAA	3540
AATCACCCAG	TTGTGCTATA	TTTTTAAAGA	AGGAGGTGCT	TTATGTGTGC	AGACAATTCT	3600
CCCTGAGGTT	AGGCCAATGG	AGAAATGAAG	CAGAGGAAGG	AAACATAGAA	AGACATGGGC	3660
TATCAGGGAG	GAGATGTGTC	AATAGAACAT	GCAAGAATTT	CTGGAAGAAA	GGCTGTGGAA	3720
GGGCCAATGG	AGAAAATGAA	TGGACAAAGC	TCAGGAATCC	CTACGCTATG	TAGAATGTTT	3780
TTGGTGTAT	CAGGTTAAG	CCCTGTAATT	ATGTAACCTA	TTTATCGCAA	CATGAATTTT	3840
TATGATTTCT	TGTGATGTAT	TCTTTTATGA	AATTAACAAG	AACCTATTAT	TTTGAGGTAG	3900
AGGAAATCA	ATGCTTTATC	TGATATGCTG	AGAAATTATT	AGATTGCCAA	TACTCATGTG	3960
CGTTTCATGT	GTTTATAAAG	GTTTGTTCCT	TTGAAGAATT	GTAGTTCCTA	GTCCACAGG	4020
GAAATGTGTA	TCTATTATTA	TATCATAGTA	TAAATCTATG	ATATATTTAT	ATCATATATA	4080
AAAGTCTGAG	TTCTCTTTCT	TAGTCCCTAA	TCAATGTTCT	CCCATAGGCT	GTGTTTACAT	4140
GGAGCTATCG	GTTTAGCCTT	TAAAGCTTCA	TTAGCTTGTC	TATTATTGAA	ATAGTTTCCA	4200
AGAAATTTTA	GATATTATCA	TAACATCTGG	GTCTACTCAA	ACACTTATTG	TTTGAAAGAC	4260
TTATGTCTTG	GACCTATCAA	AAACTGACTT	TATTTATTGC	TTAGTGAAAA	TACTAGTGGG	4320
ATCAACAATG	ATTTTCTTGA	ATGGGCATGA	ATGGAGATGC	CCGCACAGTA	ATGTAGAAAT	4380

5	GTTTCATACA	GCTATTAAAA	TGTAACGTAC	CTCCTTAGAG	GCAGATTAGT	AACTGTTTCT	4440
	ACTTTGTATA	GCTAAGTGAC	AGTCACCTAA	CTTACATGAC	TTTCTTTTTT	CACATGGGGT	4500
	CTCTGGTCTC	GTGCTCTCAG	CTCATTATTA	GCACGTCTCC	TTGATTTTTG	GTAGTATCAA	4560
	CTTCCCAAGT	ATCTGTTCAG	TTAAGTCTTT	CTCCCGTTAA	CCAGGAAGTG	CTTATTCTCT	4620
	CATCACAGTG	GGAAGAATAG	CCTATTGTCT	TTTCAATTTG	CTGAGTGTAT	TTTACTATTT	4680
	GGGCTCTGAA	ATAAAAATTA	TGAAATATGG	TGAGGTCACA	TGTTGGTGTCT	GCCTTGCTGC	4740
	ATAAAAATCT	AGGAGGGCAG	GTTAGGAGAC	AGTTATGTAT	GGCCTTTCGG	GAAAAATCAA	4800
	AGGGTGGGAT	TACAAGGGTG	TTCTCAGGC	ATGCCCTTAT	GGGCCCTATG	TGGAAGCAAG	4860
10	AAGAATTGAC	TGATTTACAG	GACTTCTCTT	TATGTCAATC	TTAAGAGGAT	GGATGAATCT	4920
	GGACATTGT	TCCACCCGAC	CTCTGACTGA	TGGTTTGGAA	AATAACTTTA	ATTAGGATCA	4980
	TATGACCATT	GAAAAAGGAA	AAATGTAGAC	TCTGACTTCC	GTCCCACTGA	AGGATTAATG	5040
	AAAAACCTTA	CTAGCATTTA	GAGCTTTTCA	GAACATCCCC	ACTGTCATGT	GTCTCAGCAG	5100
	TGGAGACTGC	AAGTAAGGCT	TTTAATTTTA	GGAGGTTTTT	TTTTTTTTTT	TTTTTCCCTC	5160
	TAAATGGTAT	GGCCAAAAGT	CAGAGTTAAA	ATATATATAG	TTAGATTCCA	ACTTCTCTCT	5220
15	TCACCTCTAA	AATAGAAATC	AAACCCACTC	TTTATATATG	CTTCCAGAAT	GGGGCTTAAG	5280
	TACCAATCTC	TGCTTTGCAA	TGGGCACAA	CTTGGTCATG	TCTTGAGGCT	CTCTAAGAAA	5340
	AGAGAGGATC	TAGGATGGGA	GAGCTAGAAA	GTTGCTAACT	GGGAAGAAC	AGGCCCTGAG	5400
	GGGTTGGTCT	TCCACCTCTG	GAAGATTGGA	AAACAAACTT	CTCGCAACTG	AAGGAAGGCT	5460
20	GAAGGCTGCT	GCAAGTCATT	GAGTGACTTT	AGGATGAGCA	AAACATGGGG	CCACTTCTTA	5520
	ATGCCCTATG	TGTATAGTAC	CAGAAGCAAG	GTCTCAGACT	TAACAGACCC	AGCTCTGTTC	5580
	CAAGGTGAGT	CTGAACCAAT	AGAAAGCAAA	CATGTGCAGA	TATCCAAACA	AGACTGCTCA	5640
	TGCAAGTCGG	GGCTGGCTAC	CCGTCTTAGG	CAGCAACAGC	AGAGCTCCAG	GGAGCTTAT	5700
	CAATATTTC	TGAGACTTCG	AAGACCCAGC	AGATGTTTAA	TGAAGTCACT	ATTTTGGCTC	5760
25	AAACCCCTCA	CTTCTCCCC	TCCCCTCAAA	AAGCCACAG	GTAACACAT	AAATGAAAGA	5820
	AACCCACAGA	AGGGGATGGG	AAATAAGAA	AATTCTCTCA	AGACTTCTCC	AGGCCCATGT	5880
	CCTGCTGAG	CGTGGTTTTT	ATGTGTATTA	GGATTGGGGG	ATGTGAAGAA	ATAAGTATCC	5940
	AGTACTTTAT	AACCAAGACA	ATTAAATGAT	ATTGGGGTAG	GGAAATGTTG	CCAGTTTGT	6000
	TTAGTTTTC	CATCAGATTG	TCACCCAGAC	CTCACCTAGC	CCCAAGTAAT	CGGGCGCCCC	6060
30	GAAGAGGGAG	ACAGAGATGT	GCCAGAGTTG	ACCCAGTGTG	CGGATGATAA	CTACTGACGA	6120
	AAGAGTCATC	GACCTCAGTT	AGTGGTTGGA	TGTAGTCACA	TTAGTTTGCC	TCTCCCATC	6180
	TTTGTCTCCC	TGCGAAGGAG	AATATGCGGG	ACATGATGCT	AAGAGCCCTG	GGTAAATGTG	6240
	GTGAGAAATG	ACCGCTGCAT	ATGCTACACA	TATGTGCTTC	TCAGTTGCAG	AAAATGAAT	6300
	GCTTTGGGAG	ATTATCAGTA	GAAAGAGTGT	TATCATATTG	GTGCTGAGTG	CTATGTGTGC	6360
35	TTATACAATT	TGTTCTTGTA	TTTAAATAAA	CTTTGAATAA	AAGAATAAAA	AAAAAATAAA	6420
	AAAAAATAAA						6429

Seq ID NO: C192 DNA Sequence  
Nucleic Acid Accession #: NM\_006549.2  
Coding sequence: 824..2590

40	1	11	21	31	41	51	
	GAGCCTGGGG	AGGTCGAGGG	TGCAGCGAGC	CGTGATCGTG	CTACTGCACT	CCAGCCTGGG	60
45	CAACACAGAG	AGACCCCTGTC	TCAAAAACAAA	CAAAACAAACA	AAACAAACAAA	CAAAAACAAAG	120
	AAAAAAAAT	GGGAGTGGGC	CGGGCGCGGT	GACTCACACC	TGTAATCCCA	GCACTTTCGG	180
	AGGCCAAGGC	GGTGGATCA	CGAGGTCAGG	AATTCAGAT	TAGCCTGGAC	AACATGGTGA	240
	AACCCATCT	TACGCAAAAA	TACAAAAATT	AGCCAAGTAT	GGTGGCCGGC	GCCTGTAATC	300
	CCAGCTACTC	GGGAGACTGA	GGCAGAGAAC	TGCTTGAACC	TGGGAGGCAG	AGGTTGCAGT	360
50	GATCCGAGAT	CGCGTCACTG	CCTCCAGCG	TGGCGCAGAG	AGCGAGACTC	CGTTTCAGAA	420
	AAGAAAAAAA	AAAAAATAAA	AAAAAGGGAG	TCGGGGTGGG	GCTCTCATTG	GCTCGTTGCA	480
	TGTGAGTGTC	CCTACGGCCT	AGAAATACCA	GAGAAGCACA	TCGGAACGGG	CTGGAATATCC	540
	ACCCAGTTAA	CTAGAGGGCT	TTGAACCTTT	TATTAACCTG	GAGGTTGACT	CTCCTGTCAA	600
	CTCGATTCCC	TTTTGGCTGT	TTGGCAGGGT	CAGTGAGACA	TCCCCTGGGT	CGCTCGACCC	660
55	CGTAGGACGG	TTTAGGGAGC	CCTCCAGGTC	TTCTTTCTC	CTCTTCCCCG	CACAGTGCTG	720
	TTATCCAGCT	GGGGGATCCA	ACGCACACTT	AAGGCTCCAG	CAAAGTGGCT	CCGCTGCGCG	780
	ATGGGAGTGC	CCAGTGTGTC	TGGATGAAGC	TGGCGCATGC	ACCATGTCTC	CATGTGTCTC	840
	TAGCCAGCCC	ATGACCAACC	GGGCCGCCCC	CCAGGATGAG	CTGGGGGGCA	GGGGCAGCAG	900
	CAGCAGCGAA	AGCCAGAAAG	CCTGTAGGGC	CCTGCGGGGC	CTCTATCTCT	TGAGCATCCA	960
60	CCTGGGCGAT	GAGTCCTTCA	TTGTGGTCAC	CGAGTGTGAG	CCGGGCTGTG	CTGTGGACCT	1020
	CGGCTTGGCG	CGGAGACCGC	CCCTGGAGGC	CGATGGCCAA	GAGGTCCCCC	TTGACTCCTC	1080
	CGGGTCCCAG	CGCCGGCCCC	ACCTCTCCGG	TCGCAAGCTG	TCTCTGCAAG	AGCGGTCCCC	1140
	GGGTGGGCTG	GCAGCCGGTG	GCAGCCTGGA	CATGAACGGA	CGCTGCATCT	GCCCGTCCCT	1200
	GCCCTACTCA	CCCGTCAAGT	CCCGCGAGTC	CTCGCCTCGG	CTGCCCCGGC	GGCCGACAGT	1260
	GGAGTCTCAC	CACGTCTCCA	TCACGGGTAT	GCAGGACTGT	GTGCAGCTGA	ATCAGTATAC	1320
65	CCTGAAGGAT	GAAATGGGAA	AGGGCTCCTA	TGGTGTCTGC	AAGTTGGCCT	ACAATGAAAA	1380
	TGACAATACC	TACTATGCAA	TGAAGGTGCT	GTCCAAAAAG	AAGCTGATCC	GGCAGGCCGG	1440
	CTTTCCACGT	CGCCCTCCAC	CCCAGGCGAC	CCGGCCAGCT	CCTGGAGGCT	GCATCCAGCC	1500
	CAGGGGCCCC	ATTGAGCAGG	TGTACCAAGG	AATTGCCATC	CTCAAGAAAG	TGGACCAACC	1560
70	CAATGTGGTG	AAGCTGGTGG	AGGTCTCTGA	TGACCCCAAT	GAGGACCATC	TGTACATGGT	1620
	GTTCGAACTG	GTCACCAAG	GGCCCGTGAT	GGAAGTGCCT	ACCCCTCAAC	CACCTCTCTG	1680
	AGACCAGGCC	CGTTTCTACT	TCCAGGATCT	GATCAAAGGC	ATCGAGTACT	TACACTACCA	1740
	GAAGATCATC	CACCGTGACA	TCAAACCTTC	CAACCTCTCT	GTCGGAGAAG	ATGGGCACAT	1800
	CAAGATCCGT	GACTTTGGTG	TGAGCAATGA	ATTCAAGGGC	AGTGACGCGC	TCTCTCCAA	1860
75	CACCGTGGGC	ACGCCCGCCT	TCAATGGCAC	CGAGTCTGCT	TCTGAGACCC	GCAAGATCTT	1920
	CTCTGGGAAG	GCCTTGGATG	TTTGGGCCAT	GGGTGTGACA	CTATACTGCT	TTGTCTTTGG	1980
	CCAGTGCCCC	TTTATGGACG	AGCGGATCAT	GTGTTTACAC	AGTAAGATCA	AGAGTCAGGC	2040
	CCTGGAAATT	CCAGACCAAG	CCGACATAGC	TGAGGACTTG	AAGGACCTGA	TCACCCGTAT	2100
	GCTGACAGAG	AACCCCGAGT	CGAGGATCGT	GGTGCCGGAA	ATCAAGCTGC	ACCCCTGGGT	2160
80	CACGAGGCAT	GGGCGGAGC	CGTTGCCGTC	GGAGGATGAG	AACTGCACGC	TGGTCGAAGT	2220
	GACTGAAGAG	GAGGTCGAGA	ACTCAGTCAA	ACACATTTCC	AGCTTGGCAA	CCGTGATCCT	2280
	GGTGAAGACC	ATGATACGTA	AACGCTCTTT	TGGGAACCCA	TTGAGGGGCA	CGCGGCGGGA	2340
	GGAAACGCTCA	CTGTCAAGCG	CTGGAACCTT	GCTCACCAAA	AAACCAACCA	GGGAATGTGA	2400
	GTCCCTGTCT	GAGCTCAAGG	AAGCAAGGCA	GCGAAGACAA	CCTCCAGGGC	ACCCAGCCGC	2460
	CCCCCGTGGG	GGAGGAGGAA	GTGCTCTTGT	GAGAGGCAGT	CCCTGCGTGG	AAAGTTGCTG	2520

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50

```

GGCCCCCGCC CCGGGCTCCC CCGCACGCAT GCATCCACTG CGGCCGGAGG AGGCCATGGA 2580
GCCCGAGTAG CTGCGTGGAT CGCTCGACCT GGCATGCGCG CCGCGTCGCC TCTGGGGGGC 2640
TGCTGCACCG CGTTTCCATA GCAGCATGTC CTACGGAAAC CCAGCACGTG TGTAGAGCCT 2700
CGATCGTCAT CTCTGTTTAT TTGTTTTTTC CTTTGTGTGT TTAAGGGGGA CAAAAAAGAA 2760
AAAAAAGGGA CTTGACTCCA TGACGTCGAC CGTGGCCGCT GGTGGCTGG ACAGGCGGGT 2820
GTGAGGAGTT GCAGACCCAA ACCACGCTGC ATTTGGGGAA ATTGCTTTT AAAAGATTTT 2880
TATGCCAAAA ATCTTCATT GTGATTTTCA GAACCACTC AGATATACCA AGTGACTGTG 2940
TGTTGGGTTT GACAACTGTG GAAAGGCGAG CAGAAAACCT CGGGGGTCTG AGGCCATGGA 3000
TGCGTTGCTC GCATTTGAGA GGGAGTAGGG GGCTAGATGT GGCTCCTAGT GCAAAACCGGA 3060
AACCATGGCA CATTCCAGAG CCGTGGTCTC AAGGAGTCAG AGCAGGGCTG GCCCTCAGTA 3120
GCTGCAGGGA GCTTTGATGC AACTTATTTG TAAGAAGGAT TTTTAAATTT TTTATGGGTA 3180
GAATTGTAGT CAGGAAAACA GAAAGGGCTT GAAATTTAAT AAGTGTCTGT GGAAGGGGAT 3240
TTTCCAAGCC TGGAGGGGTA TTCAGCAGCT GTGGTGGGGA AACATTTCTC CTGAAAGACT 3300
GAACGTGTTT CTTTCATACA GCTGCTCAAA GCAGGTTTCT GAGATAGCTG ACCGAGCTCT 3360
GGTAAATCTC TTTGTCAAA TACGAAAAC TACAGGGTGA ATCCTATGCT TTCATGTACA 3420
TTACATGGCT TAAGATTAAA CAAAAACATT TTTCAAGTCT CTAAGTAGAG TGAAGTCTAG 3480
AGCAGTAGTT TTCAGAAACT ATTTAGAGCT TCCAGGATAT ATTTACAGC TTCAAGCATG 3540
TGATCAGTTA GAGCCAGTGA AACCTATGCC CGCCTGTATA TATATTAGCA GCTTAGCTAG 3600
TTCATAACCT GTATATTCTA AAGACTGCTA AGGTTTGTGT TTTATTTTAA ATCCTAGCTG 3660
ATTGTTGTGG TCAATGAAAT ACCCAGTTTC TGAAGGGCCA GGTGGGAAAT GCTTTCAGT 3720
GACCAACACA CAAATGATCA TCCTGAGGAT CTGAGCTTCC CTAGACTCCA CAAATAAAC 3780
TTGGGGCACC CTTTTAGAGA AGACTGTGTA AACCACAGC ACTCGTTGGG GTATAGGGAA 3840
ACCAAGGCTT GGCACAGGAA GTTCCCTTTT GTAGCTAAAA GTCCAGAAAG AAAGGGTTCA 3900
TCTTTTGTAC TTCCAACGTA TATTGGGAAG TTTGGTTGAG GTTCAAGTGT GACTCCTTCC 3960
AGAGCCACAG GTAGGGGAGT GTGAAGTTGA GGGGGAGGAA AGCTGGAAGG ACTCTGCCTT 4020
GGGAGATTCC CAGCTCTGCT TTCCAGCGCT TGGTGGAAATC TGGGCTGGGG AAAGACGGCA 4080
CCGGGAAACT CTGCTTCCCC ATTGTTTCCA TCTGATCAGC TGTGGTGTGA GGACTTCTCA 4140
GACAAAGGCA AGGCCTCGTG CCCCTGCCCA GCCCATTTCAT GGAGCCCTGG GCCTTCTTGG 4200
CTTCCATAGA TCCTAAGCTC TTGACTGTAG TTTAGCCAGA CTTGTTTTGC TATCTTATAA 4260
GCAGTTTACA ATTAGGGAAT GCTGGTTTGT AAGAGCAAAG GACAGGTAGT CTAGAGAGGG 4320
TCGTCGGGCC TGCTTGTCTG GTCTTTGTAA CCCAGCACTT CCTCTGCCCC TCCTGGCTTT 4380
ATGTTTATGG GAGAGGACTC AATAGCTCCA CCCCTTCTGG CACCAGATGG GGCTTGGTTA 4440
GTTTGCATAA AGCACCCTGC AGAGGTTAAA GCCAGCGGGT CCCTAGTCTT AGGCCACGCC 4500
TGCTTGTGTG GGCTCTGGCC TGGCTGTGTC GCTGGCCAG GGGGCAGCAG TGCTTAGAGC 4560
TTCTGCAGGG CTTCTCTTGT TTACACAGCT GCATCAGACA ATGCCATTTC TCCCACCAC 4620
GGAACCTTCC ATCTAAGATT TCTTCCAGGG AATGCCAGCA ATCAGGCAGC ACCCAGCTGT 4680
GGGGGCAGTG GGGTGGGGGA GACCCACATT GATGACTTTT TTTTTCCTT TTAATGAAGA 4740
AACACCAAAG AAAGCTGTGG AAAGGACCTG CCCCACATGA AAAGGATAAG CCAAGATGGC 4800
TGTAACACA GAGCATTTGA GCTGCCACTC TTGGAGCACA TTGATTTTTC AAAAGCCAGC 4860
TCTGTCAAGG AAGGAGGTGC TGTATGACA GCTCTTCCAG TGGGCAAGA GGACGCCCAT 4920
AATTTCTTCC ATTGCTAGCT CATCTGTGGG ACCAATTGTT TGTAAGCAAC CTGTGGCCTG 4980
CACTTGTGGC TCCGAAAGGA GCACAAACCC TCCATCCACT TCCATTTTCC TCTGCCCTTT 5040
TCCACCTCCC CTTTCCATCC CACCAGCTGC CAGTGGCTCC CAGAAAGCCT TATTGAGCCC 5100
CTTGTGTACA CTTGGGGCTG CGGAGGCCCT TCCCTACTCG TCTGGCTTTT CCTGAGAGGC 5160
AGGTCTTCCG TCCTCAGAGC CTTTCTGGAA CAAGGAGAAT GCCTGTGCAG GTGGACACAC 5220
AGGCCTGGCC TGTCGTCTC ACTTGTCTTC CAGCGGGGAG CTTACAGTTG CCGAGTGGAA 5280
GAACCATGAC TCCCATTTGC TTCCAAGGTG CTAGGGAGT TTCAGGGTAC GCTGGTTTCC 5340
CTCTCCAGCT GAGAGCCGAG TTTCTGGGGA CTGCAGATT TTTACTCTG TGTGATTC 5400
AATGCCGAT GCTTCTGTTT CATTCCCAGC CTTTCTACT ATGCATTTTC CTTTATCAG 5460
GTGTATAAAG TTAAATAGT TGTATTATC ACTAAAAAGT ACATGAACCT AAGAGACAAC 5520
TAAGCCTTTC GTGTTTTTCC ACAGGTGTTT AAGCTTCTCT GTACAGTTGA AATAAACAGA 5580
CAGCAAAATG GTAAAAAATA AAAAAAATA A 5611
  
```

Seq ID NO: C193 DNA Sequence  
 Nucleic Acid Accession #: NM\_018646  
 Coding sequence: 217..2394

60  
 65  
 70  
 75  
 80

```

1 11 21 31 41 51
| | | | | |
GCTCTGCCAA GTGTAACAAA CTCACAGCCC TCTCCAAACT GGCTGGGGCT GCTGGGAGAC 60
TCCCAAGGAA CTCGTACGGA AGGCAGGAGA CAGGAGACGG GACCTCTACA GGGAGACGGT 120
GGGCGGGCCC TTGGGGGGGC TGATGTGGCC CCAAGGCTGA GTCCCGTCAG GGTCTGGCCT 180
CGGCCTCAGG CCCCCAAGGA GCCGGCCCTA CACCCCATGG GTTTGTCACT GCCCAAGGAG 240
AAAGGGCTAA TTCTCTGCCT ATGGAGCAAG TTCTGCAGAT GGTTCAGAG ACGGGAGTCC 300
TGGGCCCAGA GCCGAGATGA GCAGAACCTG CTGCAGCAGA AGAGGATCTG GGAGTCTCCT 360
CTCCTTCTAG CTGCCAAAGA TAATGATGTC CAGGCCCTGA ACAAGTTGCT CAAGTATGAG 420
GATTGCAAGG TGCAACAGAG AGGAGCCATG GGGGAAACAG CGCTACACAT AGCAGCCCTC 480
TATGACAACC TGGAGGCCGC CATGGTGTCT ATGGAGGCTG CCCCGAGCT GGTCTTTGAG 540
CCCATGACAT CTGAGCTCTA TGAGGGTCAG ACTGCACTGC ACATCGCTGT TGTGAACCA 600
AACATGAACC TGGTGCAGAG CCTGCTTGCC CGCAGGGCCA GTGTCTCTGC CAGAGCCACA 660
GGCACTGCTT TCCGCCGTAG TCCCTGCAAC CTCATCTACT TTGGGGAGCA CCCTTTGTTC 720
TTTGTGCTCT GTGTGAACAG TGAGGAGATC GTGCGGCTGC TCATTGAGCA TGGAGCTGAC 780
ATCCGGGCCCT AGGACTCCCT GGGAAACACA GTGTTACACA TCCTCATCCT CCAGCCCAAC 840
AAAACCTTTG CCTGCCAGAT GTACAACCTG TTGCTGTCTT ACGACAGACA TGGGGACCAC 900
CTGCAGCCCC TGGACCTCGT GCCCAATCAC CAGGCTCTCA CCCCTTTCAA GCTGGCTGGA 960
GTGAGGGGTA ACACATGTAT GTTTTCAGCA CTGATGCAGA AGCGGAAGCA CACCCAGTGG 1020
ACGTATGGAC CACTGACCTC GACTCTCTAT GACCTCAGAG AGATCGACTC CTAGGGGAT 1080
GAGCAGTCCC TGCTGGAAC TATCATCACC ACCAAGAAGC GGGAGGCTCG CCAGATCTCT 1140
GACCAAGACG CGGTGAAGGA GCTGGTGAGC CTCAGTGGGA AGCGGTACGG GCGGCCGTAC 1200
TTCTGCATGC TGGGTGCCAT ATATCTGCTG TACATCATCT GCTTCACCAT GTGCTGCATC 1260
TACCGGCCCC TCAAGCCCAAG GACCAATAAC CGCACGAGCC CCCGGGACAA CACCCTCTTA 1320
CAGCAGAAGC TACTTCAGGA AGCCTACATG ACCCTAAGG ACGATATCCG GCTGGTCTGG 1380
GAGCTGGTGA CTGTCAATGG GGCTATCATC ATCCTGCTGG TAGAGGTTCC AGACATCTTC 1440
AGAATGGGGG TCACTCGCTT CTTTGGACAG ACCATCCCTG GGGGCCCATT CCATGTCCTC 1500
  
```



5 ATCATCACCT ATGCTTCAT GGTGCTGGTG ACCATGGTGA TCGGGCTCAT CAGTGCCAGC 1560  
 GGGGAGGTGG TACCCATGTC CTTTGCACTC GTGCTGGGCT GGTGCAACGT CATGTACTTC 1620  
 GCCCCAGGAT TCCAGATGCT AGGCCCTTC ACCATCATGA TTCAGAAGAT GATTTTGGC 1680  
 GACCTGATGC GATTCTGCTG GCTGATGGCT GTGGTCATCC TGGGCTTTGC TTCAGCCTTC 1740  
 10 TATATCATCT TCCAGACAGA GGACCCGAG GAGCTAGGCC ACTTCTACGA CTACCCCATG 1800  
 GCCTGTTCGA GCACCTTCGA GCTGTTCCCT ACCATCATCG ATGGCCACGC CAACACAAAC 1860  
 GTGGACCTGC CCTTCATGTA CAGCATCACC TATGCTGCCT TTGCCATCAT CGCCCACTG 1920  
 CTATGCTCA ACCTCCTCAT TGCCATGATG GGCGACACTC ACTGGCGAGT GGCCCATGAG 1980  
 CGGGATGAGC TGTGGAGGGC CCAGATTGTG GCCACCACGG TGATGCTGGA GCGGAAGCTG 2040  
 CCTGCTGGCC TGTGGCTCG CTCGGGATC TCGGACGGG AGTATGGCCT GGGAGACCGC 2100  
 TGGTTCCTGC GGGTGAAGA CAGGCAAGAT CTCAACCGGC AGCGATCCA ACGTACGCA 2160  
 CAGGCTTCC ACACCGGGG CTCTGAGGAT TTGGACAAAG ACTCAGTGA AAACTAGAG 2220  
 CTGGGCTGTC CCTTCAGCCC CCACCTGTCC CTTCTATGC CCTCAGTGTC TCGAAGTACC 2280  
 15 TCCCGCAGCA GTGCCAATTG GGAAGGCTT CGGCAAGGGA CCTGAGGAG AGACCTGCGT 2340  
 GGGATAATCA ACAGGGGTCT GGAGACGGG GAGAGCTGGG AATATCAGAT CTGACTGCGT 2400  
 GTTCTCACTT CGCTTCTGAG AACTTGTCTT CATTTTCTGT GGTGCATCAA ACAAACAAA 2460  
 AACCAACAC CCAGAGGTCT CATCTCCAG GCCCAGGGG AGAAAGAGGA GTAGCATGAA 2520  
 CGCCAAGGAA TGTACGTTGA GAATCACTGC TCCAGGCTG CATTACTCT TCAGCTCTGG 2580  
 20 GGCAGAGGAA GCCCAGCCCA AGCAGGGGC TGGCAGGGCG TGAGGAACCT TCCTGTGGCC 2640  
 TGCTCATCAC CCTTCCGACA GGAGCACTGC ATGTCAGAGC ACTTTAAAA CAGGCCAGCC 2700  
 TGCTTGGCG CTGCTGTCC ACCCAGGGT CATAAAGTGGG GAGAGAGCCC TTCCAGGGC 2760  
 ACCCAGGCG GTGCAGGAA GTGCAGAGCT TGTGAAAGC GTGTGAGTGA GGGAGACAGG 2820  
 AACGGCTCTG GGGGTGGAA GTGGGCTAG GTCTTGCCA CTCCATCTTC AATAAGTCG 2880  
 25 TTTTCGGATC CCTGAAAAA AAAAAAAA AAAAAA 2918

Seq ID NO: C194 DNA Sequence  
 Nucleic Acid Accession #: NM\_021910.1  
 Coding sequence: 260..601

30 1 11 21 31 41 51  
 GTTCTCCACA ACTGCCAGCA ATCCTTCCAC CAGGCAAAAC ACATCATCTA AGGAAAAGAA 60  
 GTGAGGTTTG CTTAGGGCGT GGCAGCTTCG GATAAACGCA GGACTCCGCC TGGCAGCCCG 120  
 35 ATTTCTCCCG GAACCTCTGC TCAGCCTGGT GAACCAACA GGCAGCGCT CTGACATGCA 180  
 CCCACTCCAC GGTGCAGCTG CGGCTTATCT CTCAGCCAG CGAGATGCCA GCCTTCCTGT 240  
 CCCCAGGCG CGCTCTGACA TGCAGAAGGT GACCTGGGC CTGCTTGTGT TCCTGGCAGG 300  
 CTTTCTGTCT CTGGACGCCA ATGACCTAGA AGATAAAAA AGTCCTTTCT ACTATGACTG 360  
 GCACAGCCTC CAGGTGGCG GGCTCATCTG CGCTGGGTT CTGTGCGCCA TGGGCATCAT 420  
 40 CATCGTATG AGTGAAGTGA GGAGCTCGGG GGAGCAGGCG GGCAGGGCT GGGCTCCCC 480  
 TCCCCTGACC ACTCAGCTCT CCCCAACAGG TGCAAAATGC AAATGCAAGT TTGGCCAGAA 540  
 GTCCGCTCAC CATCCAGGGG AGACTCCACC TCTCATCACC CCCGGCTCAG CCCAAAGCTG 600  
 ATGAGGACAG ACCAGCTGAA ATTGGGTGGA GGACCGTTCT CTGTCCCCAG GTCCCTGTCT 660  
 TGCAAGAAA CTTGAACCTC AGGATGGAAT TCTTCTCTCT CTGTGGGAC TCCTTTGCAT 720  
 45 GGCAGGCGCT CATCTCACCT CTCGCAAGAG GGTCTCTTGT TTTCAATTTT TTTAATCTAA 780  
 AATGATTGTG CCTCTGCCCA AGCAGCCTGG AGACTTCCTA TGTGTGCATT GGGGTGGGGC 840  
 TTGGGGCACC ATGAGAAGGT TGGCGTGCCC TGGAGGCTGA CACAGAGGCT GGCAGTGGC 900  
 CTGCTTGTG GGAAAGGCC ACAGGCTGT TCCCTTGTGG CTTGGGACAT GGCACAGGCC 960  
 CGCCCTCTGC CTCTCAGCC ATGGGACCTC ATATGCAATT TGGGATTAC TAGTAGCCAA 1020  
 50 AAGGAATGAA AGAGAGCTCT AACCAGATGG AACACTGGAA CATTCCAGTG GACCCTGGAC 1080  
 CATTCCAGGA AAACCTGGAT ATAGGATCGT CCCGCTATGA TGGAAAGTGT CAGACAGTTT 1140  
 ATAATAGTAA GCCCTGTGTA CCCTCTCACT TACCCGAGA CTTCACTTTA TTACAAGATC 1200  
 TTTCCAAATA CCCAATATG CCTGCAAGCC CGTTAAATAA TTCCCTATGC TACCTTAAT 1260  
 AACATACAAT GACCACATAG TGTGAGAACT TCCAACAAGC CTCAAAGTCC CTTGAGACTC 1320  
 55 CCCAATACCT AATAAGGCAT GCGAAATGTT CTCATGAACT ACCCCACAAC ACGCTATAAA 1380  
 CTCAAAACAC CCAAAATAT CTCTCCAAT GTCCCTGAGAC ATGAACCCAA AAAGAGACCC 1440  
 ACAATAAACT CGTGACTTGT CCCCTC 1466

Seq ID NO: C195 DNA Sequence  
 Nucleic Acid Accession #: NM\_005971.2  
 Coding sequence: 176..439

60 1 11 21 31 41 51  
 GTTCTCCACA ACTGCCAGCA ATCCTTCCAC CAGGCAAAAC ACATCATCTA AGGAAAAGAA 60  
 GTGAGGTTTG CTTAGGGCGT GGCAGCTTCG GATAAACGCA GGACTCCGCC TGGCAGCCCG 120  
 65 ATTTCTCCCG GAACCTCTGC TCAGCCTGGT GAACCAACA GGCAGCGCT CTGACATGCA 180  
 GAAGGTGACC CTGGGCTGTC TTGTGTTCTT GGCAGGCTTT CTGTCTCTGG ACGCCAATGA 240  
 CCTAGAAGAT AAAAACAGTA CTTTCTACTA TGACTGGCAC AGCCTCCAGG TTGGCGGGCT 300  
 70 CATCTGCGCT GGGGTTCTGT GCGCCATGGG CATCATCATC GTCATGAGTG CAAATGCAA 360  
 ATGCAAGTTT GGCCAGAAGT CCGGTCAACA TCCAGGGGAG ACTCCACCTC TCATCACCC 420  
 AGGCTCAGCC CAAAGCTGAT GAGGACAGAC CAGCTGAAAT TGGGTGGAGG ACCGTTCTCT 480  
 GTCCCCAGGT CTTGTCTCTG CACAGAAACT TGAACCTCAG GATGGAATTC TTCTCTCTCT 540  
 GCTGGGACTC CTTTGCATGG CAGGGCTCA TCTCACTCT CGCAAGAGGG TCTCTTGTGT 600  
 75 CAATTTTTTT TAATCTAAAA TGATTGTGCC TCTGCCCAAG CAGCCTGGAG ACTTCTATG 660  
 TGTGCAATTG GGTGGGCTTT GGGGCACCAT GAGAAGGTTG GCGTGCCCTG GAGGCTGACA 720  
 CAGAGGCTGG CACTGAGCCT GCTTGTGGG AAAAGCCAC AGGCCTGTTT CTTTGTGGCT 780  
 TGGGACATGG CACAGGCCCG CCTCTGCCT CCTCAGCCAT GGGACCTCAT ATGCAATTTG 840  
 GGATTTACTA GTAGCCAAA GGAATGAAAG AGAGCTCTAA CCAGATGGAA CACTGGAACA 900  
 80 TTCCAGTGA CCCTGGACCA TTCCAGGAAA ACTGGGACAT AGGATCGTCC CGCTATGATG 960  
 GAAGTGTTC CACAGTTTAT AATAGTAAGC CCCTGTGACC CTCTCACTTA CCCCAGAGAC 1020  
 TCATTTTAT ACAAGATCTT TCCAATACC CAAATATCCC TGCAAGCCCG TTAATAAAT 1080  
 CCCTATGCTA CCTTAAATA CATAAATGA CCACATAGTG TGAGAAGTTC CAACAAGCCT 1140  
 CAAAGTCCCT TGAGACTCCC CAATACCTAA TAAGGCATGC GAAATGTTCT CATGAAGTAC 1200  
 CCCACAACAC GCCTAAAAC CAAAACACCC AAAAAATATCT CTCCATATGT CTGAGACAT 1260

GAACCCAAAA AGAGACCCAC AATAAACTCG TGA CTGTGTCC CCTC

1304

Seq ID NO: C196 DNA Sequence  
Nucleic Acid Accession #: NM\_004961.2  
Coding sequence: 55..1575

5

	1	11	21	31	41	51	
10	GCCAGAGCGT	GAGCCGCGAC	CTCCGCGCAG	GTGGTTCGCGC	CGGTCTCCGC	GGAAATGTTG	60
	TCCAAAGTTC	TTCCAGTCCT	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	GGTCGAGGGA	120
	CCTCAGACTG	AATCAAAGAA	TGAAGCCTCT	TCCCGTGATG	TGTCTATGG	CCCCCAGCCC	180
	CAGCCTCTGG	AAAAATCAGT	CCTCTCTGAG	GAACAAAGT	CAACTGAGAC	TGAGACTGGG	240
	AGCAGAGTTG	GCAAACTGCC	AGAAGCCTCT	CGCATCCTGA	ACACTATCCT	GAGTAATTAT	300
15	GACCACAAAC	TGCGCCCTGG	CATTGGAGAG	AAGCCCACTG	TGGTCACTGT	TGAGATCGCC	360
	GTCAACAGCC	TTGGTCTCT	CTCTATCCTA	GACATGGAAT	ACACCATGGA	CATCATCTTC	420
	TCCCAGACCT	GGTAGCAGCA	ACGCTCTCTG	TACAACGACA	CCTTTGAGTC	TCTTGTCTCG	480
	AATGGCAATG	TGGTGAGCCA	GCTATGGATC	CCGGACACCT	TTTTTAGGAA	TTCTAAGAGG	540
	ACCCACGAGC	ATGAGATCAC	CATGCCCAAC	CAGATGGTCC	GCATCTACAA	GGATGGCAAG	600
	GTGTTGTACA	CAATTAGGAT	GACCATTGAT	GCCGGATGCT	CACTCCACAT	GCTCAGATTT	660
20	CCAAATGGAAT	CTCACTCTTG	CCCTCTATCT	TTCTCTAGCT	TTTCTATATC	TGAGAATGAG	720
	ATGATCTACA	AGTGGGAAAA	TTTCAAGCTT	GAAATCAATG	AGAAGAACTC	CTGGAAGCTC	780
	TTCCAGTTTG	ATTTTACAGG	AGTGAGCAAC	AAAACTGAAA	TAATCACAAAC	CCCAGTTGGT	840
	GACTTTCATG	TCATACGAT	TTTCTTCAAT	GTGAGCAGCG	GGTTTGGCTA	TGTTGCCCTT	900
	CAAAATCATG	TCCCTTCTTC	CGTGACCACG	ATGCTCTCCT	GGGTTTCCTT	TTGGATCAAG	960
25	ACAGAGTCTG	CTCCAGCCCG	GACCTCTCTA	GGGATCACCT	CTGTTCTGAC	CATGACCACG	1020
	TTGGGCACCT	TTTCTCGTAA	GAATTTCCTG	CGTGTCTCCT	ATATCACAGC	CTTGGATTTC	1080
	TATATCGCCA	TCGTCTCTCT	CTTCTGCTTC	TGCGCTCTGT	TGGAGTTTGC	TGTGCTCAAC	1140
	TTCTGTATCT	ACAACGACAG	AAAAGCCCAT	GCTTCTCCTA	AACTCCGCCA	TCTCGTATC	1200
	AATAGCCGTG	CCCATGCCCG	TACCCGTGCA	CGTTCCCGAG	CCTGTGCCCG	CCAACATCAG	1260
30	GGAAGCTTTT	TGTGCCAGAT	TGTCAACACT	GAGGGAAGTG	ATGGAGAGGA	GGCGCCGTCT	1320
	TGCTCAGCCC	AGCAGCCCCC	TAGCCAGGTT	AGCCCTGAGG	GTCCCGCCAG	CCTCTGCTCC	1380
	AAGCTGGCCT	GCTGTGAGTG	GTGCAAGCGT	TTTAAGAAAT	ACTTCTGCAT	GGTCCCCGAT	1440
	TGTGAGGGCA	GTACCTGGCA	GCAGGGCCGC	CTCTGCATCC	ATGCTTACCG	CCTGGATAAC	1500
35	TACTCGAGAG	TTGTTTCCCT	AGTGACTTTC	TTCTTCTTCA	ATGTGCTCTA	CTGGCTTGTT	1560
	TGCCTTAATC	TGTAGGTACC	AGCTGGTACC	CTGTGGGGCA	ACCTCTCCAG	TTCCCCAGGA	1620
	GGTCCAAGCC	CCTTGCCAAG	GGAGTTGGGG	GAAAGCAGCA	GCAGCAGCAG	GAGCGACTAG	1680
	AGTTTTTCTC	GCCCCATTCC	CCAAACAGAA	GCTTGCAAGG	GGTTTGTCTT	TGCTGCCCTT	1740
	CTCCCCTACC	TGGCCCATTC	ACTGAGTCTT	CTCAGCAGAC	CATTTCAAAT	TATTAATAAA	1800
40	TGGGCCACCT	CCCTCTTCTT	CAAGGAGCAT	CCGTGATGCT	CAGTGTTCAA	AACCCAGGCC	1860
	ACTTAGTGAT	CAGCTCCCTA	AAACCATGCC	TAAGTACAGG	CGGATTAGCT	ATCTTCCAAC	1920
	AATGCTGACC	ACAGACAAT	TACTGCATTT	TTCCAGAAGC	CCACTATTGC	CTTTGTAGTG	1980
	CTTTCGGCCC	AGTTCTGGCC	TCAGCCTCAA	AGTGCACCGA	CTAGTTGCTT	GCCTATACCT	2040
	GGCACCTCAT	TAAGATGCTG	GGCAGCAGTA	TAACAGGAGG	AAGAGATCCC	TCTCCTTTGG	2100
45	TCAGATTATT	ATGTTTCTCG	TTCTCTCTCC	CTGCTACCCC	TTTCTCTGCA	GATAGATAGA	2160
	CACCTGGCATT	ATCCCTTTAG	GAAGAGGGGG	GGGCAGCAAG	AGAGCCTATT	TGGGACAGCA	2220
	TTCTCTCTCT	CTGTCTGTCT	TGACATCTCC	CTCTCCTTGC	TGGCTCCATC	TTTCGTCTGC	2280
	ACTACCAATT	CAATGCCCTT	CATCCAATGG	GTATCTATTT	TTGTGTGTGA	TTATAGTAAC	2340
	TACTCCCTGC	TTTATATGCC	ACCCTCTTCC	TTCTCTTTGA	CCCCTGTGAC	TCCTTCTGTA	2400
	ACTTTCCCGA	TGACTTCCCC	TAGCCCTGAC	CCAGGCACTA	GGCCTTGGTG	ACTTCTCTGG	2460
50	GCCCAAGAAC	TAAGGAAACT	CGGCTTTGCA	ACAGGCATTA	CTCGCCATTG	ATTGGTGCCC	2520
	ACCCAGGGCA	CACCTGTCGA	GTCTATATCA	TTGCTTGACC	CCTGGACCCA	TAAACCAAGT	2580
	CACCTGTTATA	ATGTTTCTCG	TCTAACCATC	ACAATCAATC	AATCAAAATC	CCTTAAATTT	2640
	GTATGGCACT	GGAACTTTGG	CAAAGCACTT	TTGACAAGTT	GTGTCTGATT	GGAGCTTCAT	2700
55	GATAGCCTTG	TGACATCTTT	AGGGCAGGAT	TCTTATCCCC	ATTTTGCAGA	TGAAAACCCCT	2760
	GAGTCACAGA	TTTCTGTGGG	ACTGTGGATC	TCAGTGAAGT	CTATCCAAAG	GGCCACTGTC	2820
	ACCTTCTAGA	CCACATGATA	GGGCTAGACA	GCTCAGTTCA	CCATGATTCT	CTTCTGTCTC	2880
	CTCTGCTGGC	ACCAAGGTGG	CAAGGCCGAG	AATGGCGACC	TCTCTTTAGC	TCAATTTCTG	2940
	GGCCTGAGGT	GCTCAGACTG	CCCCCAAGAT	CAAATCTCTC	CTGGCTGTAG	TAACCCAGTG	3000
60	GAATGAATTT	GGACATGCCC	CAATGCTTCT	ATATGCTAAG	TGAAATCTGT	GTCTGTAATT	3060
	TGTTGGGGGG	TGGATAGGGT	GGGGTCTCCA	TCTACTTTT	GTCCACATCA	TCTGAAATGG	3120
	GGAATATATG	AAATAAATAT	ATCAGCAAAG	CAAAAAGAAA	AAAAAAA		3168

Seq ID NO: C197 DNA Sequence  
Nucleic Acid Accession #: NM\_021984.1  
Coding sequence: 572..1753

65

	1	11	21	31	41	51	
70	GCCAGAGCGT	GAGCCGCGAC	CTCCGCGCAG	GTGGTTCGCGC	CGGTCTCCGC	GGAAATGTTG	60
	TCCAAAGTTC	TTCCAGTCCT	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	AACATGTATA	120
	CAGAGAAGTG	CTCAAATCAT	AAGGTGACAG	CTGATGAGTT	GTCAAAAAAT	GACCACAGCG	180
	GTGTAAGAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAAG	CCCCCTTTGT	240
	CACCTGCCTCC	CAGCAAGGGC	AGCACTATCC	GGACTTCTAA	CACCATCGGG	TGAGGGGACC	300
75	TCAGACTGAA	TCAAAGAATG	AAGCCTCTTC	CCGTGATGTT	GTCTATGGCC	CCCAGCCCCA	360
	GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGG	420
	CAGAGTTGGC	AAACTGCCCAG	AAGCCTCTCG	CATCCTGAAC	ACTATCCTGA	GTAATTATGA	480
	CCACAAACTG	CGCCCTGGCA	TTGGAGAGAA	GCCCCACTGT	GTCACTGTGT	AGATCTCCGT	540
	CAACAGCCTT	GGTCTCTCT	CTATCCTAGA	CATGGAATAC	ACCATTGACA	TCATCTTCTC	600
	CCAGACCTGG	TACGACGAAC	GCCTCTGTTA	CAACGACACC	TTTGAGTCTC	TTGTTCTGAA	660
80	TGGCAATGTG	GTGAGCCAGC	TATGGATCCC	GGACACCTTT	TTTAGGAATT	CTAAGAGGAC	720
	CCACAGCAT	GAGATCACCA	TGCCCAACCA	GATGGTCCGC	ATCTACAAGG	ATGGCAAGGT	780
	GTTGTACACA	ATTAGGATGA	CCATTGATGC	CGGATGCTCA	CTCCACATGC	TCAGATTTC	840
	AATGGATTCT	CACCTTTGCC	CTCTATCTTT	CTCTAGCTTT	TCCTATCTCT	AGAATGAGAT	900
	GATCTACAAG	TGGGAAATTT	TCAAGCTTGA	AATCAATGAG	AAGAACTCCT	GGAAGCTCTT	960

5  
10  
15  
20  
25  
30  
35  
40

```

CCAGTTGGAT TTTACAGGAG TGAGCAACAA AACTGAAATA ATCACAACCC CAGTTGGTGA 1020
CTTCATGGTC ATGACGATTT TCTTCAATGT GAGCAGGCGG TTTGGCTATG TTGCCTTTCA 1080
AAACTATGTC CCTTCTTCCG TGACCACGAT GCTCTCCCTGG GTTTCCTTTT GGATCAAGAC 1140
AGAGTCTGCT CCAGCCCGGA CCTCTCTAGG GATCACCTCT GTTCTGACCA TGACCACGTT 1200
GGGCACCTTT TCTCGTAAGA ATTTCCCGCG TGCTCTCCTAT ATCACAGCCT TGGATTCTTA 1260
TATCGCCATC TGCTTCGTCT TCTGCTTCTG CGCTCTGTGT GAGTTTGCTG TGCTCAACTT 1320
CCTGATCTAC AACCAGACAA AAGCCCATGC TTCTCCTAAA CTCGCCATC CTCTGATCAA 1380
TAGCCGTGCC CATGCCCGTA CCCGTGCACG TTCCCGAGCC TGTGCCCGCC AACATCAGGA 1440
AGCTTTTGTG TGCCAGATTG TCACCACTGA GGGGAAGTAT GGAGAGGAGC GCCCGTCTTG 1500
CTCAGCCGAG CAGCCCCCTA GCCCAGGTAG CCCTGAGGGT CCCCAGCAGC TCTGCTCCAA 1560
GCTGGCCTGC TGTGAGTGGT GCAAGCGTTT TAAGAAGTAC TTCTGCATGG TCCCGGATTG 1620
TGAGGGCAGT ACCTGGCAGC AGGCCCGCCT CTGCATCCAT GTCTACCGCC TGGATAACTA 1680
CTCGAGAGTT GTTTTCCGAG TGACTTTCTT CTCTTCAAT GTGCTCTACT GGCTTGTTTG 1740
CCTTAACTTG TAGGTACCAG CTGGTACCCT GTGGGGCAAC CTCTCCAGTT CCCCAGGAGG 1800
TCCAAGCCCC TTGCCAAGGG AGTTGGGGGA AAGCAGCAGC AGCAGCAGGA GCGACTAGAG 1860
TTTTTCTGTC CCCATTCCCC AAACAGAAGC TTGCAGAGGG TTTGTCTTTG CTGCCCTCT 1920
CCCCTACCTG GCCCATTCAC TGAGTTTCTT CAGCAGACCA TTCAAATTA TTAATAAATG 1980
GGCCACCTCC CTCTTCTTCA AGGAGCATCC GTGATGCTCA GTGTTCAAAA CCACAGCCAC 2040
TTAGTGATCA GCTCCCTAAA ACCATGCCCTA AGTACAGGCG GATTAGCTAT CTTCACACAA 2100
TGCTGACCAC CAGACAATTA CTGCATTTT CCAGAAGCCC ACTATTGCCT TTGCAGTGCT 2160
TTCGGGCCAG TTCTGGCCTC AGCCTCAAAG TGCACCGACT AGTTGCTTGC CTATACCTGG 2220
CACCTCATTA AGATGCTGGG CAGCAGTATA ACAGGAGGAA GAGATCCCTC TCCTTTGGTC 2280
AGATTATTAT GTTCTCAGTT CTCTCTCCCT GCTACCCCTT TCTCTGAGA TAGATAGACA 2340
CTGGCATTAT CCCTTAGGA AGAGGGGGGG GCAGCAAGAG AGCCTATTGG GGACAGCATT 2400
CCTCTCTCTC TGCTGCTGTG ACATCTCCCT CTCTTGCTG GCTCCATCTT TCGTCTGCAC 2460
TACCAATTTCA ATGCCCTTCA TCCAATGGGT ATCTATTTTT GTGTGTGATT ATAGTAACTA 2520
CTCCCTGCTT TATATGCCAC CCTCTTCTCT CTCTTTGACC CCTGTGACTC TTTCTGTAAC 2580
TTTCCAGTG CATCTCCCTA GCCCTGACCC AGGCACTAGG CCTTGGTGAC TTCCTGGGGC 2640
CAAGAACTA AGGAACTCG GCTTTGCAAC AGGCATTACT CGCCATTGAT TGGTGCCAC 2700
CCAGGGCACA CTGTCGGAGT TCTATCACTT GCTTGACCCC TGGACCCATA AACCACTCA 2760
CTGTTATACC CGGGGCACTC TAACCATCAA AATCAATCAA TCAAAATCCC TTAATTTGT 2820
ATGGCACTGG AACTTTGGCA AAGCACTTTT GACAAGTTGT GTCTGATTGG AGCTTCATGA 2880
TAGCCTTGTG ACATCTTTAG GGCAGGATTC TTATCCCCAT TTTGCAGATG AAAACCTGA 2940
GTCACAGATT TCTGTGGGAC TGTGGATCTC ACTGGAAGCT ATCCAAGAGC CCACTGTAC 3000
CTTCTAGACC ACATGATAGG GCTAGACAGC TCAGTTTACC ATGATTCTCT TCTGTACCT 3060
CTGCTGGCAC ACCAGTGGCA AGGCCAGAA TGGCGACCTC TCTTTAGCTC AATTTCTGGG 3120
CCTGAGGTGC TCAGACTGCC CCCAAGATCA AATCTCTCCT GGCTGTAGTA ACCCAGTGG 3180
ATGAATTTGG ACATGCCCCA ATGCTTCTAT ATGCTAAGTG AAATCTGTGT CTGTAATTTG 3240
TTGGGGGGTG GATAGGGTGG GGTCTCCATC TACTTTTGT CACCATCATC TGAATGGGG 3300
AAATATGTAA ATAAATATAT CAGCAAAGC 3320

```

Seq ID NO: C198 DNA Sequence  
Nucleic Acid Accession #: NM\_021987.1  
Coding sequence: 572..1657

45  
50  
55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
GCCAGAGCGT GAGCCGCGAC CTCGCGCGAG GTGGTCGCGC CGGTCTCCGC GGAAATGTTG 60
TCCAAAGTTC TTCAGTCCCT CCTAGGCATC TTATTGATCC TCCAGTCGAG AACATGTATA 120
CAGAGAAAGTG CTCAAATCAT AAGTGTACAG CTGATGAGTT GTCAAAAAT GACCACAGCG 180
GTGTAAAGAA AGCCAAATCA AGGACCCGAA TGTGAGCAGG ACCTCAGAAG CCCCCTTTGT 240
CACTGCCTCC CAGCAAAAGC AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC 300
TCAGACTGAA TCAAAGAAATG AAGCCTCTTC CCGTATGATT GTCTATGGCC CCCAGCCCCA 360
GCCTCTGGAA AATCAGCTCC TCTCTGAGGA AACAAAGTCA ACTGAGACTG AGACTGGGAG 420
CAGAGTTGGC AAACCTGCCAG AAGCCTCTCG CATCCTGAAC ACTATCCTGA GTAATTATGA 480
CCACAAACTG CGCCCTGGCA TTGAGAGAGAA GCCCACTGTG GTCACCTGTT AGATCTCCGT 540
CAACAGCCTT GGTCTCTCTC CTATCCTAGA CATGGAATAC ACCATTGACA TCATCTTCTC 600
CCAGACCTGG AATTCTAAGA GGACCCACGA GCATGAGATC ACCATGCCCA ACCAGATGGT 660
CCGCATCTAC AAGGATGGCA AGGTGTTGTA CACAATTAGG ATGACCATTG ATGCCGGATG 720
CTCACTCCAC ATGCTCAGAT TTCCAATGGA TTCTCACTCT TGCCCTCTAT CTTTCTCTAG 780
CTTTTCTCTAT CCTGAGAAATG AGATGATCTA CAAGTGGGAA AATTTCAAGC TTGAAATCAA 840
TGAGAAGAAC TCTTGAAGC TCTTCCAGTT TGATTTTACA GGAGTGAGCA ACAAACCTGA 900
AATAATCACA ACCCCAGTTG GTGACTTTCAT GGTATGACG ATTTTCTTCA ATGTGAGCAG 960
GCGGTTTGGC TATGTTGCCT TTCAAACCTA TGTCCCTTCT TCCGTGACCA CGATGCTCTC 1020
CTGGGTTTCC TTTTGGATTA AGACAGAGTC TGCTCCAGCC CGGACCTCTC TAGGGATCAC 1080
CTCTGTTCTG ACCATGACCA CGTTGGGCAC CTTTCTCTGT AAGAATTTCG CGCGTGTCTC 1140
CTATATCACA GCCTTGGATT TCTATATCGC CATCTGCTTC GTCTTCTGCT TCTGCGCTCT 1200
GTTGGAGTTT GCTGTGCTCA ACTTCTGAT CTACAACCAG ACAAAGCCC ATGCTTCTCC 1260
TAAACTCGCG CATCTCGTA TCAATAGCCG TGCCCATGCC CGTACCCGTG CACGTTCCCG 1320
AGCCTGTGCC CGCCAACATC AGGAAGCTTT TGTGTGCCAG ATTGTACCA CTGAGGGAAG 1380
TGATGGAGAG GAGCGCCCGT CTGTCTCAGC CCAGCAGCCC CCTAGCCCAG GTAGCCCTGA 1440
GGGTCCCCGC AGCCTCTGCT CCAAGCTGGC CTGCTGTGAG TGGTGCAAGC GTTTTAAGAA 1500
GTACTTCTGC ATGGTCCCGG ATTGTGAGGG CAGTACCTGG CAGCAGGGCC GCCTCTGCAT 1560
CCATGTCTAC CGCCTGGATA ACTACTCGAG AGTTGTTTTC CCAGTGACTT TCTTCTTCTT 1620
CAATGTGCTC TACTGGCTTG TTGCTCTTAA CTGTAGGTA CCAGCTGGTA CCCTGTGGGG 1680
CAACCTCTCC AGTTCCCCAG GAGGTCCAAG CCCCTTGCCA AGGGAGTTGG GGGAAAGCAG 1740
CAGCAGCAGC AGGAGCGACT AGAGTTTTC CTGCCCATT CCCCACACAG AAGCTTGACG 1800
AGGGTTTGTG TTTGCTGCC CTCTCCCTA CTGGCCCAT TCACTGAGTT TTCTCAGCAG 1860
ACCATTTCAA ATTATTAATA AATGGGCCAC CTCCCTCTTC TTCAAGGAGC ATCCGTGATG 1920
CTCAGTGTTC AAAACACACG CCACTTAGTG ATCAGCTCCC TAAAACCATG CCTAAGTACA 1980
GGCGGATTAG CTATCTTCCA ACAATGCTGA CCACCAGACA ATTACTGCAT TTTTCCAGAA 2040
GCCCACTATT GCCTTTGCAG TGCTTTGCGC CAGTTCTGG CCTCAGCCTC AAAGTGCACC 2100
GACTAGTTGC TTGCCTATAC CTGGCACCTC ATTAAGATGC TGGGCAGCAG TATAACAGGA 2160
GGAAGAGATC CCTCTCCTTT GGTCAAGATTA TTATGTTCTC AGTTCTCTCT CCCTGCTACC 2220

```

	CCTTTCTCTG	CAGATAGATA	GACACTGGCA	TTATCCCTTT	AGGAAGAGGG	GGGGGCAGCA	2280
	AGAGAGCCTA	TTTGGGACAG	CATTCTCTCT	TCTCTGCTGC	TGTGACATCT	CCCTCTCCTT	2340
	GCTGGCTCCA	TCCTTCGTCT	GCACTACCAA	TTCAATGCCC	TTTCATCCAAT	GGGTATCTAT	2400
5	TTTTGTGTGT	GATTGTAGTA	ACTACTCCCT	GCTTTATATG	CCACCTCTTT	CCTTCTCTTT	2460
	GACCCCTGTG	ACTCTTTCTG	TAACCTTTCCC	AGTGACTTCC	CCTAGCCCTG	ACCAGGCACT	2520
	AGGCCTTGGT	GACTTCTCTG	GGCCAAGAAA	CTAAGGAAAC	TCGGCTTTGC	AACAGGCATT	2580
	ACTCGCCATT	GATTGGTGCC	CACCCAGGGC	ACACTGTCCG	AGTTCTATCA	CTTGCTTGAC	2640
	CCCTGGACCC	ATAAACCACT	CCACTGTTAT	ACCCGGGGCA	CTCTAACCAT	CACAATCAAT	2700
10	CAATCAAATT	CCCTTAAATT	TGTATGGCAC	TGGAACCTTG	GCAAAGCACT	TTTGACAAGT	2760
	TGTGTCTGAT	TGGAGCTTCA	TGATAGCCTT	GTGACATCTT	TAGGGCAGGA	TTCTTATCCC	2820
	CATTTTGCAG	ATGAAAAACC	TGAGTCACAG	ATTTCTGTGG	GACTGTGGAT	CTCACTGGAA	2880
	GCTATCCAAG	AGCCCACTGT	CACCTTCTAG	ACCACATGAT	AGGGCTAGAC	AGCTCAGTTC	2940
	ACCATGATTG	TCTTCTGTCA	CCTCTGCTGG	CACACCAGTG	GCAAGGCCCA	GAATGGCGAC	3000
15	CTCTCTTTAG	CTCAATTTCCT	GGGCCTGAGG	TGCTCAGACT	GCCCCCAAGA	TCAAATCTCT	3060
	CCTGGCTGTA	GTAACCCAGT	GGAAATGAATT	TGGACATGCC	CCAATGCTTC	TATATGCTAA	3120
	GTGAAATCTG	TGTCGTGAAT	TTGTTGGGGG	GTGGATAGGG	TGGGGTCTCC	ATCTACTTTT	3180
	TGTCACCATC	ATCTGAAATG	GGGAAATATG	TAAATAAATA	TATCAGCAAA	GC	3232

20 Seq ID NO: C199 DNA Sequence  
Nucleic Acid Accession #: NM\_021990.1  
Coding sequence: 1309..2490

	1	11	21	31	41	51	
25	GCCAGAGCGT	GAGCCGCGAC	CTCCGCGCAG	GTGGTGGCGC	CGGTCTCCGC	GGAAATGTTG	60
	TCCAAAGTTC	TTCCAGTCTC	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	AACATGTATA	120
	CAGAGAAAGTG	CTCAAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAATAT	GACCACAGCG	180
	GTGTAAAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAAG	CCCCCTTTGT	240
30	CACCTGCCTCC	CAGCAAAGGC	AGCACTATCC	GGACTTCTAA	CACCATCGGT	GAGTTTCATA	300
	CCTTGGCAGA	TGGCCTTTAA	CATTTTTGTT	TAATTCAATT	ATTCTTACTA	ATCTTCTTCT	360
	TTTTCTTGGC	TGTTGTGCAT	GGCTGTGGAG	CTCAGGGTGG	ACTCTCTGTT	GGCAGCCAGT	420
	TCCTGGATGG	CTGTCTGTGG	GTGGAGGACT	CCTGCCTTTC	CTGTTTAGAC	ACCCACAAGG	480
	GCTGCTCTTT	AGCCTTCTTC	CCTTCATCCC	CTTCCCTGCG	CCCCAGTGCA	ACGAGTATTA	540
35	CACAACCAAC	AAAACCGCAA	AATATTCCCA	CAATTTTCTG	GTCCTCTCTG	GGAGAGGCCG	600
	CTCTGGCTTT	TCCTCTCAGC	CCTGGCCCTC	TGCTGTCTCC	TCACCTCTGG	TTGGTGCTGG	660
	TCAGGCTGAC	TAGAGGCCAA	GGCGACCAAC	ACTAGGCCAA	CGCGGCCAGC	GCTCAGACAT	720
	AAATGCCCTC	TTCAATTAC	GTGTAACATT	CTTTTAAAT	CTAGGTCTTG	GTTTGTGTTGA	780
	TTTTTCTT	AATAAAGAG	TGATCATAAA	AGAGGGACAG	CATAGAAAGT	CCCCAAAGAG	840
40	CAGCAAGGTT	TTAAAGAAAT	TCACAAGCCT	AATCTGTAC	TGCTTATATA	TTTGCTATTA	900
	CCAGTCACAA	TTTAACTAGG	TTTTGTGTTG	AAAACTTGTT	TGTTGTTGCT	TCTGTCCCAA	960
	GAGGCACTAG	CTGGGGCCCC	TACAGAGTGC	AGGGCAGAGC	TTCAATTTTC	GTTTGAATGT	1020
	TCTAGGGTCG	AGGGACCTCA	GACTGAATCA	AAGAATGAAG	CCTCTTCCCG	TGATGTTGTC	1080
	TATGGCCCCC	AGCCCCAGCC	TCTGAAAAAT	CAGCTCCTCT	CTGAGGAAAC	AAAGTCAACT	1140
45	GAGACTGAGA	CTGGGAGCAG	AGTTGGCCAA	CTGCCAGAA	CCTCTCGCAT	CCTGAACACT	1200
	ATCCTGAGTA	ATTATGACCA	CAAACTGCGC	CCTGGCATTG	GAGAGAAGCC	CACTGTGGTC	1260
	ACTGTTGAGA	TCTCCGTCAA	CAGCCTTGGT	CCTCTCTCTA	TCCTAGACAT	GGAAATACAC	1320
	ATTGACATCA	TCTTCTCCCA	GACCTGGTAC	GACGAACGCC	TCTGTTACAA	CGACACCTTT	1380
	GAGTCTCTTG	TTCTGAATGG	CAATGTGGTG	AGCCAGCTAT	GGATCCCGGA	CACCTTTTTT	1440
50	AGGAATTTCT	AGAGGACCCA	CGAGCATGAG	ATCACCATGC	CCAACCAAGT	GGTCCGCATC	1500
	TACAAGGATG	GCAAGGTGTT	GTACACAATT	AGGATGACCA	TTGATGCCCG	ATGCTCACTC	1560
	CACATGCTCA	GATTTCCAAT	GGATTCTCAC	TCTTGCCCTC	TATCTTTCTC	TAGCTTTTCC	1620
	TATCCTGAGA	ATGAGATGAT	CTACAAGTGG	GAAATTTTCA	AGCTTGAAT	CAATGAGAAG	1680
	AACTCCTGGA	AGCTCTTCCA	GTTTGATTTT	ACAGGAGTGA	GCAACAAAAC	TGAAATAAAT	1740
55	ACAACCCGAC	TTGGTGACTT	CATGGTCATG	ACGATTTTCT	TCAATGTGAG	CAGGCGGTTT	1800
	GGCTATGTTG	CCTTTCAAAA	CTATGTCCCT	TCTTCCGTGA	CCACGATGCT	CTCCTGGGTT	1860
	TCCTTTTGGG	CTAAGACAGA	GTCTGTCTCA	GCCCCGACCT	CTCTAGGGAT	CACCTCTGTT	1920
	CTGACATGTA	CCAGCTTTGG	CACCTTTTCT	CGTAAGAATT	TCCCGCGTGT	CTCCTATATC	1980
	ACAGCCTTGG	ATTCTTATAT	CGCCATCTGC	TTGCTTCTCT	GCTTCTGCGC	TCTGTTGGAG	2040
60	TTTGCTGTGC	TCAACTTCTT	GATCTACAAC	CAGACAAAAG	CCCATGCTTC	TCCTAAACTC	2100
	CGCCATCTCT	GTATCAATAG	CCGTGCCCAT	GCCCCGACCT	GTGCACGTTT	CCGAGCCTGT	2160
	GCCCGCCAAC	ATCAGGAAGC	TTTGTGTGTC	CAGATTGTCA	CCACTGAGGG	AAGTGATGGA	2220
	GAGGAGCGCC	CGTCTTGTCT	AGCCCAAGCAG	CCCCCTAGCC	CAGGTAGCCC	TGAGGGTCCC	2280
	CGCAGCCTCT	GCTCCAAGCT	GGCCTGCTGT	GAGTGGTGCA	AGCGTTTTAA	GAAGTACTTC	2340
	TGCATGGTCC	CCGATTGTGA	GGGCAGTACC	TGGCAGCAGG	GCCGCTCTG	CATCCATGTC	2400
65	TACCGCTGCG	ATAAATGAGT	GAGAGTTGTT	TTCCCAAGTGA	CTTTCTTCTT	CTTCAATGTG	2460
	CTCTACTGGC	TTGTTTGCTT	TAACTTGTAG	GTACCAGCTG	GTACCCTGTG	GGGCAACCTC	2520
	TCCAGTTCCC	CAGGAGGTCC	AAGCCCCTTG	CCAAGGGAGT	TGGGGGAAAG	CAGCAGCAGC	2580
	AGCAGGAGCG	ACTAGAGTTT	TTCTTGCCCC	ATTCCCCAAA	CAGAAAGCTT	CAGAGGGTTT	2640
70	GTCTTTGCTG	CCCCCTCTCC	CTACCTGGCC	CATTCACCTG	GTTTTCTCTG	CAGACCATTT	2700
	CAAAATATTA	ATAAATGGGC	CACCTCCCTC	TTCTTCAAGG	AGCATCCGTG	ATGCTCAGTG	2760
	TTCAAAACCA	CAGCCACTTA	GTGATCAGCT	CCCTAAAACC	ATGCCTAAGT	ACAGGCGGAT	2820
	TAGCTATCTT	CCAACAATGC	TGACCAACAG	ACAATTAAGT	CATTTTTCCT	GAAGCCCACT	2880
	ATTGCTTTTG	CAGTGCTTTC	GGCCCACTTC	TGGCCTCAGC	CTCAAGTGC	ACCGACTAGT	2940
75	TGCTTGCTTA	TACCTGGCAC	CTCATTAAGA	TGCTGGGCAG	CAGTATAACA	GGAGGAAGAG	3000
	ATCCCTCTCC	TTTGGTCAGA	TTATTATGTT	CTCAGTTCTC	TCTCCCTGCT	ACCCCTTTCT	3060
	CTGCAGATAG	ATAGACACTG	GCATTATCCC	TTTAGGAAGA	GGGGGGGGCA	GCAAGAGAGC	3120
	CTATTTGGGA	CAGGATTCCT	CTCTCTCTGC	TGCTGTGACA	TCTCCCTCTC	CTTGCTGGCT	3180
	CCATCTTTCT	TCTGCACTAC	CAATTCAATG	CCCTTCATCC	AATGGGTATC	TATTTTGTGT	3240
80	TGTGATTATA	GTAACACTCT	CCTGCTTTAT	ATGCCACCCT	CTTCTTCTCT	TTTGACCCCT	3300
	GTGACTCTTT	CTGTAACTTT	CCCAGTGACT	TCCCCTAGCC	CTGACCAGGC	ACTAGGCCCT	3360
	GGTGACTTCT	TGGGGCCCAAG	AAACTAAGGA	AACTCGGCTT	TGCAACAGGC	ATTACTCGCC	3420
	CTTGATTGGT	GCCCAACCCAG	GGCACACTGT	CGGAGTTCTA	TCACTTGCTT	GACCCCTGGA	3480
	CCATAAACAC	AGTCCACTGT	TATACCCGGG	GCACTCTAAC	CATCACAATC	AATCAATCAA	3540
	ATTCCTTTAA	ATTGTGATGG	CACCTGGAAT	TTGGCAAGC	ACTTTTGACA	AGTTGTGTCT	3600

GATTGGAGCT TCATGATAGC CTTGTGACAT CTTTAGGGCA GGATTCTTAT CCCCATTTTG 3660  
 CAGATGAAAA CCCTGAGTCA CAGATTCTCTG TGGGACTGTG GATCTCACTG GAAGCTATCC 3720  
 AAGAGCCAC TGTCACCTTC TAGACCACAT GATAGGGCTA GACAGCTCAG TTCCACATGA 3780  
 TTCTCTTCTG TCACCTCTGC TGGCACACCA GTGGCAAGGC CCAGAATGGC GACCTCTCTT 3840  
 TAGCTCAATT TCTGGGCTCG AGGTGCTCAG ACTGCCCCCA AGATCAAATC TCTCTGGCT 3900  
 GTAGTAACCC AGTGGAAATGA ATTTGGACAT GCCCAATGC TTCTATATGC TAAGTGAAAT 3960  
 CTGTGTCTGT AATTGTTGG GGGGTGGATA GGGTGGGTC TCCATCTACT TTTTGTCAAC 4020  
 ATCATCTGAA ATGGGGAAAT ATGTAATAA ATATATCAGC AAAGC 4065

Seq ID NO: C200 DNA Sequence  
 Nucleic Acid Accession #: NM\_021819.1  
 Coding sequence: 39..1619

1 11 21 31 41 51  
 | | | | |  
 TAGGCGCGTC GCGTAATTCG GCACGAGGGC GCTCACGTAT GCCGGCGGTC AGTGGTCCAG 60  
 GTCCCTTATT CTGCCTTCTC CTCTCTGTCC TGGACCCCA CAGCCCTGAG ACGGGGTGTG 120  
 CTCCTTACG CAGGTTTGGC TACAAGCTCA GCTTCAAAGG CCAAGGCTG GCATTGCTGT 180  
 GGGCTGGAAT ACCCTTCTGG AGCCATCATG GAGACGCCAT CCTGGGCTG GAGGAAGTGC 240  
 GGCTGACGCC ATCCATGAGG AACCGGAGTG GCGCGTGTG GAGCAGGGCC TCTGTCCCCT 300  
 TCTCTGCCCTG GGAAGTAGAG GTGCAATGA GGGTGACGG ACTGGGCGCC CGGGGAGCCC 360  
 ACCGCATGGC CGTGTGTAC ACCCGGGCA GGGGCCATGT AGGCTCTGT CTTGGGGGGC 420  
 TGGCTTCGTG GGACGGCATC GGGATCTTCT TTGACTCTCC GGCAGAGGAT ACTCAGGACA 480  
 GTCTGCCAT CCGTGTGTG GCCAGCGAC GGCACATCCC CTCTGAGCAG CTGGGGATG 540  
 GAGCTAGCCA AGGGCTGGGC TCCTGTCTATT GGGACTTCCG GAACCGGCCA CACCCCTTCA 600  
 GAGCAGGAT CACCTACTGG GGGCAGAGGC TGCATGTCT CTTGAACAGT GGCCTCACTC 660  
 CCACTGATCC AGGTGAGTTC TGTGTGGATG TGGGGCCCT GCTTTTGGTC CCTGGAGGTT 720  
 TCTTTGGGGT CTCAGCATCC ACCGSCACC TGGCAGATGA TCATGATGTC CTGTCTTCC 780  
 TGACCTTCAG CCTGAGTGAG CCCAGCCCAG AGGTTCCCC TCAGCCCTTC CTGGAGATGC 840  
 AGCAGCTCCG CTGGCGAGG CAGCTGGAAG GGTGTGGGC AAGGCTGGGC TTGGGCACCA 900  
 GGGAGGATGT AACTCCAAA TCAGACTCTG AAGCTCAAAG AGAAGGGGAA AGGCTCTTTG 960  
 ACCTGGAGGA GACGCTGGGC AGACACCGCC GGATCCTGCA GGCTCTGCGG GGTCTCTCCA 1020  
 AGCAGCTGGC CCAGGCTGAG AGACAATGGA AGAAGCAGCT GGGGCCCCCA GGCCAAGCCA 1080  
 GGCCTGACGG AGGCTGGGCC CTGGATGCTT CTGCCAGAT TCCATCCACC CCAGGGAGGG 1140  
 GTGGCCACCT CTCCATGTCA CTCAATAAGG ACTCTGCCAA GGTGGTGGC CTGTCCATG 1200  
 GACAGTGGAC TCTGCTCCAG GCCCTGCAAG AGATGAGGGA TGCAGCTGTC CGCATGGCTG 1260  
 CAGAAGCCCA GGTCTCTTAC CTGCTGTGG GCATTGAGCA TCATTCTTCA GAGCTGGACC 1320  
 ACATCTGGG CCTCTGTCAG GAGGAGCTTC GGGGCCCGGC GAAGGCAGCA GCCAAGGCC 1380  
 CCGGCCACCC TGGCCAGCCC CCAAGGGCCT CCTCGTGCT GCAGCCTGGC ATCTTCTGT 1440  
 TCTACTCTCT CATTGAGACT GTAGGCTTCT TCGGCTACGT GCATTCAGG CAGGAGCTGA 1500  
 ACAAGAGCCT TCAGAGTGT CTGTCCACAG GCAGCCTTCC TCTGGTCTCT GCACCACACA 1560  
 CCCCAGGGC CTGGGGATT CTGAGGAGGC AGCCTCTCCC TGCCAGCATG CCTGCCTGAC 1620  
 CCACCTCAGA GCCTGCTTTG CATCACTGGG AAGCAGGCAG TGTCTTGGT GGGGCTTGG 1680  
 TCAGTATCTCT CTCCTCTGG GTGCCAGCT CCCACGCACA CCTGAGCTTT CGGCATGCTC 1740  
 CCACCTCGTT AAAGTGATT TCCTCTCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1800  
 A 1801

Seq ID NO: C201 DNA Sequence  
 Nucleic Acid Accession #: XM\_117036.1  
 Coding sequence: 25..495

1 11 21 31 41 51  
 | | | | |  
 AGCCAAGAGA GGGGGGACAG ACAGATGGAA AGACGGACAC GGGGAGCTCT GGGGAGCAGG 60  
 CGGCCCCAC CCCCCTTCC AGCTCTGAGA CATTTGTGCA CAGGCCTGCA GCGGCTGGG 120  
 ATGGCTTGGC CGGGCAGCTT CTGGAGACAC ACATGCCAAG GCAGGGCCNG GGCACCCGAG 180  
 GGCCCGTGGG GCGTGTTCCT ACCACACAGG TGCCCGAGGG AGGCAGGGCA GGCCCGGTG 240  
 GGACCCAGCC CCGAAACGCA GGTGTGCGCC CACGTTTGA GCCGCGCTCG CGTGTCCGTG 300  
 GATGAGCGGG AACCGGGGGC CGGCGCTTAC GCAATGCACG TTACGCCCGG GTGGAAGGGG 360  
 TGTACCGCC ACAGCGGCGG CACCGTGGT GGTCTGTTT CCTGGAAACG TCCAGAACAG 420  
 GCAGCCCCG AGACAGGGAG GGGCCAGCG GTGCCAGGG GAAGTGGGGA TGGGAATGAG 480  
 TGGGATGGG GCTGAGGTTT TTCTGAAGG ATGAATGCTC TGAACCTGTG AATAGACACA 540  
 CGGAACCTGT CACGTTTCA GGTGAACCG GTGGGGAGTG AATCCATCTC AACAGAGCTG 600  
 TTACACAGTG AACAGAGCA CGANGGGTGG AGGCCNCTTG TCTGCTCCTG CAGATCGAGC 660  
 CGGCTGCTCA GAGCCGGGAG ATGGCCACTC AGCTCCTTTA ACTG 704

Seq ID NO: C202 DNA Sequence  
 Nucleic Acid Accession #: XM\_167803.2  
 Coding sequence: 1162..1488

1 11 21 31 41 51  
 | | | | |  
 AACATCATAC ATAGTAGGTG AATCGTTTGT TAGAGTGAAG AATGCTAATG TAAAGCAAAT 60  
 AGTCAACCCAC GTTCTTTGTA AATCCAAATG TTTCTATATT GTAGCTTTGC TTTAAATGGG 120  
 GTCGGGCCCA ACTGCATCCT CCTCTTTGGC GGGCTGGGGA GCGGCCCCCA GCGGGGACGG 180  
 GAGGGCAGCG ACCCCGAGGC CTCGTGACG TGGGAGAGAG TGTGGTGGGA AGTCTTGAGC 240  
 GAGGAGGGG ATCTGCCCTT CTCACTTCTT CTCTTGGATC CGCTCGGTT TCTGTCCCC 300  
 CCACACCCG CCTGCCCGC GGAAGACCGC CAGTGAGCC AGCCCCACC TTCCAGGCGC 360  
 CTTGCCCTG GGGATCCAA CAACTTGTAT CGAGTGGGCG GGGCAACGGC TCCCCATTTT 420  
 TCCCGAGCCC CGCCACAGA GCTCTTAGCC AATCCTATGC AGAGAGCATC TCCTGGCAGG 480  
 GGTCTCTTCC CAACCCAGAC ACATTAAGCA CCAGGCTTGG GCTTCCCGAG 540  
 CGCCCCACCA CCACACGTG CAGGTGGAGC TCTGGGATGC TATGTTGGGG CGGCAAGCGG 600  
 TGGCCGAGG GCCGGGTAGG CTAGCACGGG AGGTAAGGGT GGTATGGGAT GGGGCGGGGG 660  
 CGGTCTAGGG CAATGAGAGA GCAGAGAATG GGGGAACCTG AGGGTGGGGG GAGGGCACCG 720

GAGCCTTGCC ACCATCCCAG GACTTTGGGC AAGTCACCCG CACTCCCTGG GCCTCGGTTT 780  
 CCCCATCTGT AAAATGATGG TAATAATACT TCACCTACCT CATAGGGGAG GTTGTGAGGC 840  
 CACCATCACC TGACCTGGGG GTCAAGGCAG GAGGACTCCG AAGGTGCTAC CCGTGAGCAA 900  
 AGTGTAAATTA CCGAAATCCTG ACTGCAAGGC CCACCTGCCC CTCCCCACA GAGCCTCCAG 960  
 AGCTAGCTGA GGCCAACGCA GGCCCATCCG TCTCTTCACT CTGTCGCAGG CCCTTTTCATG 1020  
 GGCTTCGTCT GCCATCTTTG TGGGTGCCCT AGACTTAGTC CTATCTTGT CCTGGTTTCC 1080  
 TTTCTTGTGA CCATCTCCCC ATGAAAGTGC TGTACAAATT CCACCCGCC CAGGACCCCC 1140  
 GCACCTGCCC TCTGGCACC GATGCCAGGG AAGGGACAGA GGAAACAGC CACAAACAAG 1200  
 CCAGGGGGGC TCCCCGGAGC CCCAGGGGTG GGGATTGGTG GCCACTGTTT GTATGTTCTT 1260  
 GAGTGCAAGT GTTTTATAAA AAATAAAACA AAAACCCACC ATCACAAAAA AAAAAATTTT 1320  
 CGAGCGAAGA GAAATGAAGA AAAACTGAAG AAAAAAATAA AACAGGAAAA AAAGAACCAT 1380  
 ACAAAATTTT TCACACACAC ATACCTCTA AGCCAGCAAG ATTTCTCTT TGCAAAATCA 1440  
 TATTTTGTG GGAATGGGCC CTGCTTTTGTG TGCAAGGCC TGTCTGTATT AATAAAGGAT 1500  
 CGTGAAAAAG T 1511

Seq ID NO: C203 DNA Sequence  
 Nucleic Acid Accession #: NM\_024780.1  
 Coding sequence: 31..1023

1 11 21 31 41 51  
 | | | | |  
 ATTAATCTGG CCGTGCCATG CATCTACTCC ATGTTTCAGGC TTGTGGAGAG GTACGAGATG 60  
 CCACGGCACG AAGTCTACGT TCTCCTGATC CGAAACATCT TTTTGAAAAAT ATCAATCATT 120  
 GGCATTCTTT GTTACTATTG GCTCAACACC GTGGCCCTGT CTGGTGAAGA GTGTTGGGAA 180  
 25 ACCTTCATTG GCCAGGACAT CTACCGGCTC CTTCGTATGG ATTTTGTGTT CTCTTTAGTC 240  
 AATTCTCTTC TGGGGGAGTT TCTGAGGAGA ATCATTGGGA TGCAACTGAT CACAAGTCTT 300  
 GGCCTTCAGG AGTTTGACAT TGCCAGGAAC GTTCTAGAAC TGATCTATGC ACAAACTCTG 360  
 GTGTGGATTG GCATCTTCTT CTGCCCTCTG CTGCCCTTTA TCCAAATGAT TATGCTTTTC 420  
 30 ATCATGTTCT ACTCAAAAA TATCAGCCTG ATGATGAATT TCCAGCCTCC GAGCAAAGCC 480  
 TGGCGGGCCT CACAGATGAT GACTTTCTTC ATCTTCTTGC TCTTTTTCCT ATCCTTCACC 540  
 GGGGTCTTGT GCACCCCTGGC CATCACCATC TGGAGATTGA AGCCTTCAGC TGACTGTGGC 600  
 CCTTTCTCAG GTCTGCCTCT CTTCATTTCAC TCCATCTACA GCTGGATCGA CACCCTAAGT 660  
 ACACGGCCTG GCTACCTGTG GGTGTGTTGG ATCTATCGGA ACCTCATGGG AAGTGTGCAC 720  
 35 TTCTTTTCA TCCTCACCTC CATTGTGCTA ATCATCACCT ATCTTTACTG GCAGATCACA 780  
 GAGGGAAGGA AGATTATGAT AAGGCTGCTC CATGAGCAGA TCATTAAATGA GGGCAAAGAT 840  
 AAAATGTTCC TGATGAGAAA ATTGATCAAG CTGCAGGATA TGGAGAAGAA AGCAAAACCC 900  
 AGCTCACTTG TTCTGGAAAG GAGAGAGGTG GAGCAACAAG GCTTTTTCGA TTTGGGGGAA 960  
 CATGATGGCA GTCTTGACTT GCGATCTAGA AGATCAGTTC AAGAAGGTAA TCCAAGGGCC 1020  
 40 TGATGACTCT TTTGGTAACC AGACACCAAT CAAATAAGGG GAGGAGACGA AAATGGAATG 1080  
 ATTTCTTCCA TGCCACCTGT GCCTTTAGGA ACTGCCCAGA AGAAATCCA AGGCTTTAGC 1140  
 CAGGAGCCGA AACTGACTAC CATGTAATTA TCAAAGTAAA ATTGGGCATT CCATGCTATT 1200  
 TTTAATACCT GGATTGCTGA TTTTTCAGA CAAAATACTT GGGGTTTTCC AATAAAGATT 1260  
 GTTGTAATAT TGAAATGAGC CTACAAAAAC CTAGGAAGAG ATAAGTGGG AATAATGTAT 1320  
 45 ATTAATCTTA AGAAGTGTGT GCAGGAATGA TTGGTTCTTA GAAATCTCTC CTGCCAGACT 1380  
 TCCCAGACCT GGCAAGGTT TAGAAACTGT TGCTAAGAAA AGTGGTCCAT CCTGAATAAA 1440  
 CATGTAATAC TCCAGCAGGG ATATGAAGCC TCTGAATTGT AGAACCTGCA TTTATTTGTG 1500  
 ACTTTGAAC TAAAGCATCC CCCATGTCCC AAAGGTGGAA TACAACCAGA GGTCTCATCT 1560  
 CTGAACCTTC TTGCGTACTG ATTACATGAG TCTTTGGAGT CGGGGATGGA GGAGGTTCTG 1620  
 50 CCCCTGTGAG GTGTTATACA TGACCATCAA AGTCCTACGT CAAGCTAGCT TTGCACTGGC 1680  
 AGTACCGTAG CCAATGAGAT TTATCCGAGA CGCGATTATT GCTAATTGGA AATTTTCCCA 1740  
 ATACCCACCC GTGATGACTT GAAATATAAT CAGCGCTGGC AATTTTGTAG AGTCTCTACG 1800  
 GAGACTGAAT AAG 1813

Seq ID NO: C204 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 AGCGGGGTTA GATGCAGGGA GTTATGTTGT GATTTGTGTA GGGGTGGCTT TGGTGAGCTC 60  
 ATCCTGGCAT TTTAAAAATA ATGTGAATGG TGTATCCCTT TGTGATCATC ATCACTTTTT 120  
 CCCTGCGAGT CCAATCAAT GCGGGTGTGA CTGCTGTATG AAGTCTCAGG AAGCCCACCC 180  
 CAGTGGAGAA GAAGGCTTGC AGGAGGCAGG AGATGCTGTC CGATGACCAC GTGAATGAAA 240  
 TCATCATACA GGTGAGAAAT GTTTCCTCTG GGGTCCAAAG CCACCCATCC TCAATCAGA 300  
 65 TTTTCAAGA AAAGGTGCTG CTAGACTCAA GCATCAACAT GGTTTTGTCA ATATCTGACA 360  
 TTGATGTGAT AGACTCTCAG ACAGTCAGCA AAAGGAATGA CCAAAAGGGT AACCAGGTGC 420  
 TCGGGTTTTT AACATCTTTG AATGAGTCGA TGTCTCAGAC CCTTCATAGC CTAGAATGCA 480  
 TGGGCATAGA CACTCCTGGT TCTTCACATG AAACTGTTCA AGGACAGAAG TTAATCGCAT 540  
 CCCTTATACC CATGACATCC AGAGACAGAA TTAAAGCCAT CAGGAACCCAG CCAAGGACCA 600  
 70 TGGAAGAGAA AAGGAACCTT AGGAAAATAG TTGACAAAGA AAAAAAGCAA CAGACCCATC 660  
 GTATCCTTCA GCTCAATTGC TGTATTAGT GTCTGAACTC CATTTCCTCG GCTTATCGGA 720  
 GATCCAAGAA CAGCCTGTGC GAAATTCTGA ATTCCATCAG CCTGTGGCAG AAGACGCTGA 780  
 AGATCATTGG AGGCAAGTTT GGAACACGCG TCCTCTCCTA TTTCAACTTT CTGAGATGGC 840  
 75 TTTTGAAGTT CAACATTTTC TCATTATCC TGAACCTCAG CTTCATCATA ATCCCTCAGT 900  
 TTACCGTGGC CAAAAAGAAC ACCCTCCAGT TCACTGGGCT GGAGTTTTTC ACTGGGGTGG 960  
 GTTATTTTGA GGACACAGTG ATGTACTATG GCTTTTACAC CAATTCACCC ATCCAGCAGC 1020  
 GGAACAGCGG GGCATCCTAC AACATGCAGC TGGCCTACAT CTTCACAATC GGAGCATGCT 1080  
 TGACCACTGT CTCTTCTCAG TTGCTGTTCA GCATGGCCAA GTATTTCCCG AACAACCTCA 1140  
 80 TTAATCCCCA CATTTACTCC GGAGGGATCA CCAAGCTGAT CTTTGTCTGG GACTTCACTG 1200  
 TCACTCATGA AAAAGCTGTG AAGCTAAAAC AGAAGAATCT TAGCACTGAG ATAAGGGAGA 1260  
 ACCCTGTGCA GCTCCGTCAG GAGAATTCCA AGTTGACGTT CAATCAGCTG CTGACCCGCT 1320  
 TCTCTGCCTA CATGGTAGCC TGGGTGTGCT CTACAGGAGT GGCCATAGCC TGCTGTGCGA 1380  
 CCGTTTATTA CTTGGCTGAG TACAACCTAG AGTTCTGTAA GACACACAGT AACCCCTGGG 1440  
 CGGTGCTGTT ACTGCCTTTC GTTGTGTCTT GCATTAATCT GGCCGTGCCA TGCATCTACT 1500  
 CCATGTTTCA GCTTGTGGAG AGGTACGAGA TGCCACGGCA CGAAGTCTAC GTTCTCTGTA 1560

TCCGAAACAT CTTTGTGAAA ATATCAATCA TTGGCATCTT TTGTTACTAT TGGCTCAACA 1620  
 CCGTGGCCCT GTCTGGTGAA GAGTGTGGG AAACCCCTCAT TGGCCAGGAC ATCTACCGGC 1680  
 TCCTTCTGAT GGATTTTGTG TTCTCTTTAG TCAATTCCTT CCTGGGGGAG TTCTGAGGA 1740  
 GAATCATTTG GATGCAACTG ATCACAAGTC TTGGCCTTCA GGAGTTTGAC ATTGCCAGGA 1800  
 5 ACCTTCTAGA ACTGATCTAT GCACAAACTC TGGTGTGGAT TGGCATCTTC TTCTGCCCCC 1860  
 TGCTGCCCTT TATCCAAATG ATTATGCTTT TCATCATGTT CTACTCCAAA AATATCAGCC 1920  
 TGATGATGAA TTTCCAGCCT CCGAGCAAAG CCTGGCGGGC CTCACAGATG ATGACTTTCT 1980  
 TCATCTTCTT GCTCTTTTTC CCATCCTTCA CCGGGGTCTT GTGCACCCTG GCCATCACCA 2040  
 10 TCTGGAGATT GAAGCCTTCA GCTGACTGTG GCCCTTTTTC AGGTCTGCCT CTCTTCATT 2100  
 ACTCCATCTA CAGCTGGATC GACACCTTAA GTACACGGCC TGGCTACCTG TGGGTGTGTT 2160  
 GGATCTATCG GAACCTCATT GGAAGTGTGC ACTTCTTTT CATCCTCACC CTCAATTGTG 2220  
 TAATCATCAC CTATCTTTAC TGGCAGATCA CAGAGGGAAG GAAGATTATG ATAAGGCTGC 2280  
 TCCATGAGCA GATCATTAAAT GAGGGCAAAG ATAAATGTT CCTGATAGAA AAATGATCA 2340  
 15 AGCTGCAGGA TATGGAGAA GAAAGCAAAC CCAGCTCACT TGTCTTGAA AGGAGAGAGG 2400  
 TGGAGCAACA AGGCTTTTTC CATTGGGGG AACATGATGG CAGTCTTGAC TTGCGATCTA 2460  
 GAAGATCAGT TCAAGAAAGT AATCCAAGGG CCTGATGACT CTTTGTGTAA CCAGACACCA 2520  
 ATCAAATAAG GGGAGGAGAY GAAATGGA TGATTTCTTC CATGCCACCT GTGCCTTTAG 2580  
 GAACCTGCCCA GAAGAAATAT CAAGGCTTTA GCCAGGAGCG GAAACTGACT ACCATGTAAT 2640  
 TATCAAAGTA AAATTTGGGCA TTCCATGCTA TTTTAAATAC CTGGATTGCT GATTTTCAA 2700  
 20 GACAAAATAC TTGGGGTTTT CCAATAAGA TTGTGTAAAT ATTGAAWRA RMMWAMAAA 2760  
 ACCTAGGAAG AGATAACTAG GGAATAATGT ATATTATCTT CAAGAAGTGT GTGCAGGAAT 2820  
 GATTGGTTCT TAGAAATCTC TCCTGCCAGA CTTCACGAGC CTGGCAAAGG TTTAGAAACT 2880  
 GTTGTCTAAGA AAAGTGGTCC ATCCTGAATA AACATGTAAT ACTCCAGCAG GGATATGAAG 2940  
 25 CCTCTGAATT GTAGAACCTG CATTATTATT TGACTTTGAA CTAAGACAT CCCCATGTC 3000  
 CCAAAGGTGG AATAACAACA GAGGTCTCAT CTCGAACTT TCTTGCCTAC TGATTACATG 3060  
 AGTCTTTGGA GTCCGGGATG GAGGAGGTTT TGCCCTGTG AGGTGTTATA CATGACCATC 3120  
 AAAGTCCTAG GTCAGCTAG CTTTGCACTG GCAGTACCGT AGCCAATGAG ATTTATCCGA 3180  
 GACGCGATTA TTGCTAAATT GAAATTTTCC CAATACCCCA CCGTGATGAC TTGAAATATA 3240  
 30 ATCAGCGCTG GCAATTTTTC ACAGTCTCTA CGGAGACTGA ATAAG 3285

Seq ID NO: C205 DNA Sequence  
 Nucleic Acid Accession #: NM\_002250.1  
 Coding sequence: 397..1680

35 1 11 21 31 41 51  
 | | | | |  
 GTCTTCGGT GTCTGGGTGT GGTGAGTAGA GGTGTGTGTC ACAAAGTACA GACCATTGTG 60  
 TGTGACAAAG CCCATCGTGT GTCTGTGTGT GTCTTTATCC ACGTGGATGG ACGTCTCTTT 120  
 40 CTGTCTCTGC CCCAAGACAC ACCCTAGCCC CTCCTTATTC TCAAAGGGG GAGCTGGGGA 180  
 GCCTCCCCCT ACCCTGGGGC CTCCTCTGCC CCTCCCCGCC CTGCTTGGCC GTCACCACTC 240  
 CCGAGAGGGC ACAGGGCTCT GCTGTGCCTC AGAGCAAAG TCCCAGAGCC AGCAGAGCAG 300  
 GCTGACGACC TGCAAGCCAC AGTGGCTGCC CTGTGCGTGC TGGGAGGTGG GGGACCCTGG 360  
 GCAGGAAGCT GGCTGAGCCC CAAGACCCCG GGGGCCATGG GCGGGGATCT GGTGCTTGGC 420  
 45 CTGGGGGCTT TGAGAGCCCG AAAGCGCTTG CTGGAGCAGG AGAAGTCTCT GCCTGGCTGG 480  
 GCACTGGTGC TGGCAGGAAC TGGCATTGGA CTCATGGTGC TGATGTCAGA GATGCTGTGG 540  
 TTCGGGGGGT GCTCGTGGGC GCTCTACCTG TTCTGTGTTA AATGCACGAT CAGCATTTC 600  
 ACCTTCTTAC TCCTCTGCCT CATCGTGGCC TTTCATGCCA AAGAGGTCCA GCTGTTTCATG 660  
 ACCGACAAAG GGCTGCGGGA CTGGCGCGTG GCGCTGACCG GCGCGCAGG GCGCGAGATC 720  
 50 GTGCTGGAGC TGGTGGTGTG TGGGCTGCAC CCGCGCGCCG TCGGGGGCCC GCGTGCCTG 780  
 CAGGATTTAG GGGCGCCGCT GACCTCCCCG CAGCCCTGGC CGGATTCCT GGGCCAGGG 840  
 GAAGCGCTGC TGTCCTGGC CATGCTGTGT CGTCTCTACC TGGTGCCTCG CGCCGTGCTC 900  
 CTGCGCAGCG GCGTCTGCT CAACGCTTCC TACCGCAGCA TCGGCGCTCT CAATCAAGTC 960  
 CGCTTCCGCC ACTGGTTCTG TGCCAAAGCT TACATGAACA CGCACCTGG CCGCTGCTG 1020  
 55 CTCGGCCTCA CGCTTGGCCT CTGGCTGACC ACCGCTGGG TGCTGTCCGT GGCCGAGAG 1080  
 CAGGCTGTTA ATGCCACTGG GCACCTTTCA GACACACTTT GGCTGATCCC CATCACATTC 1140  
 CTGACCATCG GCTATGCTGA CGTGGTGCCG GGCACCATGT GGGGCAAGAT CGTCTGCCCT 1200  
 TGCACCTGGG TCATGGGTGT CTGCTGCACA GCCCTGCTGG TGGCCTGGT GGCCCGGAAG 1260  
 CTGGAGTTTA ACAAGGCAGA GAAGCACGTG CACAACCTCA TGATGGATAT CCAGTATACC 1320  
 60 AAAGAGATGA AGGAGTCCGC TGCCCGAGTG CTACAAGAAG CCTGGATGTT CTACAAACAT 1380  
 ACTCGCAGGA AGGAGTCTCA TGCTGCCCG AGGCATCAGC GCAAGCTGCT GGCCCGCATC 1440  
 AACCGCTTCC GCCAGGTGCG GCTGAAACAC CGGAAGCTCC GGAACAAGT GAACTCCATG 1500  
 GTGGACATCT CCAAGATGCA CATGATCCTG TATGACCTGC AGCAGAATCT GAGCAGCTCA 1560  
 CACCGGGCCC TGGAGAAACA GATTGACACG CTGGCGGGGA AGCTGGATGC CTGACTGAG 1620  
 65 CTGCTTAGCA CTGCCCTGGG GCCGAGGCAG CTTCAGAAC CCAGCCAGCA GTCCAAGTAG 1680  
 CTGGACCCAC GAGGAGGAAC CAGGCTACTT TCCCCAGTAC TGAGGTGGTG GACATCGTCT 1740  
 CTGCCACTCC TGACCCAGCC CTGAACAAAG CACCTCAAGT GCAAGGACCA AAGGGGGCCC 1800  
 TGGCTTGGAG TGGGTGGGCT TGCTGATGGC TGCTGAGGGG GACGCTGGCT AAAGTGGGTA 1860  
 70 GGCTTGGCC CACCTGAGGC CCCAGGTGGG AACATGGTCA CCCCCACTCT GCATACCCCTC 1920  
 ATCAAAACA CTCTCACTAT GCTGCTATGG ACAGCTTCCA GCTCTCAGTT ACAAGTGCAG 1980  
 GCGACTGGAG CAGGACTCTC TGGGTCCCTG GGAAGAGGG TACTAGGGG CCGGATCCAG 2040  
 GATTCTGGGA GGCTTCAAGT ACCGCTGGCC GAGCTGAAGA ACTGGGTATG AGGCTGGGGC 2100  
 GGGGCTGGAG GTGGCGCCCC CTGGTGGGAC AACAAAGAGG ACACCATTTT TCCAGAGCTG 2160  
 CAGAGAGCAC CTGGTGGGGA GGAAGAAGTG TAACCTACCA GCCTCTGCTC TTATCTTTGT 2220  
 75 AATAAATGTT AAAGCCAG 2238

Seq ID NO: C206 DNA Sequence  
 Nucleic Acid Accession #: NM\_025257.1  
 Coding sequence: 1..2139

80 1 11 21 31 41 51  
 | | | | |  
 ATGGGGGGAA AGCAGCGGGA CGAGGATGAC GAGGCCTACG GGAAGCCAGT CAAATACGAC 60  
 CCCTCTTTTC GAGGCCCCAT CAAGAACAGA AGCTGCACAG ATGTCATCTG CTGCGTCTCT 120  
 TTCCTGCTCT TCATCTCTAG TTACATCGTG GTGGGGATTG TGGCCTGGTT GTATGGAGAC 180

5  
 10  
 15  
 20  
 25  
 30  
 35

```

CCCCGGCAAG TCCTCTACCC CAGGAAGCTCT ACTGGGGCCT ACTGTGGCAT GGGGGAGAAC 240
AAAGATAAGC CGTATCTCCT GTACTTCAAC ATCTTCAGCT GCATCCTGTC CAGCAACATC 300
ATCTCAGTTG CTGAGAACGG CCTACAGTGC CCCACACCCC AGGTGTGTGT GTCTCTCTGC 360
CCGGAGGACC CATGGACTGT GGGAAAAAAC GAGTTCTCAC AGACTGTTGG GGAAGTCTTC 420
TATACAAAAA ACAGGAACTT TTGTCTGCCA GGGGTACCCCT GGAATATGAC GGTGATCACA 480
AGCCTGCAAC AGGAAGCTCTG CCCAGTTTC CTCTCCCTCT CTGCTCCAGC TCTGGGACGC 540
TGCTTTCCAT GGACCAACAT TACTCCACCG GCGCTCCAG GGATCACCAA TGACACCACC 600
ATACAGCAGG GGATCAGCGG TCTTATTGAC AGCCTCAATG CCCGAGACAT CAGTGTTAAG 660
ATCTTTGAAG ATTTTGCCCA GTCTCTGGTAT TGGATTCTTG TTGCCCTGGG GGTGGCTCTG 720
GTCTTGAGCC TACTGTTTAT CTTGCTTCTG CGCCTGGTGG CTGGGCCCCCT GGTGCTGGTG 780
CTGATCTCTG GAGTGTCTGG CGTGTGCCA TATGGCATCT ACTACTGCTG GGAGGAGTAC 840
CGAGTGTCTG GGGACAAGGG CGCCTCCATC TCCCAGCTGG GTTTCACCAC CAACCTCAGT 900
GCCTACCAGA GCGTGCAGGA GACCTGGCTG GCCGCCCTGA TCGTGTGGC GGTGCTTGAA 960
GCCATCTCTG TGCTGGTGCT CATCTTCCCT CGGCAGCGGA TTCGTATTGC CATCGCCCTC 1020
CTGAAGGAGG CCAGCAAGGC TGTGGGACAG ATGATGTCTA CCATGTTCTA CCCACTGGTC 1080
ACCTTTGTCC TCCTCTCAT CATGCAATGCC TACTGGGCCA TGACTGCTCT GTATCCTCTG 1140
CCCACGACG CAGGCATCTT TGGATATGTG CTCTGGGCAT CCAACATCAG CTCCTCCGGC 1200
TGTGAGAAAG TGGCAATAAA TACATCATGC AACCCACGG CCCACCTGT GAACTCCTCG 1260
TGCCAGGGC TGATGTGCGT CTTCCAGGGC TACTCATCCA AAGGCCATA CCAACGTCT 1320
GTCTTCAATC TGCAATCTA TGGGGTCTCT GGGCTCTTCT GGACCTTAA CTGGGTACTG 1380
GCCCTGGGCC AATGCGTCTT CGCTGGAGCC TTTGCCCTCT TCTACTGGG CTTCCACAAG 1440
CCCCAGGACA TCCCTACCTT CCCCTTAATC TCTGCCCTCA TCCGCACACT CCGTTACCAC 1500
ACTGGGTCTT TGGCATTTGG AGCCCTCATC CTGACCCCTG TGCAATAGC CCGGGTCATC 1560
TTGGAGTATA TTGACCACAA GCTCAGAGGA GTGCAGAAC CTGTAGCCCG CTGCATCATG 1620
TGCTGTTTCA AGTGTCTGCT CTGTGTCTG GAAAAATTTA TCAAGTCTCT AAACCGCAAT 1680
GCATACATCA TGATCGCCAT CTACGGGAAG AATTTCGTG TCTCAGCCAA AATGCGTTC 1740
ATGCTACTCA TGCGAAACAT TGTCAAGGTG GTCTCTCTGG ACAAGTCTAC AGACCTGCTG 1800
CTGTCTTTTG GGAAGCTGCT GGTGGTCTGA GCGTGGGGG TCCTGTCTCT CTTTTTTTTC 1860
TCCGTCGCA TCCGGGGGCT GGGTAAAGAC TTTAAGAGCC CCCACCTCAA CTATTACTGG 1920
CTGCCCATCA TGACCTCATC CCTGGGGGCC TATGTCTATG CCACGCGCTT CTTGAGCGTT 1980
TTCCGCAATG GTGTGGACAC GCTCTTCTCT TGCTTCTCTG AAGACCTGGA GCGGAACAAC 2040
GGCTCCCTGG ACCGCCCTCA CTACATGTCC AAGAGCCTTC TAAAGATTCT GGGCAAGAAG 2100
AACGAGGCGC CCCCAGGACA CAAGAAGAGG AAGAAGTGAC AGCTCCGGCC CTGATCCAGG 2160
ACTGCACCCC ACCCCACCG TCCAGCCATC CAACCTCACT TCGCCTTACA GGTCTCCATT 2220
TTGTGGTAAA AAAAGGTTT AGGCCAGGCG CCGTGGCTCA GCGCTGTAAT CCAACACTTT 2280
GAGAGGCTGA GCGGGCGGA TCACCTGAGT CAGGAGTTTC AGACCAGCT GGGCAACATG 2340
GTGAAAC
  
```

Seq ID NO: C207 DNA Sequence  
 Nucleic Acid Accession #: NM\_016180.1  
 Coding sequence: 26..1618

45  
 50  
 55  
 60  
 65  
 70

```

1 11 21 31 41 51
CAGGAAGGTT CCTCTCCCAG TGGCCATGGG TAGCAACAGT GGGCAGGCTG GCCGCCACAT 60
CTATAAATCC CTAGCTGATG ATGGCCCTCT TGACTCTGTG GAGCCGCTTA AAAGACCCAC 120
CAGCAGACTC ATCATGCACA GCATGGCCAT GTTCGGAAGA GAGTTCTGCT ACGCGGTGGA 180
GGCAGCGTAT GTGACCCAG TCCTGCTCAG CGTAGGCTCT CCCAGCAGCC TGTACAGCAT 240
TGTTGTGGTT CTCAGCCCCA TCCTGGGATT CTGTCTGCAG CCCGTGGTCT GATCGGCCAG 300
CGACCACTGC CGTCCAGGT GGGGCCGCGG GAGACCTTAC ATCCTCACCC TGGGAGTCAT 360
GATGCTCGTG GGCATGGCTC TGTACCTCAA TGGGGCTACT GTTGTAGCAG CTTTGATTGC 420
TAACCCRAGG AGGAAGCTGG TTTGGGCGAT AAGTGTCAAC ATGATAGGTG TCGTTCTCTT 480
TGATTTTGCT GCCGACTTCA TTGATGGGCC CATCAAAGCC TACTTATTTG ATGTCTGCTC 540
CCATCAGGAC AAGGAGAAGG GCCTCCACTA CCATGCCCTC TTCACAGGTT TTGGAGGTGC 600
CCTGGGTTAC CTTTTGGGTG CTATAGACTG GGCCCATCTG GAGCTGGGAA GACTGTTGGG 660
TACAGAATTC CAGGTCTGCT TCTTCTCTC TGCAATGGTG CTCACTTTGT GTTTTACTGT 720
TCATCTGTGC AGTATCTCTG AAGCCCACT TACAGAGGTT GCAAAGGGA TTCCCCACA 780
GCAAACCCCT CAGGACCCCT CATTTGTCAT AGATGGAATG TACGAGTATG GTTCTATCGA 840
GAAAGTTAAA AATGGTTACG TAAATCCAGA GCTGGCAATG CAGGGAGCAA AAAACAAAAA 900
TCATGCTGAA CAGCTCGCA GGGCAATGAC ATTAAGTCA CTGCTGAGC CACTGGTGAA 960
CATGCCCTCT CACTACCGCT ACCTTTGCAT CAGCCACCTC ATTGGATGGA CGGCCTTCCT 1020
GTCCAACATG CTGTTCTTCA CAGATTTTCT GGGCCAGATT GTGTACCGCG GGGATCCCTA 1080
TAGTGCACAC AACTCCACAG AGTTTCTCAT CTACGAAAGA GGAGTCGAGG TTGGATGTTG 1140
GGGCTTCTGC ATCAACTCCG TGTTTTCTCT ACTTTATTCT TACTTTTCTA AAGTTTGGT 1200
ATCTACATT GATTAAAGG GTCTTTACTT CACGGGATAT TTGCTGTTG GCCTGGGGAC 1260
GGGATTTATT GGGCTCTTCC CGAATGTCTA CTCCACCCTG GTCTGTGCA GCCTGTTTGG 1320
TGTAATGTCC AGCACCTGT ACCTGTGCC CTTTAACTCT ATTACTGAGT ACCACCGCGA 1380
GGAAGAAAAG GAGAGGCAGC AGGCCCCAGG AGGGGACCCA GACAACAGCG TGAGAGGGAA 1440
GGGCTATGAC TGCGCCACCC TCACATGCAT GGTGCAGCTG GCTCAGATCC TGGTCGGAGG 1500
TGGCCTGGGC TTTCTGTGCA ACACAGCCGG GACCGTTGTC GTTGTGGTGA TCACAGCGTC 1560
TGCGGTGGCA CTGATAGGCT GTTGTCTTGT CGCTCTCTT GTTAGATATG TGGATTAGGT 1620
CAATAAAGAG ACAATGACCC TAAAAAATAA
  
```

Seq ID NO: C208 DNA Sequence  
 Nucleic Acid Accession #: NM\_003273.1  
 Coding sequence: 255..2024

80

```

1 11 21 31 41 51
CGCCGCGGGG CCGGATCCTC CGCGCGGCCG AGTCCATCTC CTGGGAAATG GGGCGGACAG 60
TGTTTCTTGT ACTGACTATT GTGAGCGCCC TCTCTCTCCG GCGGAGCGGA GACCATGGCC 120
CCCACTCAGG CCCCCGGGCC CCGCTGGAAT TCGGAGGGCC CCTGGGTAAT GGGGACAGAG 180
GATGGGACCT GGGGCAAGAG CTAAGCGAAG GAGAGCTGGA GCGGGTGAAC TAAGAGCGGG 240
GGCGAGATCT GAGGATGGAA GGCTTTGGGG GTGTCCGAGG CAGAGGGACC CCGGGGTTTG 300
  
```



CAGCGAAGGG TGTCTGGAGA GGGAGAGCTG AGGAGGGGCC GGTTCCTGGGG GCTGCAGAAC 360  
 GGGGATTTAT GGTGTGCACT GGGAGCAGGA GGAGGGTCTT CGAGGGGCCT GGGGGCGGGG 420  
 GACTAAGATG GACGCTCTGGG AAGGGAACTG GGAGGCAGCG GGGTGCTCTGG GGGCCGAGGG 480  
 CTGAGGACGG GGTGCGGAGG CGCACTCTGG GAATGCCGAG AGGGTCCCGC AGAGACGTCA 540  
 GGGCGCCGTG CGGGCCGGCG GGGAGCTGGG GGGCTAGGGG GGGACGCCGA CGTGATGGCC 600  
 CTTCGCCGAG GCGCCCGCGC TCTGCTACTG CTGCTGCCCC CCACCATGTT CCACCTGCTC 660  
 CTGGCGGCCC GTTCGGGCCC CGCGCGCTG CTGGGTCCAC CCGGTCCCTC GCCCGGGCTG 720  
 GAGGTGCTGT GGAGCCACG GCGCGTCTG CTGTGGCTCG CTFGGCTCGG CTGCGAGGCG 780  
 GCCTCTTACC TACTGCCGGC GCGCAAGGTG CGGGCCCCGC TCGCGGACGC TCGGGGGAGG 840  
 GAAGCGAATG GGCTCGCGA GGGAAAGGAC GCCCGGGGCC TTATCAGAGC CCCCTTGGAC 900  
 CCGCAGTGGC CGAGGGGCGA GAATTGAAGG ACAAGAGTCG CTGCGCTAT CCTATTAAACG 960  
 GCTTCCAGGC CCTGGTGCTG ACAGCCCTGT TGGTGGGGCT GGGGATGTCA GCGGGGCTGC 1020  
 CTCTGGGGGC GCTCCCGGAA ATGCTCCTGC CCTGGGCTT TGTGCGCACC CTCACCGCTT 1080  
 TCATCTTCAG CCTCTTCTC TACATGAAGG CGCAGGTAGC CCCAGTTTCG GCCCTGGCAC 1140  
 CTGGGGGAA CTTAGGCAAT CCGATTACG ACTTTTCTT GGGACGAGAG CTCACCCCTC 1200  
 GTATCTGTTT CTTCGACTTC AAATATTCT GTGAAGTGG ACCCGGCTC ATCGGCTGGG 1260  
 TCCTCATCAA CCTGGCCCTG TTGATGAAGG AGGCAGAGCT TCGAGGCAGT CCCTCACTGG 1320  
 CCATGTGGCT GGTCAATGGC TTCCAGTTGC TCTACGTGGG TGATGCCCTC TGGCACGAGG 1380  
 AGGCCGTCTT CACCACCATG GATATCACAC ATGACGGGTG TGGCTTCATG CTGGCGTTTG 1440  
 GGGACATGGC CTGGGTGCC TTCACTTACA GCCTGCAGGC CCAGTTCTTG CTGCACCACC 1500  
 CGCAGCCCTT GGGGTTGCC ATGGCTCTG TCATCTGCCT CATCAATGCT ACTGGTTACT 1560  
 ACATCTTCCG TGGGGCGAAT TCCAGAAAA ACATTTTCCG AAAGAACTCT TCTGACCCCA 1620  
 GAGTGGCTGG GCTTGAGACC ATCTCTACAG CCACAGGCG GAAACTGCTG GTGTCTGGGT 1680  
 GGTGGGGTAT GGTCCGCCAT CCCAACTATC TTGAGACCT CATCATGGCT CTGGCTTGGT 1740  
 CCTTGCCTTG CGGGGTGTCA CACTGTGTC CCTACTTCTA CCTCTCTAC TTCACCGCGC 1800  
 TGCTGGTGCA CCGTGAGGCC CGGGATGAGC GGAGTGCTG CAGAAGTACG GCCTGGCCTG 1860  
 GCAGGAGTAC TGCCGGCGTG TGCTTACCG CATCATGCC TACATCTACT GAAGCGGCTC 1920  
 CACCACCCCA GGTGGGCGAT GTGCCACTC ATCCACCAG ACACCCAGGA CCAGGAGCCT 1980  
 CGACACACTT GGGACTCAAG GGCTTGACCC CCACCCAGCC CTGAGGATGA ACAACCTCAG 2040  
 AGAAGAGGTG GTTTAGAGCA AGGAAAAAAA TGAAACCAGT GACCAAAAAA AAAAAAAA 2100

Seq ID NO: C209 DNA Sequence  
 Nucleic Acid Accession #: NM\_015720.1  
 Coding sequence: 21..1838

1 11 21 31 41 51  
 | | | | |  
 CCAGTTCGG CACGAGGACC ATGGGCGGGC TGCTGCGGGC CGCCCGGCTG CCGCCGCTGC 60  
 TTTCGCCGT GCTGCTTCTG CTGGTTGGGG GAGCGTTCTT GGGTGCTTGT GTGGCTGGGT 120  
 CTGATGAGCC TGGCCGAGAG GGCCTCACCT CCACCTCCCT GCTAGACCTC CTGTGCCCA 180  
 CTGGCTTGA GCCACTGGAC TCAGAGGAGC CTAGTGAGAC CATGGGCTG GAGCTGGGC 240  
 TGGGAGCCCC TGGCTCAGGC TTCCCGAGCG AAGAGAATGA AGAGTCTCGG ATTCTGCAGC 300  
 CACCACAGTA CTTCTGGGAA GAGGAGGAAG AGCTGAATGA CTCAGTCTG GACCTGGGAC 360  
 CCACCTGAGA TTATGTTTTT CTGACTTAA CTGAGAAGGC AGGTTCCATT GAAGACACTA 420  
 GCCAGGCTCA AGAGCTGCCA AACCTCCCCT CTCCTTGCC CAAGATGAAT CTGGTTGAGC 480  
 CTCCTTGGCA TATGCTTCCC AGAGAGGAGG AAGAAGAGGA AGAGGAAGAG GAGGAGAGGG 540  
 AGAAGGAAGA GTTAGAGAAA CAAGAGGAGG AGGAAGAGGA GGAGCTGCTC CTTGTGAATG 600  
 GATCCCAAGA AGAAGCCAAG CCTCAGGTCC GTGACTTTT TCTCACCAGC AGCAGCCAGA 660  
 CCCCAGGGGC CACCAAAAGC AGGCATGAAG ACTCCGGGGA CCAGGCTCA TCAGGTGTGG 720  
 AGGTGGAGAG CAGCATGGGG CCCAGCTTGC TGCTGCCTTC AGTCACCCCA ACTACAGTGA 780  
 CTCGCGGGGA CCAGGACTCC ACCAGCCAAG AGGCAGAGGC CACAGTGCTG CCAGCTGCAG 840  
 GGCTTGGGT AGAGTTCGAG GCTCCTCAGG AAGCAAGCGA GGAAGCCACT GCAGGAGCAG 900  
 CTGGTTTGTG TGGCCAGCAC GAGGAGGTGC CGGCTTGCC TTCATTCCCT CAAACCAAG 960  
 CTCCTCAGTG GGCAGGACAC CCAGATGAAG ATCCCCTTGG CTCTAGAACC TCAGCTCTT 1020  
 CCCCAGTGG CCTTGAGAG ATGGAATGA CACCTTCCCT TGCTACCTTG GACCAAGAAG 1080  
 ATCTCAACCA GCAGTCTCTA GAAGGCGAGG CAGCTGAAGC TCAATCCAGG ATACCTTGG 1140  
 ATTCTACGCA GGTGATCTGC AAGGACTTGA GCAATCTGGC TGGGAAAAAC TACATCATT 1200  
 TGAACATGAC AGAGAACATA GACTGTGAGG TGTTCGGCA GCACCGGGG CCACAGCTCC 1260  
 TGGCCCTGGT GGAAGAGGTG CTGCCCCGCC ATGGCAGTGG CCACCATGGG GCCTGGCACA 1320  
 TCTCTGTAG CAAGCCAGC GAGAAGGAGC AGCACCTTCT CATGACACTG GTGGGCGAGC 1380  
 AGGGGTGGT GCCCACTCAA GATGTCTTTT CCATGCTGGG TGACATCCGC AGGAGCCTGG 1440  
 AGGAGATTGG CATCCAGAAC TATTCCACAA CCAGCAGCTG CCAGGCGCGG GCCAGCCAG 1500  
 TCGCAGCGA CTACGCGACG CTCTTCGTGG TGCTGGTGGT CATTTGGGGC ATCTGCATCA 1560  
 TCATCATTGC GCTTGGCCTG CTCTACAACT GCTGGCAGCG CCGGTGCCCC AAGCTCAAGC 1620  
 ACGTGTGCGA CGGCGAGGAG CTGCGCTTCG TGGAGAACGG CTGCCACGAC AACCCACGCG 1680  
 TGGACGTGGC CAGCGACAGC CAGTCGAGG TGCAGGAGAA GCACCCAGC CTGAACGGCG 1740  
 GCGGGGCCCT CAACGGGCCG GGGAGCTGGG GGGCGCTCAT GGGGGGCAAG CGGGACCCCG 1800  
 AGGACTCGGA CGTGTTCGAG GAGGACACGC ACCTGTGAGC GCAGCGAGGC GCAGGCGGAG 1860  
 TGGGCGGCCA GGACCAAGCG AGGTGGACCC CGAAACGGAC GGCCTGGAGC CCGCACCAGC 1920  
 CCGCGCGCTA CCGGGCCGCG CCGCGCGCTG GCCTCGGCG CGGGCTCCTT CCGCTTCCC 1980  
 CCGACTTCA ACGGCGGCTT CGGACCAACT CCTCACTCC CGCCCGAGGG CGAGGCTTCA 2040  
 AAGCCCGCTT TGGCCCGCTT TTCCCGCCCC TGAACCCCGG CCGCGCGGGC GCGGGCGCGC 2100  
 CTCCTGCGC CCGGGGACTC AATTAACCC GCGCGGAGAC CAGCGGGGCC CAGCGAAAAA 2160  
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 2220  
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 2269

Seq ID NO: C210 DNA Sequence  
 Nucleic Acid Accession #: NM\_001197.3  
 Coding sequence: 61..543

1 11 21 31 41 51  
 | | | | |  
 GACACGAAGC TCCCCGGGTG GCTTACAGAC GCTGCCAGCA TCGCCGCCGC CAGAGGAGAA 60  
 ATGTTGAAG TAAGACCCCT CTCCAGAGAC ATCTTGATGG AGACCTTCT GTATGAGCAG 120

CTCTTGGAA CCCCCGACCAT GGAGGTTCTT GGCATGACTG ACTCTGAAGA GGACCTGGAC 180  
 CCTATGGAGG ACTTCGATTC TTTGGAATGC ATGGAGGGCA GTGACGCATT GGCCTGCGG 240  
 CTGGCCTGCA TCGGGGACGA GATGGACGTG AGCCTCAGGG CCCCAGCCTT GGGCCAGCTC 300  
 TCCGAGGTGG CCAATGCACAG CCTGGGTCTG GCTTTCATCT ACGACCAGAC TGAGGACATC 360  
 5 AGGGATGTTT TTAGAAGTTT CATGGACGGT TTCACCACAC TTAAGGAGAA CATAATGAGG 420  
 TTCTGGAGAT CCCCAGAACCC CGGTCTCTGG GTGTCTCTGG AACAGGTGCT GCTGGGCTG 480  
 CTGCTGCTGC TGGCGCTGCT GCTGCCGCTG CTCAGCGGGG GCCTGCACCT GCTGCTCAAG 540  
 TGAGGCCCGG GCGGCTCAGG GCGGGGCTGG CCCCACCCCT ATGACCACTG CCCTGGAGGT 600  
 10 GCGGCTCTGC TGCTGTATAT TTTTAACTG TTTTCTCATG ATGCCTTTTT ATATTTAAAC 660  
 CCGAGATAG TGCTGGAACA CTGCTGAGGT TTTTACTCA GGTTTTTTGT TTTTCTTTA 720  
 TTCCAGTTTT CGTTTTTCT AAAAGATGAA TTCCTATGGC TCTGCAATTG TCACCGGTTA 780  
 ACTGTGGCCT GTGCCAGGA AGAGCCATTC ACTCTGCCC CTGCCACAC GGCAGGTAGC 840  
 AGGGGGAGTG CTGGTCACAC CCTGTGTGA TATGTGATGC CCTCGGCAA GAATCTACTG 900  
 15 GAATAGATTC CGAGGAGCAG GAGTGCTCAA TAAATGTTG GTTTCAGCA AAAAAAAAAA 960  
 AAA 963

Seq ID NO: C211 DNA Sequence  
 Nucleic Acid Accession #: AF272357  
 Coding sequence: 83..1060

1 11 21 31 41 51  
 | | | | |  
 GCTGCTCCCG ACGCGGAGCC CGGAGCCCGC GCCGAGCCCC TGGCCTCGCG GTGCCATGCT 60  
 GCCCCGCGGG CGGCGCTGAA GGATGGCGAC GCCGCTGCCT CCGCCTCCC CGCGGCACCT 120  
 25 CGCGCTGCTG CGGCTGCTGC TCTCCGGCCT CGTCTCTGGC GCCGCCCTGC GTGGAGCCGC 180  
 CGCCGGCCAC CGGATGTAG CCGCTGTTC CGGGAGCCTG GACTGTGCCC TGAAGAGGCG 240  
 GGCAAGGTGT CCTCTGTGT CACATGCTGT TGGGCCCTGC CTTAGCCCTT TCCAGGAGGA 300  
 CCAGCAAGGG CTCTGTGTG CCAGGATGCG CCGGCTCCA GCGGGGGGCC GGGCCAGGCC 360  
 30 CAGACTGGAA GATGAGATTG ACTTCTGGC CCAGGAGCTT GCCCGGAAGG AGTCTGGACA 420  
 ATCAACTCCG CCCCACCCA AGGACCGACA GCGGCTCCCG GAGCCTGCCA CCCTGGGCTT 480  
 CTCGGCACGG GGGCAGGGGC TGGAGCTGGG CTTCCCTCC ACTCCAGGAA CCCCACGCC 540  
 CACGCCACAC ACCTCCCTGG GCTCCCTGT GTATCCGAC CCGGTGCACA TGTCCGCCCT 600  
 GGAGCCCCGG GGAGGGCAAG GCGACGGCCT CGCCCTTGTG CTGATCCTGG CTTCTGTGT 660  
 35 GGCCGGTGCA GCCGCCCTCT CGTAGCCTC CCTCTGCTGG TGCAGGCTGC AGCGTGAGAT 720  
 CCGCCTGACT CAGAAGGCCG ACTACGCCAC TGCGAAGGCC CCGTGGCTAC CTGCGAGCTC 780  
 CCGGATCTCG CTTGGGGACC AGCGGCTGGC ACAGAGCGCG GAGATGTACC ACTACCAGCA 840  
 CCAACGGCAA CAGATGCTGT GCCTGGAGCG GCATAAAGAG CCACCCAAGG AGCTGGACAC 900  
 GGCTCTCTCG GATGAGGAGA ATGAGGACGG AGACTTCACG GTGTACGAGT GCCCGGGCCT 960  
 40 GGCCCCGACC GGGGAAATGG AGGTGCGCAA CCTCTGTTC GACCACGCCG CACTGTCCGC 1020  
 GCGCCTGCGC GCGCCAGCT CACCGCTGC ACTGCCATGA CCTGGAGGCA GACAGACGCC 1080  
 CACCTGCTCC CGACCTCGA GGCCCCCGGG GAGGGGCAGG GCCTGGAGCT TCCCACTAAA 1140  
 AACATGTTTT GATGCTGTGT GCTTTTGGCT GGGCCTCGGG CTCCAGGCCC TGGGACCCCT 1200  
 TGCCAGGGAG ACCCCGAAC CTTTGTGCCA GGACACCTCC TGGTCCCTG CACCTCTCCT 1260  
 45 GTTCGGTTTA ACCCCCAA CATGGAGGGG CATGGAGAAC CGTAGAGCGC AGGAACGGGT 1320  
 GGGTAATTCT AGAGACAAA GCCAATTAAA GTCCATTTC AAAAAAAAAA A 1371

Seq ID NO: C212 DNA Sequence  
 Nucleic Acid Accession #: NM\_004445.1  
 Coding sequence: 799..3819

1 11 21 31 41 51  
 | | | | |  
 CGGAGGGGGG GGGCCGGGCT GCGTTCGCTC CAGCCGCGGC TCTACAGCAG CGGGCGGCGG 60  
 GACCCGGGAC CCAGCTTGGC GACGGCGATT CTGACGCGG GCGCCAGGA TTCTCCCGGC 120  
 55 GCGCCACCTC TGGAGCAGCC CCTGCGGCCA GCGTCAGGTC CACCCCGGAA TCCAGGGAC 180  
 TCTCGGCGCC GAACGAGCCC GGGCCGGTGC AACGGGGTCC CCGGACTGGA GAAGACGCGG 240  
 GTGGCACCGT CGGAGCTCCA GGAGCCCGG GTCCACTGCG AGGCCTCGGG GGGCCAGAC 300  
 CTGCAGAGAC TGCGGCCAAC GGAAGAAAT AAAGGGATTA TAGTCCACCC AATTACAGA 360  
 60 CTCTGAGAC TCAGACAGCA GGAGAGATAG AGAACCGCCA ATCTCTAGAT CAACAAGCAA 420  
 AGGAGGTGCC AAGCCTGTTT GTCTTCATTG TGCACTGGA GTCTAGATGC TGGGAAGTCC 480  
 AAGATCAGGG TGCGGGCATG GTCAGTTCTT GGCAGAGCCT CTCTTCTAGG TTTTCACTG 540  
 CCCTCTCTTT TGTGTGTCC TCGAATGGCA GAAAAGGGG TGGCTGTGG AGGAAGGGAG 600  
 GAGAGTAAAT GAAGAGAAAG AACTGGAATA ACCCTTGCA GAAAAAAGG AAAAGGGAAG 660  
 65 CTAGCTGTA CACCTGAGT CTTGCAAAAG CTGACGCCCC ACCCAGGAGC AGGGTGTGTG 720  
 CTGGGGCGAT GGTGGACGCC CTGAAGATGT CCGATGGCTA CTGAAGGGGC TGCCCAATTA 780  
 GGGAACAGAG TGGCGGCAT GGTGTGTAGC CTATGGGTGC TGCTCCTGGT GTCTTCAGTT 840  
 CTGGCTCTGG AAGAGGTATT GCTGGACACC ACCGAGAGA CATCTGAGAT TGGCTGGCTC 900  
 ACCTACCCAC CAGGGGGGTG GACGAGGTG AGTGTCTGG ACGACGCGC ACGCTCTGCT 960  
 70 CGGACCTTGG AGGCATGTGA TGTGGCAGGG GCGCCTCCAG GCACCGGGCA GGACAATTGG 1020  
 TTGCAGACAC ACTTTGTGGA GCGCGCGGG GCGCAGAGG GGCACATTG ACTCCACTTC 1080  
 TCTGTGCGGG CATGCTCCAG CCTGGGTGTG AGCGGCGGCA CCTGCCGGGA GACCTTCACC 1140  
 CTTTACTACC GTCAGGCTGA GGAGCCCGAC AGCCCTGACA GCGTTTCTC CTGGCACCTC 1200  
 75 AAACGCTGGA CCAAGGTGGA CACAATTGCA GCAGACGAGA GCTTTCCTC CTCCTCTCTC 1260  
 TCCTCTCTCT CTTCTCTCTC TGCAGCGTGG GCTGTGGGAC CCCACGGGGC TGGGCGAGCG 1320  
 GCTGGACTGC AACTGAACGT CAAAGAGCGG AGCTTTGGGC CTCTCACCCA ACGCGGCTTC 1380  
 TACGTGGCCT TCCAGGACAC GGGGGCCTGC CTGGCCCTGG TCGCTGTACG GCTCTTCTCC 1440  
 TACACCTGCC CTGCGCTGCT CCGATCCTTT GCTTCTTTC CAGAGACGCA GGCAGTGGG 1500  
 80 GCTGGGGGGG CTTCCCTGGT GGCAGCTGTG GGCACCTGTG TGGCTCATGC AGAGCCAGAG 1560  
 GAGGATGGAG TAGGGGGCCA GGCAGGAGGC AGCCCCCCA GGTGCACTG CAACGGGGAG 1620  
 GGCAAGTGA TGTAGCTGT CGGGGGCTGC CGTGTCCAGC CTGGATACCA ACCAGCACGA 1680  
 GGAGACAAGG CCGTCCACGC CTGCCACGG GGGCTCTATA AGTCTTCTGC TGGGAATGCT 1740  
 CCCTGCTCAC CATGCCCTGC CCGCAGTCA GCTCCCAACC CAGCAGCCCC CGTTTGGCCC 1800  
 TGCCTGGAGG CCTTCTACCG GGCAGTTCC GACCCACCAG AGGCCCTCTG CACTGCTCCT 1860  
 CCATCGGCTC GCGAGGAGCT TTGTTTGGAG GTGCAAGGCT CAGCACTCAT GCTACACTGG 1920

	CGCCTGCCTC	GGGAGCTGGG	GGGTCGAGGG	GACCTGCTCT	TCAATGTCGT	GTGCAAGGAG	1980
	TGTGAAGGCC	GCCAGGAACC	TGCCAGCGGT	GGTGGGGGCA	CTTGTCAACG	CTGCAGGGAT	2040
	GAGGTCACCT	TCGACCTCTG	CCAGAGAGGC	CTGACTGAGA	GCCGAGTGT	AGTGGGGGGA	2100
5	CTCCGGGCAC	ACGTACCCCTA	CATCTTAGAG	GTGCAGGCTG	TTAATGGGGT	GTCTGAGCTC	2160
	AGCCCTGACC	CTCCTCAGGC	TGCAGCCATC	AATGTGAGCA	CCAGCCATGA	AGTGCCCTCT	2220
	GCTGTCCCTG	TGGTGACCA	GGTGAGCCGG	GCATCCAA	GCATCACGGT	GTCCCTGGCCG	2280
	CAGCCCGACC	AGACCAATGG	GAACATCCTG	GACTATCAGC	TCCGCTACTA	TGACCAGGCA	2340
	GAAGACGAAT	CCCACTCCTT	CACCTTGACC	AGCGAGACCA	ACACTGCCAC	CGTGACACAG	2400
10	CTGAGCCCTG	GCCACATCTA	TGGTTTCCAG	GTGCGGGGCC	GGACTGCTGC	CGGCCACGGC	2460
	CCCTACGGGG	GCAAAGTCTA	TTTCCAGACA	CTTCCTCAAG	GGGAGCTGTC	TTCCCAGCTT	2520
	CCGGAAGAGC	TCTCCTTGGT	GATCGGCTCC	ATCCTGGGGG	CTTTGGCCTT	CCTCCTGCTG	2580
	CGAGCCATCA	CCGTGCTGGC	GGTCGTCTTC	CAGCGGAAGC	GGCGTGGGAC	TGGCTACACG	2640
	GAGCAGCTGC	AGCAATACAG	CAGCCCAGGA	CTCGGGGTGA	AGTATTACAT	CGACCCCTCC	2700
	ACCTACGAGG	ACCCCTGTCA	GGCCATCCGA	GAACCTGCCC	GGGAAGTCGA	TCCTGCTTAT	2760
15	ATCAAGATTG	AGGAGTTCAT	TGGGACAGGC	TCTTTTGGAG	AAGTGCGCCA	GGGCCGCTG	2820
	CAGCCACGGG	GACGAGGGGA	GCAGACTGTG	GCCATCCAGG	CCCTGTGGGC	CGGGGGCGCC	2880
	GAAAGCCTGC	AGATGACCTT	CCTGGGCGCG	GCCGCACTGC	TGGGTCACTT	CCAGCACCCC	2940
	AAACATCTGC	GCTGTGAGGT	CGTGGTCACC	AAGAGCCGAC	CCCTCATGGT	CTGTGAGGAG	3000
	TTCATGGAGG	TTGGCCCCCT	GGACAGCTTC	CTCAGGCAGC	GGGAGGGCCA	GTTCAGCAGC	3060
20	CTGCAGCTGG	TGGCCTGTGA	GCGGGGAGTG	GCTGCTGCCA	TGCAGTACCT	GTCCAGCTTT	3120
	GCCTTCGTCC	ATCGCTCGCT	GTCTGCCAC	AGCGTGTCTG	TGAATAGCCA	CTTGGTGTGC	3180
	AAGGTGCCCC	GTCTTGCCCA	CAGTCCCTCAG	GGCCCAAGTT	GTTTGTCTCG	CTGGGCGAGCC	3240
	CCAGAGGTCA	TTGCACATGG	AAAGCATACA	ACATCCAGTG	ATGTCTGGAG	CTTTGGGATA	3300
25	CTCATGTGGG	AAGTGATGAG	TTATGGAGAA	CGGCCTTACT	GGGACATGAG	TGAGCAGGAG	3360
	TTACTAAATG	CAATAGAGCA	GGAGTTCGGG	CTGCCCCCGC	CTCCAGGCTG	TCCTCCTGGA	3420
	TTACATCTAC	TTATGTTTGA	CACTTGGCAG	AAGGACCGTG	CCCGGCGGCT	TCATTTTGAC	3480
	CAGCTGTGGG	CTGCATTGGA	CAAGATGATC	CGCAAGCCAG	ATACCCCTGCA	GGCTGGCGGG	3540
	GACCCAGGGG	AAAGGCCCTT	CCAGGCCCTT	CTGACCCCTG	TGGCCCTGGA	CTTTCCTTGT	3600
30	CTGGACTCAC	CCCAGGCTCG	GCTTTCAGCC	ATTGGACTGG	AGTGCTACCA	GGACAACTTC	3660
	TCCAAGTTTG	GCCTCTGTAC	CTTCAGTGAT	GTGGCTCAGC	TCAGCCCTAGA	AGACCTGCCT	3720
	GCCCTGGGCA	TCACCTTGGC	TGGCCACCAG	AAGAAGCTGC	TGCACCATAT	CCAGCTCCTT	3780
	CAGCAACACC	TGAGGCAGCA	GGGCTCAGTG	GAGGTCTGAG	AATGACGATA	CCCGTGACTC	3840
	AGCCCTGGAC	ACTGCTCCGA	GAAAGGACAT	GTGGGACGTG	AGCCGGGCTC	CAACAGCCTC	3900
35	TGTGAGAGAT	GCCCCACACC	AAACCCCAACC	CTCCCGATGG	CTGCATTCCC	TGGTCTCCCG	3960
	CCTCTCCACC	AGCCCCCTCC	TCATTAAAGG	GAAAGAAGGG	AATTTGCAAA		4010

Seq ID NO: C213 DNA Sequence  
Nucleic Acid Accession #: XM\_043340.4  
Coding sequence: 195..1067

40	1	11	21	31	41	51	
	GGGCGGCGCC	CAATGGGCTG	CGCGGAGCGT	CACTTCCCGG	CAGCGGGAGG	CGAGTGGCGA	60
45	GTGGCGAGTG	GCGAGTGTCA	GGGGGGCGGC	CGGCGGGGCG	GGGGCGGGCC	GAGGAGGCGT	120
	TGGCAGCGGG	CTCGGACCCA	CGCGGCGCCG	CGGCCCGCCT	GGCCTGCAGC	GCTCCCACCC	180
	CCGGCGGGCG	CACGATGCCC	TTTGACTTCA	GGAGGTTTGA	CATCTACAGG	AAGGTGCCCA	240
	AGGACCTTAC	GCGAGCCAAC	TACACCGGGG	CCATTATCTC	CATCTGCTGC	TGCCTCTTCA	300
	TCCTCTTCTC	CTTCTCTCTG	GAGCTCACC	GATTATAAAC	GACAGAAGTT	GTGAACGAGC	360
50	TCTATGTCGA	TGACCCAGAC	AAGGACAGCG	GTGGCAAGAT	CGACGTCAGT	CTGAACATCA	420
	GTTTACCCAA	TCTGCACTGC	GAGTTGGTTG	GGCTTGACAT	TCAGGATGAG	ATGGGCAGGC	480
	ACGAAGTGGG	CCACATCGAC	AACTCCATGA	AGATCCCGCT	GAACAATGGG	GCAGGCTGCC	540
	GCTTCGAGGG	GCAAGTTCAGC	ATCAACAAGG	TCCCCGGCAA	CTTCCACGTG	TCCACACACA	600
	GTGCCACAGC	CCAGCCACAG	AACCCAGACA	TGACGCATGT	CATCCACAAG	CTCTCCTTTG	660
55	GGGACACGCT	ACAGGTCACG	AACATCCACG	GAGCTTTCAA	TGCTCTCGGG	GGAGCAGACA	720
	GACTCACCTC	CAACCCCTCG	GCCTCCCACG	ACTACATCCT	GAAGATTGTG	CCCACGGTTT	780
	ATGAGGACAA	GAGTGGCAAG	CAGCGGTACT	CCTACCAGTA	CACGGTGGCC	AACAGGAAT	840
	ACGTGCGCTA	CAGCCACACG	GGCCGCATCA	TCCCTGCAAT	CTGGTTCGCG	TACGACCTCA	900
	GCCCCATCAC	GGTCAAGTAC	ACAGAGAGAC	GGCAGCCGCT	GTACAGATTTC	ATCACCACGA	960
60	TCTGTGCCAT	CATTGGCGGG	ACCTTCCACG	TGCGCGGCAT	CCTGGACTCA	TGCATCTTCA	1020
	CAGCCTCTGA	GGCCTGGAAG	AAGATCCAGC	TGGGCAAGAT	GCATTGACGC	CACACCCAGC	1080
	CTAATGGCCG	AGGACCTTGG	GCATCGCCAG	CCTTGCCCTC	AGTGCCCTGT	CTCCTTTGGC	1140
	CCTCAATCTG	GTCCCAATCT	TGGCTGTGTC	CCAAAGGGTG	TGTGGGAAGT	GGGGGGAAG	1200
	TAGAGGATGG	CTCGATGTTT	TGCAGTACC	TCTTTTCCCC	GTGTTTCTTT	TTAGACAAAT	1260
65	TACACTGCCT	GAAAGTGCAG	TTCCCCCTTC	CCTGGGGAGC	CCCAAGAAC	GAGTCAGGCA	1320
	AGGGGTGGGG	AGTCCAGGGG	AACATCCCAG	AATGCATATC	GATCAGCTCT	CAGCCAGGCT	1380
	TGCACATCT	CGCAGCCCCC	ACTAGGTGGA	CACATTAAAT	ATTGTTGTTT	TCCCCTGGGC	1440
	AGCCAACTTG	CCCCAGAGGC	ACCAGACCTG	GGCTTTTCAGC	TTTGGGACCA	GGCTGCCCAA	1500
	AGGTACTCCT	TTATACACCC	GGCACCTTCC	ACGAAAGATG	GTACTTCCCA	AGCAAGCCCC	1560
70	TATGATTGTT	CACTATAGAT	GGAAATGTGT	GGCATGCACA	TGAGTTGAAA	TTCTTTTATG	1620
	CATTTTTTTG	AAGAAAAAAA	AAAAAACCAAC	TCTGAGGACA	TAGGGGATGT	CAGTTTCCTA	1680
	TGGAAGAGAC	ACCTCTGACC	CGTTATTCTT	ATAATCAAAA	TCTGAAGGGA	AAAAAATGTT	1740
	TTAGTTCTTT	CCCCACTCGT	TGGGTTCAAC	TAGATTAAAA	GGCTGATTTT	CAG	1793

Seq ID NO: C214 DNA Sequence  
Nucleic Acid Accession #: NM\_002151.1  
Coding sequence: 246..1499

80	1	11	21	31	41	51	
	TCGAGCCCGC	TTTCCAGGGA	CCCTACCTGA	GGGCCCCACG	GTGAGGCAGC	CTGGCCTAGC	60
	AGGCCCCACG	CCACCGCCTC	TGCTCCAGG	CCGCCGCTG	CTGCGGGGCC	ACCATGCTCC	120
	TGCCCAGGCC	TGAGACTGTA	CCGACCCCGC	GCACTACCTC	GAGGCTCCGC	CCCCACCTGC	180
	TGGACCCAG	GGTCCCACCC	TGGCCCAGGA	GGTCAGCCAG	GGAATCATT	ACAAGAGGCA	240
	GTGACATGGC	GCAGAAAGGAG	GGTGGCCGGA	CTGTGCCATG	CTGCTCCAGA	CCCAAGGTGG	300

CAGCTCTCAC TGCGGGGACC CTGCTACTTC TGACAGCCAT CGGGGCGGCA TCCTGGGGCCA 360  
 TTGTGGCTGT TCTCCTCAGG AGTGACCAGG AGCCCGTGTA CCCAGTGCAG GTCAGCTCTG 420  
 CGGACGCTCG GCTCATGTGC TTTGACAAGA CGGAAGGGAC GTGGCGGCTG CTGTGCTCCT 480  
 CGCGCTCCAA CGCCAGGGTA GCCCGACTCA GCTGCGAGGA GATGGGCTTC CTCAGGGCAC 540  
 TGACCCACTC CGAGCTGGAC GTGCGAACGG CGGGCGCCAA TGGCAGCTCG GGCTCTCTCT 600  
 GTGTGGACGA GGGGAGGCTG CCCCACACCC AGAGGCTGCT GGAGGTATC TCCGTGTGTG 660  
 ATTGCCCCAG AGGCCGTTTC TTGGCCGCCA TCTGCCAAGA CTGTGGCCGC AGGAAGCTGC 720  
 CCGTGGACCG CATCGTGGGA GGCCGGGACA CCAGCTTGGG CCGGTGGCCG TGGCAAGTCA 780  
 GCCTTCGCTA TGATGGAGCA CACCTCTGTG GGGGATCCCT GCTCTCCGGG GACTGGGTGC 840  
 TGACAGCCGC CCATGCTTTC CCGGAGCGGA ACCGGGTCTT GTCCCGATGG CGAGTGTGTTG 900  
 CCGGTGCGGT GGCCCGAGGC TCTCCCCACG GTCTGCAGCT GGGGGTGCAG GCTGTGGTCT 960  
 ACCACGGGGG CTATCTTCCC TTTCCGGACC CCAACAGCGA GGAGAACAGC AACGATATTG 1020  
 CCCTGGTCCA CCTCTCCAGT CCCCTGCCCC TCACAGAATA CATCCAGCCT GTGTGCCTCC 1080  
 CAGCTGCCGG CCAGGCCCTG GTGGATGGCA AGATCTGTAC CGTGACGGGC TGGGGCAACA 1140  
 CGCAGTACTA TGGCCAAACAG GCCCGGGTAC TCCAGGAGGC TCGAGTCCCC ATAATCAGCA 1200  
 ATGATGTCTG CAATGGCGCT GACTCTATG GAAACCAGAT CAAGCCCAAG ATGTTCTGTG 1260  
 CTGGCTACCC CGAGGGTGGC ATTGATGCCT GCCAGGGCGA CAGCGTGGT CCCTTTGTGT 1320  
 GTGAGGACAG CATCTCTGGG ACGCCACGTT GCGCGCTGTG TGGCATTGTG AGTTGGGGCA 1380  
 CTGGCTGTGC CCTGGCCAG AAGCCAGGCG TCTACACCAA AGTCAGTGAC TTCCGGGAGT 1440  
 GGATCTTCCA GGCCATAAAG ACTCACTCCG AAGCCAGCGG CATGGTGACC CAGCTCTGAC 1500  
 CGGTGGCTTC TCGCTGCGCA GCCTCCAGGG CCCGAGGTGA TCCCGTGGT GGGATCCACG 1560  
 CTGGGCGGAG GATGGGACGT TTTTCTTCTT GGGCCCGGTC CACAGGTCCA AGGACACCTT 1620  
 CCCTCCAGGG TCCTCTCTTC CACAGTGGCG GGCCCACTCA GCCCCGAGAC CACCCACCTT 1680  
 CACCTCTCTG ACCCCATGT AAATATTGTT CTGCTGTCTG GGAATCCTGT CTAGGTGCCC 1740  
 CTGATGATGG GATGCTCTTT AAATAATAAA GATGTTTGT ATT 1783

Seq ID NO: C215 DNA Sequence  
 Nucleic Acid Accession #: AB037745.1  
 Coding sequence: 26..1744

1 11 21 31 41 51  
 ATGGTGGAAC ACGCTGCCCA CAAACATGGA AACGACCGTT CTCAGTGGGA TCAACTTCGA 60  
 GTACAGGGGC ATGACAGGCT GGGAGGTGGC TGGTGATCAC ATTTACACAG CTGCTGGAGC 120  
 CTCAGACAAT GACTTCATGA TTCTCACTCT GGTGTGGCCA GGATTTAGAC CTCGCGAGTC 180  
 GGTGATGGCA GACACAGAGA ATAAAGAGGT GGCCAGAAAT ACATTTGTCT TTGAGACCTT 240  
 CTGTTCTGTG AACTGTGAGC TCTACTTCAT GGTGGGTGTG AATTCTAGGA CCAACACTCC 300  
 TGTGGAGACG TGGAAAGGTT CCAAAGGCAA ACAGTCCAT ACCTACATCA TTGAGGAGAA 360  
 CACTACCACG AGCTTCACCT GGGCCTTCCA GAGGACCACT TTTTATGAGG CAAGCAGGAA 420  
 GTACACCAAT GACGTGTGCA AGATCTACTC CATCAATGTC ACCAATGTTA TGAATGGCGT 480  
 GGCTCTCTAC TGCCCTCCCT GTGCCCTAGA AGCCTCTGAT GTGGGCTCCT CTGCACTCTC 540  
 TTGTCTGTCT GGTACTATTA TTGACCGAGA TTCAGGAACC TGCCACTCCT GCCCCCTTAA 600  
 CACAATTCTG AAAGCCACCC AGCCTTATGG TGTCCAGGCC TGTGTGCCCT GTGTGCCAGG 660  
 GACCAAGAAC AACCAAGATC ACTCTCTGTG CTACAATGAT TGCACCTTCT CACGCAACAC 720  
 TCCAACGAGG ACTTTCAACT ACAACTTCTC CGCTTTGGCA AACACCGTCA CTCTGTCTGG 780  
 AGGGCCAAGC TTCACTTCCA AAGGGTTGAA ATACTTCCAT CACTTTACCC TCAGTCTCTG 840  
 TGGAAACCAG GGTAGGAAAA TGTCTGTGTG CACCGACAAT GTCAGTGACC TCCGGATTCC 900  
 TGAGGGTGAG TCAGGGTTCT CCAATCTTAT CACAGCCTAC GTCTGCCAGG CAGTCATCAT 960  
 CCCCCAGAG GTGACAGGCT ACAAGGCCGG GGTTTCTCTA CAGCCTGTCA GCCTTGCTGA 1020  
 TCGACTTATT GGGGTGACAA CAGATATGAC TCTGGATGGA ATCACTCCC CAGCTGAACT 1080  
 TTTCCACCTG GAGTCTTGGG GAATACCGGA CGTGATCTTC TTTTATAGGT CCAATGATGT 1140  
 GACCCAGTCC TGCAGTTCTG GGAGATCAAC CACCATCCGC GTCAGGTGCA GTCCACAGAA 1200  
 AACTGTCCCT GGAAGTTTGC TGCTGCCAGG AACGTGCTCA GATGGGACCT GTGATGGGCT 1260  
 CAACTTCCA TTCCGTGTGG AGAGCGCGGC TGCTTGCCCG CTCTGTCTAG TGGCTGACTA 1320  
 CCATGCTATC GTGAGCAGCT GTGTGGCTGG GATCCAGAAG ACTACTTACG TGTGGCGAGA 1380  
 ACCCAAGCTA TGCTCTGGTG GCATTTCTCT GCCTGAGCAG AGAGTCACCA TCTGCAAAAC 1440  
 CATAGATTTT TGGCTGAAGG TGGGCATCTC TGCAGGCACC TGTACTGCCA TCCTGCTCAC 1500  
 CGTCTTGACC TGCTACTTTT GGAATAAGAA TCAAAAACCTA GAGTACAAGT ACTCCAAGCT 1560  
 GGTGATGAAT GCTACTCTCA AGGACTGTGA CCTGCCAGCA GCTGACAGCT GCGCCATCAT 1620  
 GGAAGGCGAG GATGTAGAGG ACGACCTCAT CTTTACCAGC AAGAAGTCAC TCTTTGGGAA 1680  
 GATCAAATCA TTTACTTCCA AGCAGCCAGC TCCTGTCAAC ATCTCTCTTT CAGAGGACTC 1740  
 CTGATGGATT TGACTCAGTG CCGCTGAAGA CATCCTCAGG AGGCCAGAGC ATGGACCTGT 1800  
 GAGAGGCACT GGCTGCCTCA CTGCTCTCCT CACCTTGCAAT AGCACCCTTG CAAGCCTGCG 1860  
 GCGATTTGGG TGCCAGCATC CTGCAACACC CACTGCTGGA AATCTCTTCA TTGTGGCCTT 1920  
 ATCAGATGTT TGAATTTTCT ATCTTTTCTT ATAGAGTACC CAAACCTTCC TTTCTGCTTG 1980  
 CCTCAAACTT GCCAAATATA CCCACACTTT GTTTGTAAAT TATGCCCTTG CTGTATCTT 2040  
 GTTTCCTCAA ATGGCCCATC CGCCAGAGCC ATAGCTTCGT CTGCTCATAA TTCCTATAGC 2100  
 TTTGGAATGA AAATATTTCT ATCTTCTTAA GTATAGAAAC TATTTCTCTT GTCCTCTAAC 2160  
 TTAAGGGCAG AAACAGCTGG GAGTTTTCCT CGCATGCCCT CAGCTCATGA TCTCTTCAGG 2220  
 AGAGAGGCTG GGTGAGGAGG GTGTGCGGGT TCCCTGGTGG ATAATCTTCA TAGCAGCCTG 2280  
 GATCCATTTT CCTTGGATAA CCAGCTCAAA GGGAGTGAAA ATGAGTGTCT GAGGGCAAGG 2340  
 GGAGCAAGGC CTGGGTAAAG AAAGCCTTGA AAAGCATAAA AAGAGGCCGG GCGCGGTGGC 2400  
 TCACGCTGTG AATCCAGCA CTTTGGGAGG CCGAGGCCGG CAGATCATGA GGTGCGGAGA 2460  
 TTGAGACCAT CTGGGTAAAC ACGGTGAAGC CCGTCTCTTA CTGGAATAC AAAAAATTAG 2520  
 CCGGGCGTGG TGGCGGGTGC CTGTGCTCCC AGCTACTCGG GAGGCTGAGG GGGGAGAATA 2580  
 GCGTGGGCCT GGAAGCGGGA GCTTGCAGTG AGCCGAGATC GCGCCACTGC ACTCCATCCA 2640  
 GCCTGGGTGA CAGAGTGAGA CTCTGCCTCA AAAAAAAGAA AAGCAACAAG 2700  
 AGAGGCAACA AGGAAATGTT TTGTTTGA GACAGGCTCT CACTCTGTCA CCTAGGCTGG 2760  
 AGTGACAGTG CGTAATCACT GTTCAGTGCA GCCTCAAGCT CTGGGCTCA GGCTATCTCT 2820  
 CCATCTCAGC CTCTCAAGTA GCTGGGACTA CGAGTGTGCA CCACAGGCT CACTAATTTT 2880  
 TGTGTTTTTT GTAGACACGG GGTTCACCG GTGTGCCAG GCTGGTCTCC AACTCCTGGG 2940  
 CTCAAGTGAT GTGTCCGCTC CGGCCCTCCA AACTGCTGGG ATTACAGGCA TAAGCCACTG 3000  
 CACTCAGCCT TTATTTGTTT TTTTAAACCA CGTAGCTCAT TGCTTCTCT TAAGTAAATG 3060  
 ATAGATATTC TCACTGAAGC CAAAGGAATA AGTTTCATCA GAAATGCCCC AAAGCCCTGG 3120

	TGGATACATC	CTCCCTATCT	TTTTTTTAAA	CCTTCCACTA	TCACTCTATG	ACACTGAAAA	3180
	GAACCAGGTA	AGCCCCAAAC	CCAGATGTTC	CAGCCTTATC	CTCTATTGGG	TTTACCCACA	3240
	GACATAGCAA	ACCCCTGTGAG	TGAGGAAAAA	TCCCCTATCT	TGAGTGCCCC	CCTCTAGAAA	3300
5	GTTTGGGCCA	TATTTATGGAA	CAGGGGTCTC	TTATTTGAAA	AGAGCACAAAG	GAGGCCAAGA	3360
	TTTTTAATGGG	GCACTTTAGG	GGATACAGCC	CACAATGGCA	TGGGCCTGAG	GTGGCCGTGA	3420
	TGCTGTCTTC	TAAGCTTAAC	GCATCTGCTC	AGGCACAGAA	TAAACGTCTA	GGCTGGCCAA	3480
	AAAAGGAAC	GAATCCCAGG	CCCATACGCC	AGCACCAGAA	TCAAACCACT	CTTCAAGGAA	3540
	GGAAGGCTAG	GAGAGTTTAA	CAAGATTTTC	ACTGGGCCCA	GCATGGTGGC	TCACACCTGT	3600
10	AATCCCAAGG	CAGAATGGTG	GCTTGAGCTC	AGGAGTTCAA	GACCAGCCTG	GGCAACACAG	3660
	TGAGACCCCTG	TCTCTAAAAA	ATTTAAAAAT	AAACAAGGTG	TTCACCAAGC	TGGGATACTT	3720
	CTCACTATTA	AGCCCTTATC	TTTCTCTTTT	TTTCATTCTC	AATTGCTTTG	TGTGATAAAA	3780
	AACTAAAGAG	ACTTCTGGTC	CAATTTCTGG	CAACATCCCT	TCTGAAAGGT	GAGTAGAGTG	3840
	GGTGTCTTCT	ATGCCCATTT	TCCCAATTT	TACACAACT	ATTATCAATG	AACTTTTAAG	3900
15	TACCTAGAA	TGGTAAAACC	AGAGCAAGAC	TTTAAATTAC	CTTCTTCTTT	CTTCTACTGG	3960
	CAGTTCTGCC	CCCATCACTA	TCAGGCTAGG	GTGACCTTCC	CTTGGTCAAG	CCCCAATTGC	4020
	CCATGATTG	TGCCTGTGCC	CTTTCTCCAG	TGACCAATTG	GTGACCAGAT	GGTAGATATA	4080
	GAAAGGGGAT	GGCATTGTGA	AGTGACTAGT	CTGCCACAAA	ATGCTCATCT	GATTAGCCAC	4140
	TGCTGCCCTG	GCAATGGCTT	TGTAAGAGTC	AATGAGAACT	AGAGCCAGGC	TGTGGTCCCT	4200
20	GGCCATTAAC	AGTGTGGTG	ACGGCAGGGA	GTCCCTTTGG	TTTAATAAAT	CCAGTTTTTC	4260
	TTTGGGTATC	CAAAATCTCC	CCTCCTTTTG	TAGGAGTCAG	GCTCTCAGAA	CCTGTGTCCA	4320
	TGTTGGAAT	TCCCCCAGTG	TGGATGCAGA	TACGCAGCTC	CTGAGCTCCA	GCCTAAAGTC	4380
	TTCTGTAGCC	TCAGCAATAC	TTGGGCACCT	GCTGTCTCAC	TGAATAGCTT	TCTTTTGTGA	4440
	CAAGGGCCAC	AGACAGCCCT	TAGACTATT	CGGAAACAGT	AGGAAAAATT	ACATATGTCT	4500
25	TTGACTTCTT	TATTTCTGAC	CCACTGATT	TAGCCATAAT	ACTTTAAGGA	GCTACTTTTT	4560
	ACTACCCCTT	ACCGTCTGCA	CTTCTGCAGG	TCTGCCCTGT	GACCTGTGAG	GAACTCCTGA	4620
	GTTACGCTAC	TGGGGTCACC	TGTTGCTCCC	CTAGCAAGTT	AGGCATGTCA	TATATTTTTA	4680
	ACAGCTTTAT	TGAGATATAA	TTACATATT	ATACAATTCA	CCTTTAAAAAC	ATACGATTCA	4740
	ATGGTTTTC	GCAAACTCAC	AGAGTTGTCC	GCCCACTTGA	GAGCAAAAC	ATGTTCAATT	4800
30	TTCTTTTCT	TTTTTTTTTT	GAGACAGAGT	CAGCTTTGTC	GCCCAAGGCTG	GAGTGCAGTG	4860
	CCATGATCTT	GGCTCACTGC	AGCCTCCCA	TCCTGGGTTT	AAGTGATCCT	TCTGCTTCAG	4920
	CCTCCCCAGT	AGCTGGGATT	ACAGGCATGC	GCCACCACGC	CTAGCTAATT	TTTGTGTTTT	4980
	TAGTAGAGAT	GGGGTTTTC	CGTGTGGGCC	AGGCTGGTCT	CAAACTCCTG	GACTCAAGTG	5040
	ATCCACCCAC	CTCGGCTTCC	CAAAAGTCTG	GGATTGCAGG	TGTGAGCCAC	CGTGCCTGGC	5100
35	CTACGTGTTT	AATTTTCTAT	GAACAAAGGC	TTTAGTCTCT	GACCCAGGGC	TAAAGTGGTC	5160
	TGTCCAAGCT	GTGTTGGTGA	GAGGGAGTAT	GATAAAATGT	TTAAATCTCA	TTTGGTTACC	5220
	TTGAGTCTTG	GAACACGCAG	TAACTGTCT	GCTATAGTCA	TCATCTGTAT	TGGGCTGGGA	5280
	ATACAAATGA	AGATTGTGGT	GTATTCAAGC	AGTAGGGTTT	TTGCTTTTGT	TTTTGTTTTA	5340
40	GTGCCAACAA	AACTTTTTTT	TGTTCTGACT	CATTAAAGAT	AAGACTGACT	ATATTATATC	5400
	AACAGAAACT	TTGTAATAGA	TTTTTTTCAGC	TTTGTGAAAT	CGAATTTTTT	TTTATCAGGG	5460
	CTGGTTGGAT	TTCTTTTTTA	CCCTGTAATC	CAAGCGTTAA	TAGTTTGTGA	GAAGATGGGT	5520
	TATTGATGAT	CACCTTTTTT	TTTTTGTAAT	ATAAAAACAT	ACCTTAC		5567

Seq ID NO: C216 DNA Sequence

Nucleic Acid Accession #: NM\_004864.1

Coding sequence: 26-952

	1	11	21	31	41	51	
50	CGGAACGAGG	GCAACCTGCA	CAGCCATGCC	CGGGCAAGAA	CTCAGGACGG	TGAATGGCTC	60
	TCAGATGCTC	CTGGTGTGTC	TGGTGTCTCT	GTGGCTGCCG	CATGGGGGCG	CCCTGTCTCT	120
	GGCCGAGGCG	AGCCGCGCAA	GTTTCCCGGG	ACCCTCAGAG	TTGCACTCCG	AAGACTCCAG	180
	ATTCCGAGAG	TTGCGGAAAC	GCTACGAGGA	CCTGCTAACC	AGGCTGCGGG	CCAACGAGAG	240
	CTGGGAAGAT	TCGAACACCG	ACCTCGTCCC	GGCCCCGTGA	GTCCGGATAC	TCACGCCAGA	300
55	AGTGCAGCTG	GGATCCGGCG	GCCACCTGCA	CCTGCGTATC	TCTCGGGCCG	CCCTTCCCGA	360
	GGGGCTCCCC	GAGGCTTCCC	GCCTTCCACG	GGCTCTGTTC	CGGCTGTCCC	CGACGGCGTC	420
	AAGGTCTGTT	GACGTGACAC	GACCGCTGCG	GCGTCAGCTC	AGCCTTGCAA	GACCCCAAGC	480
	GCCCGCGCTG	CACCTGCGAC	TGTGCGCGCC	GCCGTGCGAG	TCGGACCAAC	TGCTGGCAGA	540
	ATCTTCTGTC	GCACGGCCCC	AGCTGGAGTT	GCACTTGCGG	CCGCAAGCCG	CCAGGGGGCG	600
60	CCGCGAGAGC	CGTGCAGCGA	ACGGGACGGA	CTGTCCGCTC	GGGCCCGGGC	GTTGCTGCGC	660
	TCTGCACACG	GTCCGCGCGT	CGCTGGAAGA	CCTGGGCTGG	GCCGATTGGG	TGCTGTGCGC	720
	ACGGGAGGTT	CAAGTGACCA	TGTGCAATCG	CGCGTGCCCG	AGCCAGTTCC	GGGCGGCAAA	780
	CATGCAACGC	CAGATCAAGA	CGAGCCTGCA	CCGCTGAAG	CCCGACACGG	AGCCAGCGCC	840
	CTGCTGCGTG	CCGCCAGACT	ACAATCCCAT	GGTGCTCATT	CAAAAGACCG	ACACCGGGGT	900
65	GTGCTCCAG	ACCTATGATG	ACTTGTAGC	CAAAGACTGC	CACTGCATAT	GAGCAGTCCT	960
	GGTCCCTTCA	CTGTGCACCT	GCGCGGGGGA	GGCGACCTCA	GTTGTCTGTC	CCTGTGGAAT	1020
	GGGCTCAAGG	TTCTGTAGAG	ACCCGATTCC	TGCCCAACA	GCTGTATTTA	TATAAGTCTG	1080
	TTATTTATTA	TTAATTTTAT	GGGTGACCT	TCTTGGGGAC	TCGGGGGCTG	GCTGTATGGA	1140
	ACTGTGTATT	TATTTAAATC	TCTGGTGATA	AAAATAAAGC	TGTCTGAAC	GTTAAAAAAA	1200
70	AAAA						1204

Seq ID NO: C432 DNA Sequence

Nucleic Acid Accession #: NM\_052858.1

Coding sequence: 54..1259

	1	11	21	31	41	51	
75	GGCAGGAGGT	GTTGCCCTCA	GGTCTGCTCC	GGGCGCGGAC	ACGGAACCCG	GCCATGGAAG	60
	ATCCGTCGGG	GGCTCGCGAG	CCCGGGGCCC	GGCCGAGAGA	GCGGGACCCG	GGACGGCGCC	120
	CCCAACCCAGA	CCAAGGCGCG	ACCCACGATC	GACCGCGGGA	CCGACCCGGG	GACCCGCGCA	180
80	GGAAGCGAAG	CAGCGACGGG	AACCGGCGAA	GGGACGGGGA	CCGGGACCCG	AAGAGAGACC	240
	AGGAGAGGGA	CGGGGAACCG	GACCGGAACC	GGGACGGGGA	GAGGGAGAGA	GAGAGGGAAA	300
	GAGACCCGGA	CCGAGGCCCC	CGCCGGGACA	CACACAGGGA	CGCGGGCCCT	CGCGCAGGTG	360
	AACACGAGAT	TTGGGAAAAA	CCGCGCCAAA	GCCGGACGCG	GGACGGAGCC	CGGGGACTGA	420
	CCTGGGACGC	AGCCGCGCCT	CCTGGGCCCG	CGCCCTGGGA	AGCCCCGGAG	CCGCCGACGC	480

CGCAGAGGAA GGGAGACCCC GGGCGCCGCA GACCCGAAAG TGAACCCCTT TCGGAGAGAT 540  
 ATCTGCCCTC GACCCCAAGG CCTGGACGAG AGGAGGTGGA ATATTACCAG TCAGAGGCGG 600  
 AAGGACTCCT GGAATGCCAC AAATGCAAAAT ACTTGTGCAC TGGGAGAGCC TGCTGCCAAA 660  
 TGCTGGAGGT TCTCTGAAC TTGCTGTATCC TGGCCTGCAG CTCTGTGTCT TACAGTTCCA 720  
 CAGGGGGCTA CACGGGCATC ACCAGCTTGG GGGGCATTTA CTACTATCAG TTCGGAGGGG 780  
 CTTACAGTGG CTTTGTATGGT GCTGACGGGG AGAAGGCCCA GCAACTGGAT GTCCAGTTCT 840  
 ACCAGCTAAA GCTGCCATG GTCACCTGTGG CAATGGCCTG TAGTGGAGCC CTCACAGCCC 900  
 TCTGCTGCTT CTTGCTTGCC ATGGGTGTCC TGCGGGTCCC GTGGCATTGT CCACGTGTTC 960  
 TGGTGACCGA AGGCTTGTGG GACATGCTCA TCGCGGGGGG GTACATCCCG GCCTTGTACT 1020  
 TCTACTTCCA CTACTCTCT GCTGCCTATG GCTCTCCTGT GTGTAAAGAG AGGCAGGCGC 1080  
 TGTACCAAGG CAAAGGCTAC AGCGGTTTCG GCTGCAGTTT CCACGGAGCA GATATAGGAG 1140  
 CTGGAATCTT TGCTGCCCTG GGCATTGTGG TCTTTGCCCT GGGGGCGGTC CTGGCCATAA 1200  
 AGGGCTACCG AAAAGTTAGG AAGCTAAAAG AGAAGCCAGC AGAAATGTTT GAATTTTAAAG 1260  
 GGTTTCTAAA ACCTCTGAC AGATGCAAGT GGTGTGTGGA GGTAGTCTGA GCCACTGCCT 1320  
 TTCCCAAGAA TCCCTGTGTG TGGAAAGTTT CAATGCTGGA AAAGCAGCGA GCCAGCGTTG 1380  
 GTGTGTGGG CGGAGCTCCC AGTCGCATGG AGCGGTGTTT ATGGATGCAA CAGACCTGG 1440  
 CTTCTGAGT CCTCTGTGAG TGAGGGACCA ATCAAAATTA TTTTTCAAA AGCAAAAAA 1500  
 TGGCGGCGCT CGCGGCTCA CACCTGTAA CCGAGCACTT TGGGAGGCTG AGGTGGGTGG 1560  
 ATCACTTGA GTACAGGAGT CGAGACGAGC TTGGCCAAAC TGGTGAGCCC CCGTCTCTAC 1620  
 TAAATAACAA AAAAATTAGC CAGGCGTGGT GCGGGCGGCG TGTAATCCCA GCTACTTGGG 1680  
 AGGCTGAGGC AGGAGAATCG CTTGAATCTG GGAGGCGGAG ATTGCACTGA GCCGAGATCC 1740  
 CGCCACTGCA CTCCAGCCCA GGTGACAGAG CGAGACTCCA TCTCAAAAAA AAAAAA 1800

Seq ID NO: C434 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 261..2861

1 11 21 31 41 51  
 | | | | | |  
 30 | | | | | |  
 GAGCTAGCGC TCAAGCAGAG CCCAGCGCGG TGCTATCGGA CAGAGCCTGG CGAGCGCAAG 60  
 CGGCGCGGGG AGCCAGCGGG GCTGAGCGCG GCCAGGCTCT GAACCCAGAT TTTCCAGACT 120  
 AGCTACCACT CGCTTGCCCC AGCCCCGGG AGCTCGCGGC GCCTGCGCGT CAGCGACCAAG 180  
 ACGTCCGGGG CGCTGCGCT CCTGGCCCCG GAGGCGTGAC ACTGTCTCGG CTACAGACCC 240  
 35 | | | | | |  
 AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GGACTTCCCT TTCAAGGCCA 300  
 TGCTGACCAT CAGCTGGCTC ACTCTGACCT GCTTCCTTGG GGCACATCC ACAGTGGCTG 360  
 CTGGGTGCCC TGACCAGAGC CCTGAGTTGC AACCTGGAA CCCTGGCCAT GACCAAGACC 420  
 ACCATGTGCA TATCGGCCAG GGCAAGACAC TGCTGCTCAC CTCTCTGCC ACGGTCTATT 480  
 CCATCCACAT CTCAGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG CCGATTGTTT 540  
 40 | | | | | |  
 TGCGAACCAG ACACATCCTG ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTGCCCTCT 600  
 GCCCTTTCCA GGGCAATTTT ACCATCAATT TGATGGAAG GGCTGATGAA GGTATTTCAGC 660  
 CGGATCCTTA CTATGCTCTC AAGTACATTG GGGTTGGTAA AGGAGCGCT CTGAGTTGC 720  
 ATGGACAGAA AAAGCTCTCC TGGACATTTT TGAACAAGAC CCTTCACCCA GGTGGCATGG 780  
 CAGAAGGAGG CTATTTT TTTT GAAAGGAGCT GGGGCCACCG TGGAGTTATT GTTCATGTCA 840  
 45 | | | | | |  
 TCGAACCACAA ATCAGGCACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAAGA 900  
 AAGAGAGTGA ACGTCTGGTC CAGTATTGTA ACGCGGTGCC CGATGGCAGG ATCCTTTCTG 960  
 TTGCAGTGAA TGATGAAGGT TCTCGAAATC TGGATGACAT GGCACGGAAG GCGATGACCA 1020  
 AATTGGGAAG CAAACACTCT CTGCACCTTG GATTAGACA CCCTTGGAGT TTTCTAACTG 1080  
 TGAAAGGAAA TCCATCATCT TCAGTGGGAG ACCATATTGA ATATCATGGA CATCGAGGCT 1140  
 50 | | | | | |  
 CTGCTGCTGC CCGGTTATTC AAATTGTTCC AGACAGAGCA TGGCGAATAT TTCAATGTTT 1200  
 CTTTGTCCAG TGAGTGGGTT CAAGACGTGG AGTGGACGGA GTGGTTCGAT CATGATAAAG 1260  
 TATCTCAGAG TAAAGGTGGG GAGAAAATTT CAGACCTCTG GAAAGCTCAC CCAGGAAAAA 1320  
 TATGCAATCG TCCCATGTAT ATACAGGCCA CTACAATGGA TGGAGTTAAC CTCAGCACCG 1380  
 AGGTGTGCTA CAAAAAAGGC CAGGATTATA GGTGTGCTTG CTACGACCGG GGCAGAGCCT 1440  
 55 | | | | | |  
 GCCGGAGCTA CCGTGTACGG TTCCTCTGTG GGAAGCCTGT GAGGCCCAA CTCACAGTCA 1500  
 CCATTGACAC CAATGTGAAC AGCAACCTTC TGAACCTGGA GGATAATGTA CAGTCATGGA 1560  
 AACCTGGAGA TACCCTGGTC ATTGCCAGTA CTGATTACTC CATGTACCAG GCAGAAAGAT 1620  
 TCCAGGTGCT TCCCTGCAGA TCCTGCGCCC CCAACCAGGT CAAAGTGGCA GGGAAACCAA 1680  
 TGTACCTGCA CATCGGGGAG GAGATAGACG GCGTGGACAT GCGGGCGGAG GTTGGGCTTC 1740  
 60 | | | | | |  
 TGAGCCGGAA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC 1800  
 ACATCTGCAA TTTCTTTGAC TTTCGATACT TTGGGGGCCA CATCAAGTTT GCTCTGGGAT 1860  
 TTAAGGCAGC ACCTTGGAG GGCACGGAGC TGAAGCATAT GGGACAGCAG CTGGTGGGTC 1920  
 AGTACCCGAT TCACTTCCAC CTGGCCGTG ATGTAGACGA AAGGGAGGT TATGACCCAC 1980  
 CCACATACAT CAGGACCTC TCCATCCATC ATACATTCTC TCGCTGCTC ACAGTCCATG 2040  
 65 | | | | | |  
 GCTCCAATGG CTTGTTGATC AAGGACGTTG TGGGCTATAA CTCTTGGGC CACTGCTTCT 2100  
 TCACGGAAGA TGGGCGGAG GAACGCAACA CTTTGAACCA CTGTCTTGGC CTCCTTGTCA 2160  
 AGTCTGGAAC CCTCTCCCC TCGGACCGTG ACAGCAAGAT GTGCAAGATG ATCAGAGAGG 2220  
 ACTCTACCC AGGTACATC CCCAAGCCCA GGCAAGACTG CAATGCTGTG TCCACCTTCT 2280  
 GGATGGCCAA TCCCAACAAC AACCTCATCA ACTGTGCCGC TGCAGGATCT GAGGAAACTG 2340  
 70 | | | | | |  
 GATTTTGGTT TATTTTTCAC CACGTACCAA CGGGCCCCC CTGTGGGAATG TACTCCCCAG 2400  
 GTTATTGAGA GCACATTCCA CTGGGAAAT TCTATAACAA CCGAGCACAT TCCAACTACC 2460  
 GGGCTGGCAT GATCATAGAC AACGGAGTCA AAACCACCGA GGCCTCTGCC AAGGACAAGC 2520  
 GGCGGTTCTT CTCAATCATC TCTGCCAGAT ACAGCCCTCA CCAGGACGCC GACCCGCTGA 2580  
 AGCCCCGGGA GCCCGCATC ATCAGACACT TCAATGCTTA CAAGAACCAG GACCAAGGGG 2640  
 75 | | | | | |  
 CCTGGCTGCG CGCGGGGAT GTGTGGCTGG ACAGCTGCCA TTTCAAGGG GAGGCTCAGG 2700  
 AAGGCTTCTT GCTTACAGGA ATGAAGGCTG GGGGCATTTT GCTGGGGGGA GATGAGGCAG 2760  
 CCTCTGGAAT GGCTCAGGA TTCAGCCCTC CTGCGCTGAG CTGTCTGAAG CTGGTGACTA 2820  
 CGGGGTCGCC CTTTGTCTAC GTCTCTCTGG CCCACTCATG ATGGAGAAGT GTGGTCAGAG 2880  
 GGGAGCAATG GGCTTTGCTG CTTATGAGCA CAGAGGAATT CAGTCCCAG GCAGCCCTGC 2940  
 80 | | | | | |  
 CTCTGACTCC AAGAGGGTGA AGTCCACAGA AGTGAGCTCC TGCTTAGGG CCTCATTTGC 3000  
 TCTTCATCGA GGAATCTGAG CACAGGGGGC CTCCAGGAGA CCTAGATGT GCTCGTACTC 3060  
 CCTCGGCTTG GGAATTGAGA GCTGGAATA TAGAAAAATAT CTAGCCCAAA GCCTTCATT 3120  
 TAACAGATGG GGAAGGTGAG CCCCCAAGAT GGGAAAGAAC CACACAGCTA AGGGAGGGCC 3180  
 TGGGGAGCCC CACCTTAGCC CTTGCTGCCA CACCACATTG CCTCAACAAC CGGCCCCAGA 3240  
 GTGCCAGGC ACTCTGAGG TAGCTTCTGG AAATGGGGAC AAGTCCCCTC GAAGGAAAGG 3300

5 AAATGACTAG AGTAGAATGA CAGCTAGCAG ATCTCTTCCC TCCTGCTCCC AGCGCACACA 3360  
 AACC CGCCTT CCCC TTGGTGTG TTGGCGGTCC CTGTGGCCTT CACTTTGTTC ACTACCTGTC 3420  
 AGCC CAGCCT GGGTGCACAG TAGCTGCAAC TCCCATTTGG TGCTACCTGG CTCTCCTGTC 3480  
 TCTG CAGCTC TACAGGTGAG GCCCAGCAGA GGGAGTAGGG CTCGCCATGT TTCTGGTGAG 3540  
 CCAATT TGGC TGATCTTGGG TGTCTGAACA GCTATTGGGT CCACCCCACT CCCTTTCAGC 3600  
 TGCTGCTTAA TGCCCTGCTC TCTCCCTGGC CCACCTTATA GAGAGGCCAA AGAGCTCCTG 3660  
 TAAGAGGGAG AACTCTATCT GTGGTTTATA ATCTTGACAG AGGCACCAGA GTCTCCCTGG 3720  
 GTCTTGTGAT GAATACATT TATCCCTTTT CCTGCCCCAA CCACAAACTC TTTCTTCAA 3780  
 10 AGAGGGCCTG CCTGGCTCCC TCCACCCAAC TGCACCCATG AGACTCGGTC CAAGAGTCCA 3840  
 TTCCCCAGGT GGGAGCCAAC TGTGAGGGAG GTCTTTCCCA CCAACATCT TTCAGCTGCT 3900  
 GGGAGGTGAC CATAGGGCTC TGCTTTTAAA GATATGGCTG CTTCAAAGGC CAGAGTCACA 3960  
 GGAAGGACTT CTTCCAGGGA GATTAGTGGT GATGGAGAGG AGAGTTAAA TGACCTCATG 4020  
 TCCTTCTTGT CCACGGTTTT GTTGAGTTTT CACTCTTCTA ATGCAAGGCT CTCACACTGT 4080  
 15 GAACCACTTA GGATGTGATC ACTTTCAGGT GGCCAGGAAT GTTGAATGTC TTTGGCTCAG 4140  
 TTCAATTTAAA AAAGATATCT ATTTGAAAGT TCTCAGAGTT GTACATATGT TTCACAGTAC 4200  
 AGGATCTGTA CATAAAGTT TCTTTCCTAA ACCATTCAAC AAGAGCCAAT ATCTAGGCAT 4260  
 TTTCTTGGTA GCACAAATTT TCTTATTGCT TAGAAAAATG TCCTCTTGT TATTCTGT 4320  
 TGTAAAGACT AAGTGAGTTA GGTCTTTAAG GAAAGCAACG CTCCTCTGAA ATGCTTGTCT 4380  
 20 TTTTCTCTTT GCCGAAATAG CTGGTCCTTT TTCGGGAGTT AGATGTATAG AGTGTGTGTA 4440  
 TGTAAACATT TCTTGTAGGC ATCACCATGA ACAAAGATAT ATTTCTATT TATTATTAT 4500  
 ATGTGCACTT CAAGAAGTCA CTGTGACAGA AATAAAGAT TGTCTTAAAT GTCATGATTG 4560  
 GAGATGTCTT TTGCATTGCT TGGAAAGGGT GTACCTAGAG CCAAGGAAAT TGGCTCTGGT 4620  
 TTGGAATAAT TTTGCTGTTA TTATAGTAAA CATACAAAGG ATGTCAAAAA AAAAAAATAA 4680  
 25 AAAAAAATAA AAAAAAATAA AA 4702

Seq ID NO: C217 Protein Sequence  
Protein Accession #: NP\_005805.1

30 1 11 21 31 41 51  
 | | | | | |  
 MVGKMPVILW TLCAVRVTVD AISVETPQDV LRASQKSVT LPCTYHTSTS SREGLIQWDK 60  
 LLLTHTERVV IWPFSNKNYI HGELYKNRVS ISNNAEQSDA SITIDQLTMA DNGTYECSVS 120  
 LMSDLGNWTK SRVRLVLVLP PSKPECGIEG ETIIIGNNIQL TCQSKEGSPF PQYSWKRYNI 180  
 35 LNQEQLAQP ASGQPVSLKN ISTDTSGYII CTSSNEEGTQ FCNITVAVRP PSMNVALYVG 240  
 IAVGVVAALI IIGIIYYCCC CRGKDDNTED KEDARPNREA YEEPEQLRE LSREEREEDD 300  
 YRQEQQRSTG RESPHLDQ 319

Seq ID NO: C218 Protein Sequence  
Protein Accession #: Eos sequence

40 1 11 21 31 41 51  
 | | | | | |  
 MGSRTPEPSP HAVQLRWGPR RRPPLPLLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60  
 45 GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVLYCP WGASPTQCTP IEFDSKGSRL 120  
 LESSLSSESG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYLS 180  
 DNFRTRILEYA PCRSDFSWAA GGQYCGGGFS AEFTKTGRVV LGPGSYFWQ GQILSATQEQ 240  
 IAESYYPEYL INLVQGLQQT RQASSIYDSS YLGYSVAVGE FSGDDTEDFV AGVPKGNLTY 300  
 GVVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360  
 50 EVGRVYVYLQ HPAGIEPTPT LTLTGHDDEFG RFGSSLTPLG DLDDQDGYNDV AIGAPFGGET 420  
 QQGVVVFVFP GPQGLGSKPS QVLQPLWAAS HTPDFFGSAL RGRDLDGNG YPDLVGSFG 480  
 VDKAVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540  
 GFTVELQLDW QKQKGGVRRR LFLASRQATL QTQLLIQNGA REDCREMKIY LRNESEFRDK 600  
 LSPIHIALNF SLDPQAPVDS HGLRPAHLYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660  
 55 GEQNHVYLG D KVALNITFHA QNVGEGGAYE AELRVTPAPE AEYSGLVRHP GNFSSLSCDY 720  
 FAVNQSRLLV CDLGNPMKAG ASLWGGRLFT VPHLRDTKKT IQPDFQILSK NLNNSQSDVV 780  
 SFRLSVEAQA QVTILNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840  
 SQGVLELSCP QALEGGQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLSHH QQKREAPSR 900  
 SASSGPQILK CPBAECFRLR CELGPLHQQE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV 960  
 60 YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020  
 YKLGFFKRSL PYGTAMEKAQ LKPPATSDA 1049

Seq ID NO: C219 Protein Sequence  
Protein Accession #: NP\_002412.1

65 1 11 21 31 41 51  
 | | | | | |  
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60  
 VEKLRQMDEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTURIEN 120  
 70 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180  
 LAHAQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSGLGSHST DIGALMYP 240  
 TFGSDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFPKDR 300  
 FYMRTNPFYP EVELNFISVF WPQLPNGLA AYEFADRDEV RFFKGNKYWA VQGNVLHGY 360  
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRY DEYKRSMDPG YPKMIAHDFP 420  
 75 GIGHKVDADF MKDGGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN 469

Seq ID NO: C220 Protein Sequence  
Protein Accession #: Eos sequence

80 1 11 21 31 41 51  
 | | | | | |  
 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60  
 VEKLRQMDEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTURIEN 120  
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180  
 LAHAQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHAL GHSGLGSHST DIGALMYP 240

TFSGDVQLAQ DDIDGIQAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300  
 FYMRNPFYP EVELNFISVF WFQLENGLEA AYEFAADRDEV RFFKGNKYWA VQGQNVLHGY 360  
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFVANKYWRY DEYKRSMDFG YPKMIAHDFP 420  
 GIGHKVDADF MKDGFFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN 469

Seq ID NO: C221 Protein Sequence  
 Protein Accession #: NP\_055146.1

1 11 21 31 41 51  
 MVRKPVVSTI SKGGYLQGNV NGRLPSPGNK EPPGQEKVQL KRKVTLLRGV SIIIGTIIGA 60  
 GIFISPKGVL QNTGSSVGMSL TIWTVCGVLS LFGALSYAEL GTTIKSGGGH YTYILEVFGP 120  
 LPAFVRVWVE LLIIIRPAATA VISLAFGRYI LEPPFFIQCEI PELAIKLITA VGITVVMVLN 180  
 SMSVSWASARI QIFLTFCKLT AILIIIVPGV MQLIKGQTQN PKDAFSGRDS SITRLPLAFY 240  
 YGMAYAGWGF YLNFVTEEEVE NPEKTIPLAI CISMAITIGV YVLTNVAYFT TINAEEELLS 300  
 NAVAVTFSEER LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV 360  
 RKHTPLPAVI VLHPLTMIML FSGDLDSLNL FLSFARWLF GLAVAGLIYL RYKCPDMHRP 420  
 FKVPLFIPAL FSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM 480  
 SEKITRTLQI ILEVVPEDK L 501

Seq ID NO: C222 Protein Sequence  
 Protein Accession #: NP\_003237.1

1 11 21 31 41 51  
 MGLAWGLGVL FLMHVCGTNR IPESGGDNSV FDIFELTGAA RKGSGRRLVK GPDPSPPAFR 60  
 IEDANLIPPV PDDKFDQLVD AVRAEKGFLL LASLRQMKKT RGTLLALERK DHSGQVFSV 120  
 SNGKAGTLDL SLTVQKGQHV VSVEEALLAT GQWKSITLFV QEDRAQLYID CEKMEAEELD 180  
 VPIQSVFTRD LASIARLRIA KGGVNDNFQO VLQNVRFVFG TTPEDILRNK GCSSTSVLL 240  
 TLDNNVNGS SPAIRTNIGY HKTDLQAIC GISCEDELSSM VLELRGLRTI VTTLQDSIRK 300  
 VTEENKELAN ELRRPPLCYH NGVQYRNNEE WTVDSCTECH CQNSVTICKK VSCPIMPSCN 360  
 ATPVDGECPP RCWPSDADD GWSFWSEWTS CSTSCGNGIQ QGRSCDSLNL NRCEGSSVQT 420  
 RTCHIQECDK RFKQDGGWSH WSPWSSCSVT CGDGVITRIR LCNSPSPQMN GKPCGEARE 480  
 TKACKDACP INGGWGPWSP WDICSVTCGG GVQKRSRLCN NPAPQFGGKD CVGDVTENQI 540  
 CNKQDCPIDG CLSNPCFAGV KCTSYPDGSW KCGACPPGYS GNGIQCTDVD ECKEVPDADF 600  
 NHNGEHRCEH TDPGYNCLPC PPRFTGSQPF GQVEHATAN KQVCKPRNPC TDGTHDCNKN 660  
 AKCNYLGHYS DPMYRCECKP GYAGNGIICG EDTDLDGWPN ENLVCVANAT YHCKKDNCPN 720  
 LPNSGQEDYD KDGIQDADDD DDDNDKIPDD RDNCPPHYNP AQYDYDRDDV GDRCDNCPYN 780  
 HNPQADTDN NGEQDACAAD IDGDGILNER DNCQYVYNVD QRDMDMDGVG DQCDNCPLEH 840  
 NPDQLDSDSD RIGTCDNNQ DIEDDGHQNN LDNCPYVFNQ NQADHDKDGK GDACDHDDDN 900  
 DGIPDDKDNK RLVPNPQDK SDGDRGDAC KDDFDHDSVP DIDDICPENV DISETDFRRF 960  
 QMIPLDPKGT SQNDPNWVVR HQGKELVQTV NCDPGLAVGY DEFNAVDFSG TFFINTERDD 1020  
 DYAGFVFGYQ SSSRFYVVMW KQVTSYWDY NPTRAQGYSG LSVKVVNSTT GPGEHLRNAL 1080  
 WHTGNTPGQV RTLWHDPRHI GWKDFATYRW RLSHRPKTGF IRVVMYEGKK IMADSGPIYD 1140  
 KTYAGGRGLG FVFSQEMVFF SDLKYECRDP 1170

Seq ID NO: C223 Protein Sequence  
 Protein Accession #: NP\_002183.1

1 11 21 31 41 51  
 MPLLWLRLGFL LASCWIIIVRS SPTPGSEGHS AAPDCPSCAL AALPKDVPNS QPEMVEAVKK 60  
 HILNMLHLKK RPDVTQPPVK AALLNAIRKL HVGKVGENG YVEIEDDIGR AEMNELMEQT 120  
 SEIITFAESG TARKTLHFEI SKEGSDLSVV BRAEVWLFLK VPKANRTRTK VTIRLFQQQK 180  
 HPQGSLDTGE EAEVGLKGE RSELLSEKV VDARKSTWHV FVSSSIQRL LDQKSSLDV 240  
 RIACEQCQES GASVLLGKIK KKEEKEEGEK KKGKGEGGAG ADEEKEQSHR PFLMLQARQS 300  
 EDHPRHRRRR GLECDGKVINI CCKKQFFVSF KDIGWNDWII APSGYHANYC EGECPSHIAG 360  
 TSGSSLSFHS TVINHYMRG HSPFANLKSC CVPTKLRPMS MLYYDDGQNI IKKDIQNMIV 420  
 EECGCS 426

Seq ID NO: C224 Protein Sequence  
 Protein Accession #: NP\_000086.1

1 11 21 31 41 51  
 MVDPTACVLL LTLAALGASG QQSPLGSDL GPQMLRELQE TNAALQDVRD WLRQQVREIT 60  
 FLKNTVMECD ACGMQQSVRT GLPSVRPLLH CAPGFCFPV ACIQTESGGR CGPCPAGFTG 120  
 NGSHCTDVNE CNAHPCFPV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180  
 INECETGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDAQSG CQGAQRFCP DGSPSECEHE 240  
 ADCVLERDGS RSCVCRVGA GNGILCGRDT DLDGFPDEKL RCPEPQCRKD NCVTVPNSGQ 300  
 EDVDRDGIAD ACDPDADGDG VNEKDNCPV VRNPDQRNTD EDKWDACDN CRSQKNDQK 360  
 DTDQDGRGDA CDDIDIGDRI RNQADNCPRV PNSDQKSDG DGIQDADNC PQKSNPDQAD 420  
 VDHFVGDGAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQDQDAD DDDNDGVPS 480  
 RDNCRLVPPN GQEDADRDGV GDVCQDDFDA DKVVDKIDVC PENAETVLT DFRFQTVVLD 540  
 PEGDAQIDPN WVLNQGREGI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600  
 FGQDSSSFY VVMWQMEQT YWQANPFRV AEPGIQLKAV KSSTGPEQL RNALWHTGDT 660  
 ESQVRLWKD PRNVGWKDKK SYRWFLQHRP QVGYIRVRFY EGPELVADSN VVLDTMTMGG 720  
 RLGVFCFSQE NIWIANLRYR CNDTIPEDYE THQLRQA 757

Seq ID NO: C225 Protein Sequence  
 Protein Accession #: NP\_612464

1 11 21 31 41 51



MRPQGPAAASP QRLRGLLLLL LLQLPAPSSA SEIPKGKQKA QLRQREVVDL YNGMCLQGPA 60  
 GVPGRDGSFG ANGIPGTGPI PGRDGFKEGK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120  
 GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECGSL PIEAIIYLDQ 180  
 GSPMNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240  
 LPK 243

Seq ID NO: C226 Protein Sequence  
 Protein Accession #: NP\_003216.1

1 11 21 31 41 51  
 MATMENKVIC ALVLVSMAL GTLAEAQTTET CTVAPRERQN CGFPGVTPSQ CANKGCCFDD 60  
 TVRGVPWCYF PNTIDVPPEE ECEF 84

Seq ID NO: C227 Protein Sequence  
 Protein Accession #: NP\_056234.1

1 11 21 31 41 51  
 MPKRAHWGAL SVVLILLWGH PRVALACPHP CACYVPSEVH CTFRSLASVP AGIARHVERI 60  
 NLGFNSIQAL SETSFAGLTK LELLMIHNE IPSIPDGALR DLSSLQVFKF SYNKLRLVITG 120  
 QTLQGLSNLM RLHIDHNKIE FTHPQAFNGL TSLRLHLLEG NLLHQLHPST FSTFTFLDYF 180  
 RLSTIRHLYL AENMVRTLPA SMLRNMPLE NLYLQGNPWT CDCEMRWFLE WDAKSRGILK 240  
 CKKDKAYEGG QLCAFCFSK KLYKHEIHKL KDMTCLKPSI ESPLRQNRSR SIEEEQEQUE 300  
 DGGSQILILEK FQLPQWSISL NMTDEHGNMV NLVCDIKKPM DVYKIHNLQT DPPDIDINAT 360  
 VALDFECPMT KSGGLPSKRG IAYSEVPVK LHRELMLSKD PRVSYQYRQD ADEEALYYTG 420  
 VRAQILAEPE WVMQPSIDIQ LNRQRSTAKK VLLSYTYQYS QTISTKDTRQ ARGSRVWMIE 480  
 PSQAVQRDQT VLEGGPCQLS CNVKASESPS IFWVLPDGS LKAPMDPDS KFSILSSGWL 540  
 RIKSMEPSDS GLYQCIQAVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGKN PGESVTLPCN 600  
 ALALPEAHL WILPNRIIN DLANTSHVM LPNGTSLIPK VQVSDSGYYR CVAVNQGGAD 660  
 HFTVGTITVK KSGGLPSKRG RRPQAKALSR VREDIVEDEG GSGMGDEENT SRLLHPKQD 720  
 EVFLKTKDDA INGDKKAKKG RRLKLLWKHS EKEPETNVAE GRRVFESRRR INMANKQINP 780  
 ERWADILAKV RGNLPLKGT VPPLIKTTSP PSLSEVTPP FPAVSPSPAS PVQTVTSAGE 840  
 SSADVPLLE EHVLTGISS ASMGLEHNNH GVILVEPEVT STPLEEVVDD LSEKTEEITS 900  
 TEGDLKGTA PTLISEPYEP SPLTLTLDVT YEKPTHEETA TEGWSAADVG SSPEPTSSEY 960  
 EPPLDAVSLA ESSEMQYFDP DLETKSQPDE DKMKEDTFAH LTPPTIWN DSSTSOLFED 1020  
 STIGEPGVPG QSHLQGLTDN IHLVKSSLST QDTLLIKKGM KEMSQTLQGG NMLEGDPHTS 1080  
 RSSESEGGES KSITLPDSTL GIMSSMSPVK KPAETTVGTL LDKDTTITVT TPRQKVAPSS 1140  
 TMSTHPSRRR PNRRRLRPN KFRHRHKQTP PTTFAPSETF STQPTQAPDI KISSQVSSSL 1200  
 VPTAWVDNTV NTPKQLEMEK NAEPTSKGTP RRRKHGKREN HRYTPSTVSS RASGSKPSPS 1260  
 PENKHNIVT PSSETILLPR TVSLKTEGYP DSDYMTTTR KIYSSYPKVQ ETLPTVTKPT 1320  
 SDGKEIKDDV ATNVDKHKSD ILVTGESITN AIPTSRSLVS TMGEFKEESS PVGFPPTPTW 1380  
 NPSRTAQPR LQTDIPVTS GENLTDPPLL KELEDVDFTS EFLSSLTVST PFHQEEAGSS 1440  
 TLLSSIKVEV ASSQAETTL DQDHLETTVA ILLSETRPQN HTPTAARMKE PASSSPSTIL 1500  
 MSLGQTTTITK PALPSRISQ ASRDSKENVF LNYVGNPETE ATPVNEGTO HMSGNELST 1560  
 PSSDRDAFNL STKLELEKQV FGSRSLPRGP DSQRQDGRVH ASHQLTRVPA KPILPTATVR 1620  
 LPEMSTQAS RYFVTQSQR HTWNKPEITT YPSGALPENK QFTTPRLSST TIPLPLHMSK 1680  
 PSIPSKFTDR RTDQFNGYSK VFGNNNIEPA RNPVGKPPSP RIPHYSNGRL PFFTKNTLSF 1740  
 PQLGVTRRPQ IPTSPAVMR ERKVIPGSYN RIHSHSTFHL DFGPPAPPLL HTPQTGSPS 1800  
 TNLQNPVMS STQSSISFIT SSVQSSGSFH QSSSKFFAGG PPASKFWSLG EKPQILTKSP 1860  
 QTVSVTAETD TVFPCEATGK PKPFVWTWKV STGALMTPT RIQRFVLEKN GTLVIRKQVQ 1920  
 QDRGQYMCTA SNLHGLDRMV VLLSVTVQOP QILASHYQDV TVYLGDTIAM ECLAKGPAP 1980  
 QISWIFPDRR VQVTVSPVES RITLHENRTL SIKEASFSDR GYKCVASNA AGADSLAIRL 2040  
 HVAALPPVIH QEKLENISLP PGLSIHICT AKAAPLPSVR VVLGDGTQIR PSQFLHGNLF 2100  
 VFPNGTLYIR NLAPKDSGRY ECVAAANLVS ARRTVQLNVQ RAAANARITG TSPRRTDVRY 2160  
 GGTLKLDCA SGGPWPRILW RLPSKRMIDA LFSFDSRIK FANGTLVVKV VTDKADGYL 2220  
 CVARNKVGDD YVVLKVDVVM KPAKIEHKEE NDHKVFYGGD LKVDCAVTLG PNPEISWSLP 2280  
 DGSLVNSFMQ SDDSGGRTRK YVVFNNGTLY FNEVGMRERG DYTCAENQV GKDEMRVRVK 2340  
 VVTAPATIRN KTYLAVQVPY GDVVTVACEA KGEPMKVTW LSPTNKVPT SSEKYQIYQD 2400  
 GTLLIQKAQR SDGNYTCLV RNSAGEDRKT VVHVNVPQP KINGNPNPIT TVREIAAGGS 2460  
 RKLIDCKAEG IPTPRVLWAF PEGVVLPAFY YGNRITVHGN GSLDIRSLRK SDSQVLVCMA 2520  
 RNEGGEARLI VQLTVLEPME KPIFHDPIS KITAMAGHTI SLNCSAAGTP TPSLVVVLN 2580  
 GTDLQSGQQL QRIFYHKADGM LHISGLSSVD AGAYRCVARN AAGHTERLVS LKVGLKPEAN 2640  
 KQYHNLVSI NGETLKLPT PPGAGQGRFS WTLPNMGHLE GPQTLGRVSL LDNGTLTVRE 2700  
 ASVFDRTGYV CRMETEYGPS VTSIPVIVIA YPPRITSEPT PVIYTRPGNT VKLNCMAMGI 2760  
 PKADITWELP DKSHLKAGVQ ARLYGNRFLH PQGSLTIQHA TQRDAGFYKC MAKNILGSDS 2820  
 KTTYIHVF 2828

Seq ID NO: C228 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MPGTKLIRTG APADYRVILK TSQEDELDPV DDISVRVMSS QSVLVSVDV VLEKQKKVVA 60  
 SRQYTVRYRE KGEARLWDYK QIANRRVLIE NLIPDTVYEF AVRISQGERD GKWSTSVFQR 120  
 TPESAPTAP ENLNVVPVNG KPTVVAASWD ALPETEGKVK VCLLDGLFS VSSFQPSAKS 180  
 FQNTFFHTPR LSNHLEQSPS PILETLLLPW WMVCSLGNAI FSKSGPQTGE AWDLTPKPSL 240  
 SLCQCECST QKDFSLCLAYL IDIQTKQVKN DPQLEGSVFG PCFLFYFLT MLDIGGFSFI 300  
 MCYEDP?VSS LTGNSLKSVA ASKADVQONT EDNGKPEKPE PSSPSRAPA SSQHPSVPAS 360  
 PQGRNAKDL LDKNLKILAN GGAPRKQLR AKKAEELDLQ STEITGEEEL GSREDSPMSP 420  
 SDTQDKQRTL RPPSRHGSV VAPGRTAVRA RMPALPRRG VDKPGFSLAT QPRPGAPPSA 480  
 SASPAHHAST QGTSHRPSLP ASLNDNDLVD SDEDERAVGS LHPKGAFAPQ RPALSPSRQS 540  
 PSSVLDRSS VHGAPKASP ARRTPHSGAA EEDSSASAPP SRLSPHGGG SRLLPQPHL 600  
 SSPLSKGGKD GEPAPATNSN APSRSTMSSS VSSHLSRTQ VSEGAASDG ESHGDGDRED 660

GGRQAEATAQ TLRARPASGH FHLLRHKFFA ANGRSPSRFS IGRGPRLQPS SSPQSTVPSR 720  
 AHPRVPSHSD SHPKLSSGIH GDEDEKPLP ATVVNDHVPS SSRQPISRGW EDLRRSPQRG 780  
 ASLHHRKEPI ENPKSTGADT HFQGYSSLA SKAQDVQQST DADTEGHSPK AQPGSTDRHA 840  
 SPARPPAARS QQHPSVPRRM TPGRAPQQP PPPVATSQHH PGFQSRDAGR SPSQPRLSLT 900  
 QAGRPRPTSQ GRSHSSSDPY TASSRGMLEP ALQNQDEDAQ GSYDDDDSTEV EAQDVRAPAH 960  
 AARAKEAAS LPHKQQVESV TGAGAGGDHR SQRGHAASPA RPSRPGGPQS RARVPSRAAP 1020  
 GKSEPPSKRP LSSKQQSVS AEDEEEDAG FFKGGKEDLL SSSVPKWPSS STPRGGKDAD 1080  
 GSLAKEEREP AIALAPRGGS LAPVKRPLPP PPGSSPRASH VPSRPPPSA ATVSPVAGTH 1140  
 PWPRYTTRAP PGHFSTTPLL SLRQRMHAR FRNPLSRQPA RPSYRQGYNG RPNVEGKVLP 1200  
 GSNKPNQGR IINGQVCSPE VVDLDRGLVL NAEGRYLQDS HGNPLRIKLG GDGRTIVDLE 1260  
 GTFVVSPEGL PLFGQGRHGT PLANAQDKPI LSLGGKPLVG LEVIKKTTHP PTTTMMQPTT 1320  
 TTPLPTTTTP RPTTATTMQP TTTTTPLETT TPRPTTATTR RTTTRRPTTT VRTTTRTTTT 1380  
 TTPKPTTPIP TCPPGTLEPH DDDGNLIMSS NGIPECYAEE DEFSGLETDI AVPTTEAYVI 1440  
 YDEDEYFETS RPTTTEPST TATTPRVPE EGAISSFPPE EFDLAGRKRF VAPYVTYLNK 1500  
 DPSAPCSLTD ALDHFOVDL DELIPNDLKK SLPQPHAPR NITVVAVEGC HSFVIDWDK 1560  
 ATPGDLVTGY LVYSASYEDF IRNKFTQAS SVTHLPIENL KPNTYFYFKV QAQNPHGYGP 1620  
 ISPSVSFVTE SDNPLLVVRP PGGELSGSHS LSNMIPATRT AMDGNM 1666

Seq ID NO: C229 Protein Sequence  
Protein Accession #: NP\_003005.1

1 11 21 31 41 51  
 MFLSILVALC LNLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ 60  
 YEELVDVNCV AVLRFFFCAM YAPICTLEFL HDPIKPKCSV CQRARDDCEP LMKMYNHSWP 120  
 ESLACDELFP YDRGVCISPE AIVTDLEPVD KWIDITPDMM VQERPLDVC KRLSPDRCK 180  
 KKVKPTLATY LSKNYSYVIH AKIKAVQORS CNEVTTVVVD KEIFKSSSPI PRTQVPLITN 240  
 SSCQCPHILP HQDVLIMCYE WRSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRVTQD 300  
 KKKTAGRTSR SNPPKPKGKP PAKPKASPKK NIKTRSAQKR TNPKRV 346

Seq ID NO: C230 Protein Sequence  
Protein Accession #: NP\_005931.1

1 11 21 31 41 51  
 MAPAAWLRSR AARALLPPML LLLLQPPPLL ARALPPDVHH LHAERRGPQP WHAALPSSPA 60  
 PAPATQEAAP PASSLRPPRC GVPDPSDGLS ARNRQKRFLV SGGRWKTDL TYRILRFPWQ 120  
 LVQEQVRQTM AEALKVWSDV TPLTFTVEVHE GRADIMIDFA RYWHGDDLFP DPGGILAHA 180  
 FFPKTHREGD VHFYDYDETWT IGDDQGTDL LQVAAHEFGHV LGLQHTTAAK ALMSAFYTFR 240  
 YPLSLSPDDC RGQVHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300  
 VSTRGELFF FKAGFVWRLR GGQLQPGYPA LASRHWQGLP SPVDAAFEDA GQHIWFFQGA 360  
 QYWYDGEKPP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVDS 420  
 VPPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFD P VKVKALEGFP RLVGPDFFGC 480  
 AEPANTFL 488

Seq ID NO: C231 Protein Sequence  
Protein Accession #: NP\_076927

1 11 21 31 41 51  
 MCENDEPAVE APFSFRSLFG LDDLKISPPA PDADAVAAQI LSLPLKFFFP IIVIGIILI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF 120  
 TAASWKTMCV DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180  
 VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQFQGYH 240  
 LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFNEMI QPVCLPNSSE NFPDGKVCWT SGWGATEDGG DASVNLHAA 360  
 VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSCQGDS GGPLVCQERR LWKLVGATSF 420  
 GIGCAEVNKP GVTYRTVSFL DWIHEQMERD LKT 453

Seq ID NO: C232 Protein Sequence  
Protein Accession #: NP\_003211

1 11 21 31 41 51  
 MLWKLTDNIK YEDCEDRHDG TSNGTARLPQ LGTVGQSPYT SAPPLSHTPN ADFQPPYFPP 60  
 PYQPIYPQSQ DPFYSHVNDPY SLNPLHAQPQ PQHPGWPGQR QSQESGLLHT HRGLPHQLSG 120  
 LDPRRDYRRH EDLLHGPHAL SSGLGDLISIH SLPHAIIEVP HVEDPGINIP DQTVIKKGPV 180  
 SLSKSNNAV SAIPINKDNL FGGVVNNEV FCSVPGRLSL LSSTSXYKVT VAEVQRRLSP 240  
 PECLNASLLG GVLRRRAKSKN GGRSLREKLD KIGLNLPAQR RKAANVTLLT SILVEGEAVHL 300  
 ARDFGYVCET EFPKAVAEF LNRQHSDPNE QVTRKNMLLA TKQICKEFTD LLAQDRSPLG 360  
 NSRPNPILEP GIQSCSLTFHN LISHGFGSPA VCAAVTALQN YLTEALKAMD KMYLSNNPNS 420  
 HTDNNAKSSD KEEKHRK 437

Seq ID NO: C233 Protein Sequence  
Protein Accession #: NP\_002979.1

1 11 21 31 41 51  
 MKGLAAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKFIVDYSET SPQCCKPGVI 60  
 LLTKRGRQIC ADPNKKWVQK YISDLKLNA 89

Seq ID NO: C234 Protein Sequence  
Protein Accession #: NP\_004054.1

	1	11	21	31	41	51	
5	MILQAHLSL	CLLMYLATG	YGQEGKFSGP	LKPMFTSIYE	GQEPSQIIFQ	FKANPPAVTF	60
	ELTGEDTNIF	VIEREGLLYY	NRALDRETRS	THNLQVAALD	ANGIIVEGPV	PITIEVKDIN	120
	DNRPTFLQSK	YEGSVRQNSR	PGKPFLYVNA	TDLDDPATPN	GQLYYQIVIQ	LPMINNVMYF	180
	QINNKTGAIS	LTREGSQELN	PAKNPSYNLV	ISVKDMGGQS	ENSFSDTTSV	DIIVTENIWK	240
	APKPVEMVEN	STDHPPIKIT	QVRWNDPGAQ	YSLVDKEKLP	RFFPSIDQEG	DIYVTQPLDR	300
10	EKDAYVFYA	VAKDEYKPL	SYPLEIHVKV	KDINDNPPTC	PSPVTVFVQ	ENERLGNSIG	360
	TLTAHRDEE	NTANSFLNYR	IVEQTPKLP	DGLFLIQTYA	GMLQLAKQSL	KKQDTPQYNL	420
	TIEVSDKDFK	TLCFVQINVI	DINDQIPIFE	KSDYGNLTAL	EDTNIGSTIL	TIQATDADEP	480
	FTGSSKILYH	IIKGDSEGR	GVDTDPHTNT	GYVVIKKPLD	FETAAVSNIV	FKAENPEPLV	540
	FGVKYNASSF	AKFTLIVTDV	NEAPQFSQHV	FQAKVSEDVA	IGTKVGNVTA	KDPEGLDISY	600
15	SLRGDTRGWL	KIDHVTGEIF	SVAPLDREAG	SPYRVQVAT	EVGGSSLSV	SEFHLILMDV	660
	NDNPPRLAKD	YTGLFFCHPL	SAPGSLIFEA	TDDQHLFRG	PHFTFSLGSG	SLQNDWEVSK	720
	INGTHARLST	RHTEFEEREY	VVLIRINDGG	RPPLEGIVSL	PVTFCSCEVG	SCFRPAGHQT	780
	GIPTVGMAVG	ILLTTLVLIG	IILAVVFIRI	KKDKGKDNVE	SAQASEVKPL	RS	832

Seq ID NO: C235 Protein Sequence  
Protein Accession #: NP\_004434.1

	1	11	21	31	41	51	
25	MARARPPPPP	SPPFGLPLLL	PPLLLPLLLL	LPAGCRALAE	TLMDTKWVTS	ELAWTSHPES	60
	GWEEVSGYDE	AMNPRTYQV	CNVRESSQNN	WLRTGFIWRR	DVQRVVELK	FTVRDCNSIP	120
	NIPGSCKETF	NLFYIEADSD	VASASSPFWM	ENPYVKVDTI	APDESFSRLD	AGRVNTKVR	180
	FGPLSKAGFY	LAFOQDQACM	SLISVRAFYK	KCASTTAGFA	LFPETLTGAE	PTSLVIAPGT	240
	CIPNAVEVS	PLKLYCNGDG	EMWVPVGACT	CATGHEPAAK	ESQCRPCPPG	SYKAKQEGEP	300
30	CLPCPPNSRT	TSPAASICTC	HNNFYRADSD	SADSACTTVP	SPPRGVISNV	NETSLILEWS	360
	EPRLDGRDD	LLYNVICCKK	HGAGGASACS	RCDDNVEFVP	RQLGLTERRV	HISHLAHTR	420
	YTFEVQAVNG	VSGSKPLFPR	YAAVNITNQ	AAPSEVPTLR	LHSSSGSLT	LSWAPPERPN	480
	GVILDYEMKY	FEKSEGIAS	VTSQMNSVQL	DGLRPDARYV	VQVRARTVAG	YGQYSRPAEF	540
	ETTSESGGA	QQLQEQLPLI	VGSATAGLVF	VVAVVVIAIV	CLRKQRHGSD	SEYTEKLQQY	600
35	IAPGMKVYID	PFTYEDPNEA	VREFAKEIDV	SCVKIEEVIG	AGEFGEVCRG	RLKQPGRRREV	660
	FVAIKTLKVG	YTERQRDFL	SEASIMGQFD	HPNIIRLEGV	VTKSRPVMIL	TEFMENCALD	720
	SFLRLNDGQF	TVIQLVGLMR	GIAAGMKYLS	EMNYVHRDLA	ARNILVNSNL	VCKVSDFGLS	780
	RFLEDDPSDP	TYTSSLGSKI	PIRWTAPPAI	AYRKFTSASD	VWSYGIWMVE	VMSYGERPYW	840
	DMSNQDVINA	VEQYRLPPP	MDCPTALHQL	MLDCWVRDRN	LRPKFSQIVN	TLDKLIRNAA	900
40	SLKVIASQS	GMSQPLLDRT	VPDYTTFTTV	GDWLDIAKMG	RYKESFVSAG	FASFDLVAQM	960
	TAEDLLRIGV	TLAGHQKKIL	SSIQDMRLQM	NQTLFVQV			998

Seq ID NO: C236 Protein Sequence  
Protein Accession #: NP\_001795.1

	1	11	21	31	41	51	
45	MYVGYVLDDK	SPVYPGPAPR	ASLGLGPANY	GPPAPPPAPP	QYPDFSSSYH	VEPAPAPPTA	60
	WGAPFPAPKD	DWAAAYGPGP	AAPASPASL	AFGPPPDFSP	VPAPPGPGFG	LLAQPLGGFG	120
50	TPSSPGAQRP	TPYEMRRSV	AAGGGGSGSK	TRTKDKYRVV	YTDHQRLELE	KEFHYSRYIT	180
	IRRKSELAAN	LGLTERQVKI	WFQNRRAKER	KVNKKKQQQQ	QPPQPPMAHD	ITATPAGPSL	240
	GGLCPSTSL	LATSSPMPVK	EEFLP				265

Seq ID NO: C237 Protein Sequence  
Protein Accession #: NP\_068813.1

	1	11	21	31	41	51	
60	MGSDRARKGG	GPKDFGAGL	KYNSRHEKVN	GLEEGVEFLP	VNNVKKVEKH	GPGRWVVLAA	60
	VLIGLLLVLL	VGFLVWHLQ	YRDVRVQKVF	NGYMRITNEN	FVDAYENSNS	TEFVSLASKV	120
	KDALLLYSYG	VPFLGYPHKE	SAVTAASEGS	VIAIYWSEFS	IPQHLVEEAE	RVMAEERVVM	180
	LPFRARSLKS	FVVTSVVAF	TDSKTVQRTQ	DNSCSFGLHA	RGVELMRFTT	PGFPDSPYPA	240
	HARCQWALRG	DADSVLSLTF	RSFDLASCDE	RGSDLVTVYN	TLSPMEPHAL	VQLCGTYPPS	300
65	YNLTFHSSQN	VLLITLITNT	ERRHPGFEEAT	FFQLPRMSSC	GGRLRKAQGT	FNSPYYPGHI	360
	PPNIDCTWNI	EVENNQHVKV	RFKFFYLLEP	GVPAAGTCPKD	YVEINGEKYC	GERSQFVVT	420
	NSNKITVRFH	SDQSYTDTGF	LAELYLSYDSS	DPCPGQFTCR	TGRCIRKELR	CDGWADCTDH	480
	SDELNCSCDA	GHQFTCKNKF	CKPLFWVCD	VNDCGDNSE	QGCSCPAQTF	RCSNGKCLSK	540
	SQCCNGKDDC	GDGSDASCP	KVNVTCTKH	TYRCLNGLCL	SKGNPECDGK	EDCSGSGDEK	600
70	DCDCGLRSFT	RQARVVGGTD	ADEGEWFWQV	SLHALGQGHI	CGASLISPWN	LVSAAHCYID	660
	DRGFRYSIPT	QWTAFLGLHD	QSQRSAAGVQ	ERRLKRIISH	PFFNDFTFDY	DIALLELEKP	720
	AEYSSMVRPI	CLPDASHVFP	AGKAIWVTGW	GHTQYGGTGA	LILQKGEIRV	INQTTCCENLL	780
	PQQITPRMMC	VGLSLGGVDS	CQDGSGLPLS	SVEADGRIFQ	AGVVSWDGDC	AQRNKGVTY	840
	RLPLFRDWIK	ENTGV					855

Seq ID NO: C238 Protein Sequence  
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
80	MPPFLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAQFSSSTPH	LEFPLDSFST	QOEVKARIKR	120
	MVFKGGRTE	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
	FAVGVRFPFR	EELHALASEP	RQGHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCEHRTLEMV	REPAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTTHPATC	YRTTCGPGCD	300
	SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVLLFLDLS	SAGTTLDGFL	360

RAKVFKRVFV RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420  
 LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVG 480  
 EAVRAELEEI TGSPKHMVMY SDPQDLFNQI PELQGLKCSR QRPQCRTQAL DLVFMMLDTSA 540  
 SVGPENFAQM QSFVRSALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 APYLVGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVL T GGRGAEDAAV PAQKLRRNGI 660  
 SVLVVGVGPFV LSEGLRRLAG PRDSLHVA YADLRHQDV LIEWLCGEAK RPNVNLCKPSP 720  
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR FLRRP 755

Seq ID NO: C239 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 MPFFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60  
 SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120  
 MVFKGRTTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180  
 FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240  
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPPFYSWK RVFLTHPATC YRTTCPGPCD 300  
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360  
 RAKVFKRVFV RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420  
 LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVG 480  
 EAVRAELEEI TGSPKHMVMY SDPQDLFNQI PELQGLKCSR QRPQCRTQAL DLVFMMLDTSA 540  
 SVGPENFAQM QSFVRSALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600  
 APYLVGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVL T GGRGAEDAAV PAQKLRRNGI 660  
 SVLVVGVGPFV LSEGLRRLAG PRDSLHVA YADLRHQDV LIEWLCGEAK RPNVNLCKPSP 720  
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780  
 RTPPSNYREG LGTEMVPTFW NVCAPGP 807

Seq ID NO: C240 Protein Sequence  
 Protein Accession #: XP\_097386.1

1 11 21 31 41 51  
 | | | | |  
 MPKSEPLGCL SPASRAPGSA AATGAWLPAA SGGPGPLGPP CTCPPRSLGR GRAGSRAGSS 60  
 PSGCVCVSGI LRVVSVGDPA SRRWVDLDSN SEDLSLLLT MIVGTGGVGG GWARGWVPAQ 120  
 EKEVAEGSGH AGRNGRRRLQ RVVGARSWIL GRKPCQLRLL PASGGPVQPP PCPSPATACR 180  
 WGFKFGVAFV GAAQHPPLCR LGGGRAVPFA TRTLDGF 217

Seq ID NO: C241 Protein Sequence  
 Protein Accession #: CAC03433

1 11 21 31 41 51  
 | | | | |  
 MLSSTDFTFA SWELVVRVDH PNEEQQKQDV LRVSGDLHVG GVMLKLVEQI NISQDWSDF 60  
 LWWEQKHCHW LKTHWTLDDY GVQADAKLLF TPQHKMLRLR LPNLKMYRLR VSFSAVVFKA 120  
 VSDICKILNI RRSEELSLK PSGDYFKKKK KKDKNKEPI IEDILNLESS PTASGSSVSP 180  
 GLYSKTMTPY YDPINGTPAS STMTWFSDSP LTEQNCSILA FSQPPQSPEA LADMYQPRSL 240  
 VDKAKLNAGW LDSSRSLEMEQ GIQEDDEQLL RFKYYSFFDL NPKYDAVRIN QLYEQARWAI 300  
 LLEEDICTEE EMLIFAALQY HISKLSLAE TQDFAGESEV DEIEAALSNL EVTLEGGKAD 360  
 SLEEDITDIP KLANLKLFR PKLLPKAFK QYWFIFKDT S IAYFKNKELE QGEFLEKLNL 420  
 RGCEVVPDYN VAGRKFGIKL LIPVADGMNE MYLRCDHENQ YAQWMAACML ASKGKTMADS 480  
 SYQPEVLNII SFLRMKNRNS ASQVASSLEN MDMNPECFVS PRCACKHKSQ QLAARILEAH 540  
 QNVAQOMPLVE AKLRFIOAW SLPEFGLTY LVRFKGSKKD DILGVSYNRL IKIDAATGIP 600  
 VTTWRFTNIK QWNVNWETRP VVIEFDQNVF TAFTCLSDAC KIVHEYIGGY IFLSTRSKDQ 660  
 NETLDEDLFH KLTGGQD 677

Seq ID NO: C242 DNA Sequence  
 Nucleic Acid Accession #: NM\_005170  
 Coding sequence: 337..918

1 11 21 31 41 51  
 | | | | |  
 GGGCGTGAGA AAGGCGACGG CGGCGGCGCG GAGGAGGGTT ATCTATACAT TAAAAACCA 60  
 GCCGCCTGCG CCGCGCCTGC GGAGACCTGG GAGAGTCCGG CCGCACGCGC GGGACACGAG 120  
 CGTCCACGCG TCCCTGGCGC GTACGCGCTG CCACCACTAG GCCTCCTATC CCCGGGCTCC 180  
 AGACGACCTA GGACGCGTGC CCTGGGGAGT TGCTGCGCG CGCCGTGCCA GAAGCCCCCT 240  
 TGGGGCGCCA CAGTTTTCCT CGTCGCTTCC GGTTCCTCTG CCTGCACCTT CCGCGGCGC 300  
 GCCGGGACCT GGAGCGGCGG GGTGGATGCA GGCAGCATGG ACGGCGGCAC ACTGCCAGG 360  
 TCCGCGCCCC CTGCGCCCCC CGTCCCTGTC GGCTGCGCTG CCGGCGGAG ACCCGCTCC 420  
 CCGGAAGTGT TGCCTGTCAG CCGGCGGCGG CGACCGGCCA CCGCAGAGAC CGGAGGCGGC 480  
 GCAGCGGCGG TAGCGCGGCG CAATGAGCGC GAGCGCAACC GCGTGAAGCT GGTGAAGTGT 540  
 GGCTTCCAGG CGCTGCGGCA GCACGTGCGG CACGGCGGCG CCAGCAAGAA GCTGAGCAAG 600  
 GTGGAGACGC TGCCTGTCAG CGTGGAGTAC ATCCGCGCGC TGCAGCGCCT GCTGGCCGAG 660  
 CACGACGCCG TGCCTGTCAG GCTGGCGGGA GGGCTGAGGC CGCAGGCCGT GCGGCCGTCT 720  
 GCGCCCCGCG GCGCGCCAGG GACCAACCCG GTCGCGGCTT CGCCCTCCCG CGCTTCTTCG 780  
 TCCCGGGGCG GCGGGGGCAG CTCGGAGCCC GGCTCCCGCG GTTCCGCTCA CTCGTCCGAC 840  
 GACAGCGGCT GCGAAGCGCG GCTGAGTCTT GCGGAGCGCG AGCTACTCGA CTCTCCAGC 900  
 TGGTTAGGGG GCTACTGAGC GCCCTCGACC TA 932

Seq ID NO: C243 Protein Sequence  
 Protein Accession #: NP\_060233.1

1 11 21 31 41 51

	MSGGHQLQLA	ALWPLLMAT	LQAGFGRTGL	VLAAAVESER	SAEQKAVIRV	IPLKMDPTGK	60
	LNLTLLEGVFA	GVAEITPAEG	KLMQSHPLYL	CNASDDDNLE	PGFISIVKLE	SPRRAPRPL	120
5	SLASKARMAG	ERGASAVLFD	ITEDRAAAEQ	LQQPLGLTWP	VVLIWGNDAE	KLMEFVYKNQ	180
	KAHVRIELKE	PPAWPDYDVW	ILMTVVGTIF	VILLASVLRI	RCRPRHSRPD	PLQORTAWAI	240
	SQLATRRYQA	SCRQARGEWP	DSGSSCASSAP	VCAICLEEPS	EQQELRVISC	LHEFHRCNVD	300
	PWLHQHRTCP	LCVFNITEGD	SFSQSLGPSR	SYQEPGRRLH	LIRQHPGHAH	YHLPAAYLLG	360
	PSRSAVARPP	RPGFPLPSQE	PGMGRPHRRF	PRAAHPRAPG	EQQLLAGAQH	PYAQGWGMSH	420
10	LQSTSQHAAA	CPVPLRRARP	PDSSGSGESY	CTERSGYLAD	GPASDSSSGP	CHGSSSDSVV	480
	NCTDISLQGV	HGSSSTFCSS	LSSDFDPLVY	CSFKGDPQRV	DMQPSVTSRP	RLSDSVVPTG	540
	ETQVSSHVHY	HRHRHHHYKK	RFQWHGRKPG	PETGVPSQSR	PIPTQPOQPE	PSPDQQVVTG	600
	SNSAAPSGR	SNPQCPRALP	EPAPGPVDAS	SICPSTSSLF	NLQKSSLSAR	HPQRKRGGP	660
	SEPTGSRPQ	DATVHPACQI	FPHYTPSVAY	PWSPEAHPLI	CGPPGLDKRL	LPETPGPCYS	720
15	NSQPVLCLT	PRQPLEPHPP	GEGPSEWSSD	TAEGRPCYP	HCQVLSAQPG	SEEELEELCE	780
	QAV						783

Seq ID NO: C244 DNA Sequence  
Nucleic Acid Accession #: NM\_004289  
Coding sequence: 493..1695

	1	11	21	31	41	51	
	GCCGCCGCCCT	CGTCCACCGG	AGGAGCCGGC	GCCAGCGTGG	ACGGCGGCAG	CCAGGCTGTG	60
25	CAGGGGGGCG	GCGGGGACCC	CCGAGCGGCT	CGGAGTGCC	CCTTGGACGC	CGGGGAAGAG	120
	GAGAAGGCAC	CCGCGGAACC	GACGGCTCAG	GTGCCGACG	CTGGCGGATG	TGCGAGCGAG	180
	GAGAATGGGG	TACTAAGAGA	AAAGCACGAA	GCTGTGGATC	ATAGTTCCCA	GCATGAGGAA	240
	AATGAAGAAA	GGGTGTGAGC	CCAGAAGGAG	AACTCACTTC	AGCAGAATGA	TGATGATGAA	300
	AACAAAATAG	CAGAGAAACC	TGACTGGGAG	GCAGAAAAGA	CCACTGAATC	TAGAAATGAG	360
30	AGACATCTGA	ATGGGACAGA	TACTTCTTTC	TCTCTGGAAG	ACTTATTCCA	GTTGCTTTCA	420
	TCACAGCCTG	AAAATTCAC	GGAGGGGATC	TCATTGGGAG	ATATTCCTCT	TCCAGGCAGT	480
	ATCAGTGATG	GCATGAATTC	TTCAGCACAT	TATCATGTAA	ACTTCAGCCA	GGCTATAAGT	540
	CAGGATGTGA	ATCTTCATGA	GGCCATCTTG	CTTTGTCCCA	ACAATACATT	TAGAAGAGAT	600
	CCAACAGCAA	GGACTTCACA	GTCACAGAA	CCATTTCTGC	AGTTAAATTC	TCATACCACC	660
35	AATCCTGAGC	AAACCCCTTC	TGGAACATA	TTGACAGGAT	TTCTTTTACC	GGTTGACAAT	720
	CATATGAGGA	ATCTAACCA	CCAAGACCTA	CTGTATGACC	TTGACATAAA	TATATTGTAT	780
	GAGATAAACT	TAATGTCTAT	GGCCACAGAA	GACAACTTTG	ATCCAATCGA	TGTTTCTCAG	840
	CTTTTGTGAT	AACCAGATTC	TGATTCTGGC	CTTTCTTTAG	ATTCAAGTCA	CAATAATACC	900
	TCTGTCTATCA	AGTCTAATTC	CTCTCACTCT	GTGTGTGATG	AAGGTGCTAT	AGGTTATTGC	960
40	ACTGACCATG	AATCTAGTTC	CCATCATGAC	TTAGAAGGTG	CTGTAGGTGG	CTACTACCCA	1020
	GAACCCAGTA	AGCTTTGTCA	CTTGGATCAA	AGTGATTCTG	ATTTCCATGG	AGATCTTACA	1080
	TTTCAACACG	TATTTTCATA	CCACACTTAC	CACTTACAGC	CACTGTCACC	AGAATCTACT	1140
	TCTGAACCTT	TTCCGTGGCC	TGGGAAGTCA	CAGAAGATAA	GGAGTAGATA	CCTTGAAGAC	1200
	ACAGATAGAA	ACTTGAGCCG	TGATGAACAG	CGTGCTAAAG	CTTTGCATAT	CCCTTTTTCT	1260
45	GTAGATAGAA	TTGTCCGCAT	GCCTGTTGAT	TCTTTCAATA	GCATGTTAAG	TAGATATTAT	1320
	CTGACAGACC	TACAAGTCTC	ACTTATCCGT	GACATCAGAC	GAAGAGGGAA	AAATAAAGTT	1380
	GCTGCGCAGA	ACTGTCGTAA	ACGCAAAATG	GACATAATTT	TGAATTTAGA	AGATGATGTA	1440
	TGTAACCTTG	AAGCAAAAGAA	GGAAACTCTT	AAGAGAGAGC	AAGCACAAATG	TAACAAAGCT	1500
	ATTAACATAA	TGAACAGAAA	ACTGCATGAC	CTTTATCATG	ATATTTTATG	TAGATTAAGA	1560
50	GATGACCAAG	GTAGGCCAGT	CAATCCCAAC	CACTATGCTC	TCCAGTGTC	CCATGATGGA	1620
	AGTATCTTGA	TAGTACCCAA	AGAACTGGTG	GCCTCAGGCC	ACAAAAAGGA	AACCCAAAAG	1680
	GGAAAGAGAA	AGTGAGAGAA	AACTGAAGAT	GGACTCTATT	ATGTGAAGTA	GTAATGTTCA	1740
	GAAACTGATT	ATTTGGATCA	GAAACCATTC	AAACTGCTTC	AAGAATTGTA	TCTTTAAGTA	1800
	CTGCTACTTG	AATAACTCAG	TTAACGCTGT	TTTGAAGCTT	ACATGGACAA	ATGTTTAGGA	1860
55	CTTCAAGATC	ACACTTGTGG	GCAATCTGGG	GGAGCCACAA	CTTTTCATGA	AGTGCAATTGT	1920
	ATACAAAATT	CATAGTTATG	TCCAAAGAA	AGGTTAACAT	GAAAACCCAG	TAAGACTTTC	1980
	CATCTTGGCA	GCCATCCTTT	TTAAGAGTAA	GTGTGTTACT	TCAAAAAGAG	CAAAACACTGG	2040
	GGATCAAAAT	ATTTTAAGAG	GTATTTCAGT	TTTAAATGCA	AAATAGCCTT	ATTTTCATT	2100
60	AGTTTGTGTT	CACTATAGTG	AGCTTTTCAA	ACACTATTTT	AATCTTTATA	TTTAACTTAT	2160
	AAATTTTGCT	TTCT					2174

Seq ID NO: C245 Protein Sequence  
Protein Accession #: NP\_004433

	1	11	21	31	41	51	
65	MALRRIGAAL	LLLPLLAAVE	ETLMDSTTAT	AELGWMVHPP	SGWEEVSGYD	ENMNTIRTQ	60
	VCNVFESSQN	NWLRTKFIRR	RGAHRIHVEM	KFSVRDCSSI	PSVPGSCKET	FNLYYYEADF	120
	DSATKTFPNW	MENPFWKVDT	IAADESFSQV	DLGGRVMKIN	TEVRSFGPV	RSGFYLAQD	180
70	YGGCMLIAV	RVFYRKCPRI	IQNGAIFQET	LSGAESTSLV	AARGSCIANA	EEVDVPIKLY	240
	CNGDGEWLVP	IGRCMKAGF	EAVENGTVCR	GCPSGTFKAN	QGDEACTHCP	INSRTTSEGA	300
	TNCVCRNGYY	RADLDPLDMP	CTTIPSAPOA	VISSVNETS	MLEWTPPRDS	GGREDLVYNI	360
	ICKSCGSGRG	ACTRCGDNVQ	YAPRQLGLTE	PRIYISDLLA	HTQYTFEIQ	VNGVTDQSPF	420
	SPQFASVNIT	TNQAAPSAVS	IMHOVSRTVD	SITLSWSQPD	QPNQVILDYE	LQYYEKELSE	480
75	YNATAIKSPT	NTVTVQQLKA	GAIVVFQVRA	RTVAGYGRYS	GKMYFQIMTE	AEYQTSIQEK	540
	LPLLIGSSAA	GLVFLIAVVV	IAIVCNRRRG	FERADSEYTD	KLQHYTSGHM	TPGMKIYIDP	600
	FTYEDPNEAV	REPAKEIDIS	CVKIEQVIGA	GEFGEVCSGH	LKLPKREIF	VAIKTLKSGY	660
	TEQQRDFLS	EASIMGQFDH	PNVILHLEGV	TKSTPVMIT	EFMENGSLDS	FLRQNDGQFT	720
	VIQLVGLMRG	IAAGMKYLAD	MNVVHRDLAA	RNILLVNSLV	CKVSDGLSR	FLEDDTSDPT	780
80	YTSALGGKIP	IRWTAPBAIQ	YRKFTASDV	WSYGIWMWEV	MSYGERPYWD	MINQDVINAI	840
	EQDYRLPPP	DCPSALHQLM	LDCWQKDRNH	RPKFGQIVNT	LDKMIRNPNS	LKAMAPLSSG	900
	INLPLLDRTI	PDYTSFNTVD	EWLEAIKMGQ	YKESFANAGF	TSFDVVSQMM	MEDILRVGLT	960
	LAGHQKKILN	SIQVMRAQMN	QIQSVEV				987

Seq ID NO: C246 Protein Sequence

Protein Accession #: NP\_114148.1

1	11	21	31	41	51	
MDARRVPQKD	LRVKKNLKKF	RYVKLISMET	SSSSDDSCDS	FASDNFANTR	LQSVREGCRT	60
RSQCRHSGPL	RVAMKFPARS	TRGATNKKAE	SRQPSSENSVT	DSNSDSEDES	GMNPLEKRAL	120
NIKQNKAMLA	KLMSELESFP	GSFRGRHPLP	GSDSQSRRPR	RRTFPGVASR	RNPERRARPL	180
TRSRSRILGS	LDALPMEEEE	EEDKYMLVRK	RKTVDGYMNE	DDLPRSSRRS	SSVTLPFIIR	240
PVEITEGGV	GERLQQFSKR	RYITVHWALL	VINAVRRLLI	PKQTAETQTA	GAFEASSVAP	300
AFETVMVKRS	GMLCWIRTGI	ARLVEESATA	VSAGSEMDGV	RLGSLCI		347

Seq ID NO: C247 Protein Sequence  
Protein Accession #: NP\_036577.1

1	11	21	31	41	51	
MENPSPAAL	GKALCALLLA	TLGAAGQPLG	GESICSARAP	AKYSITFTGK	WSQTAFPKQY	60
PLFRPPAQWS	SLLGAHSSD	YSMWRKNQYV	SNGLRDFAER	GEAWALMKEI	EAAGEALQSV	120
HAVFSAPAVP	SGTGQTSABL	EVQRRHSLVS	FVVRIVPSPD	WFGVDSLDL	CDGDRWREQA	180
ALDLYPYDAG	TDSGFTFSSP	NFATIPQDTV	TEITSSSPSH	PANSFYYPRL	KALPPIARVT	240
LVRLRQSPRA	FIPPAVPLPS	RDNEIVDSAS	VPETPLDCEV	SLWSSWGLCG	GHCGRGLGTS	300
RTRYVRVQPA	NNGSPCFELE	EEAECVPDNC	V			331

Seq ID NO: C248 Protein Sequence  
Protein Accession #: NP\_063947.1

1	11	21	31	41	51	
MLQDPDSQDP	LNSLDVKPLR	KPRIPMETFR	KVGIPIIIAL	LSLASIIIVV	VLIKVILDKY	60
YFLCGQPLHF	IPRKLQCDGE	LDCPLGEDDE	HCVKSFPEGP	AVAVRLSKDR	STLQVLDSAT	120
GNWFSACFDN	FTALAEATAC	RQMGYSKPT	FRAVEIGPDQ	DLDVVEITEN	SQELMRNNS	180
GPCLSGSLVS	LHCLACGKSL	KTRPVVGEE	ASVDSWPQV	SIQYDKQHC	GGGILDPHWV	240
LTAACHFRKH	TDVFNWKVRA	GSDKLGSPFS	LAVAKIIIE	FNPMPKND	IALMKLQFPL	300
TFSGTVRPIC	LPFFDEELTP	ATPLWIIWGW	FTKQNGGKMS	DILLQASVQV	IDSTRCNADD	360
AYQGEVTEKM	MCAGIPEGGV	DTQCGDGGP	LMYQSDQWHV	VGIVSWGYGC	GGPSTPGVYT	420
KVSAYLNIWY	NVWKAEI					437

Seq ID NO: C249 Protein Sequence  
Protein Accession #: NP\_003036.1

1	11	21	31	41	51	
MGCKVLLNIG	QQMLRRKVVD	CSREETRLSR	CLNTFDLVAL	GVGSLGAGV	YVLGAVARE	60
NAGPAIVISF	LIAALASVLA	GLCYGEFGAR	VPKTGSAYLY	SYVTVGELWA	FITGWNLLIS	120
YIIGTSSVAR	AWSATFDELI	GRPIGEFSRT	HMTLNAPGVL	AENPDIFAVI	IILILTGLLT	180
LGVKESAMVN	KIFTCINVLV	LGFMVSGFV	KGSVKNWQLT	EEDFGNTSGR	LCLNNDTKEG	240
KPGVGGFMFP	GFSGVLGSAV	TCFYAFVGF	CIATTGEEVK	NPQKAI PVGI	VASLLICFIA	300
YFGVSAALTL	MMPYFCLDNN	SPLPDAFKHV	GWEGAKYAVA	VGSLCALAS	LLGSMFPMR	360
VIYAMAEDGL	LFKFLANVND	RTKTPIIATL	ASGAAVAVMA	FLFDLKDLVD	LMSIGTLAY	420
SLVAACVLVL	RYQPEQPNLV	YQMASTSDLE	DPADQNELAS	TNDSQLGFLP	EAEMFSLKTI	480
LSPKNMEPSK	ISGLIVNIST	SLIAVLIITF	CIVTVLGRE	LTKGALWAVF	LLAGSALLCA	540
VVTGVIWRQP	ESKTKLSFKV	PFLPVLPLS	IFVNVYLMQ	LDQGTWVRFA	VWMLIGFIY	600
FGYGLWHSEE	ASLDADQART	PDGNLDQCK				629

Seq ID NO: C250 Protein Sequence  
Protein Accession #: NP\_002767.1

1	11	21	31	41	51	
MRAPHLHLSA	ASGARALAKL	LPLLMAQLWA	AEAALLPQND	TRLDPAYGA	PCARGSQPWQ	60
VSLFNLGLSFH	CAGVLVDQSW	VLTAACHGKN	PLWARVGGDH	LLLLQGEQLR	RTTRSVVHPK	120
YHQGGSPILP	RRTDEHDLML	LKLARPVVPG	PRVRALQLPY	RCAQPGDQCQ	VAGWGTTAAR	180
RVKYNKGLTC	SSITILSPKE	CEVFYPGVVT	NNMICAGLDR	GQDPCQSDSG	GPLVCDTELQ	240
GILSWGVYPC	GSAQHFAVYT	QICKYMSWIN	KVIRSN			276

Seq ID NO: C251 Protein Sequence  
Protein Accession #: XP\_095088.3

1	11	21	31	41	51	
MTRAATAEPG	RVSPASPARS	TAGLPRAFLQ	SLRTLDDILD	DWQRGCVHLR	EIQSLWVEAR	60
ELPSGVLEGL	SQRRGPPQGA	AVRSRRGGAV	PRGARAVPER	CAGTETRRGR	RCSGLQRLGG	120
GFRGCPADPC	ARGEHRRHTI	TSGVDCGLLK	QMKELEQEKE	VLLQGLEMM	QGRDWYQQQL	180
QQVQERQCRL	GQSRASADFG	AVGSPRPLGR	LLPKVQEVAR	WLGELLAEAC	AGRALPTSSS	240
GPPCSALTST	SSPGWQQIIE	LMLEQNRLL	TQEVTEKSER	ITQLEQKSAL	IKQLFEARAL	300
SQQDGGLSPA	GPHIEPLTRF	RLPVLTWAGA	LLSPHSFQLL	LPLSADSGGP	LHELPTWFP	360
AVLLWVSPG	KRTAHARLHF	HQRPAEGAWQ	LGCGAEAAPE	TCGTLPHFES	HKTTCPEDSL	420
GGPCPQEGDR	SWSHLGAADF	VAPAVAKVTP	NREDAAGSRH	GDICPLCPKG	LLTFRDIAIE	480
FSLAEWQCLD	HAQQNLYRDV	MLENYRNLF	LGMTVSKPDL	IACLEQNKPE	QNIKRNEMAA	540
KHPVTCSHFN	QDLQPEQSIK	DSLQKVIPT	YGKCGHENLQ	LKCKCKRVDE	CEVHKGGYND	600
LNQCLNTQNT	KIQPTKCVK	VFSKFSNSNR	HNARYTGKHH	LKCKKYGKSF	CMFSLNLQHQ	660
IIHTKEKSYK	CEECGKSFNH	SSSGTTHKRI	LTGEKPYRCE	ECGKAFRWPS	NLTRHKRIHT	720
GEKPYACEEC	GQAFRRSSTL	TNHRKRIHTGE	RPYKCECGK	AFSVSSALIY	HKRIHTGEKPT	780
YTCEECGKAF	NCSSTLTKTH	IIHTGEKPYT	CEECGRFTNC	SSTVKAHKRI	HTGEKPYKCE	840

ECDKAFKWHK SLAKHKIIHT GEKPYKCSDS KALAKSSEVQ KVVSGDGENG IRVHKKKETQ 900  
 GWLVRNKNEN RTGLFQIRAA VRPNRDPSPWG QOEGSLTDPI QRKEEPLQON HYDHQNALED 960  
 QRNTGVGGLL TFRDVVIEFS LEEWQCLDHA QONLYRDMVL ENYRNLVSLG IAVSKPDLIT 1020  
 CLEQNKPEWN IKRNMVTKH PDLPELGIK DSLQKVIPRR YGKSGHDNLQ VKTCKSMGEC 1080  
 EVQKGGCNEV NQCLSTTQNK IFQTHKCVKV FGKFSNSNRH KTRHTGKKHF KCKKYGKSFC 1140  
 MVSQHLQHQI IHTRENSVQC EECGKPFNCS STLSKHKRIH TGEKPYRCCE CGKAFWSSST 1200  
 LTKHRRHTGT EKPYTECECG QAFSRSTLA NHKRIHTGEK PYTCEECGKA FSLSSSLTYH 1260  
 KRIHTGEKPY TCEECGKAFN CSSTLKKHKI IHTGEKPYKC KECGKAFAPS STLNTHKRIH 1320  
 TGEEPYKCEE CDKAFKWSST LANHKSMTGT EKPYPKE 1357

Seq ID NO: C252 Protein Sequence  
Protein Accession #: NP\_114433.1

1 11 21 31 41 51  
 MASRSMRLLL LLCLAKTGV LGDIIMRPSG APGWFYHKSQ CYGYFRKLRL WSDAELECCS 60  
 YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLYRSWSG 120  
 KSMGGNKHCA EMSNNNFLT WSSNECNKRQ HFLCKYRP 158

Seq ID NO: C253 Protein Sequence  
Protein Accession #: XP\_051860.2

1 11 21 31 41 51  
 MDGVNLSTEV VYKKGQDYRF ACYDRGRACR SYRVRFLCGK PVRPKLTVTI DTNVNSTILN 60  
 LEDNVQSWKP GDTLVIASDT YSMYQAEFFQ VLPSCRSCAPN QVKVAGKPMY LHIGEEIDGV 120  
 DMRAEVGLLS RNIIIVGEME DKCYPYRNHI CNFFDFDTFG GHIKFGALFK AAHLEGTELK 180  
 HMGQQLVGQY PIHFHLAGDV DERGGYDPPT YIRDLISIHHT FSRCVTVHGS NGLLIKDVVG 240  
 YNLSLGHCFPT EDGPEERTPT DHCLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300  
 DCNAVSTFWM ANFNNNLINC AAAGSEETGF WFIFHHVPTG PSVGMYSPPY SEHIPGLKGY 360  
 NNRAHSNYRA GMIIDNGVKT TEASAKDKRP FLSTISARYS PHQDADPLKP REPAIRHFI 420  
 AYKNQDHGAW LRGGDVWLDS CRFADNGIGL TLASGGTFPY DDGSKQETKN SLFVGESGNV 480  
 GTEMMDNRIW GPGLDLHSGR TLPIGQNFPPI RGIQLYDGPI NIQNTFRKF VALEGRHTSA 540  
 LAFRLNNAWQ SCPHNNVTGI AFEDVPITSR VFFGEPGPWF NQLDMDGDKT SVFHDVDGSV 600  
 SEYPGSYLTK NDNLVLRHPD CINVPDWRGA ICSGCIYQMY IQAYKTSNLR MKIINKDFPS 660  
 HPLYLEGALT RSTHYQQYQP VVTLQKGYTI HWDQTAPAEI AIWLINENKG DWIRVGLCYP 720  
 RGTTFSLSD VHNRLKQTS KTGTVFVRTLQ MDKVEQSYPG RSHYYWDEDS GLLFLKLKQA 780  
 NEREKFAFCS MKGCERIKIK ALIPKNAGVS DCTATAYPKF TERAVIDVPM PKKLFGSQLK 840  
 TKDHFLEVKM ESSKQHFHFL WNDFAIEVD GKKYPSSSEDG IQVVVIDGNQ GRVVSHTSFR 900  
 NSILQGIWQ LFNVVATIPD NSIVLMAKSG RYVSRGPWTR VLEKLGADRG LKLEQMAFV 960  
 GFKGSFRPIW VTLDTEHKA KIFQVVPVPV VKKKKL 996

Seq ID NO: C254 Protein Sequence  
Protein Accession #: NP\_055188.1

1 11 21 31 41 51  
 MTALSSENC FQYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLGMRRKNT QCNFMEYFCI 60  
 SLAFVLLLLL VNISIIYFR DFVLLSIRFT KYHICLFTQI ISFTYGLFHY PVFLTACIDY 120  
 CLNFSKTKL SFKQKLFYF FTVILIWISV LAYVLGDPPI YQSLKAQNAV SRHCPFYVSI 180  
 QSYWLSFFMV MILFVAFITC WEEVTLVQA IRTSYMMNET ILYFPFSSHS SYTVRSKKIF 240  
 LSKLIVCFLS TWLPFVLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHKLN 300  
 LKDIGLPLDP FVNWKCCFIP LTIPLNEQIE KPISIMIC 338

Seq ID NO: C255 Protein Sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MALVLGSLLL LGLCGNSFSG GQPSSTDAPK AWNYELPATN YETQDSHKG PIGILFELVH 60  
 IFLYVVQPRD FPDRTLKFL QKAYESKIDY DKIVYEEAGI ILCCVLGLLF IILMPLVGYP 120  
 FCMCRCKNC GGMHQQRKE NGPFLRKCA ISLLVICIII SIGIFYGFVA NHQVRTRIKR 180  
 SRKLADSNFK DLRTLLNETP EQIKYILAQY NTKDKAFTD LNSINSVLGG GILDRLRPNI 240  
 IPVLDIEKSM ATAIKEKEA LENMNSTLKS LHQQSTQLSS SLTSVKTSR SSLNDPLCLV 300  
 HPSSETCNSI RLSSLQNSN PELRQLPFVD AELDNVNNVL RTDLDGLVQV GYQSLNDIPD 360  
 RVQRQTITV AGIKRVLSNI GSDIDNVTQR LPIQDILSAF SVYVNNTESE IHRNLPTELE 420  
 YDSYWWLGGI VICSLTLIV IFYYLGLLCG VCGYDRHATP TTRGCVSNTG GVFLMVGVGL 480  
 SFLEFCWILMI IIVLTFVFGA NVEKLICEPY TSKELFRVLD TPYLLNEDWE YYLSGKLFNK 540  
 SKMKLTPEQV YSDCKQNRGT YGTLHLQNSF NISEHLNINE HTGSISSELE SLKVNLNIFL 600  
 LGAAGRKNLQ DFAACGIDRM NYDSYLAQTG KSPAGVNNLS FAYDLEAKAN SLPPGNLRNS 660  
 LKRDQAQTIK IHQQRVLPIE QSLSTLYQSV KILQRTGNGL LERVTRILAS LDFAQNFTIN 720  
 NTSSVIBET KKYGRITIGY FEHYLQWIEF SISEKVASCK PVATALDTAV DVFLCSYIID 780  
 PLNLFWFGIG KATVFLPAL IFAVKLAKYY RMDSEDVVD DVETIPMKNM ENGNNGYHKD 840  
 HVYGIHNPVM TSPSQH 856

Seq ID NO: C256 Protein Sequence  
Protein Accession #: NP\_149038.1

1 11 21 31 41 51  
 MKAIHLTLT ALLSVNTATN QGNSADAVTT TETATSGPTV AAADTTETNF PETASTTANT 60  
 PSFPTATSPA PPIIHTHSSS TIPTAPPPII STHSSSTIPI PTAADSESTI NVNSLATSDI 120  
 ITASSPNDGL ITMVPSETQS NNEMSPPTED NQSSGPPTGT ALLETSTLNS TGPSNQCQDD 180  
 PCADNSLCVK LHNTSFCLCL EGYYYNSSTC KKGKVFPGKI SVTVSETFDP EEKHSMAVQD 240

LHSEITSLFK DVFGTSVYQGV TVILTVSTSL SPRSEMRADD KFVNVTIVTI LAETTS DNEK 300  
 TVTEKINKAI RSSSSNFLNY DLTLRCDYYG CNQTADDCLN GLACDCKSDL QRPNPQSPFC 360  
 VASSLKCPDA CNAQHKQCLI KKSOGAPECA CVPGYQEDAN GNCQKCAFQY SGLDCKDKFQ 420  
 LILTVGTIA GIVILSMIIA LIVTARSNNK TKHIEENLI DEDFQNLKLR STGFTNLGAE 480  
 GSVFPKVRIT ASRDSQMNP YSRHSSMPRP DY 512

Seq ID NO: C257 Protein Sequence  
 Protein Accession #: NP\_001423.1

1 11 21 31 41 51  
 | | | | |  
 MTAGRRMEML CAGRPVALL CLGFHLLQAV LSTTVIPSCI PGESSDNCTA LVQTEDNPRV 60  
 AQVSITKCSS DMNGYCLHGQ CIYLVDMSON YCRCEVGYTG VRCEHFFLTV HQPLSKEYVA 120  
 LTVILILFL ITVVGSTYYF CRWYRNKRSK EPKKEYERV TSGDPELPQV 169

Seq ID NO: C258 Protein Sequence  
 Protein Accession #: AAC63902.1

1 11 21 31 41 51  
 | | | | |  
 MDRSKENCIS GPFVKATAPVG GPKRVLVTTQ IPCQNPLPVN SGQAQRVLCP SNSSQVRVLPQ 60  
 AQKLVSSHKP VQNKQKQLQ ATSVPHVPSR PLNNTQKSKQ PLPSAPENNP EEELASKQKN 120  
 EESKKRQWAL BDFEIGRPGL KGKFGNVYLA REKQSKFILA LKVLFAQLE KAGVEHQLRR 180  
 EVEIQSHLRH FNILRLGYF HDATRVYLIL EYAPLGTVYR ELQKLSKFDE QRTATYITEL 240  
 ANALSYCHSK RVIHRDIKPE NLLLSGAGEL KIADFGWSVH APSSRRTTLC GTLDYLPPEM 300  
 IEGRMHDEKV DLWSLGVLCY EFLVGKPPFE ANTYQETYKR ISRVEFTFPD FVTEGARDLI 360  
 SRLKHNPSQ RPMLREVLEH PWITANSSKP SNCQNKESAS KQS 403

Seq ID NO: C259 Protein Sequence  
 Protein Accession #: NP\_037504.1

1 11 21 31 41 51  
 | | | | |  
 MSRTAYTVGA LLLLLGTLLP AAEKGKKGSQ GAIPPPDKAQ HNDSEQTQSP QQPGSRNRGR 60  
 QQGRGTAMPB BEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCYG 120  
 QCNSFYIPRH IRKEEGSFQS CSFCKPKKFT TMMVTLCNPE LQPPTKKKRV TRVKQCRCIS 180  
 IDLD 184

Seq ID NO: C260 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 MKVGVWLWIS FFTFTDGHGG FLGKNDGIKT KKELVNKKK HLGPVVEEYQL LLQVTRYDSK 60  
 EKRDLENFLEK LKPPPLWWSH GLIRIIRAKA TDCNSLNGV LQCTCEDSYT WFPSPCLDPQ 120  
 NCYLHTAGAL PSCECHLNNL SQSVNFCERT KIWGTFKINE RFTNDLLNSS SAIYSKYANG 180  
 IEIQLKKAYE RIQGFESVQV TQFRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALHK 240  
 LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YTLPCSSGYR GNITAKCESS GWQVIRETCV 300  
 LSLLEELNKN FFMIVGNATE AAVSSFVQNL SVIIRQNPT TVGNLASVVS ILSNISSLSL 360  
 ASHFRVSNST MEDVISIADN ILSASVTNW TVLLREEKYA SSRLLETLEN ISTLVPTTAL 420  
 PLNFSRKFID WKGIPVNSQ LKRGYSYQIK MCPQNTSIPI RGRVLIGSDQ FQRSLPETII 480  
 SMASLTGNI LNVSKNGNAQ VNGPVISTVI QNYSINEVFL FFSKIESNLS QPHCVFWDPS 540  
 HLQWNDAGCH LVNETQDIVT CQCTHLTSFS ILMSPFVPST IFPVVKNITY VGLGISIGSL 600  
 ILCLIIEALF WQIKKSQTS HTRRICMVNI ALSLLIADV FIVGATVDT VNP SGVCTAA 660  
 VFTTHFFYLS LFFWMLMGI LLAYRIILVF HHMAQLMMA VGFCCLGYGCP LIISVITIAV 720  
 TQPSNTYKRR DVCWLNWSNG SKPLLAFFVPE ALAIVAVNFV VVLLVLTCLW RPTVGERLSR 780  
 DDKATIIIRG KSLILITPLL GLTWGFGIGT IVDSQNLAWH VIFALLNAFQ GFFILCFGIL 840  
 LDSKLRQLLF NKLSALSSWK QTEKQNSSDL SAKPKFSKPF NPLQNKHYA FSHGTGSSDN 900  
 IMLTQFVSNE 910

Seq ID NO: C261 Protein Sequence  
 Protein Accession #: NP\_000575.1

1 11 21 31 41 51  
 | | | | |  
 MTSKLAVALL AAFLISAALC EGAVLPRSAK ELRCQCIKTY SKPFHPKFIK ELRVIESGPH 60  
 CANTEIIVKL SDGRELCLDP KENWVQRVVE KFLKRAENS 99

Seq ID NO: C262 Protein Sequence  
 Protein Accession #: NP\_005594.1

1 11 21 31 41 51  
 | | | | |  
 MSTERDSETT FDEDSQPNDE VVPYSDDETE DELDDQGS AV EPEQNRVRE AEENREPFRK 60  
 ECTWQVKAND RKYHEQPHFM NTKFLCIKES KYANNAIKTY KYNAFTFIM NLFEQFKRAA 120  
 NLYFLALLIL QAVPQISTLA WYTTLVPLLV VLGVTAIKDL VDDVARHKMD KEINNRTCEV 180  
 IKDGRFKVAK WKEIQVGDI RLKKNDFVPA DILLSSSEPN NSLCYVETAE LDGETNLKFK 240  
 MSLEITDQYL QREDTATFD GFIECEPNP RLDKFTGTLF WRNTSFPLDA DKILLRGCVI 300  
 RNTDFCHGLV IFAGADTKIM KNSGKTRFKR TKIDYLMNYM VYTFVVLIL LSLAGLAIGHA 360  
 YWEAQVGNSS WYLYDGEDDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLGQSHFIN 420  
 WDLQMYAEK DTPAKARTTT LNEQLGQIHY IFSDKTGTLT QNIMTFKCC INGQIYGDHR 480  
 DASQHNHNI EQVDFSWNTY ADGKLAFYDH YLIEQIQSGK EPEVRQFFFL LAVCHTVMVD 540  
 RTDGQLNYQA ASFDEGALVN AARNFGFAFL ARTQNTITIS ELGTERTYNV LAILDENS DR 600  
 KRMSIIVRTP EGNIKLYCKG ADTVIYERLH RMNPTKQETQ DALDIFANET LRLCLCLCYKE 660



IEEKEFTWEN KKFMAASVAS TNRDEALDKV YEEIEKDIL L GATAIEDKL QDGVPEITISK 720  
 LAKADIKIIV LFGDKKETAE NIGFACELLT EDTTICYGED INSLHARME NQRNRGGVYA 780  
 KFAPPVQESF FPPGGNRLI ITGSWNLIEL LEKTKRKNKI LKLFKPRTEE ERMRMQSKR 840  
 RLEAKKEQRQ KNFVDLACEC SAVICRCVTP KQKAMVVDLV KRYKKAITLA IGDGANDVNM 900  
 IKTAHIGVGI SQEQEQMAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMCKF LRYFFYKNAF 960  
 FTLVHFVYSF FNGYSAQTAY EDWFTILYNV LYTSPLVLLM GLDDQDVSDK LSLRFPGLYI 1020  
 VGQRDLLFNY KRFFVSLHLG VLTSMILFFI PLGAYLQTVG QDGEAPSDYQ SFAVTIASAL 1080  
 VITVNFQIGL DTSYWTFFNA FSIFGSIALY FGIMFDFHSA GIHVLFPSEAF QFTGTASNAL 1140  
 RQPYIWLITII LTVAVCLLPV VAIRFLSMTI WPSESDKIQK HRKRLKAEQ WQRQVQVFR 1200  
 GVSTRRSAYA FSHQRGYADL ISSGRSIRKK RSPLDAIVAD GTAEYRRTGD S 1251

Seq ID NO: C263 Protein Sequence  
 Protein Accession #: XM\_044533

1 11 21 31 41 51  
 | | | | |  
 MLRTAMGLRS WLAAPWGALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPFL 60  
 RFEAEHISNY TALLLSRDRG TLYVGAREAL FALSSNLSFL PGGEYQELLW GADAEKKQQC 120  
 SFKGDQFQRD CQNYIKILLP LSGSHLFTCG TAAFSMPCTY INMENFTLAR DEKGNVLLED 180  
 QKGRCPFDPN FKSTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAF 240  
 VASAYIPESL GSLQGGDDKI YFFPSETQGE FEFENTIVS RIARICKGDE GGERVLQQRW 300  
 TSFLKAQLLC SRPDDGFFFN VLQDVFTLSP SPQDWRDTLF YGVFTSQWHR GTTEGSAVCV 360  
 FTMKDQVRVF SGLYKEVNRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420  
 NFLKDHFLMF QVRSRMLLL QPQARYQVVA VHRVPLGHHT YDVLFLGTGD GRLLHKAIVSVG 480  
 PRVHITEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540  
 PYCAWSGSSC KHVSLYQFQL ATRPWIQDIE GASAKDLCSA SSVVSPSPFVP TGEKPCQVQ 600  
 FQNTVNTLA CPLLSNLATV LWLNRGAPVN ASASCHVLPT GDLLLVGTQQ LGFEFCWSLE 660  
 EGQQLVASV CPEVVEDGVA DQDEGGSPV VIISTRVSA PAGGKASWGA DRSYWKFEFLV 720  
 MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNGLGPPST 780  
 PLDHGRGYQSL SDSPPGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS BIRDSVV 837

Seq ID NO: C264 Protein Sequence  
 Protein Accession #: NP\_008950.1

1 11 21 31 41 51  
 | | | | |  
 MASQNRDPA TSVAAARKGA EPSGGAARGP VGKRLQQLM TLMMSGDKGI SAFPESDNLF 60  
 KWVGTIHGAA GTVYEDLRYK LSLEFPSPGY YNAPTIVKFLT PCYHPNVDTQ GNICLDILKE 120  
 KWSALYDVRT ILLSIQSLG EPNIDSPLNT HAAELWKNPT AFKKYLQETY SKQVTSQEP 179

Seq ID NO: C265 Protein Sequence  
 Protein Accession #: NP\_055399.1

1 11 21 31 41 51  
 | | | | |  
 MGRGWGFLFG LLGAVWLLSS GHGEEQPPET AAQRFCFCQVS GYLDDCTCDV ETIDRFNNYR 60  
 LFPRRLQKLE SDYFRYKYVN LKRPCPFWMD ISQCGRRDCA VKPCQSDEVP DGIKSASYKY 120  
 SEENANLIEE CEQAERLGAV DESLSEETQK AVLQWTKHDD SSDNFCEADD IQSPEAEYVD 180  
 LLLNPERVTG YKGPDAWKI NVIYENCCK PQTIKRPLNP LASGGGTSEE NTFYSWLEGL 240  
 CVEKRAFYRL ISGLHASINV HLSARYLLQE TWLEKKWGHN ITEFQQRFDG ILTEGEGPRR 300  
 LKNLYFLYLI ELRLSKVLVP FFERPDFQLF TGNKIQDEEN KMLLEILHE IKSFLPHFDE 360  
 NSFFAGDKKE AHKLKEDFRL HFRNISRIMD CVGCFKCRWL GKLTQGLGT ALKILFSEKL 420  
 IANMPESGFS YEFHLTRQEI VSLFNAFGRI STSVKELENF RNLLQNIH 468

Seq ID NO: C266 Protein Sequence  
 Protein Accession #: NP\_002879.1

1 11 21 31 41 51  
 | | | | |  
 MQPRRQRLPA PWSGPRGRFP TAPLLALLL LAPVAAPAGS GGPDDPGQPQ DAGVPRRLQ 60  
 QKARAALHFF NFRSGSPSAL RVLAEVQEGR AWINPKEGCK VHVVFSTERY NPESLLQEGE 120  
 GRLGKCSARV FFKNQKPRPT INVTCTRLIE KKKRQEDYL LYKQMKQLKN PLEIVSIPDN 180  
 HGHIDPSLRL IWDLAFLGSS YVMWEMTTQV SHYYLAQLTS VRQWVRKT 228

Seq ID NO: C267 Protein Sequence  
 Protein Accession #: NP\_005400.1

1 11 21 31 41 51  
 | | | | |  
 MSVKGMAIAL AVILCATVVQ GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPSNNCDKI 60  
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF 94

Seq ID NO: C268 Protein Sequence  
 Protein Accession #: FGENSEH predicted

1 11 21 31 41 51  
 | | | | |  
 MLRQVLRRGL QSFCHRLGLC VSRHPVFFLT VPAVLTITFG LSALNRFQPE GDLERLVAPS 60  
 HSLAKIERSL ASSLFPLDQS KSQLYSDLHT PGRYGRVILL SPTGDNILLQ AEGILQTHRA 120  
 VLEMKVNHKG YNYTFSHLCV LRNQDKKCVL DDIISVLEDL RQAAVSNKTT ARVQVRYPN 180  
 KLVCSFCML LPIKEAALHF LP 202

Seq ID NO: C269 Protein Sequence  
 Protein Accession #: NP\_002429.1

	1	11	21	31	41	51	
5	MRLPLLVLFA	SVIPGAVLLL	DTROFLIYNE	DHKRCVDAVS	PSAVQTAACN	QDAESQKFRW	60
	VSESQIMSV	FKLCLGVPSK	TDWVAITLYA	CDSKSEFQKW	ECKNDTLLGI	KGEDLFFNYG	120
	NRQEKIMLY	KGSGLWSRWK	IYGTDDNLCS	RGYEAMYTL	GNANGATCAF	PPKFENKWYA	180
	DCTSAGRS	WLWCGTTT	DTDKLFGYCP	LKFEGSESLW	NKDPLTSVSY	QINSKSALTW	240
	HQARKSCQQ	NAELLSITEI	HEQTYLTGLT	SSLTSGLWIG	LNSLSFNSGW	QWSDRSPFRY	300
10	LNWLPGPSA	EPGKSCVSLN	PGKNAKWENL	ECVQKGLYIC	KKGNTTLLNSF	VIPSESDVPT	360
	HCPSQWNPYA	GHCYKIHRE	KKIQRDALTT	CRKEGGDLTS	IHTIEELDFI	ISQLGYEPND	420
	ELWIGLNDIK	IQMYFEWSDG	TPVTFTKWLR	GEPHENNRQ	EDCVVMKGKD	GYWADRGEW	480
	PLGYICKMKS	RSQGFPEIVE	EKGCRCGWKK	HHFYCYMIGH	TLSTFAEANO	TCNNENAYLT	540
	TIEDRYEQAF	LTSFVGLRPE	KYFWTGLSDI	QTKGTQFQWTI	EEEVRFTHWN	SDMPGRKPGC	600
15	VAMRTGIAGG	LWDVLKCDCK	AKFVCKHWAE	GVTHTPPKPTT	TPEPKCPEDW	GASSRTSLCF	660
	KLYAKGKHEK	KTFWESRDFC	RALGGDLASI	NNKEEQOTIW	RLITASGSYH	KLFWLGLTYG	720
	SPSEGFTWSD	GSPVSYENWA	YGEPPNNYQNV	EYCGELKGDP	TMSWNDINCE	HLNNWICQIQ	780
	KGQTPKPEPT	PAPQDNPPVT	EDGWVIYKDY	QYYFSKEKET	MDNARAFCKR	NFGDLVSIQS	840
	ESSEKPLWKY	VNRNDQAQSA	FIGLLISLDK	KFAWMDGSKV	DYVSWATGEP	NFANEDENCV	900
20	TMYSNSGFNW	DINGCYPNAF	ICQRHNSIN	ATTVMPTMPS	VPSGCKEGBW	FYSNKCCKIF	960
	GMEEERKNW	QEARAKCIGF	GGNLVSIQNE	KEQAFITYHM	KDSTFSAWTG	LNDVNSEHTF	1020
	LWTDGRGVHY	TNWKGYGPGG	RRSSLSYEDA	DCVVIIGGAS	NEAGKWMDDT	CDSKRGYICQ	1080
	TRSDPSLTNP	PATITQDGFV	KYKSSSYSLM	RQKQWHEAE	TYCKLHNSLI	ASILDPSYNA	1140
	FAWLQMETSN	ERVWIALNSN	LTDNQYTWD	KWRVRYTNWA	ADEPKLKSAC	VYLDLDGYWK	1200
25	TAHCNESFYF	LCKRSDEIPA	TEPPQLPGRC	PESDHTAWIP	FHGHICYIES	SYTRNWQOAS	1260
	LECLRMGSSL	VSIESAAESS	FLSYRVEPLK	SKTNFWIGLF	RNVEGTWLWI	NNSPVSVFVNW	1320
	NTGDPGGERN	DCVALHASSG	FWSNIHCSSY	KGYICKRPKI	IDAKPTHELL	TTKADTRKMD	1380
	PSKPSNNVAG	VVIIVILLIL	TGAGLAAIFY	YKRRRVHLPO	EGAFENTLYF	NSQSSPGTSD	1440
	MKDLVGNIEQ	NEHSVI					1456

Seq ID NO: C270 Protein Sequence  
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
35	MVLLHWCLLW	LLFPLSSRTQ	KLPTREDELF	QMQRDKAFF	HDSSVIPDGA	EISSYLFRDT	60
	PKRYFFVVEE	DNTPLSVTVT	PCDAPLEWKL	SLQELPEDRS	GEGSGDLEPL	EQQKQIINE	120
	EGTELFYSYG	NDVEYFISSS	SPSGLYQLDL	LSTEKDTDFK	VYATTPESD	QPYPELPYDP	180
	RVDVTSLGRT	TVTTLAWKPS	TASLLKQPIQ	YCVVINKEHN	FKSLCAVEAK	LSADDAFMMMA	240
40	PKPGLDFSPF	DFAHGFPPSD	NSGKERSFQA	KPSPKLGRHV	YSRPKVDIQK	ICIGNKNIFT	300
	VSDLKPDQYQ	YFDVVEVNN	SNMSTAYVGT	FARTKBEAKQ	KTVBLKDGKI	TDVVFVKRGA	360
	KFLRFAPVSS	HQKVTFIFIH	CLDAVQIQVR	RDGKLLLSQN	VEGIQQFQLR	GKPKAKYLVR	420
	LKGNKKGASM	LKILATTRPT	KQSFPSLPED	TRIKAFDKLR	TCSSATVAWL	GTQERNKFCI	480
	YKKEVDDNYN	EDQKKREQNQ	CLGPDIRKKS	EKVLCKYFHS	QNLQKAVTTE	TIKGLQPGKS	540
45	YLLDVYVIGH	GGHSVKYQSK	VVKTRKFC				568

Seq ID NO: C271 Protein Sequence  
Protein Accession #: AAH34229.1

	1	11	21	31	41	51	
50	MEKVQLEFEN	QEMEKKLQEF	RSTRNKEKED	RESSEYYWKS	GKVGKLVNQS	YMSQNKGNV	60
	VKFSAGKVKL	KLLKEQIQEP	VKPTVNYKMA	NSSECEKPKI	NGKVCQCEN	KAALLVCLEC	120
	GEDYCSGCPA	NVHQGALKL	HRTTLLQARS	QILFNVLDA	HQFIKDVND	EPKEENNSTK	180
55	ETSKIQHKKP	SVLLQRSSSE	VEITTMKRAQ	RTKPKRSLLC	EGSFDEEASA	QSFQEVLSQW	240
	RTGNHDDNKK	QNLHAAVKDS	LEECEVQTNL	KIWREPLNIE	LKEDILSYME	KLWLKHHRR	300
	PQEQLFKCQ	IRSHIHMKPL	VMHSVLKMK	MKIVMVRPK	YNTQLFYCQ		349

Seq ID NO: C272 Protein Sequence  
Protein Accession #: NP\_078963.1

	1	11	21	31	41	51	
60	MEKLWLKKHR	RTPQEQLFKM	LSDTFPPHPE	TTGDAQCSQN	ENEDSDGEE	TKVQHTALL	60
	PVETLNIERP	EPSLKIVELD	DTYEEFEFA	ENIVPYKVKL	ADADSQRSCA	FHDCQKNSFP	120
65	YENGIHQHHV	FDKGRDFLN	LCLRNSSTYY	KDNSKGETSN	TDFDNIVDPD	VYSSDIEKIE	180
	ESTSFERNLK	EKNIGLESNQ	KSDDCSVSLE	SKDTLLGRDL	EKAPIEEKLS	QDIKESLELS	240
	NLYKRPSPFE	SKITTKSSLL	QEIACRSKPI	TKQYQGLERF	FIFDTNERLN	LLPSHRLECN	300
	NSSTRITLAE	DREWIPDHS	SEYADNAIVL	GVLQGAQSPS	SSRKQKQMGQ	KSQRPSTANF	360
70	PLSNSVKESS	SCLSSSHPRS	RSAAAQSSSR	AASEISEIEY	IDITDQNELS	LDTTDQHTL	420
	DNLEKELQVL	RLADTSEKL	YSLTSEFFPD	FSSQSLNISQ	IDTDFLKTSH	VRGPGCQVEEL	480
	SCSGRDTIKQ	SLLSLESST	DEEEEDFLNK	QHVITLPWSK	ST		522

Seq ID NO: C273 Protein Sequence  
Protein Accession #: NP\_005399.1

	1	11	21	31	41	51	
75	MKVSAYLLCL	LLMTAAFPNQ	GLAQPDALNV	PSTCCFTFSS	KKISLQRLKS	YVITTSRCPQ	60
80	KAVIFRTKLG	KEICADPKEK	WVQNYMKHLG	RKAHTLKT			98

Seq ID NO: C274 Protein Sequence  
Protein Accession #: BAC05158.1

1	11	21	31	41	51
---	----	----	----	----	----

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55  
60  
65  
70  
75  
80

MFLLTGGVSL	KSAEKNPDPT	WLQDKSWEEI	CRASEFPAPR	GLRQHFCEHI	YEWREIYDSK	60
EPHNAKFAP	MDKNLNLQK	IIILRCRLPD	KITPAITNVV	TDKLGKKFVE	PPFFDLTKSY	120
LDSNCTIPLI	FVLSPGADPM	ASLLKFANDK	SMSGNKFAQI	SLGQGGQPIA	AKMIKAAIEE	180
GTWVCLQNC	LAVSWMPMLE	KICEDFTSET	CNSSFRLWLT	SYPSKFFPVT	ILQNGVKMTN	240
EPPTGLRLNL	LQSYLTDPVS	DPEFFKGCGR	KELLFINEYD	TIPFEAISYL	TGECNYGGRV	300
TDDWDRRLLL	TMLADFNLY	IVENPHYKFS	PSGNYFAPPK	GTEDYIEFI	KKLPFTQHPE	360
IFGLHENVDI	SKDLQQTCTL	FESLLLTQGG	SKQTGASGST	DQILLEITKD	ILNKLPSDFD	420
IEMALRKYPV	RYEESMNTVL	VQEMERFNLL	IIITIRNTLRD	LEKAIKGVVV	MDSALEALSS	480
SLLVGKVPEI	WAKRSYPSLK	PLGSYITDFL	ARLNFLQDWY	NSGKPCVFWL	SGFFFTQAFI	540
TGAMQNYARK	YTPPIDLLGY	EFEVIPSDDT	DTSPEDGVYI	HGLYLDGARW	DRESGLLAEQ	600
YPKLLFDLMP	IIWIKETQKS	RIIKSDAYVC	PLYKTSERKG	TLSTTGHSTN	FVIAMLLKTD	660
QPTRHWIKRG	VALLCQLDD					679

Seq ID NO: C275 Protein Sequence  
Protein Accession #: AAA60212.1

1  
11  
21  
31  
41  
51

MAESHLQLWL	LLLLLPTLCGP	GTAAWTSSSL	ACAQGPFWC	QSLQALQCR	ALGHCLQEVW	60
GHVGADLLCQ	ECEDIVHILN	KMAKEAIFQD	TMRKFLEQEC	NVLPLKLLMP	QCQVLDLDF	120
PLVIDYFQNG	TDNNGTCHML	GLCKSRQPEP	EQEPGMSDPL	PKPLRDPLPD	PLLDKLVLPV	180
LPGALQARPG	PHTQDLSEQQ	FPIPLPYCWL	CRALIKRIQA	MIPKALAVA	VAQVCRVVP	240
VAGGICQCLA	ERYSVILLDT	LLGRMLPQLV	CRVLVLRCSMD	DSAGPRSETG	EWLPRDSECH	300
LCMSVTQAG	NSSEQAIPQA	MLQACVGSWL	DREKCKQFVE	QHTPQLLTLV	PRGWDATTC	360
QALGVCGTMS	SPLQCIHSPD	L				381

Seq ID NO: C276 Protein Sequence  
Protein Accession #: NP\_631911.1

1  
11  
21  
31  
41  
51

MLGCGIPALG	LLLLLQGSAD	GNGIQGFYFP	WSCEGDIWDR	ESCGGQAAD	SPNLCLRLRC	60
CYRNGVCYHQ	RPDENVRKH	MWALVWTCSG	LLLLSCSICL	FWWAKRRDVL	HMPGFLAGPC	120
DMKSVSLLS	KHRGTKKTSP	TGSVPVALSK	ESRDVEGGTE	GEGTEEGEET	EGEEEEED	177

Seq ID NO: C277 Protein Sequence  
Protein Accession #: NP\_473364.1

1  
11  
21  
31  
41  
51

MKLVTIFLLV	TISLCSYSAT	AFLINKVPLP	VDKLAPLPLD	NILPFMDPLK	LLLKTLGISV	60
EHLVEGLRKC	VNELGPEASE	AVKKLLEALS	HLV			93

Seq ID NO: C278 Protein Sequence  
Protein Accession #: FGENESH predicted

1  
11  
21  
31  
41  
51

MPLSYAYKNA	ETLAGRHTSS	WMSRGAYQRR	NTRAAGRPEE	CTDRNWHAGR	TRGIWLGQLE	60
ERCSDVFGVS	FFWVVRGLAG	SGAKLQTFPT	AQEGAPTQVR	QAEALLKCRQ	SGRPGRGGA	120
SERARDASML	SPLSAAMRNY	PTSTIPPRR	SYSPTEIAHK	SYSCSLPDMK	ISMAESGPSL	180
DSLDTLEDGE	SGSPFLVTHL	YFLGVVTTGM	EQLDFETGPN	IFDLQIYVKD	EVGVTDLQVL	240
TVQVTDVNEP	PQFQGNLAED	HLRADQPHFN	AHSHTYVRVV	ATALARHRLR	SSIGSPFLGT	300
FCVVVMQYF	LISPPKSRFM	SANGTLFSTT	ELDFEAGHRS	FHLIVEVRDS	GGLKASTELQ	360
VNIVNLNDEV	PRFTSPTRVY	TVLEELSPGT	IVANITAEDP	DDEGFPSHLL	YSITTVSKYF	420
MINQLTGTIQ	VAQRIDRDAG	ELRQNPTISL	EVLVKDRPYG	GQENRIQITF	IVEDVNDNPA	480
TCQKFTFRSS	LHPALCSKTL	TWMDTVLDCF	HAADKDIPVT	GRFTKERGLI	GLTVPHGWGS	540
LTIMAEKKEE	QVTSYMDGSR	QDRACVGLK	LLIKPSDLMR	LSHYHENSNG	KTCPHDSISS	600
YQVPTTCRN	SRIQATNNED	TSSVTVTVNI	LEENDEKPIK	TPNSYFLALP	VDLKVGTNIQ	660
NFKLTCTDLD	SSPRSFYRSI	GPGNVNNHFT	FSPNAGSNVT	RLLLTSRFDY	AGGFDKIWDY	720
KLIVVVTDDN	LMSDRKKAEA	LVETGTVTLS	IKVIPHPPTI	ITTTTPRPRT	YQVLRKNVYS	780
PSAWYVPFVI	TLGSILLGLL	LVYLVVLLAK	AIHRHCPCKT	GKNKEPLTKK	GETKTAERDV	840
VVETIQMNTI	FDGEAIDPEP	EQASLELYAL	LPSCCDPSPV	TLRKVQVCGE	SEETQCSCGH	900
ITLPGKIPVD	DRKQETGLQ	GDFEVWTLCP	AVKVVVGSPP	AERCIRLALS	LKKYSSD	957

Seq ID NO: C279 Protein Sequence  
Protein Accession #: XP\_168571.1

1  
11  
21  
31  
41  
51

MINQLTGTIQ	VAQRIDRDAG	ELRQNPTISL	EVLVKDRPYG	GQENRIQITF	IVEDVNDNPA	60
TCQKFTFSIM	VPERTAKGLT	LDDLKFCFD	DDSEAPNNRF	NFTMPSGVGS	GSRLQDQDPA	120
SGKIVLIGDL	DYENPSNLAA	GKNYTVIIQV	QDVAPPYYKN	NVYVYILTSP	ENEFPLIFDR	180
PSYVFDVSR	RPAQGHLSGP	EKRLLSICM	VRACHHFLGL	HIASGSPRPV	GRPIQGSHPQ	240
TLPLQDWEQ	GTSDKERNE	DCRERRRGNN	YPDEHYL			277

Seq ID NO: C280 Protein Sequence  
Protein Accession #: NP\_005257.2

1  
11  
21  
31  
41  
51

MGDWSFLGNF	LEEVHKHSTV	VGVVWLTVLV	IFRMLVLGTA	AESSWGDEQA	DFRCDTIQPG	60
CQNVCYDQAF	PISHIRYVWL	QIIFVSTPSL	VYMGHAMHTV	RMQEKRLKLE	AERAKEVRGS	120

GSYEYPVAEK AELSCWEEGN GRIALQGTLL NTYVCSILIR TTMEVGFIVG QYFIYGIFLT 180  
 TLHVCRRSPC PHPVNCYVSR PTEKNVFFIVF MLAVAALSL LSLAELYHLG WKKIRQRFVK 240  
 PRQMAKQCL SGPSVGIVQS CTPPPDFNQC LENGPGGKFF NPFSSNMASQ QNTDNLVTEQ 300  
 VRGQEQTPEE GFIVRYGQK PEVPNGVSPG HRLPHGYHSD KRRLSKASSK ARSDDLSV 358

Seq ID NO: C281 Protein Sequence  
 Protein Accession #: NP\_055274.2

1 11 21 31 41 51  
 | | | | |  
 MYLSICCCFL LWAPALT LKN LNYSVP EEG AGTVIGNIGR DARLQPGLEP AERGGGGRSK 60  
 SGSYRVLENS APHLLD VAD SGLLYTKQRI DRESLCRHNA KCQLSLEVFA NDKEICMIKV 120  
 EIQDINDNAP SFSSDQIEMD ISENAAPGTR FPLTSAHDPD AGENGLRTRYL LTRDDHGLFG 180  
 LDVKS RGDGT KFPPELVIQKA LDREQQNHHT LVLTLALDGGE PPRSATVQIN VKVIDSNDNS 240  
 PVFEAPSYLV ELPENAPLGT VVIDLNATDA DEGPNGEVLY SFSSYVPDRV RELFSIDPKT 300  
 GLIRVKGNLD YEENGMLEID VQARDLGPNP IPAHCKVTVK LIDRNDNAPS IGFVSVRQGA 360  
 LSEAAPPGTV IALVRVTD RD SGKNGQLQCR VLGGGGTGGG GGLGGPGGSV PFKLEENYDN 420  
 FYTIVTDRLP DRETQDEYNY TIVARDGSGP PLNSTKSFAT KILDENDNPP RFTKGLYVLQ 480  
 VHENNIPGEY LGSVLAQDPD LGQNGTVSYS ILPSHIGDVS IYTVSVNPT NGAIYALRSF 540  
 NFEQTKAFEF KVLAKDSGAP AHLESNATVR VTVLDVNDNA PVIVLPTLQN DTAELOVPRN 600  
 AGLGYLVSTV RALDSDFGES GRLTYEIVDG NDDHLFEIDP SSGEIRTLHP FWEDVTPVVE 660  
 LVVKTVDHKG PTLSSAVAKLI IRSVSGSLPE GVPFVNGEQH HWDMSLPLIV TLSTISIIIL 720  
 AAMITIAVKC KRENKEIRTY NCRIAEYSHP QLGGGKGKKK KINKNDIMLV QSEVEERNAM 780  
 NVMNVSSPS LATSPMYFDY QTRLPLSSPR SEVMYLKPAS NNLTVPQGHG GCHTSFTGQG 840  
 TNASETPATR MSIIQTDNFP AEPNYMGSRQ QFVQSISVAP RLRTQKEPA 889

Seq ID NO: C282 Protein Sequence  
 Protein Accession #: NP\_005592.1

1 11 21 31 41 51  
 | | | | |  
 MELCRSLALL GGSGLMFLCL IALSTDFWFE AVGPTHSAHS GLWPTGHGDI ISGYIHVTQT 60  
 FSIAMVLWAL VSVSFLVLSC FPSLFPPGHG PLVSTTAFAA AAISMVVAMA VYTSERWDQP 120  
 PHPQIQTFSS WSFYLGWVSA ILLCTGALS LGAHCGGPRP GYETL 165

Seq ID NO: C283 Protein Sequence  
 Protein Accession #: NP\_006424.2

1 11 21 31 41 51  
 | | | | |  
 MATWALLLLA AMLLGNPGLV FSRLSPEYYD LARAHLRDEE KSCPCLAQEG PQGDLLTKTQ 60  
 ELGRDYRTCL TIVQKLKKMV DKPTQRSVSN AATRVCR TGR SRWRDVC RNF MRRYQSRVTQ 120  
 GLVAGETAQQ ICDLRLCIP STGFL 145

Seq ID NO: C284 Protein Sequence  
 Protein Accession #: NP\_005594.1

1 11 21 31 41 51  
 | | | | |  
 MKVSAALAV ILIATALCAP ASASPYSSDT TPCCFAYIAR PLPRAHIKEY FYTSGKCSNP 60  
 AVVFVTRKNR QVCANPEKKW VREYINSLEM S 91

Seq ID NO: C285 Protein Sequence  
 Protein Accession #: NP\_071437.1

1 11 21 31 41 51  
 | | | | |  
 MAPGRAVAGL LLLAAAGLGG VAEGPGLAFS EDVLSVFGAN LSLSAAQLQH LLEQMGAASR 60  
 VGVPEPGQLH FNQCLTAEI FSLHGFSNAT QITSSKFSVI CPAVLQQLNF HPCEDRPKHK 120  
 TRPSHSEVWG YGFLSVTIIN LASLLGLILT PLIKKSYPFK ILTFVVLAI GTLFSNAIFQ 180  
 LIPEAFGFDP KVDSYVEKAV AVFGGFYLLF FFERMLKMLL KTYGQNGHHT FGNDNFGPQE 240  
 KTHQPKALPA INGVTYANP AVTEANGHIH FDNVSVVSLQ DGKKEPSSCT CLKGPKLSEI 300  
 GTIAWMITLC DALHNFIDGL AIGASCTLSL LQGLSTSAI LCEEFPHELG DFVILLNAGM 360  
 STRQALLFNF LSACSCYVGL AFGILVGNNF APNIIFALAG GMFLYISLAD MFPENMDMLR 420  
 EKVTGRKTDF TFFMIQNAGM LTGFTAILLI TLYAGEIELE 460

Seq ID NO: C286 Protein Sequence  
 Protein Accession #: NP\_004175.1

1 11 21 31 41 51  
 | | | | |  
 MPNSEPASLL ELFNISIATQG ELVRS LKAGN ASKDEIDS AV KMLVSLKMSY KAAAGEDYKA 60  
 DCPPGNPAPT SNHGPDAT EA EEDFVD PWT V QTS SAKGIDY DKLIVRFSGS KIDKELINRI 120  
 ERATGQRPHH FLRRGIFFSH RDMNQVLDA Y ENK KPFYLYT GRGPSSEAMH VGH LIPFIFT 180  
 KWLQDVFNVP LVIQMTDDEK YLWKDLTLDQ AYGD AVENAK DIIACGFDIN KTFIFSDLDY 240  
 MGMSSGFYKN VVKIQKHVTF NQVKGIFGFT DSDCIGKISF PAIQAAPSPS NSFPQIFRDR 300  
 TDIQCLIPCA IDQDPYFRMT RDVAPRIGYP KPALLHSTFF PALQGAQTKM SASDPNSSIF 360  
 LTDTAQIKT KVNKHAFFSG RDTIEEHRQF GGNCDVDVSF MYLTFLEDD DKLEQIRKDY 420  
 TSGAMLTGEL KKALIEVLQP LIAEHQARRK EVIDEIVKEF MTPRKLSFDF Q 471

Seq ID NO: C287 Protein Sequence

Protein Accession #: NP\_004929.1

	1	11	21	31	41	51	
5	MTVFRQENVD	DYYDTGEELG	SGQFAVVKKC	REKSTGLQYA	AKFIKKRRTK	SSRRGVSRED	60
	IEREVSILKE	IQHPNVITLH	EVYENKTDVI	LILELVAGGE	LFDFLAEKES	LTEEEATEFL	120
	KQILNGVYYL	HSLQIAHFDL	KPENIMLLDR	NVPKPRIKII	DFGLAHKIDF	GNEFKNIFGT	180
	PEFVAPEIVN	YEPLGLEADM	WSIGVITYIL	LSGASPLFGD	TKQETLANVS	AVNYEFEDEY	240
10	FSNTSALAKD	FIRRLVKDP	KKRMTIQDSL	QHPWIKPKDT	QQALSRKASA	VNMEKFKKFA	300
	ARKKWKQSVR	LISLCQRLSR	SFLSRSNMSV	ARSDDTLDEE	DSFVMAKIIH	AINDDNVPGI	360
	QHLLGSLSNY	DVNQPNKHGT	PPLLIAAGCG	NIQILQLLIK	RGSRIDVQDK	GGSSNAVYWA	420
	RHGHVDTLKF	LSENKCLPDV	KDKSGEMALH	VAARYGHADV	AQVTCASAAQ	IPISRTKEEE	480
	TPLHCAAWHG	YYSVAKALCE	AGCNVNIKNR	EGETPLLTAS	ARGYHDIVCE	LAEHGADLNA	540
15	CDKDGHIHAL	LAVRRQMEV	IKTLLSQGCF	VDYQDRHGNT	PLHVACKDGN	MPIVVALCEA	600
	NCNLDISNKY	GRTPLHLAAN	NGILDVVRYL	CLMGASVEAL	TTDGKTAEDL	ARSEQHEHVA	660
	GLLARLRKDT	HRGLFIQQLR	PTQNLQPRIK	LKLFHSGSGS	KTTLVESLKC	GLLRSFFRRR	720
	RPRLSSTNSS	RFPSPSLASK	PTVSVSINNL	YPGCENVSVR	SRSMMFEPGL	TKGMLEVFVA	780
	PTHHPHCSAD	DQSTKAIDIQ	NAYLNGVDF	SVWEFSGNPV	YFCYDYFAA	NDPTSIVVVV	840
20	FSLEEPYBIQ	LNPVIFWLSF	LKSLVPVEEP	IAFGGKLKNP	LQVVLVATHA	DIMNVPRPAG	900
	GEFGYDKDTS	LLKEIRNRFG	NDLHISNKL	VLDAGASGSK	DMKVLNRHLQ	EIRSQIVSVC	960
	PPMTHLCEKI	ISTLPSWRKL	NGPNQLMSLQ	QFVYDVQDQL	NPLASEEDLR	RIAQQHLSTG	1020
	EINIMQSETV	QDVLILLDRW	LCTNVLGKLL	SVETPRALHH	YRGRTYVEDI	QRLVPDSVDE	1080
	ELLQILDAMD	ICARDLSSGT	MVDVPAIKT	DNLHRSWADE	EDEVMMVYGGV	RIVPVEHLTP	1140
	FPCGIFHKVQ	VNLRCRWIQQ	STEGDADIRL	WVNGCKLANR	GAELLVLLVN	HGQGIQVQVR	1200
25	GLETEKIKCC	LLDSVSCSTI	ENVMATTLPG	LLTVKHYLSP	QQLREHHEPV	MIYQPRDFFR	1260
	AQTLKETSLT	NTMGYKESF	SSIMCFGCHD	VYSQASLGMD	THASDLNLLT	RRKLSRLDDP	1320
	PDPLGKDWCL	LAMNLGLPDL	VAKYNTNNGA	PKDFLPSPLH	ALLREWTYP	ESTVTGLMSK	1380
	LRELGRDDAA	DLKLKASSVF	KINLDGNGQE	AYASSCNSGT	SYNSISSVVS	R	1431

Seq ID NO: C288 Protein Sequence

Protein Accession #: NP\_002072.1

	1	11	21	31	41	51	
35	MELRARGWWL	LCAAAALVAC	ARGDPASKSR	SCGEVRQIYG	AKGFSLSDVP	QAEISGEHLR	60
	ICPGYTCCT	SEMENLANR	SHAELETALR	DSSRVLQAML	ATQLRSFDDH	FQHLNDSER	120
	TLQATPPGAF	GELYTQNARA	FRDLYSELRL	YRGANLHLE	ETLAEFWARL	LERLFKQLHP	180
	QLLLPDDYLD	CLGKQAEALR	PFGEAPREL	LRATRAFVAA	RSFVQGLGVA	SDVVRKVAQV	240
40	PLGPECSRVA	MKLVCYCAHL	GVPGARPCPD	YCRNVLGKCL	ANQADLDAEW	RNLDSMVL	300
	TDKFWGTSGV	ESVIGSVHTW	LAEAINALQD	NRDTLTAKVI	QCGCNPKVNP	QGPPEEKRR	360
	RGKLAPREPR	PSGTEKLVIS	EAKAQLRDVQ	DFWISLPGTL	CSEKMALSTA	SDRCWNGMA	420
	RGRYLPVVMG	DGLANQINNP	EVEVDITKPD	MTIRQQIMQL	KIMTNRLRSA	YNGNDVDFQD	480
	ASDDGSGSGS						490

Seq ID NO: C289 Protein Sequence

Protein Accession #: AAH30205.1

	1	11	21	31	41	51	
50	MIILYLFLL	LWEDTQGWGF	KDGIFHNSIW	LERAAQVYHR	EARGSKYKLT	YAEAKAVCEF	60
	EGGHLATYKQ	LEAARKIGFH	VCAAGWMAGK	RVGYPIVKG	PNCGFGKTGI	IDYGIKLNRS	120
	ERWDAYCYNP	HAKECCGVFT	DPKQIFKSPG	FPNEYEDNQI	CYWHIRLKYG	QRIHLSFLDF	180
	DLEDDPGCLA	DYVEIYDSYD	DVHGFGVGRYC	GDELPPDIIS	TGNVMTLKFL	SDASVTAGGF	240
55	QIKYVAMPDV	SKSSQKGKNTS	TTSTGNKNFL	AGRFSHL			277

Seq ID NO: C290 Protein Sequence

Protein Accession #: NP\_001973.1

	1	11	21	31	41	51	
60	MRANDALQVL	GLLFSLARGS	EVGNSQAVCP	GTLNGLSVTG	DAENQYQTL	KLYERCEVVM	60
	GNLEIVLTGH	NADLSFLQWI	REVTGYVLVA	MNEFSTLPLP	NLRVVRGTQV	YDGKFAIFVM	120
	LNNTNNSHA	LRQLRLTQLT	EILSGGVYIE	KNDKLCHMDT	IDWRDIVRDR	DAEIVVKDNG	180
65	RSCPPCHEVC	KGRCCWPGSE	DCQTLTKTIC	APQCNGHCFG	PNNPQCCHDE	CAGGCSGPQD	240
	TDCAFACRFN	DSGACVPRCP	QPLVYNKLT	QLEPNPHTKY	QYGGVVCVASC	PHNFVVDQTS	300
	CVRACPPDKM	EVDKNGKLMC	EPCGGGLCPKA	CEGTGSGSRF	QTVDSNIDG	FVNCTKILGN	360
	LDFLITGLNG	DPWHKIPALD	PEKLNIVRTV	REITGYLNIQ	SWPPHMHNFS	VFSNLTITIG	420
	RSLYNRGFSL	LIMKNLNVTS	LGFRSLKEIS	AGRIYISANR	QLCYHHSNLN	TKVLRGPTEE	480
70	RLDIKHNRP	RDCVABGKVC	DPLCSSGGCW	GPGEQCLSC	RNYSRGVCV	THCNFLNGEP	540
	REFAHEAECF	SCHPECQPMG	GTATCNGSGS	DTCAQCAHRF	DGPHCVSSCP	HGVLGAKGPI	600
	YKYPDVQNEC	RPCHENCTQG	KCGPELQDCL	GQTLVLIGKT	HLTMALTVIA	GLVVFIMMLG	660
	GTFLYWRGRR	IQNKRAMRRY	LERGESIEPL	DPSEKANKVL	ARIFKETELR	KLKVLGSGVF	720
	GTVHKGVWIP	EGESIKIPVC	IKVIEDKSGR	QSFQAVTDHM	LAIGSLDHAH	IVRLGLCPG	780
75	SSLQLVTQYL	PLGSLLDHVR	QHRGALGPQL	LLNWGVQIAK	GMYYLEEHGM	VHRNLAARNV	840
	LLKSFSQVQV	ADFGVADLLP	PDDKQLLYSE	AKTPIKWMAL	ESIHFGKYTH	QSDVWSYGVT	900
	VWELMTFGAE	PYAGLRLAEV	PDLEKGERL	AQPQICTIDV	YVMVMKCMWI	DENIRPTFKE	960
	LANEFTRMAR	DPPIRYLVIKR	ESGPGIAPGP	EPHGLTNKKL	EEVELEPELD	LDLDEAEED	1020
80	NLATTTLGSA	LSLPVGTINR	PRGSQSLLSP	SSGYMPMNQ	NLGSCQESA	VSGSSERCP	1080
	PVSLHPMPRG	CLASESSEGH	VTGSEAELE	KVSMCRSRSR	SRSRPRGRDS	AYHSQRHSL	1140
	TPVTPLSPPG	LEEDVDNNGV	MPDTHLKGTP	SSREGTLLSV	GLSSVLGTTE	EDEDEEYEM	1200
	NRRRRHSPPH	PPRPSLEEL	GYEYMDVGS	LSASLGSTQS	CPLHEVPIMP	TAGTTPDEEDY	1260
	EYMNRRQDGG	GFGGDYAAAG	ACPASEQGYE	EMRAFQGP	QAPHVHYARL	KTLRSLEATD	1320
	SAFDNPDYWH	SRLFFKANAQ	RT				1342

Seq ID NO: C291 Protein Sequence  
Protein Accession #: NP\_001207.1

```

5      1      11      21      31      41      51
|      |      |      |      |      |
MAPLCPSPWL PLLIPAPAFG LTVQLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL 60
GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG 120
DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180
ELLGFQLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240
10  VEGHRFPABI HVVHLSTAFR RVDEALGRPG GLAVLAAFL EGPENSAEY QLLSRLEEIA 300
EESSTQVPG LDISALLPSD FSRYPQYEGS LTPPCAQGV IWTVFNQTM LSAKQLHTLS 360
DTLWGPQDSR LQLNFRATQP LNGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420
GLLFAVTSVA FLVQMRQRHR RGTGKGVSYR PAEVAETGA 459

```

Seq ID NO: C292 Protein Sequence  
Protein Accession #: NP\_004198.1

```

20      1      11      21      31      41      51
|      |      |      |      |      |
MGGAVVDEGP TGVKAPDGGW GWAFLFGCFV ITGFSYAFPK AVSVFFKELI QEFGIGYSdT 60
AWISSILLAM LGTGTPLCSV CVNRFGRPV MLVGGFLFASL GMVAASFCRS IIQVYLTTGV 120
ITGLGLALNF QPSLIMLNRY FSKRRPMANG LAAAGSPVFL CALSPLGQLL QDRYGWRGGF 180
LILGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRLLDL SVFRDRGFVL YAVAASVMVL 240
25  GLFVPPVFFV SYAKDLGVPD TKAAPLLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSS 300
SMFFNGLADL AGSTAGDYGG LVVFCIFFGI SYGMVGALQF EVLMAIVGTH KFSIAIGLVL 360
LMEAAVVLVG PPSGGKLLDA THVYMYVFIL AGAEVLTSSL ILLGNFFCI RKKPKPEQPE 420
VAAABEEKLH KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETS V 465

```

Seq ID NO: C293 Protein Sequence  
Protein Accession #: NP\_000349.1

```

30      1      11      21      31      41      51
|      |      |      |      |      |
MALFVRLAL ALALALGPAA TLAGPAKSPY QLVQLHSRLR GRQHGPNVCA VQKVIQTNRK 60
YFTNCKQWYQ RKICGKSTVI SYECCPGYEK VPGEKGCPAA LPLSNLNYETL GUVGSTTTQL 120
YTDRTKLRP EMEGPGSFTI FAPSNEAWAS LPAEVLDSL SVNVIELLNA LRYHVMGRRV 180
LTDLKHGMT LTSMYQNSNI QIHHPNGIV TVNCARLLKA DHATNGVVH LIDKIVSTIT 240
NNIQIIEIE DTFETLRAAV AASGLNTMLE GNGQYTLAP TNEAFKIPS ETLNRLIGDP 300
EALRDLNNH ILKSAMCAEA IVAGLSVETL EGTLEVGCS GDMLTINGKA IISNKDILAT 360
40  NGVIHYIDEL LIPDSAKTLF ELAASDVST AIDLFRQAGL GNHLSGSERL TLLAPLNSVF 420
KDGTPPIDAH TRNLLRNHII KDQLASKYLY HGQTLETGG KKLRFVYVRN SLCIENSCIA 480
AHDKRGRYGT LFTMDRVLTP PMGTVMVLK GDNRFSLMVA AIQSAGLTET LNREGVYTVF 540
APTNEAFRAL PPRERSRLG DAKELANILK YHIGDEILVS GGIGALVRLK SLQGDKLEVS 600
LKNVSVSNK EPVAEPDIMA TNGVVHVITN VLQPPANRPQ ERGDELADSA LEIFKQASAF 660
45  SRASQSRVRL APVYQKLLER MKH 683

```

Seq ID NO: C294 Protein Sequence  
Protein Accession #: NP\_006527.1

```

50      1      11      21      31      41      51
|      |      |      |      |      |
MTQRSIAGPI CNLKFVTLV ALSELPLFG AGVQLQDNGY NGLLIAINPQ VPENQNLISN 60
IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAH 120
GDDPYTLQYR GCGKEGYIY FTFNELLNDN LTAGYGSRRG VFVHEWAHLR WGVFDEYNND 180
55  KPFFYINGQK IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240
MFMQSLSSVV EFCNASTHNO EAPNLQNMCM SLRSADWDVIT DSADFHSFPP MNGTELPPPP 300
TFSLVQAGDK VVCLVLDVSS KMAEADRLQ LQQAABFYLM QIVEIHTFVG IASFDSKGEI 360
RAQLHQINSN DDRKLLVSYL PTTVSAKTDI SICSGLKKGF EVVEKLNKGA YGSVMILVTS 420
GDDKLLGNCL PTVLSSSGSTI HSIALGSSAA PNLEELSRIT GGLKFFVPDI SNSNSMIDAF 480
60  SRISSTGDI PQHQIQUEST GENVKPHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL 540
FDPDGRKYYT NNFITNLTFR TASLWIPGTA KPGHWYTYLN NTHHSLQALK VTVTSRASNS 600
AVPPATVEAF VERDSLHFPF PVMYIANVKQ GFYPILNATV TATVEPETGD PVTLRLLDDG 660
AGADVINKDG IYSRYFFSFA ANGRYSLKVH VNHSPSISTP AHSIPGSHAM YVPGYTANGN 720
65  IQMNAPRKSV GRNEEERKNG FSRVSSGGSF SVLGVPAGPH PDVFPCKII DLEAVKVEEE 780
LTLSTWAPGE DFDQQAQTSY EIRMSKSLQN IQDDFNAIL VNTSKRNPQQ AGIREIFTFS 840
PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
LILKGVLTAM GLIGIICLI VVTHHTLSRK KRADKKENG KLL 943

```

Seq ID NO: C295 Protein Sequence  
Protein Accession #: Eos sequence

```

70      1      11      21      31      41      51
|      |      |      |      |      |
MKFLLILLQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHFF REMPGGPVWR KHYITYRINN 120
YTPDMNREDV DYAIRKAFV WSNVTPKFVS KINTGMADIL VVFARGAHD FHAFDGKGGI 180
LAHAFPGSGG IGGDAHFEDF EFWTTHSGGT NLFLTAVHEI GHSLGLGHSS DPKAVMFPTY 240
75  KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF 300
FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360
80  EPNYPKSIHS FGFPNFVKKI DAAVNPRFY RTYFFVDNQY WRYDERRQMM DPGYPKLITK 420
NFQIGIGPKID AVFYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC 470

```

Seq ID NO: C296 Protein Sequence  
Protein Accession #: Eos sequence

1 11 21 31 41 51  
 5 MKFLILLLLQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60  
 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHVF REMPGGPVWR KHYITYRINN 120  
 YTPDMNREDV DYAIRKAFQV WSNVTPCLKFS KINTGMADIL VVFARGAHGD FHAFDGGKGGI 180  
 LAHAFGPSG IGGDAHDEED EFWTTHSGGT NLFLTAVHAI GHSLGLGHSS DPKAVMFPTY 240  
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFF 300  
 FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLFKDD KYWLISNLRP 360  
 10 EPNYPKSIHS FGPFNFVKKI DAAVFNPRFY RTYFFVDNQY WRyderRQMM DPGYPKLITK 420  
 NFQIGIPKID AVFYSKNKY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC 470

Seq ID NO: C297 Protein Sequence  
 Protein Accession #: NP\_008883.1

1 11 21 31 41 51  
 15 MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAW 60  
 IGIFVGLICLF CLSLVGLVGI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDFFTFNL 120  
 20 FLKQMLERYQ NNSPPNDDQ WKNGVTKTW DRMLQDNCC GVNPGSDWQK YTSAFRTENN 180  
 DADYPWRQC CVMNKLKEPL NLEACKLGV GFYHNQGCYE LISGPMNRHA WGVAVFGFAI 240  
 LCWTFWVLLG TMFWWSRIEY 260

Seq ID NO: C298 Protein Sequence  
 Protein Accession #: NP\_001784.2

1 11 21 31 41 51  
 30 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60  
 QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120  
 KGPPFQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK 180  
 YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 35 TDMDGDGSTT TAVAVVEILD ANDNAPMFDQ QKYEAHVPEA AVGHEVQRLT TADLDAPNSP 360  
 AWRATYLING GDDGDHFTIT THPESNQGIL TTRKGLDFFA QNQHLYVEV TNEAFFVLKL 420  
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NOKISYRILR 480  
 DPAGWLAMPD DSGQVAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLLD 540  
 VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPTSFPQ AQLTDDSDIY WTAEVNEEGD 600  
 40 TVVLSLKKFL KQDITYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL 660  
 GAVLALLFL LVLVLLVRK RKIKEPLLLP EDDTRDNVY YGEEGGGEED QDYDITQLHR 720  
 GLEARPEVVL RNDVAPTIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780  
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYL EWGSRFKKLA DMYGGGEDD 829

Seq ID NO: C299 Protein Sequence  
 Protein Accession #: NP\_005620.1

1 11 21 31 41 51  
 50 MAKSAENGI YSVSGDEKKK PLIAPGPDGA PAKGDGPVGL GTPGGRLAVP PRETWTRQMD 60  
 FMSCVGFVAV GLGNVWRFPY LCYKNGGGVF LIPYVLIALV GGIIPIFFLEI SLGQFMKAGS 120  
 INVWNICPLF KGLGASPMVI VFYCNTRYIM VLAAGFYLV KSFTTTLFPA TCGHTWNTPD 180  
 CVEIFRHEDC ANASLANLTC DQLADRRSPV IEFWENKVLV LSGGLEVPQA LNWEVTLCLL 240  
 ACWVLVYFCV WKGVKSTGKI VYFTATFPYV VLVVLLVRGV LLPGALDGI YLKPDSWKL 300  
 55 GSPQVWIDAG TQIFFSYAIG LGALTAGLSY NRFNNNCYKD AILALINSQ TSFFAGFVVF 360  
 SILGFMAAEQ GVHISKVAES GPGLAFIAYP RAVTLMFPAP LWAAALFFML LLLGLDSQFV 420  
 GVEGFITGLL DLLPASYYFR FOREISVALC CALCFVIDLS MVTDDGMYVF QLFDDYASAG 480  
 TTLLWQAFWE CVVAVVYGA DRFMDDIACM IGYRCPWMK WCWSFETPLV CMGIFIFNVV 540  
 YVEPLVYNT YVYPWNGEAM GWAFALSSML CVPLHLLGL LRAKGTMAER WQHLTQPIWG 600  
 60 LHHLEYRAQD ADVRGLTTLT PVSESKVVV VESVM 635

Seq ID NO: C300 Protein Sequence  
 Protein Accession #: NP\_006507.1

1 11 21 31 41 51  
 65 MEPSSKKLTG RLMLAVGGAV LGSLLQFGYNT GVINAPQKVI EEFYNQTVH RYGESILPTT 60  
 LTTLWLSLVA IFSVGMIGS FSVGLFVNRF GRRNSMLMMN LLAFVSAVLM GFSKLKGSFE 120  
 MLILGRFIIIG VYCGLTGTFV PMYVGEVSPT AFRGALGTLH QLGIIVGILI AQVFGLDSIM 180  
 70 GNKDLWPLLL SIIFIPALLQ CIVLPFCPEP PRFLINRNE ENRAKSVLKK LRGTADVTHD 240  
 LQEMKESRQ MMREKKVTIL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV FYYSTSIFEK 300  
 AGVQPPVYAT IGSQIVNTAF TVVSLFVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ 360  
 LPWMSYLSIV AIFGFVAFFE VGPGPPIWFI VAELEFSQGP PAALAVAGFS NWTSNFIVGM 420  
 CFQYVEQLCG PYVFIIFTVL LVLFFIFTYF KVPETKGRTE DEIASGFRQG GASQSDKTPE 480  
 75 ELFHPLGADS QV 492

Seq ID NO: C301 Protein Sequence  
 Protein Accession #: XP\_035292.2

1 11 21 31 41 51  
 80 MAGAGPKRRA LAAPAAEKEE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60  
 GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYAEALGTTI SKSGGDYAYM 120  
 LEVYGSLEPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPPTCPVPEEA AKLVACLCLV 180  
 LLTAVNCYSV KAATRVQDAF AAARKLALAL IILLGFVQIG KGDVSNLDPN FSFEGTKLDV 240

GNIVLALYSG LFAYGGWNYL NRVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300  
 STEQMLSSSEA VAVDFGNYHL GVMWSIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360  
 SILSMIHPQL LTPVPSLVFT CVMITLLYAFS KDIFSVINFF SFFNWLCVAL AIIGMIWLRH 420  
 RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWVWKN 480  
 KPKWLLQGIF STTVLCQKLM QVVPQET 507

Seq ID NO: C302 Protein Sequence  
 Protein Accession #: NP\_005259.1

1 11 21 31 41 51  
 | | | | |  
 MNWSIFEGLL SGVKNYSTAF GRIWLSLVFI FRVLVYLVT A ERVWSDDHKD FDCNTRQPGC 60  
 SNVCFDEFFP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKRRHREAHG ENSGRLYLNP 120  
 15 GKKRGGWLWT YVCSLVFKAS VDIAPLYVFH SFYPKYLPP VVKCHADPCP NIVDCFISKP 180  
 SEKNIFTLFM VATAICILL NLVELIYLV KRCHECLAAR KAQAMCTGHH PHGTSSCKQ 240  
 DLLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL 273

Seq ID NO: C303 Protein Sequence  
 Protein Accession #: NP\_005121.1

1 11 21 31 41 51  
 | | | | |  
 MKKICSLTLLS FLLLAQVLL VEGKKVKNG LHSKVSEQK DTLGNTQIKQ KSRPGNKKGK 60  
 VTKDQANCRW AATQEEGSI LKVECTQLDH EFSCVFAGNP TSCLKLKDER VYWKQVARNL 120  
 25 RSQKDICRYS KTAVKTRVCR KDFPESSLKL VSSTLFGNTK PRKEKTEMSP REHIKKGKETT 180  
 PSSLAVTQTM ATKAPCEVED PDMANQRKTA LEFCGETWSS LCTFFLSIVQ DTSC 234

Seq ID NO: C304 Protein Sequence  
 Protein Accession #: AAH22542

1 11 21 31 41 51  
 | | | | |  
 MCSEIILRQE VLKDCGHRDL LIKVKFGESI EDLHTCRLLI KQDIPAGLYV DPYELASLRE 60  
 RNITEAVMVS ENFDIEAPNY LSKSEVLIY ARDSQCIDC FQAFLPVHCR YHRPHSEDEGE 120  
 35 ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFPILK CWAHSEVAAP CALENEDICQ 180  
 WNKMKYKSVY KNVILQVPVG LTVHTSLVCS VTLLITILCS KKKKK 225

Seq ID NO: C305 Protein Sequence  
 Protein Accession #: NP\_004985.1

1 11 21 31 41 51  
 | | | | |  
 MSLWQPLVLV LVLVGCFAA PRQRQSTLVL FPGDLRTNLT DRQLAEEYLY RYGYTRVAEM 60  
 RGEKSLGPA LLLQKQLSL PETGELDSAT LKAMRTPRCG VPDLGRFQTF EGDLLKWHHN 120  
 45 ITYWTQNYSE DLFRAVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP 180  
 FDGKDGLLAH AFPPGPGIQG DAHFDDDELW SLGKGVVVPT RFGNADGAAC HFPFIFEGRS 240  
 YSACTDGRS DGLPWCSTTA NYDTDDRFGF CPSERLYTRD GNADGKPCQF PFIFQGQSYS 300  
 ACTTDGRSDG YRWCAATTANY DRDKLFGFCP TRADSTVMGG NSAGELCVFP FTFGLKEYST 360  
 CTSEGRGDRG LWCATSNFD SDDKMGFCPD QGYSLELVAA HEFGHALGLD HSSVPEALMY 420  
 50 PMYRFTEGPP LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSE 480  
 PTAGPTGPPS AGPTGPPTAG PSTATTVPLS PVDDACNVNI FDAIAEIGNQ LYLFPKDGKYW 540  
 RFSEGRGSRP QQPFLIADKV PALPRKLDV FEEPLSKLF FFSGRQVWVY TGASVLGPRR 600  
 LDKLGLGADV AQVTGALRSR GKMMLFSGR RLWRFDVKAQ MVDPRSASEV DRMPFGVPLD 660  
 55 THDVQYREK AYFCQDRFYW RVSSRSELNQ VDQVGVTYD ILQCPED 707

Seq ID NO: C306 Protein Sequence  
 Protein Accession #: NP\_000204

1 11 21 31 41 51  
 | | | | |  
 MAGPRPSPWA RLLAALISV SLSGTLANRC KKAPVKSCTE CVRVDKDCAY CTDEMFRDRR 60  
 CNTQAELLAA GCQRESIVM ESSFQITEET QIDTTLRSQ MSPQGLRVRL RPGEERHFEL 120  
 EVFEPLESPV DLYILMDFSN SMSDDLNLK KMGQNLARVL SOLTSDYTIG FGKFDVKVSV 180  
 65 PQTDMRPEKL KEPWNSDDP FSFKNVISLT EDVDEFNRKL QGERISGNLD APEGGFDAI 240  
 QTAVCTRDIG WRPDSTHLLV FSTESAFHYE ADGANVLAGI MSRNDERCHL DTTGTYTQYR 300  
 TQDYPVSPTL VRLAKHNII PIPAVTNYSY SYEKLHTYF PVSSLGVLQE DSSNIVELLE 360  
 EAFNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGVGIYQV QLRALHVDG 420  
 THVCQLPEDQ KGNHILKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480  
 70 CSEGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYEGGR YEGQFCEYDN 540  
 FQCPRTSGFL CNDGRGRCSMG QCVCEPGWTG PSCDCPLSNA TCIDSNGGIC NGRGHCECGR 600  
 CHCQQQLSYT DTICEINYS A IHPGLCEDLR SCVQCQAWGT GEKKGRTCEE CNFKVKMVE 660  
 LKRAEEVVVR CSFRDEDDDC TYSYTMEDG APGPNSTVLV HKKDCPPGS FWWLIPLLL 720  
 75 LFLLLALLLL LCWKYCACCK ACLALLPCCN RGHMVGFKEH HYMLRENLMA SDHLDTFPLR 780  
 SGNLKGKRDVW RWKVNTNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTRC 840  
 AQLRQVEEEN LNEVYRQISG VHLKQQTFR QPNAGKKQD HTIVDTVLMA PRSAKPALLK 900  
 LTEKQVEQRA FHDLVKAPGY YTLTADQDAR GMVEFQEGVE LVDVRVPLFI RPEDDDEKQL 960  
 LVEAIDVPAG TATLGRRLVN ITIIEQARD VVSFEQPEFS VSRGDQVARI PVIRRVLDGG 1020  
 KSQVSVYRTQD GTGQGNRDYI PVEGELFQV GEAWKELQVK LLELQEVDSL LRGRQVRRFH 1080  
 80 VQLSNPKFGA HLGQPHSTTI IIRDPDELDR SFTSQMLSSQ PPPHGDLAG QNPNAKAAGS 1140  
 RKTHFNWLP SGKPMGYRVK YWIQGDESE AHLSDSKVPS VELTNLYPYC DYEMKVCAYG 1200  
 AQGEGPYSSL VSCRTHQEVV SEPGRFAFNV VSSTVTQLSW AEPAETNGEI TAYEVCYGLV 1260  
 NDDNRPIGPM KKVLDVNPKN RMLLIENLRE SQPYRYTVKA RAGAGWGPER EAIINLATQP 1320  
 KRPMSPPIIP DIPIDVDAQS EDYDSFLMYS DDVLRSPSGS QRPVSDDTG CGWKFEPLLG 1380  
 EEIDLRRVTV RLPELIPRL SASSGRSSDA EAPTAPRTTA ARAGRAAVP RSATPGPPGE 1440



HLVNGRMDFA FPGSTNSLHR MTTTSAAAYG THLSPHVPHR VLSTSSLTTR DYNLSLRSEH 1500  
 SHSTTLPRDY STLTSSVSSHD SRLTAGVPDT PTRLVFSALG PTLRLVSWQE PRCEPLQGY 1560  
 SVEYQLNGG ELHRNINPNP AQTSSVVVDEL LPNHSYVFRV RAQSQEGWGR EREGVITIES 1620  
 QVHPQSPCLP LFGSAFTLST PSAPGFLVFT ALSPDSLQLS WERPRRPNGD IVGYLVTCM 1680  
 AQGGGPGATF RVDGDSPESE LTVPGLSNV PYKFKVQART TEGFGPEREG IITIESQDGG 1740  
 PFPQLGSRAG LFQHPQLQSEY SSITTTHTSA TEPFLVDGLT LGAQHLEAGG SLTRHVTQEF 1800  
 VSRITLTSGT LSTHMDQQFF QT 1822

Seq ID NO: C307 Protein Sequence  
 Protein Accession #: NP\_076404.1

1 11 21 31 41 51  
 MGFNLTAKL PNNELHGOES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60  
 GLAVWIFFHI RNKTSFIFYL KNIVVADLIM TLTFPFRIHV DAGFGPWYFK FILCRYTSVL 120  
 FYANMYTSIV FLGLISIDRY LKVVKFPFGDS RMYSTFTTKV LSVCVWVIMA VLSLPNIILT 180  
 NGQPTEDNIH DCSKIKSPLG VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240  
 ISQSSRKRKH NQSIRVVAV FETCFLPYHL CRIPFTFSLH DRLLESAQK ILYYCKEITL 300  
 FLSACNVCLD PIIFYMCRS FSRRLFKSN ITRSESIRS LQSVRRSEVR IYYDYTDV 358

Seq ID NO: C308 Protein Sequence  
 Protein Accession #: NP\_065840.1

1 11 21 31 41 51  
 MVWCLGLAVL SLVISQGDG RGKPEVVSUV GRAEESVVLG CDLLPPAGRP PLHVIEWLRF 60  
 GFLLPIFIQF GLYSRIDPD YVGRVRLQKG ASLQIEGLRV EDQGWYECRV FFLDQHIPED 120  
 DFANGSWHL TNNSPPQOE TPAVLEVQE LEPVTLRCVA RGSPLPHVTW KLRGKDLGQG 180  
 QQQVQVQNT LRIRIVERGS SGVYTCQASS TEGSATHATQ LLVLGPPVIV VPPKNSTVNA 240  
 SQDVSLACHA EAYPANLTVS WFQDNINVFH ISRLQPRVQI LVDGSLRLLA TQPDAGCYT 300  
 CVPSNGLLHP PSASAYLTVL CMFVIRCPV RANPPLLFVS WTKDGKALQL DKFPQWSQGT 360  
 EGSLLIALGN EDALGEYST PYNSLGTAGP SPVTRVLLKA PPAFIERPKE EYFQEVGREL 420  
 LIPCSAQGD PVPVSWTKVG RGLQQAQVD SNSSLILRPL TKEAHGHWEC SASNAVARVA 480  
 TSTNVVVLGT SPHVVTNVSV VALPKGANVS WEPGFDGGYL QRFSVWYTPL AKRPDRMHHD 540  
 WVSLAVPVA AHLLVFGLPQ HTQYQFSVLA QNKLGSPPFS EIVLSAPEGL PTPAAPGLP 600  
 PTEIPPLSP PRGLVAVRTP RGVLLHWDPP ELVPKRLDGY VLEGRQGSQG WEVLDPVAVG 660  
 TETELLVPLG IKDVLVEFRL VAFAGSFVSD PSNTANVSTS GLEVYPSRTQ LPGLLPQPV 720  
 AGVVGGVCLF GVAVLVSLA GCLLNRRRAA RRRRKRLRQD PPLIFSETGK SAAPSALGSG 780  
 SPDSVAKLKL QGSPVPSLRQ SLLWGDPAQT PSPHPDPPSS RGFLPLEPIC RGPDRFVVG 840  
 PTVAAPQERS GREQAEPTP AQRLARSFDC SSSSPSGAPQ PLCIEDISPV APPPAAPPSP 900  
 LFGPGPLLQY LSLPFFREM VDGWPFLEE PSPAAPPDYM DTRRCPTSSF LRSPETPPVS 960  
 PRESLEGAUV GAGATAEPY TALADWTLRE RLLPGLLPAA PRGSLTSQSS GRGSASFRLP 1020  
 PSTAPSAGGS YLSPAPGDT SWASGPERWP RREHVTVSK RRNTSVDENY EWDSEFPDGM 1080  
 ELLETLLHLG ASSRLRPEAE TELGVKTPEE GCLLNTAHVT GPEARCAALR EEFLAFRRRR 1140  
 DATRARLPAY RQPVHPPEQA TLL 1163

Seq ID NO: C309 Protein Sequence  
 Protein Accession #:

1 11 21 31 41 51  
 MLTKPLQGGP APPGTPTPPP GKKDREAFAE EYRLGPLL GKFGTVFAGH RLTDRLQVAI 60  
 KVIPRNRVLG WSPLSDSVTC PLEVALLWKV GAGGGHPGVI RLLDWFETQE GFMLVLERPL 120  
 PAQDLFDYIT EKGPLGEGPS RCFFGQVVA IQHCHSRGVV HRDIKENIL IDLRRCACKL 180  
 IDFGSGALLH DEPYTDFDGT RVYSPPewis RHQYHALPAT VWSLGILLYD MCGDIPFER 240  
 DQEILEAEHL FPAHVSPDCC ALIRRCCLAPK PSSRPSLEEI LDLPWMQTPA EDVTPQPLQR 300  
 RCPFFGLVLA TSLAWFGLA PNGQKSHMA MSQG 334

Seq ID NO: C310 Protein Sequence  
 Protein Accession #: NP\_002501.1

1 11 21 31 41 51  
 MECLYYFLGF LLLAARLPLD AAKRFHDVLG NERPSAYMRE HNQLNGWSSD ENDWNEKLYP 60  
 VWKRGDMRWK NSWKGGRVQA VLTSDSPALV GSNITFAVNL IFPRCQKEDA NGNIVYEKNC 120  
 RNEAGLSADP YVYNWTAWSE DSDGENGTOG SHHNVPFDGK PFPHPGWRR WNFIVVFHTL 180  
 GQYFQKLGRG SVRVSVNTAN VTLGPQLMEV TVYRRHGRAY VPVIAQVKDY VVTDIQIPV 240  
 TMFQKNDRNS SDETFLKDLF IMFVDLIHDP SHFLNYSTIN YKWSFGDNTG LRVSTNHTVN 300  
 HTYVNLGTF LNLTVKAAAP GPCPPPPPPP RPSKPTPSLG PAGDNPLELS RIPDENCQIN 360  
 RYGHFQATIT IVEGILEVNI IQMTDVLMPV WPPESSLIDF VVTCQGSIPT EVCTIISDPT 420  
 CEITQNTVCS PVDVDEMCLL TVRRTFNGSG TYCVNLTLGD DTSALTSTL ISVPDRDPAS 480  
 PLRMANSALI SVGCLAIFVT VISLLVYKHH KEYNPNIENSP GNVVRSKGLS VFLNRAKAVF 540  
 FPGNQEKDPL LKNQEFKGV 560

Seq ID NO: C311 Protein Sequence  
 Protein Accession #: Eos seq

1 11 21 31 41 51  
 MRILKRLFLAC IQLLCVCRLD WANGYRQR KLVVEIGWSY TGALNQKNWG KKYPTCNPK 60  
 QSPINIDBL TQVNVNKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITFWH GKCNMSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KKGKGLRALS 180  
 ILFEVGTEN LDFKALIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240  
 TDTVDWIVFK DTVSISESQL AVFCEVLTMQ QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300

Seq ID NO: C312 Protein Sequence  
Protein Accession #: XP\_031379

Seq ID NO: C313 Protein Sequence  
Protein Accession #: NP\_002842

1355

PLVIVSALTFL ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840  
 PIKHFPPKHVA DLHASSGFTE EFETLKEFYQ EVQSCCTVDLG ITADSSNHPD NKHKNRYINI 900  
 VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960  
 VEVIVMITNL VEKGRRKCDQ YWPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020  
 GSQKGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080  
 TGTIYVLDLM LQIQHEGTV NIFGFLKHIR SQRYNLVQTE EQYVFIHDTL VEAILSKETE 1140  
 VLDSDHSHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200  
 VERSRVGISS LSGEGTDYIN ASYIMGYYS NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260  
 MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320  
 VLEVRHFQCP KWNPNPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTT 1380  
 MHQLEKENSVDVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440  
 AALPDGNIAE SLESILV 1456

Seq ID NO: C314 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 MVFKASKITF HWGKCNMSSD GSEHSLEGQK FPLEMQIYCF DADRFSSEFE AVKGKGLRA 180  
 LSLFEEVGTE ENLDFKAIID GVESVSRFGK QAALDPFILL NLLFNSTDKY YIYNGSLTSP 240  
 PCTDTDWIVF KDTVSISESQ LAVFCEVLTM QSGYVMLMD YLQNNFREQQ YKFSRQVFSS 300  
 YTGKEEIHFA VCSSEPENVO ADPENYTSLL VTWERPRVYV DTMIEKFAVL YQQLDGEDQT 360  
 KHEFLTIDGY DLGAILNNLL PNMSYVLQIV AICTNGLYK YSDQLIVDMP TDNPELDLFP 420  
 ELIGTEEIIK EEEEGKDIIE GAIVNPGRDS ATNQIRKKEP QISTTHYNR IGTKYNEAKT 480  
 NRSPTRGSEF SGKGDVPNTS LNSTSQPVTK LATEKDISLT SQTVTELPHP TVEGTSASLN 540  
 DSGKTVLRSP HMNLSGTAES LNTVSITEYE EESLLTSFKL DTGAEDSSGS SPATSAIPFI 600  
 SENISQGIYF SSENPEITTY DVLIPESARN ASEDSTSSGS EESLKDPSME GNVWFPSSDT 660  
 ITAQPDVGS GRESFLQNTY EIRVDESEKT TKSFSAGPVM SQGPSVTDLE MPHYSTFAYF 720  
 PTEVTPHAPT PSSRQQLVLS TVNVVYSQTT QPVYNEASNS SHESRIGLAE GLESEKKAVI 780  
 PLVIVSALTFL ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840  
 PIKHFPPKHVA DLHASSGFTE EFETLKEFYQ EVQSCCTVDLG ITADSSNHPD NKHKNRYINI 900  
 VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960  
 VEVIVMITNL VEKGRRKCDQ YWPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020  
 GSQKGRPSGR VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080  
 TGTIYVLDLM LQIQHEGTV NIFGFLKHIR SQRYNLVQTE EQYVFIHDTL VEAILSKETE 1140  
 VLDSDHSHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIP 1200  
 VERSRVGISS LSGEGTDYIN ASYIMGYYS NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260  
 MIPDQGNMAE DEFVYWPNDK EPINCESFKV TLMAEEHKCL SNEEKLIQD FILEATQDDY 1320  
 VLEVRHFQCP KWNPNPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTT 1380  
 MHQLEKENSVDVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440  
 AALPDGNIAE SLESILV 1456

Seq ID NO: C315 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITFWH GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSEFEAV KGKGLRALS 180  
 ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240  
 TDTVDWIVF KDTVSISESQ LAVFCEVLTM QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300  
 TGKEEIHFAV CSSEPENVO ADPENYTSLL TWERPRVYV TMIEKFAVL YQQLDGEDQT 360  
 HEFLTIDGYD LGAILNNLLP NMSYVLQIVA ICTNGLYGY SDQLIVDMPT DNPELDLFE 420  
 LIGTEEIIKE EEEEGKDIIEG AIVNPGRDSA TNQIRKKEPQ ISTTHYNR IGTKYNEAKT 480  
 RSPTRGSEFS KGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPHP TVEGTSASLN 540  
 GSKTVLRSPH MNLSGTAESL NTVSITEYEE EESLLTSFKL DTGAEDSSGS PATSAIPFIS 600  
 ENISQGIYF SSENPEITTY DVLIPESARNA SEDSTSSGSE EESLKDPSME GNVWFPSSDT 660  
 TAQPDVGSGR ERESFLQNTY EIRVDESEKT TKSFSAGPVM SQGPSVTDLE MPHYSTFAYF 720  
 TEVTPHAPT SSRQQLVLS TVNVVYSQTT QPVYNEASNS HESRIGLAE GLESEKKAVI 780  
 LVIVSALTFL ICLVVLVGIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840  
 IKHFPPKHVA DLHASSGFTE EFETLKEFYQ EVQSCCTVDLG ITADSSNHPD NKHKNRYINI 900  
 AYDHSRVKLA QLAEKDGKLT DYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMIWEHN 960  
 EVIVMITNLV EKGRRKCDQ YWPADGSEY GNFLVTQKSV QVLAYYTVRN FTLRNTKIKK 1020  
 SQKGRPSGRV VVTQYHYTQW PDMGVPEYSL PVLTFVRKAA YAKRHAVGPV VVHCSAGVGR 1080  
 GTIYVLDLM LQIQHEGTV NIFGFLKHIR SQRYNLVQTE EQYVFIHDTL VEAILSKETE 1140  
 LDSDHSHAYV NALLIPGPAG KTKLEKQFQL TSPRLRCRG TISAHCNLPL PGLTDPPTSA 1200  
 SRVAGTILLS QSNIQQSDYS AALKQCNR NRTSSIIPVE RSRVGISSLS GEGTDYINAS 1260  
 YIMGYYSQNE FIITQHPLH TIKDFWRMIW DHNAQLVPMI PDQGNMAEDE FVYWPNDKDEP 1320  
 INCESFKVTL MAEEHKCLSN EELKLIQDFI LEATQDDYV EVRHFQCPKW PNPDPSPISK 1380  
 FELISVIKE AANRDGPMIV HDEHGGVTAG TFCALTTLMH QLEKENSVDV YQVAKMINLM 1440  
 RGVVFADIEQ YQFLYKVI LSGVTRQENP STSLDSNGAA LPDGNIAESL ESLV 1494

Seq ID NO: C316 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNLKKL KFQGWDKTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITFWH GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSEFEAV KGKGLRALS 180  
 ILFEVGTEEN LDFKAIIDGV ESVSRFGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240

TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300  
 TGKEEIHAEV CSSEPENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360  
 HEFLTGDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPEASNSH 420  
 ESRIGLAEGE ESEKKAVIPL VIVSALTFIC LVVLVGLIY WRKCFQTAHF YLEDSTSPRV 480  
 ISTPPTPIFP ISDDVGAIP I KHFPKHVADL HASSGFTEEF ETLKEFYQEV QSCITVDLGIT 540  
 ADSSNHPDNK HKNRYINIVA YDHSRVKLAQ LAEKDQGLTD YINANYVDGY NRPKAYIAAQ 600  
 GPLKSTAEDF WRMIWEHNVE VIVMITNLVE KGRRKCDQYW PADGSEBYGN FLVTQKSVQV 660  
 LAYYTVRNFIT LRNTKIKKGS QKGRPSGRVY TQYHYTQWPD MGVPEYSLPV LTFVRKAAYA 720  
 KRHAVGVPVV HCSAGVGRTG TYIVLDSMLQ QIQHEGTVNI FGFLKHRSQ RNYLVQTEEQ 780  
 YVFIHDTLVE AILSKETEVL DSHIHAYVNA LLIPGPAGKT KLEKQFQLLS QSNIQQSDYS 840  
 AALKQCNREK NRTSSIIPEV RSRVGISLS GEGTDYINAS YIMGYQSNE FIITQHPLH 900  
 TIKDFWRMIW DHNAQLVVM I PDGQNMMAEDE FVYWPKNDEP INCESFKVTL MAEEHKCLSN 960  
 EEKLIQDIFI LEATQDDYVL EVRHFQCPKW PNPDSPISKT FELISVKEE AANRDGPMIV 1020  
 HDEHGGVTAG TFCALTLMH QLEKENSVDV YQVAKMINLM RGVFADIEQ YQFLYKVILS 1080  
 LVSTRQEENP STSLDSNGAA LPDGNIAESL ESL 1113

Seq ID NO: C317 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNLKKL KFGQWDKTSI ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KGKGLRALS 180  
 ILFEVGTEN LDFKAIIDGV ESVSRFQKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240  
 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300  
 TGKEEIHAEV CSSEPENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360  
 HEFLTGDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE 420  
 LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNI GTKYNEAKTN 480  
 RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540  
 GSKTVLRSPH MNLSTGAESL NTVSITYEE ESSLTSFKLD TGAEDSSGSS PATSAIPFIS 600  
 ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSTDI 660  
 TAQPDVSGSR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720  
 TEVTPHAFIP SSRQDQDLVST VNVVYSQTTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780  
 LVIVSALTFI CLVVLVGLI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840  
 IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCITVDLGI TADSSNHPDN KHKNRYINIV 900  
 AYDHSRVKLA QLAEKDQGLT DYINANYVDG YNRPKAYIAA QGPLKSTAED FWRMIWEHNV 960  
 EVIVMITNLV EKGRRKCDQY WPADGSEBYG NFLVTQKSVQ VLAYYTVRNF TLRNTKIKKG 1020  
 SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFRKAAY AKRHAVGPVV VHCAGVGRT 1080  
 GTYIVLDSML QIQHEGTVN IFGFLKHRS QRYLVQTEE QYVFIHDTLV EAILSKEDEV 1140  
 LDASHIAYVN ALLIPGPAGK TKLEKQFQGL TSPRLCECRG TISAHCNLPL PGLTDPPTSA 1200  
 SRVARTILLS QSNIQQSDYS AALKQCNREK NRTSSIIPEV RSRVGISLS GEGTDYINAS 1260  
 YIMGYQSNE FIITQHPLH TIKDFWRMIW DHNAQLVVM I PDGQNMMAEDE FVYWPKNDEP 1320  
 INCESFKVTL MAEEHKCLSN EEKLIQDIFI LEATQDDYVL EVRHFQCPKW PNPDSPISKT 1380  
 FELISVKEE AANRDGPMIV HDEHGGVTAG TFCALTLMH QLEKENSVDV YQVAKMINLM 1440  
 RGVFADIEQ YQFLYKVILS LVSTRQEENP STSLDSNGAA LPDGNIAESL ESL 1493

Seq ID NO: C318 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60  
 QSPINIDEDL TQVNVNLKKL KFGQWDKTSI ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120  
 FKASKITFHW GKCNMSSDGS EHSLEGQKFP LEMQIYCFDA DRFSSFEAV KGKGLRALS 180  
 ILFEVGTEN LDFKAIIDGV ESVSRFQKQA ALDPFILLNL LPNSTDKYYI YNGSLTSPPC 240  
 TDTVDWIVFK DTVSISESQL AVFCEVLTMO QSGYVMLMDY LQNNFREQQY KFSRQVFSSY 300  
 TGKEEIHAEV CSSEPENVQA DPENYTSLLV TWERPRVVDY TMIEKFAVLY QQLDGEDQTK 360  
 HEFLTGDGYQD LGAILNNLLP NMSYVLQIVA ICTNGLYGKY SDQLIVDMPT DNPELDLFPE 420  
 LIGTEEIIKE EEEGKDIEEG AIVNPGRDSA TNQIRKKEPQ ISTTTHYNI GTKYNEAKTN 480  
 RSPTRGSEFS GKGDVPNTSL NSTSQPVTKL ATEKDISLTS QTVTELPPT VEGTSASLND 540  
 GSKTVLRSPH MNLSTGAESL NTVSITYEE ESSLTSFKLD TGAEDSSGSS PATSAIPFIS 600  
 ENISQGYIFS SENPETITYD VLIPESARNA SEDSTSSGSE ESLKDPSMEG NVWFPSTDI 660  
 TAQPDVSGSR ESFLQNTYTE IRVDESEKTT KSFSAGPVMS QGPSVTDLEM PHYSTFAYFP 720  
 TEVTPHAFIP SSRQDQDLVST VNVVYSQTTQ PVYNEASNS HESRIGLAEG LESEKKAVIP 780  
 LVIVSALTFI CLVVLVGLI YWRKCFQTAH FYLEDSTSPR VISTPPTPIF PISDDVGAIP 840  
 IKHFPKHVAD LHASSGFTEE FETLKEFYQE VQSCITVDLGI TADSSNHPDN KHKNRYINIV 900  
 AYDHSRVKLA QLAEKDQGLT DYINANYVDG YNRPKAYIAA QGPLKSTAED FWRMIWEHNV 960  
 EVIVMITNLV EKGRRKCDQY WPADGSEBYG NFLVTQKSVQ VLAYYTVRNF TLRNTKIKKG 1020  
 SQKGRPSGRV VTQYHYTQWP DMGVPEYSLP VLTFRKAAY AKRHAVGPVV VHCAGVGRT 1080  
 GTYIVLDSML QIQHEGTVN IFGFLKHRS QRYLVQTEE QYVFIHDTLV EAILSKEDEV 1140  
 LDASHIAYVN ALLIPGPAGK TKLEKQFQGL QSNIQQSDY SAALKQCNRE KNRTSSIIPEV 1200  
 ERSRVGISLS GEGTDYINA SYIMGYQSN EFIIITQHPL HTIKDFWRMI WDHNAQLVVM 1260  
 IPDQNMMAED EFVYWPKNDE PINCESFKVT LMAEEHKCLS NEEKLIQDIF ILEATQAWRS 1320  
 DGRNFLCSDN PYAPTRKRKF RGCLFGSQDD QSDEARSLC 1359

Seq ID NO: C319 Protein Sequence  
 Protein Accession #: XP\_002914.4

1 11 21 31 41 51  
 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRF TRPLECQDAL ETAARAEGLS 60  
 LDASMSQLR ILDEHPKPK YHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSLAR 120  
 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEBELNEV GPDAASLRRV VWIFCRTRLI 180

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

LSIVCLMITQ LAGFSGPAPM VKHLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW 240  
 ALNYRTGVRL RGAILTMAFK KILKLNKIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300  
 PVVAILGMIY NVIILGPTGF LGSASFILFY PAMMFASRLT AYFRKRCVAA TDERVQKMNE 360  
 HMTLGFDLTA AQAFTVTVTF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEVEHMKI 480  
 NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTEHQA 540  
 VLAQKQGHLL LDSDERPSPE EEEGKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVSGG 600  
 KTSLSAISLG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660  
 CCLRPDLAIL PSSDLTEIGE RGANLGGQQR QRISLARALY SDRSIYILDD PLSALDAHVG 720  
 NHIFNSAIRK HLKSKTVLFV THQLQYLVDV DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780  
 FNNLLGETP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKQGS 840  
 VPWSVYGVYI QAAGGPLAFV VIMALFMLNV GSTAFSTWWL SYWIKQSGN TTVTRGNETS 900  
 VSDSMKDNPH MQYYASIAL SMAMVLILKA IRGVVFKGT LRASSRLHDE LFRRLRSPM 960  
 KFFDTTPTGR ILNRFKMD EVDVRLPFQA EMFIQNVILV FFCVGMIAV FPWFLVAVGP 1020  
 LVILFVSLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL 1080  
 LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140  
 GLFOFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDPQGE GEVTFENAEM 1200  
 RYRENLPVLV KKVSTFIKPK EKIGIVGRTG SGKSSLGMAF FRLVELSGGC IKIDGVRISD 1260  
 IGLADLRSLK SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHMEK CIAQLPLKLE 1320  
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT 1380  
 MLTIAHRLHT VLGSDRIMVL AQQQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVK 1437

Seq ID NO: C320 Protein Sequence  
Protein Accession #: NP\_005679.1

1 11 21 31 41 51  
 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFR TRPLECQDAL ETAARAEGLS 60  
 LDASMHSQRL IDDEEHPKSG YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSLAR 120  
 VAHKGELISM EDVWSLSKHE SSDVNCRRLE RLWQELNEV GPDAASLRV VWIFCRTL 180  
 LSIVCLMITQ LAGFSGPAPM VKHLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW 240  
 ALNYRTGVRL RGAILTMAFK KILKLNKIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG 300  
 PVVAILGMIY NVIILGPTGF LGSASFILFY PAMMFASRLT AYFRKRCVAA TDERVQKMNE 360  
 HMTLGFDLTA AQAFTVTVTF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEVEHMKI 480  
 NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTEHQA 540  
 VLAQKQGHLL LDSDERPSPE EEEGKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVSGG 600  
 KTSLSAISLG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS 660  
 CCLRPDLAIL PSSDLTEIGE RGANLGGQQR QRISLARALY SDRSIYILDD PLSALDAHVG 720  
 NHIFNSAIRK HLKSKTVLFV THQLQYLVDV DEVIFMKEGC ITERGTHEEL MNLNGDYATI 780  
 FNNLLGETP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKQGS 840  
 VPWSVYGVYI QAAGGPLAFV VIMALFMLNV GSTAFSTWWL SYWIKQSGN TTVTRGNETS 900  
 VSDSMKDNPH MQYYASIAL SMAMVLILKA IRGVVFKGT LRASSRLHDE LFRRLRSPM 960  
 KFFDTTPTGR ILNRFKMD EVDVRLPFQA EMFIQNVILV FFCVGMIAV FPWFLVAVGP 1020  
 LVILFVSLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL 1080  
 LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT 1140  
 GLFOFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDPQGE GEVTFENAEM 1200  
 RYRENLPVLV KKVSTFIKPK EKIGIVGRTG SGKSSLGMAF FRLVELSGGC IKIDGVRISD 1260  
 IGLADLRSLK SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHMEK CIAQLPLKLE 1320  
 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT 1380  
 MLTIAHRLHT VLGSDRIMVL AQQQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVK 1437

Seq ID NO: C321 Protein Sequence  
Protein Accession #: NP\_005553.1

1 11 21 31 41 51  
 MPALWLGCCF CFSLLPAAR ATSRREVCDG NGKSRQCIFD RELHRQTGNG FRCILNCNDNT 60  
 DGIHCEKCKN GFYRHRERDR CLPCNCSKSG SLSARCDNSG RCSCKPGVTG ARCDRLPGPF 120  
 HMLTDAGCTQ DQRLDLSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDGNG 180  
 PEGCTQCFCY GHSASCRSSA EYSVHKITST FHQVDVGWKA VQRNGSPAKL QWSQRHQDVF 240  
 SSAQRQLDPV FVAPAKFLGN QQVSYGQSLT FDIRVDRGGR HPSAHDVILE GAGLRITAPL 300  
 MPLGKTLPCG LTKYTFRLN EHPSNNWSEF LSYPEYRRL RNLTLALIRA TYGEYSTGYI 360  
 DNVTLISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLGPF GTICPCNCQG 420  
 GGACDPDTGD CSGDENPDI ECADCPIGFY NPDHDPSCSK PCPCNHGFSV SVMPETEEVV 480  
 CNNCPFGVTG ARCELCAADY FGDPPFGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCCLK 540  
 CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCPMGS EPVGCSDGT CVCKPGFPGP 600  
 NCEHGAFSCP ACYNQVKIQM DQFMQQLQRM EALISKAQGG DGVDPDELE GRMQQAEQAL 660  
 QDILRDAQIS EGASRSLGLQ LAKVRSQENS YQSRLDDLKM TVERVRALGS QYQNRVRDTH 720  
 RLITQMLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR 780  
 ETEDYSKQAL SLVRKALHEG VSGSGSPDG AVVQGLVEKL EKTSLAQQL TREATQAEIE 840  
 ADRSYQHSIR LLDVSRLQG VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EFKRTQKNLG 900  
 NWKEEAQQLL EMKRLSYIS QKVSDASDKT QQAERALGSA AADAQRAKNG AGEALEISSE 960  
 QVDNRKAEAE EAMKRLSYIS QKVSDASDKT QQAERALGSA AADAQRAKNG AGEALEISSE 1020  
 IQEIGSLNL EANTADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDAVQMVITE 1080  
 AQKVDTRAKN AGVTIQDTLN TLDGLHLMD QPLSVDEEGL VLLEQKLSRA KTQINSQLRP 1140  
 MMSELEERAR QQRGHLHLE TSIDGILADV KNLENIRDNL PPGCYNTQAL EQQ 1193

Seq ID NO: C322 Protein Sequence  
Protein Accession #: NP\_066924.1

1 11 21 31 41 51  
 MANAGLQLLG FILAFLGWIG AIVSTALPQW RIYSYAGDNI VTAQAMYEGE WMSCVSQSTG 60

QIQCKVFDLS LNLSTLTQAT RALMVVGILL GVIAIFVATV GMKCMKCLED DEVQKMRMAV 120  
 IGGAIFLLAG LAILVATAWY GNRIVQEFYD PMTPVNARYE FGQALFTGWA AASLCCLLGA 180  
 LLCSCSPRKT TSYPTPRPYF KPAPSSGKDY V 211

5 Seq ID NO: C323 Protein Sequence  
 Protein Accession #: AAM77876

10 1 11 21 31 41 51  
 | | | | |  
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120  
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLPASN LAAPNLTVEE GKSTILSCSV AGDPVPNMYW DVGNLVSKHM 240  
 NETSHTQGS L RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300  
 15 WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

20 Seq ID NO: C324 Protein Sequence  
 Protein Accession #: NP\_006171.1

25 1 11 21 31 41 51  
 | | | | |  
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120  
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLPASN LAAPNLTVEE GKSTILSCSV AGDPVPNMYW DVGNLVSKHM 240  
 NETSHTQGS L RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300  
 30 WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGPASV ISNDDDSASP 480  
 LHHISNGSNT PSSSEGGPDA VIIGMTKIPV IENPQYFGIT NSQLKPDFTV QHIKRHNIVL 540  
 KRELGEAGFG KVFLAECYNL CPEQDKILVA VKTLKDASN ARKDFHREAE LLTNLQHEHI 600  
 35 VKFYGVCEVEG DPLIMVFYEM KHGDLNKLFLR AHGPDAVLMA EGNPPTLTQ SQMLHIAQQI 660  
 AAGMVYLASQ HPVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYRVG GHTMLPIRWM 720  
 PPESIMYRKF TTSDVWSLG VVLWEIFTYG KQPWYQLSNN EVIECITQGR VLQRPRTCPQ 780  
 EVVELMLGCW QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG 822

40 Seq ID NO: C325 Protein Sequence  
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51  
 | | | | |  
 MSSWIRWHGP AMARLWGFCW LVVGFWRAAF ACPTSCCKCSA SRIWCSDPSP GIVAFPRLEP 60  
 NSVDPENITE IFIANQKRLE IINEDDVEAY VGLRNLITVD SGLKFVAHKA FLKNSNLQHI 120  
 NFRTRNKLTS SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180  
 SKNIPLANLQ IPNCGLPASN LAAPNLTVEE GKSTILSCSV AGDPVPNMYW DVGNLVSKHM 240  
 NETSHTQGS L RITNISSDDS GKQISCVAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300  
 50 WCIPFTVKGN PKPALQWFYN GAILNESKYI CTKIHVTNHT EYHGCLQLDN PTHMNGDYT 360  
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420  
 DVTDKTGREH LSVYAVVVIA SVVGFCLLVM LFLKLARHS KFGMKGFVLF HKIPLDG 477

55 Seq ID NO: C326 Protein Sequence  
 Protein Accession #: NP\_570843.1

60 1 11 21 31 41 51  
 | | | | |  
 MPLKHYLLLL VGCQAWGAGL AYHGCPSSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60  
 LNTHTIELNE SPFLNISALI ALRIEKNELS RITPGAFRNL GSLRYLSLAN NKLQVLPIGL 120  
 FQGLDSLES L LLSNQQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFF HLVLTKLNL 180  
 GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQQ NQIGLLSPGL 240  
 FHNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGLFG PMPNLRELWL 300  
 YDNHISSEPD NVFSNLRQLQ VLILSRNQIS FISPFAFNGL TELRELSLHT NALQDLQDGNV 360  
 FRMLANLQNI SLQNNRLRLQ PGNIFANVNG LMAIQLQNNQ LENLPLGIFD HLGLCELRL 420  
 65 YDNFWRCDSD ILPLRNWLLL NQPRLGTDITV PVCFSANVR GQSLIIINVN VAVPSVHVPE 480  
 VPSYPETPWY PDTSPYPTTT SVSSTTELTS PVEDYDILTIT IQVTDDRSVW GMTQAQSGLA 540  
 IAAIVIGIVA LACSLAACVG CCCCCKRSQA VLMQMKAPNE C 581

70 Seq ID NO: C327 Protein Sequence  
 Protein Accession #: NP\_002649.1

75 1 11 21 31 41 51  
 | | | | |  
 MRALLARLLL CVLVVSDSKG SNEHLQVPSN CDCLINGGTCV SNKYFSNIHW CNCPKKFGGQ 60  
 HCEIDKSKTC YBGNHGFYRG KASTDTMGRP CLPWSNATVL QQTYHAHRSD ALQLGLGKH 120  
 YCRNPDNRRR PWCYVQVGLK PLVQECMVHD CADGKPPSP PEELKFQCGQ KTLRPRFKII 180  
 GGEFTTIENQ PWFAAIYRRH RGSVTVYVCG GSLISPCWVI SATHCFIDYP KKEDYIVYLG 240  
 RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHNNDIALLK IRSKEGRCAQ PSRTIQTICL 300  
 80 PSMYNDPQFG TSCEITGFGK ENSTDYLYPE QLKMTVVVKLI SHRECOQPHY YGSEVTTKML 360  
 CAADPQWKTD SCQGDGGGGL VCSLQGRMTL TGIWSWGRGC ALKDKPGVYT RVSHFLPWIR 420  
 SHTKEENGLA L 431

Seq ID NO: C328 Protein Sequence  
 Protein Accession #: XP\_087254.1

	1	11	21	31	41	51	
5	MQFRECSING	MKYQEINGRL	VPEGPTPDSS	EGNLSYLSSL	SHLNNLSHLT	TSSSFRTSPE	60
	NETELIKEHD	LFFKAVSLCH	TVQISNVQTD	CTGDGPWQSN	LAPSQLYYA	SSPDEKALVE	120
	AAARIGIVFI	GNSEETMEVK	TLGKLERYKL	LHILEFSDSR	RRMSVIVQAP	SGEKLLFAKG	180
	AESSILPKCI	GGIEKTRIH	VDEFALKGLR	TLCTIAYRKFT	SKEYEEDDKR	IFEARTALQQ	240
	REEKLAAVFQ	FIEKDILLG	ATAVEDRLQD	KVRETIEALR	MAGIKVWVLT	GDKHETAVSV	300
10	SLSCGHFHRN	MNILELINQK	SDSECAEQLR	QLARRITEDH	VIQHGLVVDG	TSLSLALREH	360
	EKLMEVCRN	CSAVLCCRMA	PLQKAKVIRL	IKISPEKPIT	LAVGDGANDV	SMIQEAHVGI	420
	GIMKKEGRQA	ARNSDYAAR	FKFLSKLLEF	HGHFYIIRIA	TLVQYFFYKN	VCFITPQFLY	480
	QFYCLFSQQT	LYDSVYLTL	NICFTSLPIL	IYSLLEQHV	PHVLQNKPTL	YRDISKNRLL	540
	SIKTFLYWTI	LGFSHAFIF	FGSYLLIGKD	TSLGNGQMF	GNWTFGTLVF	TVMVITVTVK	600
	MALETHFTW	INHLVTWGS	IFYFVFSLFY	GGILWPFLGS	QNMVYFVFIQ	LSSGSAWFAI	660
15	ILMVVTCLEF	DIKKKVFDRH	LHPTSTAKAQ	LTETNAGIKC	LDSMCCFPEG	EACASVGRM	720
	LERVIGRCSP	THISRSWSAS	DPFYTNDRSI	LTLSTMSST	C		761

Seq ID NO: C329 Protein Sequence  
Protein Accession #: XP\_087461.1

	1	11	21	31	41	51	
20	MLPLLAALLA	AACPLPPVRG	GAADAPGLLG	VPSNASVNAS	SAASPSPRGC	WPRRPPGPPS	60
	ARARRRRRRR	RRLCNISVQR	QMLSSLLVRW	GRPRGFQCDL	LLFSTNAHGR	AFFAAAFHRV	120
25	GPPLLIIEHLG	LAAGGAQDQL	RLCVGCGWVR	GRRTGRLRPA	AAPSAATA	GAPTALPAYP	180
	AAEPPGPWLW	QGEPLHFCCL	DFSLEELQGE	PGWRLNRKPI	ESTLVACFMT	LVIVVWSVAA	240
	LIWPVPIIAG	FLPNGMEQRR	TTASTTAATP	AAVPAGTTAA	AAAAAAAAAA	AVTSGVATK	299

Seq ID NO: C330 Protein Sequence  
Protein Accession #: XP\_051522.2

	1	11	21	31	41	51	
35	MDLHLFDYSE	PGNFSDISWP	CNSSDCIVVD	TVMCPNMPNK	SVLLYTLSEI	YIFIFVIGMI	60
	ANSVVVVVNI	QAKTGYDYTH	CYILNLAIAD	LWVVLTIPTV	VVSLVQHNQW	PMGELTCKVT	120
	HLIFSINLFG	SIFFLTICMSV	DRYLSITYFT	NTPSSRKKMW	RRVVCILVWL	LAFCVSLPDT	180
	YYLKTVTSAS	NNETYCRSFY	PEHSIKEWLI	GMELVSVVLG	FAVPFSIIAV	FYFLLARAI	240
	ASSDQKHSS	RKIIFSIVVV	FLVCWLPYHV	AVLLDIFSL	HYIPTCRLE	HALFTALHVT	300
40	QCLSLVHCCV	NPVLYSFINR	NYRYELMKAF	IFKYSAKTGL	TKLIDASRVS	ETEYSALEQS	360
	TK						362

Seq ID NO: C331 Protein Sequence  
Protein Accession #: NP\_000341.1

	1	11	21	31	41	51	
45	MGEFVRQIQL	LWKNWTLRKR	QKIRFVVELV	WPLSLFLVLI	WLRNANPLY	HHECHFENKA	60
	MPSAGMLPWL	QGIFCNVNNP	CFQSPTPGES	PGIVSNYNNS	ILARVYRDFQ	ELLMNAPESQ	120
50	HLGRIWTEHL	ILSQFMDTLR	THPERIAGRG	IRIRDILKDE	ETLTFLIKN	IGLSDSVVYL	180
	LINSQVRPEQ	FAHGVPDLAL	KDIACSEALL	ERFIIFSQR	GAKTVRYALC	SLSQGTILQWI	240
	EDTLANVDF	FKLFRVLPTL	LDERSQGINL	RSWGGILSDM	SPRIQEFIRH	PSMQDLLWVT	300
	RPLMQNGGPE	TFTKLGMILS	DLLCGYPEGG	GSRLVSPNWY	EDNNYKAFGL	IDSTRKDIPI	360
	SYDRRTTSFC	NALIQSLESN	PLTKIAWRRA	KPLLMGKILY	TPDSPAARRI	LKNANSTFEE	420
	LEHVRKLKVA	WEEVGPQIY	FFDNSTQMNM	IRDTLGNPTV	KDFLNRLQGE	EGITAEAILN	480
55	FLYKGPRESQ	ADDMANFDWR	DIFNITDRTL	RLVNQYLECL	VLDKFESYND	ETQLTQRALS	540
	LLEENMFWAG	VVFPDMYPWT	SSLPPHVYK	IRMDIDVVEK	TNKIKDRYWD	SGPRADPVED	600
	FRYIWGGFAY	LQDMVEQGIT	RSQVQAEAPV	GIYLQMPYP	CFVDDSFMI	LNRCFFPIFMV	660
	LAWIYSVSM	VKSIVLEKEL	RLKETLKNQG	VSNVAVICTW	FLDSFSIMSM	SIFLLTIFIM	720
	HGRILHYSDF	FILEFLFLAF	STATIMLCFL	LSTFFSKASL	AAACSGVIYF	TLYLPHILCF	780
60	AWQDRMTAEL	KKAVSLFLSPV	AFGFGTEVLV	RFEEQGLGLQ	WSNIGNSPTE	GDEFSFLLSM	840
	QMMLDAACY	GLLAWYLDQV	PPGDYGTPLP	WYFLLQESY	LSGEGCSTRE	ERALEKTEPL	900
	TEETEDPEHP	EGIHDSFFER	EHPGWVPGVC	VKNLVKIFEP	CGRPAVDRLN	ITFYENQITA	960
	FLGHNGAGKT	TTLILTGLL	PPTSGTVLVG	GRDIETSLDA	VRQSLGMCPQ	HNILFHHLT	1020
	AEHMLFYAQL	KGKSQEEAQL	EMEAMLEDTG	LHHKRNEEAQ	DLSGGMQRKL	SVAIAFVGDA	1080
65	KVVILDEPTS	GVDPYSSRSI	WDLCLKYRS	RTIIMPTHMM	DEADHQGDRI	AIIAQGRLYC	1140
	SGTPLFLKNC	FGTGLYLTIV	RKMKNISQSR	KGSEGTCS	SKGFSTTC	HVDDLTPQV	1200
	LDGDVNELMD	VVLHHVPEAK	LVEICIGQEL	FLLPKNKFKH	RAYASLFREL	EETLADLGLS	1260
	SFGISDTPLE	EIFLKVTEDS	DSGPLFAGGA	QOKRENVNPR	HPCLGPKEKA	GQTPQDSNVC	1320
70	SPGAPAAHPE	GQPPPEPECP	GPQLNTGTQL	VLQHVQALLV	KRFQHTIRSH	KDFLAQIVLP	1380
	ATFVFLALML	SIVILPFGFY	PALTILHPWI	GQQYTFSSMD	EPGSEQFTVL	ADVLLNKPFG	1440
	GNRCLKEGWL	PEYPCGNSTP	WKTPSVSPNI	TQLFQKQKWT	QVNPSPSCRC	STREKLTMLP	1500
	ECPEGAGGLP	PPQRTQRSTE	ILQDLTDRNI	SDFLVKTYPA	LIRSSLKSKF	WVNEQRYGGI	1560
	SIGGKLFPVP	ITGEALVGFL	SDLGRIMNVS	GGPITREASK	BIPDFLKHLE	TEDNIKVWFN	1620
	NKGWHALVSF	LNVAHNAILR	ASLPKDRSPE	EYGITVISQP	LNLTKQLSE	ITVLTTSVDA	1680
75	VVAICVIFSM	SFVPASFLVY	LQERVNKS	HLQFISGVSP	TTYWVTNFW	DIMNYSVSAG	1740
	LVLVFIGFQ	KHAYTSPENL	PALVALLLLY	GWAVIFMMYP	ASFLEFVDPST	AYVALSCANL	1800
	FIGINSSAIT	FILELFDNDR	TLLRFNAVLR	KLLIVFFHFC	LGRGLIDLAL	SQAVTDVYAR	1860
	FGEEHSANPF	HWDLIGKNLF	AMVVEGVVYF	LLTLLVQRHF	FLSQWIAEPT	KEPIVDEDD	1920
	VAAERQRIIT	GONKTDILRL	HELTKIYLG	SSPAVDRLCV	GVRPGECFGL	LGVNAGAGKT	1980
80	TFKMLTGDIT	VTSGDATVAG	KSILTNISEV	HQNMGYCPCQ	DAIDELLTGR	EHLVLYARLR	2040
	GVPAEBIEKV	ANWSTKSLGL	TVYADCLAGT	YSGGNKRKLS	TAIALIGCPP	LVLLEPTTG	2100
	MDPQARRMLW	NVIVSIIRKG	RAVVLTSHSM	EECEALCTRL	AIMVKGAFCR	MGTIQHLKSK	2160
	FDGDIYVTMK	IKSPKDDLLP	DLNPVEQFFQ	GNFPGSVQRE	RHYNMLQFQV	SSSSLARIFQ	2220
	LLLSHKDSLL	IEBYSVTQIT	LDQVFVNFAK	QQTESHDLP	HPRAAGASRQ	AQD	2273

Seq ID NO: C332 Protein Sequence  
Protein Accession #: NP\_006662.2

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
MVPHAILARG RDVCRRNGLL ILSVLSVIVG CLLGFFLRTR RLSPQEISYF QFPGELLMRM 60
LKMMLPLVV  SSLMSGLASL DAKTSSRLGV LTVAYYLWTT FMAVIVGIFM VSIHFGSAA 120
KQETTEQSGK PIMSSADALL DLIRNMFAN LVEATFKQYR TKTTTPVVKSP KVAPEEAPPR 180
10    RILYGVQEE  NGSHVQNFAL DLTPPEVVY KSEPGTSDGM NVLGIVFFSA TMGIMLGRMG 240
DSGAPLVGFC QCLNESVMKI VAVAVWYFF GIVFLIAGKI LEMDDPRAVG KKLGFYSVTV 300
VCGVLVHGLF ILPLLYFFIT KKNPIVFIRG ILQALLIALA TSSSSATLFI TFKCLENNH 360
IDRRIRFVL  PVGATINMDG TALYEAVAAI FIAQVNNYEL DFGQIITISI TATAASIGAA 420
GIPOAGLVTM VIVLTSVGLP TDDITLIIAV DWALDRFRMT INVLDALAA GIMAHICRKD 480
15    FARDTGTCKL LPECETKPVSL QEIVAAQQNG CVKSVAEASE LTLGPTCPHH VPVQVERDEE 540
LPAASLNHCT IQISELETNV

```

Seq ID NO: C333 Protein Sequence  
Protein Accession #: NP\_005680.1

```

20    1      11      21      31      41      51
      |      |      |      |      |      |
MVTVGNVCEA EGFVGPWAMQ DGLSPCFFFT LVPSTRMALG TLALVLALPC RRRERFAGAD 60
SLSWGAGPRI SPYVLQLLLA TLQALPLAG LAGRVGTARG APLPSYLLLA SVLESAGAC 120
25    GLWLLVVERS QARQRLAMGI WIKFRHSPGL LLLWTVAFAA ENLALVSWNS PQWWARADL 180
QQVQVSLWV  LRYVVSGLF VLGWLWAPGLR PQSYTLQVHE EDQDVERSQV RSAAQOSTWR 240
DFGRKLRLLS GYLWPRGSPA LQLVVLICLG LMGLERLALNV LVPIFYRNIV NLLTEKAPWN 300
SLAWTVTSYV FLKFLQGGGT GSTGFVSNLR TFLWIRVQQF TSRRVELLIF SHLHELRLRW 360
HLGRRTGVL  RIADRGTSV TGLLSYLVFN VIPTLADIII GIIYFSMFFN AWFGLIVFLC 420
30    MSLYLTTLTV VTEWRTKFRR AMNTQENATR ARAVDSLLNF ETVKYNAES YEVEYREAL 480
IKYQGLEWKS SASVLLNQI QNLVIGLGLL AGSLLCAYFV TEQKLQVGDY VLFGTYYIQL 540
YMPLNWFQTY YRMIQTNFID MENMFDLLKE ETEVKDLPGA GPLRFQKGRI EFENVHFSYA 600
DGRETLQDVS FTVMPQTLA LVGPSGAGKS TILRLFRFY DISSGCIRID QQDISQVTOA 660
35    SLRSHIGVVP QDTVLFNDDI ADNIRYGRVT AGNDEVEAAA QAAGIHDAIM AFPEGYRTQV 720
GERGLKLSGG EKQRAIART ILKAPGIILL DEATSALDTS NERAIQASLA KVCANRTTIV 780
VAHRLSTVFN ADQILVIKDG CIVERGRHEA LLSRGVGYAD MWQLQQQEE TSEDTKPQTM 840
ER

```

Seq ID NO: C334 Protein Sequence  
Protein Accession #: NP\_000667.1

```

40    1      11      21      31      41      51
      |      |      |      |      |      |
MLLETQDALY VALELVIAAL SVAGNVLVCA AVGTANTLQT PTNYFLVSLA AADVAVGLFA 60
45    IPFAITISLG FCTDFYGLCF LACFVLVLTQ SSIFSLAVA VDRYLAICVP LRYKSLVTGT 120
RARGVIAVLW VLAFIGILTP FLGWNSKDSA TNNCTEPWDG TTNESSCLVK CLFENVVPM 180
YMYVFNFFGC VLPPLLIMLV IYIKIFLVAC RQLQRTLEMD HSRTTLQREI HAAKSLAMIV 240
GIFALCNLHV HAVNCVTLFQ PAQGNKPKW AMNMAILSH ANSVVNPVIV AYRNRDFRYT 300
50    FHKIISRYLL CQADVKSNGG QAGVQPALGV GL

```

Seq ID NO: C335 Protein Sequence  
Protein Accession #: NP\_443164

```

55    1      11      21      31      41      51
      |      |      |      |      |      |
MGLGARGAWA ALLGLTLQVL ALLGAAHESA AMAETLQHVP SDHTNETSNS TVKPPTSVAS 60
DSSNTTVTM  KPTAASNTT PGMVSTNMTS TTLKSTPKTT SVSQNTSQIS TSTMTVTHNS 120
SVTSAASSVT ITTTHMSEAK KGSKFDTGSF VGGIVLTLGV LSILYIGCKM YYSRRGIRYR 180
60    TIDEHDAII

```

Seq ID NO: C336 Protein Sequence  
Protein Accession #: NP\_004186.1

```

65    1      11      21      31      41      51
      |      |      |      |      |      |
MAQHGMAGAF RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTARCC RVHTTRCCRD 60
YPGECCSEW  DCMCVQPEFH CGDPCCTTCR HHPCPPGQGV QSQGFSGF QCIDCASGTF 120
SGGHEGHCKP WTDCTQFGFL TVFPGNKTHN AVCVPGSPPA EPLGWLTVVL LAVAACVLLL 180
70    TSAQLGLHIW QLSQCMWPR ETQLLLEVPP STEDARSCQF PEEERGERSA EEKRLGLDW 240
V

```

Seq ID NO: C337 Protein Sequence  
Protein Accession #: BAC03767.1

```

75    1      11      21      31      41      51
      |      |      |      |      |      |
MGCDGRVSGL LRRNLQPTLT YWSVFFSFG L CIAFLGPTLL DLRCQTHSSL PQISWVFFSQ 60
QLCLLGSAL  GGVFKRTLQ SLWALFTSSL AISLVFAVIP FCRDVKVLAS VMALAGLAMG 120
CDDTVANMQL VMYQKDSAV FLQVLHFFVG FGALLSPLIA DPFLSEANCL PANSTANTTS 180
80    RGHLFHVSRV LQOHVDAKP WSNQTFPGLT PKDGAGTRVS YAFWIMALID LPVPMVAVML 240
LSKERLLTCC PQRRLPLLSA DELALETQPP EKEDASSLPP KFQSHLGHD LFSCCQKRLN 300
RGAPYSFFAI HITGALVLFM TDGLTGAYSA FVYSYAVEKP LSVGHKVAGY LPSLFWGFI 360
LGRLLSIPIS SRMKPATMVF INVVGVVVTF LVLLIFSINV VPLFVGTASL GLFLSSTFPS 420
MLAYTEDSLQ YKGCATTVLV TGAGVGEMVL QMLVGSIFQA QGSYSFLVCG VIFGCLAFTF 480

```



YILLLFFHRM HPGLPSVPTQ DRSIGMENSE CYQR

514

Seq ID NO: C338 Protein Sequence  
 Protein Accession #: NP\_002194.1

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50

1	11	21	31	41	51	
MGPERTGAAP	LPLLLVLALS	QGILNCCLAY	NVGLPEAKIF	SGPSSEQFGY	AVQQFINPKG	60
NWLLVGSFWS	GFENRMGDV	YKCPVDLSTA	TCEKLNLTQS	TSIPNVTEMK	TNMSLGLILT	120
RNMTGGFLT	CGPLWAQCCG	NQYTTGVCS	DISPDFQLSA	SFSPATQPCP	SLIDVVVVCD	180
ESNSIYPWDA	VKNFLEKFVQ	GLDIGPTKTQ	VGLIQYANNP	RVVFNLTNYK	TKEEMIVATS	240
QTSQYGGDLT	NTFGAIQYAR	KYAYSAAAGG	RRSATKVMVV	VTDGESHGDS	MLKAVIDQCN	300
HDNILRFGIA	VLGYLNRNAL	DTKNLIKEIK	AIASIPTERY	FFNVSDAAL	LEKAGTLGEQ	360
IFSIEGTVQG	GDNFQMEMSQ	VGFSADYSSQ	NDILMLGAVG	AFGWSGTIVQ	KTSHGHLIFP	420
KQAFDQILQD	RNHSSYLQYS	VAAISTGEST	HFVAGAPRAN	YTGQIVLYSV	NENGNITVIQ	480
AHRGDQIGSY	FGSVLCSDVD	DKDITITDVL	VGAPMYMSDL	KKEEGRVYLF	TIKKGILGQH	540
QFLEGPEGIE	NTRFGSAIAA	LSDINMDGFN	DVIVGSPLEN	QNSGAVYIYN	GHQGTIRTQY	600
SQKILGSDGA	FRSHLQYFGR	SLDGYDLNG	DSITDVSIGA	FGQVVQLWSQ	SIADVAIEAS	660
FTPEKITLVN	KNAQIILKLC	FSAKFRPTKQ	NNQVAIVYNI	TLDADGFSSR	VTSRGLFKEN	720
NERCLQKNMV	VNQACSCEH	IYIQEPSDV	VNSLDLRVDI	SLNPGTSPA	LEAYSETAKV	780
FSIPFHKDCG	EDGLCISDLV	LDVRQIPAAQ	EQPFIVSNQN	KRLTFSVTLK	NKRESAYNTG	840
IVVDFSENLF	FASPSLPVDG	TEVTCQVAAS	QKSACDVGY	PALKREQQVT	FTINFDNLQ	900
NLQNAQSLSF	QALSESQEEN	KADNLVNLKI	PLLYDAEIH	TRSTNINFYE	ISSDGNVPSI	960
VHSPEDVGP	FIFSLKVTITG	SVPVSMATVI	IHIPQYTKK	NPLMYLTGVQ	TDKAGDISCN	1020
ADINPLKIQG	TSSSVSFKSE	NFRHTKELNC	RTASCSNVTC	WLKDVHMKGE	YFVNVTTRI	1080
NGTFASSTFQ	TVQLTAAAEI	NTYNPEIYVI	EDNTVTIPLM	IMKPDKEAEV	PTGVIIGSII	1140
AGILLLLALV	AILWKLGF	FFKRYEKM	TKNPDEIDET	TELS	S	1181

Seq ID NO: C339 Protein Sequence  
 Protein Accession #: NP\_113648.1

35  
 40  
 45  
 50

1	11	21	31	41	51	
MYRPRARAAP	EGRVRGCAVP	STVLLLLAYL	AYLALGTGVF	WTLEGRAAQD	SSRSFQDKW	60
ELLQNFTCLD	RPALDSLIRD	VVQAYKNGAS	LLSNTTSMGR	WELVGSFFFS	VSTITTIGYG	120
NLSPTMAAR	LFCIFALVGF	IFLNLVVLNR	LGHLMQQGVN	HWASRLGGTW	QDPDKARWLA	180
GSGALLSGLL	FLPLLPLLF	SHMEGWSYTE	GFYFAFITLS	TVGFGDYVIG	MNPSQRYPLW	240
YQNMVSLWIL	FGMAWLALII	KLILSQLETP	GRVCSCCHHS	SKEDFKSQSW	RQGPDPREPES	300
HSPQGCYPE	GPMGIQHLIE	PSAHAAGCGK	DS			332

Seq ID NO: C340 Protein Sequence  
 Protein Accession #: NP\_004145.1

45  
 50

1	11	21	31	41	51	
MEWDNGTGQA	LGLPPTTCVY	RENFKQLLLP	PVYSAVLAAG	LPLNICVITQ	ICTSRRALTR	60
TAVYTLNLAL	ADLLYACSLP	LLIYNYAQGD	HWPFGDFACR	LVRFLFYANL	HGSILFLTCT	120
SPQRYLGICH	PLAPWHKRG	RRAAWLVCVA	VWLAVTTQCL	PTAIFAATGI	QRNRTVCYDL	180
SPPALATHYM	PYGMALTVIG	FLLPFAALLA	CYCLLACRLC	RQDGPAPFVA	QERRGKAARM	240
AVVAAAFAI	SFLPFHITKT	AYLAVRSTPG	VPCTVLEAFA	AAKYGTFRPA	SANSVLDPIL	300
YFYTQKKFRR	RPHELLQKLT	AKWQRQGR				328

Seq ID NO: C341 Protein Sequence  
 Protein Accession #: NP\_009128.1

55  
 60  
 65

1	11	21	31	41	51	
MQRPGPRLWL	VLQVMGSCAA	ISSMDMERPG	DGKCQPIEIP	MCKDIGYNTM	RMPNLMGHEN	60
QREAAIQLHE	FAPLVEYGCH	GHLRFFLCSL	YAPMCTEQVS	TIPIACRVMC	EQARLKCSP	120
MEQFNFKWPD	SLDCRKLPNK	NDPNYLCMEA	PNNGSDEPTR	GSGLFPPFLR	PQRPHSAQEH	180
PLKDGPGPRG	GCDNPGKFHH	VEKSASCAPL	CTPGVDVYWS	REDKRFAVVW	LAIWAVLCFF	240
SSAFTVLTF	IDPARFRYPE	RPIIFLSMCY	CVYSVGYLIR	LFAGAESTAC	DRDSGQLYVI	300
QEGLESTGCT	LVFLVLVYFG	MASSLWVVVL	TLTWFLAAGK	KWGHEATEAN	SSYFHLLAANA	360
IPAVKTIIL	VMRRVAGDEL	TGVCYVGSMD	VNALTGFVLI	PLACYLVIGT	SFILSGFVAL	420
FHIRRVMTG	GENTDKLEKL	MVRIGLFSVL	YTVPATCVIA	CYFYERLNMD	YWKILAAQHK	480
CKMNNQTKTL	DCLMAASIPA	VEIFMVKIFM	LLVVGITSGM	WIWTSKTLQS	WQQVCSRRLLK	540
KKSRKPPASV	ITSGGIYKKA	QHPQKTHHGK	YEIPAQSPTC	V		581

Seq ID NO: C342 Protein Sequence  
 Protein Accession #: NP\_005752.1

70  
 75  
 80

1	11	21	31	41	51	
MEVSRRKAPP	RPPRPAAPLP	LLAYLLALAA	PGRGADEPVW	RSEQAIGAIA	ASQEDGVFVA	60
SGSCLDQLDY	SLEHSLSRLY	RDQAGNCTEP	VSLAPPARFR	PGSSFSKLLL	PYREGAAGLG	120
GLLLTGWTFD	RGACEVRPLG	NLSRNSLRNG	TEVVVSCHPQG	STAGVVYRAG	RNNRWYLAVA	180
ATYVLPEPET	ASRCNPAASD	HDATALKDT	EGRSLATQEL	GRLLKCEGAG	SLHFFVDAFLW	240
NGSIYFPPYP	VNYTSGAATG	WPSMARIAQS	TEVLFQGGAS	LDCCGHGHPDG	RRLLLSSSLV	300
EALDVWAGVF	SAAAGEGQER	RSPTTALCL	FRMSEIQARA	KRVSWDFKTA	ESHCKEGDQP	360
ERVQPIASST	LIHSDLTSVY	GTVMNRTVL	FLGTGQGQLL	KVILGENLTS	NCPEVIYBIK	420
EETPVFYKLV	PDPVKNIIYI	LTAGKEVRR	RVANCNKHKS	CSECLTATDP	HCGWCHSLQR	480
CTFQGDCHVS	ENLENWLDIS	SGAKCKPKIQ	IIRSSKEKTT	VTMVGFSFSPR	HSKCMVKNVD	540
SSRELCONKS	QPNRTCTCSI	PTRATYKDV	VVNVMFSFGS	WNLSDRFNFT	NCSSSLKECPA	600
CVETGCWCK	SARRCIHPFT	ACDPSDYERN	QBQCPVAVEK	TSGGGRPKEN	KGNRTNQALQ	660
VFYIKSIEPQ	KVSTLGKSNV	IVTGANFTRA	SNITMLKGT	STCDKDVIVQ	SHVLNDTHMK	720

FSLPSSRKEM KDVCIQFDGG NCSSVGSLSY IALPHCSLIF PATTWISGGQ NITMMGRNFD 780  
 VIDNLIISHE LKGNINVSEY CVATYCGFLA PSLKSSKVRT NVTVKLRVQD TYLDCGTLQY 840  
 REDPRTGYR VESEVDTELE VKIQKENDNF NISKKDIEIT LFHGENGQLN CSFENITRNQ 900  
 DLTTILCKIK GIKTASTIAN SSKKVRVKLG NLELYVEQES VPSTWYFLIV LPVLLVIVIF 960  
 AAVGVTRHKS KELSRKQSQQ LELLESELRK EIRDGFaelQ MDKLDVVDSE GTVPFLDYKH 1020  
 FALRTFFPES GGFTHIFTED MHNRDANDKN ESLTALDALI CNKSFLVTVI HTLEKQKNFS 1080  
 VKDRCLFASF LTIALQTKLV YLTSILEVLT RDLMEQCSNM QPKMLLRTE SVVEKLLTNW 1140  
 MSVCLSGFLR ETVGEPFYLL VTTLNQKINK GPVDVITCKA LYTLNEDWLL WQVPEFSTVA 1200  
 LNVVFEKIPE NESADVCRNI SVNVLDCDTI GQAKEKIFQA FLKNGSPYG LQLNEIGLEL 1260  
 QMGTRQKELL DIDSSSVILE DGITKLNTIG HYEISNGSTI KVFKKIANFT SDVEYSDHHC 1320  
 HLLLPDSEAF QDVQGRHRG KHKFKVKEMY LTKLLSTKVA IHSVLEKLFER SIWSLPNSRA 1380  
 PFAIKYFFDF LDAQAENKKI TDPDVVHIWK TNSLPLRFVW NILKNPQFVF DIKKTPHIDG 1440  
 CLSVIAQAFM DAFSLTEQQL GKEAPTNNKL YAKDIPTYKE EVKSYYKAIR DLPPLSSEM 1500  
 EEFLTQESKK HENEFNEEVA LTEIYKYIVK YFDEILNKLE RERGLEEAQK QLLHVKVLF 1560  
 EKKKCKWM 1568

Seq ID NO: C343 Protein Sequence  
 Protein Accession #: NP\_002176.1

1 11 21 31 41 51  
 | | | | |  
 MTILGTTFGM VFSLQVVSQ ESGYAQNGDL EDAELDDYSF SCYSQLEVNG SQHSLTCAFE 60  
 DDPVNTTNLE FEICGALVEV KCLNFRKLQE IYFIETKKFL LIGKSNICVK VGEKSLTCKK 120  
 IDLTTIVKPE APFDLSVIYR EGANDFVVT FNTSHLQKKYV KVLMDHVAYR QEKDENKWT 180  
 VNLSTKLTL LQRKLQPAAM YEIKVRSIPD HYFKGFSEW SPSYFRTPE INNSSGEMDP 240  
 ILLTISILSF FSVALVILA CVLWKKRIK IVWPSLPDHK KTLHLCKKP RKNLNVSFNP 300  
 ESFLDCQIHR VDDIARDEV EGFLQDTFFQ QLESEKQRL GGDVQSPNCP SEDVVTPES 360  
 FGRDSSLTCL AGNVASADAP ILSSRSRLDC RESGKNQPHV YQDLLSLGT TNSLPPFFS 420  
 LQSGILTLPN VAQQQPILTS LGSNQEEAYV TMSSFYQNG 459

Seq ID NO: C344 Protein Sequence  
 Protein Accession #: NP\_002713.1

1 11 21 31 41 51  
 | | | | |  
 MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPEQMAQYA ADLRRYINML 60  
 TRPRYGRHK EDTLAFSEWG SPAAVPREL SPLDL 95

Seq ID NO: C345 Protein Sequence  
 Protein Accession #: NP\_115934.1

1 11 21 31 41 51  
 | | | | |  
 MTWRHHVRL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSHFGE 60  
 VTGSAEGWGP EEPLPYRAF GEGASARPRC CRNGGTCVLG SFCVCPAHFT GRYCEHDQRR 120  
 SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL 180  
 LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRPVPSVPLG HRL 223

Seq ID NO: C346 Protein Sequence  
 Protein Accession #: NP\_006524.1

1 11 21 31 41 51  
 | | | | |  
 MARSLVCLGV IILLSAFSGP GVRGGPMPKL ADRKLCADQE CSHPISTMAVA LDYMAPDCR 60  
 FLTIHRGQVV YVFSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD 120  
 VKTDKWDFYC Q 131

Seq ID NO: C347 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 | | | | |  
 MTQVTEKSTE HPEKTTSTTE KTRTPPEKPT LYSEKTICTK GKNTVPPEKP TENLGNTTTL 60  
 TETIKAPVKS TENPEKTA AV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI 120  
 TSRTKLSSIT SEATGNESH P YLNKDGSKG IHAGQMGEN D SFPWAIVIV VLVAVILLV 180  
 FLGLIFLVSY MMRTRRTLTQ NTQYNDAEDE GGPNSYPVYL MEQQLNGMGQ IPSR 235

Seq ID NO: C348 Protein Sequence  
 Protein Accession #: NP\_543146.1

1 11 21 31 41 51  
 | | | | |  
 MTQVTEKSTE HPEKTTSTTE KTRTPPEKPT LYSEKTICTK GKNTVPPEKP TENLGNTTTL 60  
 TETIKAPVKS TENPEKTA AV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI 120  
 TSRTKLSSIT SEATGNESH P YLNKDGSKG IHAGQMGEN D SFPWAIVIV VLVAVILLV 180  
 FLGLIFLVSY MMRTRRTLTQ NTQYNDAEDE GGPNSYPVYL MEQQLNGMGQ IPSR 235

Seq ID NO: C349 Protein Sequence  
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51  
 | | | | |

	MWPRLAFCCW	GLALVSGWAT	FQOMSPSRNF	SFRLFPETAP	GAPGSIPAPP	APGDEAAGSR	60
	VERLGQAFRR	RVRLLRELSE	RLELVFLVDD	SSSVGEVNFR	SELMFVRKLL	SDFPVVPTAT	120
	RVAIVTFSSK	NYVVRVRYDI	STRRARQHKC	ALLLQEIPAI	SYRGGGTYTK	GAFAQAAQIL	180
5	LHARENSTKV	VFLITDGYSN	GGDPRIIAAS	LRDSGVEIFT	FGIWQGNIRE	LNDMASTPKE	240
	EHCYLLHSFE	EFEALARRAL	HEDLPSGSFI	QDDMVHCSYL	CDEGKDCCDR	MGSCCKGTHT	300
	GHFECICEKG	YYGKGLQYEC	TACPSGTYKP	EGSPGGISSC	IPCPDENHTS	PPGSTSPEDC	360
	VCREGYRASG	QTCELVHCPA	LKPPENGYFI	QNTCNNHFNA	ACGVRCHPGF	DLVGSSIIIC	420
	LPNGLWSGSE	SYCRVTRCPH	LRQPKHGHIS	CSTREMLYKT	TCLVACDEGY	RLEGSCKLTC	480
10	QGNQSQWDGPE	PRCVERHCST	FQMPKDVIIIS	PHNCGKQPAK	FGTICYVSCR	QGFILSGVKE	540
	MLRCTTSGKW	NVGVQAAVCK	DVEAPQINCP	KDIEAKTLEQ	QDSANVTWQI	PTAKDNSGEK	600
	VSVHVHPAFT	PPYLFPIGDV	AIVYTATDLS	GNQASCFIHI	KVIDAEPPVI	DWCRSPFPVQ	660
	VSEKVHAASW	DEPQFSDNSG	AELVITRSHT	QGDLPFQGET	IVQYTATDPS	GNNRTCDIHI	720
	VIKGSFCEIP	FTPUNGDFIC	TPDNTGVNCT	LTCLEGYDFT	EGSTDKYYCA	YEDGVVKPTY	780
15	TTEWPDCAKK	RFANHGFKSF	EMFYKAARCD	DTDLMKKFSE	AFETTLGKMV	PSFCSDAEDI	840
	DCRLEENLTK	KYCLEYNYDY	ENGFAIGPGG	WGAANRLDYS	YDDFLDTVQE	TATSIGNAKS	900
	SRIKRSAPLS	DYKIKLIFNI	TASVPLPDER	NDTLEWENQ	RLQLTLETIT	NKLRKTLNKO	960
	PMYSFQLASE	ILIADSNMLE	TKKASPFRCR	GSVLRGRMCV	NCPLGTYYNL	EHFTCESCRI	1020
	GSYQDEEGQL	ECKLCPSGMY	TEYIHSRNIS	DCKAQCKQGT	YSYSGLETCE	SCPLGTYQPK	1080
20	FGSRSCLSGP	ENTSTVKRGA	VNISACGVPC	PEGKFSRSLG	MPCHPCPRDY	YQPNAGKAFK	1140
	LACPFYGTTP	PAGSRSITEC	STSVLNTITF	GGFGHLELLN	CPSEVFHECF	FNPCHNSGTC	1200
	QQLGRGYVCL	CPLGYTGLKC	ETDIDECSP	PCLNNGVCKD	LVGEFICECP	SGYTQQRCEE	1260
	NINECSSSPC	LNKGTICVDGV	AGYRCTCVKG	FVGLHCETE	NECQSNPCLN	NAVCEQVGG	1320
	FLCKCPGGFL	GTRCGKNVDE	CLSQPKCKNGA	TCKDGANFR	CLCAAGFTGS	HCELNINECQ	1380
25	SNPCRNQATC	VDELNSYSCK	CQPGFSGKRC	ETEQTSGFNL	DFEVSGIYGY	VMLDGMPLSL	1440
	HALTCTFWMK	SSDDMNYGTP	ISYAVDNGSD	NTLLLTIDYNG	WVLYVNGREK	ITNCPSVNDG	1500
	RWHHIAITWT	RNGWVWKVYI	DGKLSDDGAG	LSVGLPIPGG	GALVLGQEQD	KKEGEGFSPA	1560
	SFVGSISQLN	LWDYVLSQPY	VKSLATSCPE	ELSKGNVLAW	PDFLSGIVGK	VKIDSKSIFC	1620
	SDCPRLGGSV	PHLRTASEDL	KPGSKVNLFC	DPGFQLVGNP	VQYCLNQGGW	TQPLPHCERI	1680
30	SCGVPPPLEN	GFHSADDFYA	GSTVTYQCN	GYLLGDSRM	FCTDNGSWNG	VSPSCLDVIDE	1740
	CAVGSDCSEH	ASCLNVGDSY	ICSCVPPYTG	DGKNCAEPIK	CKAPGNPENG	HSSGEIYTVG	1800
	AGVTFSCQEG	YQLMGVTKIT	CLESGEWNHL	IPYCKAVSCG	KPAIPENGCI	EELAFTFGSK	1860
	VTYRCNKGYT	LAGDKESSCL	ANSSWSHSP	VCEPVKCSSP	ENINNGKYIL	SGLTYLSTAS	1920
	YSCDTGYSLQ	GPSIIETIAS	GIWDRAPPAC	HLVFCGEPPA	IKDAVITGNN	FTFRNTVITYT	1980
35	CKEGYTLAAG	DTIECLADGK	WSRSDQQLA	VSCDEPPIVD	HASPETAHRL	FGDIAFYICS	2040
	DGYSLADNAG	LLCNAQGWV	PPEGQDMPRC	IAHFCEKPPS	VSYSILESVS	KAKFAAGSVV	2100
	SFKCMGFFVL	NTSAKIECMR	GGQWNPSPMS	IQCIIPVRCGE	PPSIMNGYAS	GSNYSFGAMV	2160
	AYSCNKGFYI	KGEKKSTCEA	TGQWSSPIPT	CHPVSCGEPP	KVENGFLHT	TGRIFESEVR	2220
	YQCNPGYKSV	GSVPFVCQAN	RHHHSESPML	CVPLDCGKPP	PIQNGFMKGE	NFEVGSKVQF	2280
40	FCNEGVELVG	DSSWTCKQSG	KWNKKSNEPK	MPAKCPEPPL	LENQLVLKEL	TTEVGVTTF	2340
	CKEGHVLQGP	SVLKLCLPSQ	WNDSFPVCKI	VLCTPPPLIS	FGVPIPPSAL	HFGSTVKYSC	2400
	VGGFFLRNGS	TTLCQPDGTW	SSPLPECVPV	ECPOPEELPN	GIIDVQGLAY	LSTALYTCKP	2460
	GFELVGNNTT	LCGENGHWLG	GKPTCKAIEC	LKPKEILNGK	FSYTDLHYGQ	TVTYSCNRGF	2520
	RLBGPALTC	LETGDDWDVA	PSCAIHCDS	PQPIENGFEV	GADYSYGAI	IYSCFPFGFQV	2580
45	AGHAMQICEE	SGWSSSIPTC	MPIDCGLPPH	IDFGDCTKLK	DDQGYFQED	DMMEVPVYTP	2640
	HPPYHLGAVA	KTWENTKESP	ATHSSNFLYG	TMVSYTCNPG	YELGPNVLI	CQEDGTWNGS	2700
	APSCISIECD	LPTAPENGFL	RFTETSMGSA	VQYSCKPGHI	LAGSDLRLCL	ENRWKSGASP	2760
	RCEAISCKKP	NPVMNGSIKG	SNYTYLSTLY	YECDPGVVLN	GTERRTCQDD	KNWDEDEPIC	2820
	IPVDCSSPPV	SANGQVRGDE	YTFQKEIET	CNEGFLLEGA	RSRVCLANGS	WSGATPDCVP	2880
50	VRCATPPQLA	NGVTEGLDYG	FMKEVTFHCH	EGYILHGAPK	LTCQSDGNWD	AEIPLCKPVN	2940
	CGPPEDLAHG	FPNGFSFIHG	GHIQYQCFPG	YKLHGNSSRR	CLSNWSWSGS	SPSCLPCRCS	3000
	TPVIEYGTVN	GTDFDCGKAA	RIQCFKGFKL	LGLSEITCEA	DGQWSSGFPH	CEHTSCGSLP	3060
	MIPNAFISET	SSWKENYIQC	SCRSGYVIQG	SSDLICTEKG	VWSQPYPVCE	PLSCGSPPSV	3120
	ANAVATGEAH	TYSEVKLRC	LEGYTMDDTD	DTFTCQKDR	WFERISCSP	KKCPLPENIT	3180
55	HILVHGDDFS	VNRQVSVSCA	EGYTFEGVNI	SVCQLDGTWE	PPFSDSCSP	VSCGKPESPE	3240
	HGFVVGSKYT	FESTIYQCE	PGELEGNRE	RVCQENRQWS	GGVAICKETR	CETPLFLNG	3300
	KADIENTTGT	PNUVYSCNRG	YSLEGPSEAH	CTENGTSWHP	VPLCKPNPCP	VPFVIPENAL	3360
	LSEKEFYVDQ	NVSIKCRBGF	LLQGHGIITC	NPDETWTQTS	AKCEKISCGP	PAHVENAIAR	3420
	GVHYQYGDMI	TYSYCSGYML	EGFLRSVCLC	NGTWTSPPIC	RAVCRFPQCN	GGICQRPNAC	3480
60	SCPEGWMLRL	CEEPICILPC	LNGGRCVAPY	QCDCPPGWTG	SRCHTAVCQS	PCLNGGKCVR	3540
	ENRCHCLSSW	TGHNCSTR					3557

Seq ID NO: C350 Protein Sequence  
Protein Accession #: FGENESH predicted

65	1	11	21	31	41	51	
	MRFSVSGMRT	DYPRSVLAPA	YVSVCLLLLC	PREVIAPAGS	EPWLCQPAPR	CGDKIYNPLE	60
	QCCYNDAIVS	LSETRQCGPP	CTFWPCFELC	CLDSFGLTND	FVVKLKVQGV	NSQCHSSPIS	120
70	SKCERGRIC						129

Seq ID NO: C351 Protein Sequence  
Protein Accession #: AAH35671.1

75	1	11	21	31	41	51	
	MVPARGGGGA	LARAAGRGLL	ALLLAVSAPL	RLQAEELGDG	CGHLVITYQDS	GTMTSKNYPG	60
	TYPNHTVCEK	TITVPKGRKL	ILRLGLDLIE	SQTCASDYLL	FTSSSDQYGF	YCGSMTVPKE	120
	LLLNTSEVTV	RFESGSHISG	RGFLITYASS	DHPDLITCLE	RASHYLKTEY	SKFCPAGCRD	180
80	VAGDISGNMV	DGYRDTSLLC	KAAIHAGIIA	DELGGQISVL	QRKGISRYEG	ILANGVLSRD	240
	GSLSDKRFLF	TNNGCSRSLS	FEPDQIRAS	SSWQSVNESG	DQVHWSFGQA	RLQDQGPSWA	300
	SGDSSNNHKP	REWLEIDLGE	KKKITGIRTT	GSTQSNFNFY	VKSFVNMFKN	NNSKWKTYKG	360
	IYNNBEKVFO	GMSNFRDPVQ	NNFIPPIVAR	YVRVVPQTWH	QRIALKVELI	GCQITQGNDS	420
	LWVRKTSQST	SVSTKKEDET	ITRPIPSEET	STGINITTVA	IPLVLVLVLV	FAGMGIFAAP	480
	RKKKKKGSPY	GSAEAQKTDK	WKQIKYFFAR	HQSAEFTISY	DNEKEMTQKL	DLITSDMAG	539

Seq ID NO: C352 Protein Sequence  
Protein Accession #: Eos sequence

5  
10  
15  
20

1	11	21	31	41	51	
MGFGAGQRLR	PVPAPRSSAE	EAARPGQLRL	GIRRGEAELA	KLAPSGVMVP	GARGGGALAR	60
AAGRGLLALL	LAVSAPLRLO	AEELGDGCGH	LVTYQDSGTM	TSKNYPGTYP	NHTVCEKTIT	120
VPKGRLLLR	LGDDIESQT	CASDYLLFTS	SSDQYGPYCG	SMTVPKELLL	NTSEVTVRFE	180
SGSHISGRGF	LLTYASSDHP	DLITCLERAS	HYLKTEYSKF	CPAGCRDVAG	DISGNMVDGY	240
RDTSLLCKAA	IHAGIIADEL	GGQISVLQRK	GISRYEGILA	NGVLSRDGSL	SDKRFLFTSN	300
GCSRSLSEFP	DGQIRASSSW	QSVNESGDQV	HWSPGQARLQ	DQGSPWASGD	SSNNHKPREW	360
LEIDLGEKKK	ITGIRTTGST	QSNFNFYVKS	FVMNFKNNNS	KWKTYKGIVN	NEEKVFQGNS	420
NFRDPVQNNF	IPPIVARYVR	VVPQFWHQRI	ALKVELIGCQ	ITQGNDSLWV	RKTSQSTSVS	480
TKKEDETITR	PIPSEETSGT	INITTVAIPL	VLLVVLVFAV	MGIFAAFRKK	KKKGSPYGSA	540
EAQKTDCWKQ	IKYPFARHQS	AEFTISYDNE	KEMTQKLDLI	TSDMAG		586

Seq ID NO: C353 Protein Sequence  
Protein Accession #: FGENESH predicted

25  
30  
35  
40

1	11	21	31	41	51	
MFQRQERFLD	LSSAEAVAAM	ILHQHPDIIN	KGDGCGHLVT	YQDSGMTSTK	NYPGTYPNHT	60
VCEKTITVPK	GKRLILRLGD	LDIESQTCAS	DYLLFTSSSD	QYGMQKEEET	EVLCLSVAGA	120
QRVDIPVQLL	PSFLEGWKGH	ADARGPYCGS	MTVPKELLN	TSEVTVRFES	GSHISGRGFL	180
LTASSDHPD	LITCLERASH	YLKTEYSKFC	PAGCRDVAGD	ISGNMVDGYR	DTSLCKAAI	240
HAGIIADELG	QQISVLQRKG	ISRYEGILAN	GVLSRDGSL	DKRFLFTSNG	CSRSLSEFPD	300
GQIRASSSQW	SVNESGDQVH	WSPGQARLQD	QGPSWASGDS	SNNHKPREWL	EIDLGEKKKI	360
TGIRTTGSTG	SNFNFYVKS	VNMNFKNNNS	WKTYKGIVN	EKVFQGNSN	FRDPVQNNFI	420
PIVARYVRV	VPQFWHQRI	LKVELIGCQI	TQGNDSLWVR	KTSQSTSVST	KKEDETITRP	480
IPSEETSTDA	MPVQIVGDHT	QMISQRENLG	PDEGKIPFKG	TAESMVRVVF	AVVNDLGLML	540
FLAHTPEEDI	DHYCWQIKY	PFARHQSABF	TISYDNEKEM	TQKLDLITSD	MADYQQPLMI	600
GTGTVTRKGS	TFRPMDDAE	EAGVSTDAGG	HYDCPQRAGR	HEYALPLAPP	EPEYATPIVE	660
RHVLRAHTFS	AQSGYRVPGP	QPGHKHSLSS	GGFSPVAVVG	AQDGDYQRP	SAQPADRGYD	720
RPKAVSALAT	ESGHPDSQKP	PTHPGTSDSY	SAPRDCLTPL	NQTAMTALL		769

Seq ID NO: C354 Protein Sequence  
Protein Accession #: NP\_004607.1

45

1	11	21	31	41	51	
MAGVSACIKY	SMFTFNFLFW	LCGILILALA	IWVRVSNDSD	AIFGSEDVGS	SSYVAVDILI	60
AVGAIIMILG	FLGCCGAIKE	SRCMLLLFFI	GLLLILLLQV	ATGILGAVFK	SKSDRIVNET	120
LYENTKLLSA	TGESEKQFQE	AIIVFQBEFK	CCGLVNGAAD	WGNFNQHYPE	LCACLDKQRP	180
CQSYNGKQVY	KETCISFIKD	FLAKNLIIVI	GISFGLAVIE	ILGLVFSMVL	YCQIGNK	237

Seq ID NO: C355 Protein Sequence  
Protein Accession #: NP\_004608.1

50  
55

1	11	21	31	41	51	
MCTGGCARCL	GGTLIPLAFF	GFLANILLFF	PGGKVIDDND	HLSQEIWFFG	GILGSGVIMI	60
FPALVFLGLK	NNDCCGCCGN	EGCGKRFAMF	TSTIFAVVGF	LGAGYSFIIS	AISINKGPCK	120
LMANSTWGYF	FHDGIDYLNDE	ALWNKCREPL	NVVPWNLTFL	SILLVVGGIQ	MVLCAIQVVN	180
GLLGTLCGDC	QCCGCCGGDG	PV				202

Seq ID NO: C356 Protein Sequence  
Protein Accession #: NP\_002372.1

60  
65  
70

1	11	21	31	41	51	
MPRPAPARRL	PGLLLLLLWPL	LLLPSAAPDP	VARPGFRRLE	TRGPGGSPGR	RPSAAPDGA	60
PASGTSEPRG	ARGAGVCKSR	PLDLVFIIDS	SRSVRPLEFT	KVKTFVSRII	DTLDIGPADT	120
RVAVVNYAST	VKIEFQLQAY	TDKQSLKQAV	GRITPLSTGT	MSGLAIQTAM	DEAFTVEAGA	180
REPSSNIPKV	AIIVTDGRPQ	DQVNEVAARA	QASGIELYAV	GVDRADMASL	KMMASEPLEE	240
HVFVETYGV	IEKLSRRFQE	TFCALDPCVL	GTHQCQHVCI	SDGEGKHHCE	CSQGYTLNAD	300
KKTCALDRG	ALNTHGCEHI	CVNDRSGSYH	CECYEGYTLN	EDRKTCSAQD	KCALGTHGCQ	360
HICVNDRTGS	HHCECYEGYT	LNADKKTCVS	RDKCALGSHG	CQHICVSDGA	ASYHCDCYPG	420
YTLNEDKKTC	SATEBARRLV	STEDACGCEA	TLAFQDKVSS	YLQRLNTKLD	DILEKLKINE	480
YQIHR						486

Seq ID NO: C357 Protein Sequence  
Protein Accession #: NP\_057723.1

75  
80

1	11	21	31	41	51	
MARGSLRRL	RLVLGLWLA	LLRSVAGEQA	PGTAPCSRGS	SWSADLDKCM	DCASCRRAPH	60
SDFCLGCAA	PPAPFRLWLP	ILGGALSLTF	VLGLLSGFLV	WRRCRREKRF	TPPIETGGE	120
GCPAVALIQ						129

Seq ID NO: C358 Protein Sequence  
Protein Accession #: NP\_001810.1

1 11 21 31 41 51  
 | | | | |  
 MQPTLLLSLL GAVGLAAVNS MPVDNRNHNE GMVTRCIEEV LSNALSKSSA PPITPECRQV 60  
 LKTSRKDVVD KETTENENTK FEVRLLRDPA DASEAHESSE RGEAGAPGEE DIQGTAKADT 120  
 5 EKWAEGGGHS RERADKPQWS LYPSDSQVSE EVKTRHSEKS QREDEEEEG ENYQKGERGE 180  
 DSSEKHLLEE PGETQNAFLN ERKQASAIKK EELVARSETH AAGHSQEKTH SREKSSQESG 240  
 BEAGSQENHP QESKGQPRSQ ESEEGEEDA TSEVDKRRT PRHHHGRSRP DRSSQGGSLP 300  
 SEEKGHPQEE SEESNVSMAS LGEKRDHST HYRASEEPE YGEEIKGYFG VQAPEDLEWE 360  
 10 RYRGRGSEY RAPRPQSEES WDEEDKRNYP SLELDKMAHG YGEESEEEERG LEPGKGRHHR 420  
 GRGGEPRAYF MSDTREEKRF LGEHHRVQE NQMDKARRHP QGAWKELDRN YLNYGEEGAP 480  
 GKWQQQDQL DTKEENREAR FQDKQYSSH TAEKRRLGE LFNPPYDPLQ WKSSHFERRD 540  
 NMNDNFLGE EENELTLNEK NFFPEYNYDW WEKKPFSEDV NWGYEKNLA RVPKLDLKRQ 600  
 YDRVAQLDQL LHYRKSAEF PDFYDSEEPV STHQEAENEK DRADQTVLTE DEKKELENLA 660  
 15 AMDLELQKIA EKFSQRG 677

Seq ID NO: C359 Protein Sequence  
 Protein Accession #: XP\_093082.1

1 11 21 31 41 51  
 | | | | |  
 MKLLCEGLKQ PNCVLQTLRW YRCLISSASC GALAAVLSTS QWLTELEFSE TKLEASALKL 60  
 LYGGKLDPMC KLQKLNLFQS LSVTAAKLPV GMVGNCSGFS GSLVQSHFGY CQDSSFKCDL 120  
 CKLLWPSTRV AAACDCGSPK SFLSEGLNWA GRLEAVEEVL GLGVLVQPGD PASQGGHCE 180  
 25 NYGSRDLVD LEVKAESPLR KGGMDLQRP LQVLLCKIF SLKFLFLIAL PNSPGQSVV 240  
 QVTIPDGPNV VTVGSNVTI CIYTTTVASR EQLSIQWSPF HKKEMEPISS PWEEGKWDV 300  
 EAVKTLDDGQ QALQIYFSQ GQQAIAIGQF KDRITGSNDP GNASTISHM QPADSGIYIC 360  
 DVNNPPDFLG QNGILNVSV LVKPSKPLCS VQGRPETGHT ISLSCLSLG TSPVYVWHK 420  
 LEGRDIVPVK ENFNPTTGL VIGNLTNFEQ GYYQCTAINR LGNSSCEIDL TSSHPEVGII 480  
 30 VGALIGSLVG AAIISVVCV ARNKAKAKAK ERNSKTIAEL EPMTKINPRG ESEAMPREDA 540  
 TQLEVTLPSS IHETGPDITQ EPDYEPKPTQ EPAPEPAPGS EPMAPDLDI ELELEPETQS 600  
 ELEPEPEPEP ESEPGVVVEP LSEDEKGVVK A 631

Seq ID NO: C360 Protein Sequence  
 Protein Accession #: FGENSEH predicted

1 11 21 31 41 51  
 | | | | |  
 MVFAFWKVFL ILSCLAGQVS VVQVTIPDGF VNVTVGSNVT LICITYTTVA SREQLSIQWS 60  
 FFHKEMEPI SSPWEEKWP DVEAVKGTLD GQQAELQIYF SQGGQAVAIG QFKDRITGSN 120  
 40 DPGNASITIS HMQPADSGIY ICDVNNPPDF LGQNQGLNV SVLVKPSKPL CSVQGRPETG 180  
 HTISLSCLSA LGTPSPVYVW HKLEGRDIVP VKENFNPTTG ILVIGNLTNF EQGYQCTAI 240  
 NRGNSSCEI DLTSSHEPVG IIVGALIGSL VGAAIIISVV CFARNKAKAK AKERNSKTIA 300  
 ELEPMTKINP RGSEAMPRE DATQLEVTLP SSIHETGPDITQ EPDYEPKP TQEPAPAPAP 360  
 45 GSEPMAPVDL DIELELEPET QSELEPEPEP EPSEPGVVV EPLSEDEKGV VKA 413

Seq ID NO: C361 Protein Sequence  
 Protein Accession #: NP\_003011.1

1 11 21 31 41 51  
 | | | | |  
 MVSRMVSTML SGLLFWLASG WTPAFAYSPP TPDRVSEADI QRLHGVMEQ LGIARPRVEY 60  
 PAQAMNLVG PQSIEGGAHE GLQHLGPFGN IPNIVAEITG DNIPKDFSED QGYDPPNPPC 120  
 55 PVGKTDDGCL ENTPDTAEFS REFQLHQHLE DPEHDYPGLG KWNKLLYEK MKGGERRKRR 180  
 SVNPLYQQQR LDNVVAKKSV PHFSDEKDP E 211

Seq ID NO: C362 Protein Sequence  
 Protein Accession #: NP\_076926.2

1 11 21 31 41 51  
 | | | | |  
 MTTMQGMEQA MPGAGPGVPQ LGNMAVIHSH LWKGLQEKFL KGEPKVLGVV QILTALMSLS 60  
 MGITMMCMAS NTYGSNPISV YIGYTIWGSV MFIISGSLSI AAGIRTTKGL VRGSLGMNIT 120  
 65 SSVLAASGIL INTFSLAFYS FHHPYCNYYG NSNNCHGTMS ILMGLDGMVL LLSVLEFCIA 180  
 VLSAFGCKV LCCTFGGVVL ILPSHSHMAE TASPTPLNEV 220

Seq ID NO: C363 Protein Sequence  
 Protein Accession #: NP\_002082.1

1 11 21 31 41 51  
 | | | | |  
 MRGSELPLVL LALVLCAPR GRAVPLPAGG GTVLTMYPR GNHWAVGHLM GKKSTGESSS 60  
 70 VSERGSLKQ LREYIRWEA ARNLLGLIEA KENRNHQPQ PKALGNQPS WDSSESSNFK 120  
 DVSGKGVGR LSAPGSQREG RNPQLNQ 148

Seq ID NO: C364 Protein Sequence  
 Protein Accession #: NP\_036393.1

1 11 21 31 41 51  
 | | | | |  
 MDLQGRGVPS IDRLRVLLML FHTMAQIMAE QEVENLSGLS TNPEKDIFVV RENGTTCLMA 60  
 80 EFAAKFIVP DWWASNYVDL ITEQADIALT RGAEVKGRG HSQSELQVFW VDRAYALKML 120  
 FVKESHNSK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHHLS ALVTPAGKSY 180  
 ECQAQQTISL ASSDPKQTVT MILSAVHIQ FDIISDFVS EEHKCPVDER EQLEETPLPI 240  
 LGLILGLVIM VTLAIYVHH KMTANQVQIP RDRSQYKHM 280

1                    11                    21                    31                    41                    51

5	1	11	21	31	41	51	
	MRQSHQLPLV	GLLLFSFIPS	QLCEICEVSE	ENYIRLKPLL	NTMIQSNYNR	GTSAVNVVLS	60
	LKLVGIQIQT	LMQKMIQIQ	YNVKSRLSDV	SSGELALIL	ALGVCRNAEE	NLIYDYHLTD	120
	KLENKFQAEI	ENMEAHNGTP	LTNYQLSLD	VLALCLFNGN	YSTAEVNVHF	TPENKNYYFG	180
	SQFSVDTGAM	AVLALTCVKK	SLINGQIKAD	EGSLKNISYI	TKSLVEKILS	EKKENGLIGN	240
10	1	11	21	31	41	51	
	TFSTGEAMQA	LFVSSDYNE	NDWNCQQTIN	TVLTEISQGA	FSNPNAQAQV	LPALMGKTFL	300
	DINKDSSCVS	ASGNFNISAD	EPITVTPDS	QSYISVNYSV	RINETYFTNV	TVLNGSVFLS	360
	VMEKAQKMND	TIFGFTMEER	SWGPYITCIQ	GLCANNNDRT	YWELLSGGEP	LSQGAGSYVV	420
	RNGENLEVRW	SKY					433
Seq ID NO: C371 Protein Sequence Protein Accession #: NP_004582.1							
15	1	11	21	31	41	51	
	MCCTKSLLLA	ALMSVLLHL	CGESEASNF	DCCLGYTDRI	LHPKFIVGFT	RQLANEGCDD	60
	NAIIFHTKKK	LSVCANPKQT	WVKYIVRLLS	KKVKNM			96
Seq ID NO: C372 Protein Sequence Protein Accession #: NP_037403.1							
20	1	11	21	31	41	51	
	MAGSPLLWGP	RAGGVGLLV	LLLGLFRPPP	ALCARPVKEP	RGLSAASPPL	AETGAPRRFR	60
	RSVPRGEAAG	AVQELARALA	HLEAERQER	ARAEAQEAED	QCARVLAQLL	RVWGAPRNSD	120
	PALGLDDDDP	APAAQLARAL	LRARLDPAAL	AAQLVPAPVP	AAALRP RPVP	YDDGPAGPDA	180
	EEAGDETPDV	DELLRLYLLG	RILAGSADSE	GVAAPRRLRR	AADHDVGSEL	PPEGVLGALL	240
25	1	11	21	31	41	51	
	RVKRLETPAP	QVFARLLFP					260
Seq ID NO: C373 Protein Sequence Protein Accession #: NP_002236.1							
30	1	11	21	31	41	51	
	MLQSLAGSSC	VRIVERHRSA	WCFGFLVLGY	LLYLVP GAVV	FSSVELPYED	LLRQELRKLK	60
	RRFLEEHECL	SEQQLEQFLG	RVLEASNYGV	SVLSNASGNW	NWDFTSALFF	ASTVLSTTGY	120
	GHTVPLSDGG	KAFCIISVSI	GIPFTLLELT	AVVQRITVHV	TRRPVLYFHI	RWGFSGQVVA	180
	IVHAVLLGFV	TVSCFFFIAP	AVFSVLEDDW	NFLESFYFCF	ISLSTIGLGD	YVPGEGYNQK	240
35	1	11	21	31	41	51	
	FRELYKIGIT	CYLLGLLIAM	LVVLETFCEL	HELKKFRKMF	YVKKDKDEDQ	VHIEHDQLS	300
	FSSITDQAAG	MKEDQKQNEP	FVATQSSACV	DGPANH			336
Seq ID NO: C374 Protein Sequence Protein Accession #: NP_005463.1							
40	1	11	21	31	41	51	
	METTINGTETW	YESLHVLKA	LNATLHSNLL	CRPGPGLGPD	NQTEERRASL	PGRDDNSYMY	60
	ILFVMFLFAV	TVGSLILGYT	RSRKVDKRSD	PYHVYIKNRV	SMI		103
Seq ID NO: C375 Protein Sequence Protein Accession #: NP_005236.1							
45	1	11	21	31	41	51	
	MGRHLALLLL	LLLLFQHFQD	SDGSQRLEQT	PLQFTHLEYN	VTVQENSAAK	TYVGHVPKMG	60
	VYITHPAWEV	RYKIVSGDSE	NLFKAEEYIL	GDFCFLRIRT	KGGNTAILNR	EVKDYHTLIV	120
	KALEKNTNVE	ARTKVRVQVL	DTNDRPLFS	PTSYSVSLPE	NTAIRTSIAR	VSATDADIGT	180
	NGEFYYSFKD	RTDMFAIHPT	SGVIVLTGRL	DYLETKLYEM	EILAADRGMK	LYGSSGISSM	240
50	1	11	21	31	41	51	
	AQLTVHIEQA	NECAPVITAV	TLSPSELDRD	PAYAIVTVDD	CDQGANGDIA	SLSIVAGDLL	300
	KQFRTVRSEF	GSKEYKVKAI	GDIDWDSHPF	GYNLTQAKD	KGTPPQFSSV	KVIHVTSPQF	360
	KAGPVKFEKD	VYRAIEISEFA	PENTPVVMVK	AIPAYSHLRY	VFKRTPGKAK	FSLNNTGLI	420
	SILEPVKRQQ	AAHFELEVTT	SDRKASTKVL	VKVLGANSNP	PEFTQTAYKA	AEDENVPIGT	480
55	1	11	21	31	41	51	
	TIMSLSAVDP	DEGENGYVTY	SIANLNHVPF	AIDHFTGAVS	TSENLDYELM	PRVYTLRIRA	540
	SDWGLPYRRE	VEVLATITLN	NLNDNTPLFE	KINCEGTIPR	DLGVGEQITT	VSAIDADELQ	600
	LVQYQIEAGN	ELDLFSLNPN	SGVLSLKRSL	MDGLGAKVSF	HSLRITATDG	ENFATPLYIN	660
	ITVAASHKLV	NLQCEETGVA	KMLAEKLLQA	NKLHNQGEVE	DIFFDSSHVN	AHIPQFRSTL	720
60	1	11	21	31	41	51	
	PTGIQVKENQ	PVGSSVIFMN	STDLDITGFNG	KLIVYAVSGGN	EDSCFMIDME	TGMLKILSPL	780
	DRETTDKYTL	NITVYDLGIP	QKAAWRLLHV	VVDANDNPP	EFLQESYFVE	VSEDKEVHSE	840
	IIQVEATDKD	LGPNGHVTYS	ILTDITDTFSI	DSVTGVVNIA	RPLDRELQHE	HSLKIEARDQ	900
	AREEPQLFST	VVVKVSLDEV	NDNPPTFIPP	NYRVKVRDEL	PEGTVIMWLE	AHDPLDQSGG	960
65	1	11	21	31	41	51	
	QVRYSLLDHG	EGNFVDVKLS	GAVRIVQQLD	FEKKQVYNLT	VRAKDKGKPV	SLSSTCYVEV	1020
	EVVDVNEHLH	PPVFSFVEK	GTVKEDAPVG	SLVMTVSAHD	EDAGRDGEIR	YSIRDGSGVG	1080
	VFKIGEETGV	IETSDRLDRE	STSHYWLTVF	ATDQGVVPLS	SFIEIYIEVE	DVNDNAPQTS	1140
	EPVYYPEIME	NSPKDVSUVQ	IEAFDPDSSS	NDKLMYKITS	GNPQGFSSIH	PKTGLITTS	1200
70	1	11	21	31	41	51	
	RKLDREQQDE	HILEVTVDN	GSPPKSTIAR	VIVKILDEND	NKPQFLQKPY	KIRLPEREKP	1260
	DRERNARREP	LYRVIAATDK	EGPNAEISYS	IEDGNEHGKF	FIEPKTGVVS	SKRFSAAAGEY	1320
	DILSIKAVDN	GRPKQSSTTR	LHIEWISKPK	QSLPISFEE	SFFTFTVMES	DPVAHMIGVI	1380
	SVEPPGIPLW	FIDITGNNYDS	HFDVDKGTGT	IIVAKPLDAE	QKSNYNLTVE	ATDGTITILT	1440
75	1	11	21	31	41	51	
	QVFIKVIDTN	DHRPQFSTSK	YEVVIPEDTA	PETEILQISA	VDQDEKNKLI	YTLQSSRDPL	1500
	SLKKFRLLDP	TGSLYTSEKL	DHEAVSPAHL	TVMVRDQDVP	VKRNFARIVV	NVSDTNDHAP	1560
	WFTASSYKGR	YLESAAVGSV	VLQVTALDKD	KGKNAEVLYS	IESGNIGNIG	NSFMDPVLG	1620
	SKTKAKELDR	SNQAEYDLMV	KATDKGSPPM	SEITSVRIFV	TIADNASPKF	TSKEYSVELS	1680
80	1	11	21	31	41	51	
	ETVSIGSFVG	MVAHLSQSSV	VYEIKDNGTG	DAFDINPHSG	TIITQKALDF	ETLPIYTLII	1740
	QGTNMAGLST	NTTVLVLHQD	ENDNAPVFMQ	AEYTGILISE	ASINSVVLTD	RNVPLVIRAA	1800

	DADKDSNALL	VYHIVEPSVH	TYFAIDSSTG	AIHTVLSLDY	EETSIFHFTV	QVHDMGTPRL	1860
	FAEYAAANVTV	HVIDINDCPP	VFAKPLYEAS	LLLPYKGVK	VITVNATDAD	SSAFSGLIYS	1920
	ITEGNIGKFK	SMDYKTGALT	VQNTTQLRSR	YELTVRASDG	RFAGLTSVKI	NVKESKESHL	1980
5	KFTQDVYSAV	VKENSTEAE	LAVITAIGSP	INEPLFYHIL	NPDRRFKISR	TSGLVSTGT	2040
	PFDRQQEAF	DVVVEVIEEH	KPSAVAHVVV	KVIVEDQNDN	APVFNLPYY	AVVKVDTEVG	2100
	HVIRYVTAVD	RDSGRNGEVH	YYLKEHHEHF	QIGPLGEISL	KKQFELDTLN	KEYLVTVVAK	2160
	DGGNPAFSAE	VIVPITVMNK	AMPVEKPFY	SAEIAESIQV	HSPVVHVQAN	SPEGLKVFYS	2220
	ITDGDPPFSQF	TINFNTGVIN	VIAPLDPEAH	PAYKLSIRAT	DSLTGAHAEV	FVDIIVDDIN	2280
10	DNPPVFAQQS	YAVTLSEASV	IGTSVVQVRA	TDSDSEPNRG	ISYQMFGNHS	KSHDHFHVD	2340
	STGLISLLRT	LDYEQSRQHT	IFVRAVDGGM	PTLSSDVIPT	VDVTDLNGNP	PLFEQQIYEA	2400
	RISEHAPHGH	FVTCVKAYDA	DSSDIDKLQY	SILSGNDHKK	FVIDSATGII	TLSNLHRHAL	2460
	KPFYSLNLSV	SDGVFRSSTQ	VHVTVIGGNL	HSPAFLQNEY	EVELAENAPL	HTLVMEVKT	2520
	DGDSGIYGHV	TYHIVNDFAK	DRFYINERGO	IFTLEKLDR	TPAEKVISVR	LMAKDAGGKV	2580
15	AFCTVNVILT	DDNDNAPQFR	ATKYEVNIGS	SAAKGTSVVK	SASDADEGSN	ADITYAIEAD	2640
	SESVKENLEI	NDNLSGVITTK	ESLIGLENEF	FTFFVRAVDN	GSPSKESVVL	VYVKILPPEM	2700
	QLPKFSEPPY	TFTVSEDVPV	GTEIDLIRAE	HSGTVLYSLV	KGNTPESNRD	ESFVIDRQSG	2760
	RLKLEKSLDH	ETTKWYQFSI	LARCTQDDHE	MVASVDVSIQ	VKDANDNSPV	FESSPYEAFI	2820
	VENLPGGSRV	QIRASDADS	GTNGQVMYSL	DQSQSVEVIE	SFAINMETGW	ITTLKELDHE	2880
20	KRDNYQIKV	ASDHGEKIQ	SSTAIVDVT	TDVNDSPPRF	TABIYKGTVS	EDDPQGGVIA	2940
	ILSTTDADSE	EINRQVTYFI	TGGDPLGQFA	VETIQNEWKV	YVKKPLDREK	RDNYLLTTA	3000
	TGDTFSSKAI	VEVKVLDAND	NSPVCEKTLV	SDTIPEDVLP	GKLIMQISAT	DADIRSNAEI	3060
	TYTLGLSGAE	KFKLNPDTGE	LKTSTPLDRE	EQAVYHLVLR	ATDGGGRFCQ	ASIVVTLEDV	3120
	NDNAPFESAD	PYAITVFENT	EPGTLTRVQ	ATDADAGLNR	KILYSLIDSA	DGQFSINELS	3180
25	GIIQLEKPLD	RELQAVYTIS	LKAVDQGLPR	RLTATGTIV	SVLDINDNPP	VEFYREYGAT	3240
	VSEDILVGT	VLQVYAASRD	IEANAEITYS	IISGNEHGKF	SIDSKTGAVF	IIENLDYESS	3300
	HEYYLTVEAT	DGGTSPSLSDV	ATVNVNVTDI	NDNTPVFSQD	TYTTVISED	VLEQSVITVM	3360
	ADDADGPSNS	HIHYSIDGN	QSSSFTIDPV	RGEVKVTKLL	DRETISGYTL	TVQASDNGSP	3420
	PRVNTTTVNI	DVSDVNDNAP	VFSRGNYSVI	IQENKPVGFS	VLQLVVTDED	SSHNGPPFF	3480
30	TIVTGNDEKA	FEVNPQGVLL	TSSAIKRKEK	DHYLLQVKVA	DNGKPOLSSL	TYIDIRVIEE	3540
	SIYPPAILPL	EIFITSSGEE	YSGGVIGKIH	ATDQDVYDTL	TYSLDPQMDN	LFSVSSTGGK	3600
	LIAHKLDIG	QYLLNVSVD	GKFTTVADIT	VHIRQVTQEM	LNHTIAIRFA	NLTPEEFVGD	3660
	YWRNFQRLR	NILGVRNRDI	QIVSLQSSSE	HPHLDVLLFV	EKPGSAQIST	KQLLHKINSS	3720
	VTDIEEIGV	RILNVFQKLC	AGLDPCWKFC	DEKVSVDSEV	MSTHSTARLS	FVTPRHHRRA	3780
35	VCLCKEGRCP	PVHGCEDDD	CPEGSECVSD	PWEEKHTCVC	PSGRFGQCPG	SSSMTLTGNS	3840
	YVKYRLTENE	NKLEMLKTM	LRTYSTHAVV	MYARGTDYSI	LEIHHGRLQY	KFDCGSGPGI	3900
	VSVQSIQVND	GQWHAVALV	NGMYARLVLD	QVHTASGTAP	GLTKLTNLND	YVFFGGHIRQ	3960
	QGTRHGRSPQ	VGNNGFRGCM	SIYLNGQELP	LNSKPRSYAH	IEESVDVSPG	CFLTATEDCA	4020
	SNPCQNGGVC	NPSAPAGYYC	KCSALYIGTH	CEISVNPCSS	NPCLYGGTCV	VNNGGFVCQC	4080
40	RGLYTGQRQC	LSPYCKDEPC	KNGGTCFDSL	DGAVCQCDSD	FRGERCQSDI	DECSGNPCLH	4140
	GALCENTHGS	YHCNCSEHYR	GRHCEDAAPN	QYVSTPWNI	LAEGIGIVVF	VAGIFLLVVV	4200
	FVLCRKMISR	KKKHQAEPKD	KHLGPATAFL	QRPYFDSKLN	KNIYSDIPPQ	VPVRPISTYP	4260
	SIPSDSRNNL	DRNSFECSAI	PEHPEFSTFN	PESVHGHRKA	VAVCVAPNLP	PPPPPSNSPS	4320
	DSDSIQKPSW	DFDYDTKVVD	LDPCLSKKPL	EEKPSQPYSA	RESLSEVQSL	SSPQSESCDD	4380
45	NGVHWDTSW	MPGVLPEDIQ	EFPNYEVIDE	QTPLYSADPN	AIDTDYVPGG	YDIESDFPPP	4440
	PEDFPAADEL	PPLPPEFSNQ	FESIHPPRDM	PAAGSLGSSS	RNRQRFLNLQ	YLPNFYPLDM	4500
	SEPTQKTGTE	NSTCREPHAP	YPPGYQRHFE	APAVESMFMS	VYASTASCSD	VSACCEVESE	4560
	VMMSDYESGD	DGHFEVITIP	PLDSQQHTEV				4590

Seq ID NO: C376 Protein Sequence  
Protein Accession #: NP\_055035.1

	1	11	21	31	41	51	
55	MCYKGCARCI	GHSVLGLALL	CIAANILLYF	PNGETKYASE	NHLSRFVWFF	SGIVGGGLLM	60
	LLPAFVFIGL	EQDDCCGCCG	HENCGKRCAM	LSSVLAAALIG	IAGSGYCVIV	AALGLAEGPL	120
	CLDSLQWQNY	TFASTEGQYL	LDTSTWSECT	EPKHIVEWNV	SLFSILLALG	GIEFILCLIQ	180
	VINGVLGGIC	GFCCSHQQYQ	DC				202

Seq ID NO: C377 Protein Sequence  
Protein Accession #: NP\_003750.1

	1	11	21	31	41	51	
65	MSTENVEGKP	SNLGERGRAR	SSTFLRVVQP	MFNHSIFTS	VSPAARIRIF	ILGEEDDSPA	60
	PPQLFTELDE	LLAVDQEME	WKETARWIKF	EEKVEQGGER	WSKPHVATLS	LHSLFELRTC	120
	MEKGSIMLDR	EASSLFPQV	MIVDHIQETG	LLKPELKDKV	TYTLRKRHRH	QTKKSNLRS	180
	ADIGKTVSSA	SRMFTNPNG	SPAMTHRNLT	SSSLNDISDK	PEKQQLKNKF	MKKLPRDAEA	240
	SNVLVGEVDF	LDTPFIAFVR	LQQAIVMLGAL	TEVPVPTRFL	FILLGPKGKA	KSYHEIGRAI	300
70	ATLMSDEVFH	DIAYKAKDRH	DLIAGIDEFL	DEVIVLPPGE	WDPAIRIEPP	KSLPSSDKRK	360
	NMYSGGENVQ	MNGDTPHDGG	HGGGGHGDCE	ELQRTGRFCG	GLIKDIKRKA	PPFASDFYDA	420
	LNIQALSAIL	FYILATVTNA	ITFGGLLGD	TDNMQGVLES	FLGTAVSGAI	FCLFAGQPLT	480
	ILSSGTGPVIV	FERLLENFSK	DNNFDYLEFR	LWIGLWSAFL	CLILVATDAS	FLVQYVTRFT	540
	EEGFSSLSIF	IFIYDAFKKM	IKLADYYPIN	SNFKVGYNTL	FSCTCVPPDP	ANISISNDTT	600
75	LAPEYLPTMS	STDYHNTTF	DWAFLSKKEC	SKYGGNLVGN	NCNFVPDITL	MSFILFLGTY	660
	TSSMALKKFK	TSYPFTTAR	KLISDFAILL	SILIFCVIDA	LVGVDPKPLI	VPSEFKPTSP	720
	NRGWFPVPPG	ENPWWVCLAA	AIPALLVTIL	IFMDQQTAV	IVNRKHEKLL	KGAGVHLDLF	780
	WVAILMVICS	LMALPWYVAA	TVISIAHIDS	LKMETETSAP	GEQPKFLGVR	EQRVGTGLVF	840
	ILTGLSVFMA	PILKFIPIPV	LYGVFLYMGV	ASLNGVQFMD	RLKLLMLPLK	HQPDFIYLRH	900
80	VPLRRVHLFT	FLQVLCALAL	WILKSTVAAL	IFPVMILALV	AVRKGMDYLF	SQHDLSFLDD	960
	VIPEKDKKKK	EDEKDKKKKK	GSLDSDNDDS	DCPYSEKVP	IKIPMDIMEQ	QPFLSDSKPS	1020
	DRERSPTFLE	RHTSC					1035

Seq ID NO: C378 Protein Sequence  
Protein Accession #: NP\_000949.1



1 11 21 31 41 51  
 5 MSTPGVNSSA SLSPDRLNSP VTIPAVMFIF GVVGNLVAIV VLCKSRKEQK ETTFFYTLVCG 60  
 LAVTDLLGTL LVSPVTIATY MKGQWPGGQP LCEYSTFILL FFSLSGLSII CAMSVERYLA 120  
 INHAYFYSHY VDKRLAGLTL FAVYASNVLFCALPNMGLGS SRLQYPTDTC FIDWTTNVTA 180  
 HAAYSIMYAG FSSFLILATV LCNVLVCGAL LRMHRQFMRR TSLGTEQHHA AAAASVASRG 240  
 HPAASPALPR LSDFRRRRSF RRIAGAEIQM VILLIATSLV VLICSIPLVV RVFVNQLYQP 300  
 10 SLEREVSXNP DLQAIRIASV NPILDPIYI LLRKTVLSKA IEKIKCLPCR IGGSRRRRSRG 360  
 QHCSDSQRTS SAMSGHSRSF ISRELKEISS TSQTLPLDLS LPDLSENGLG GRNLLPGVFG 420  
 MGLAQEDTTS LRTLRISETS DSSQGDSES VLLVDEAGGS GRAGPAPKGS SLQVTFPSET 480  
 LNLSEKCI 488

Seq ID NO: C379 Protein Sequence  
 Protein Accession #: NP\_002650.1

1 11 21 31 41 51  
 20 MGHPPLLPLL LLHTCVPAS WGLRCMCCKT NGDCRVEECA LGQDLCRTTI VRLWEEGEEL 60  
 ELVEKSCTHS EKTNRSLSYR TGLKITSLTE VVCGLDLCNQ GNSGRAVTYS RSRYLECISC 120  
 GSSDMSCERG RHQSLQCRSP EQCLDVVTH WIQEGEEGRP KDDRHLRGCG YLPGCPGNSG 180  
 FHNNDTFHFL KCCNTTKCNE GPILLENLFP QNGRCQYSCK GNSTHGCSSE ETFLIDCRGP 240  
 MNQCLVATGT HEPKNQSYMV RGCATASMCQ HAHLGDAFSM NHIDVSCCTK SGCNHPDLV 300  
 25 QYRSGAAPQP GPAHLSLTIT LLMTARLWGG TLLWT 335

Seq ID NO: C380 Protein Sequence  
 Protein Accession #: BAB55406.1

1 11 21 31 41 51  
 30 MDEFSGQVDP LASVILPPNL LENLSPEDSV LVRRQAQTFE NKTGLFQDVG PQRKTLVSYV 60  
 MACSIGNITI QNLKDPVQIK IKHTRTQEVH HPICAFWDNL KSKSFGGWNT SGCAVHRDSD 120  
 ASETVCLCNH FTHFGVIMDL PRSASQLDAR NTKVLTFISY ICGGISAIFS AATLLTYVAF 180  
 35 EKLRRDYPSPK ILMNLSLALL FLNLLFLLDG WITSFNVNGL CIAVAVLLHF FLATFTWMG 240  
 LEAHHMYIAL VKVFNTYIRR YILKFCIIGW GLPALVSVV LASRNNNEVY GKESYGKEKG 300  
 DEFQWIDQPV IFYVTCAGYF GVMFFLNIAI FIVVMVQICG RNGKRSNRTL REEVLNRLRS 360  
 VVSLTFLLGM TWGFAFFAWG PLNIPFMYLF SIFNSLQGLF IFIFHCAMKE NVQKQWRRLH 420  
 CCGRFRLLADN SDWSKTATNI IKKSSDNLGK SLSSSSISGN STYLTSSKSKS SSTTYFKRNS 480  
 40 HTDNVSYEHS FNKSGSLRQC FHGQVLVKTG PC 512

Seq ID NO: C381 Protein Sequence  
 Protein Accession #: NP\_000565.1

1 11 21 31 41 51  
 45 MTVARPSVPA ALPLLGLPRL LLLLVLCLLP AVWGDCGLPP DVPNAQPALE GRTSFPEDTV 60  
 ITYKCEESFV KIPGEKDSVI CLKGSQWSDI BEFCNRSCEV PTRLNSASLK QPYITQNYFP 120  
 VGTVVEYECR PGYRREPSLS PKLTCLQNLK WSTAVEFCKK KSCPMPGEIR NGQIDVPGGI 180  
 LFGATISFSC NTGYKLFGST SSFCLISGSS VQWSDPLPEC REIYCPAPPQ IDNGIIQGER 240  
 50 DHYGYRQSVT YACNKGFTMI GEHSIYCTVN NDEGEWSGPP PECRGKSLTS KVPPTVQKPT 300  
 TVNVPTTEVS PTSQKTTTKT TTPNAQATRS TPVSRRTTKH HETTPNKGSG TTSQTTRLLS 360  
 GHTCFTLTGL LGTLVTMGLL T 381

Seq ID NO: C382 Protein Sequence  
 Protein Accession #: Eos sequence

1 11 21 31 41 51  
 60 MDTSLRGLVLL SLPVLLQLAT GGSSPRSGVL LRGCPHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNNISQ LLNPLPLSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120  
 LQNNQLRHVP TEALQNLRS LSLRLDANHI SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD 240  
 LNYNNLDEFP TAIRTLNLSK ELHFYDNPIQ FVGRSAFQHL PELRTLTLNG ASQITEFPDL 300  
 65 TGTANLESIT LTGAQISSLP QTVCNQLPNL QVLDLSYNLL EDLPSEFVCQ KLQKIDLRHN 360  
 EIYEIKVDTF QQLLSLRSIN LAWNKIAIHH PNAFSTLPSL IKDLSSNLL SSFPITGLHG 420  
 LTHLKLGTNH ALQSLISSEN FPELVIEIMP YAYQCCAFGV CENAYKISNQ WNKGDNSMMD 480  
 DLHKKDAGMF QAQDERDLED FLDDFEEDLK ALHSVQCSPS PGPFKPEHL LDGWLIRIGV 540  
 WTIAVLALTC NALVTSTVFR SPLYISPIKL LIGVIAAVNM LTGVSSAVLA GVDATFGSGF 600  
 70 ARHGAWWENG VGCHVIGFLS IFASESSVFL LTLAALERGF SVKYSKAFET KAPFSSLKVI 660  
 ILLCALLALT MAAVPLLGGS KYGASPLCLP LPFGEPSTMG YMALILLNS LCFLMMTIAY 720  
 TKLYCNLDKG DLENINDCSM VKHIALLLFT NCILNCPVAF LSFSSLINLT FISPEVIKFI 780  
 LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS 840  
 TQALVTFTSS SITYDLPPSS VSPAYPVTE SCHLSSVAFV PCL 883

Seq ID NO: C383 Protein Sequence  
 Protein Accession #: NP\_003658.1

1 11 21 31 41 51  
 80 MDTSLRGLVLL SLPVLLQLAT GGSSPRSGVL LRGCPHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSVFTSY LDLSMNNISQ LLNPLPLSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120  
 LQNNQLRHVP TEALQNLRS LSLRLDANHI SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD 240  
 LNYNNLDEFP TAIRTLNLSK ELGFHSNNIR SIPEKAFVGN PSLITIHFDY NPIQFVGRSA 300

FQHLPELRTL TLNGASQITE FPDLTGTANL ESLLTLGAQI SSLPQTVCNQ LPNLQVLDLS 360  
 YNLLEDLPSPF SVCQKLKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIHPNAPST 420  
 LPSLTKLDLS SNLLSSFPIT GLHGLTHLKL TGNHALQSLI SSENFPFLKV IEMPYAYQCC 480  
 AFGVCENAYK ISNQWNKGDN SSMDDLHKKD AGMFQAQDER DLEDFLDDE EDLKALHSVQ 540  
 CSPSPGPFKP CEHLDDGWL I RIGVWTIAVL ALTICNALVTS TVFRSPLYIS PIKLLIGVIA 600  
 AVNMLTGVSS AVLAGVDAFT FGSFARHGAW WENGVCCHVI GFLSIFASES SVFLLTLAAL 660  
 ERGFSVKYSA KPETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEF 720  
 STMGYMVALI LLNSLCFLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LFTNCILNC 780  
 VVAFLSFSSL INLTFSPEV IKFILLVVVP LPACLNPLLY ILFNPHFKED LVSLRKQTYV 840  
 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVSPSPAY PVTESCHLSS 900  
 VAFVPC 907

Seq ID NO: C384 Protein Sequence  
 Protein Accession #: NP\_003497.1

1 11 21 31 41 51  
 MEMFTFL LTC IFLLPLRGHS LFTCEPITVP RCMKMAYNMT FFPNLMGHYD QSIAAVEMEH 60  
 FLPLANLECS PNIEFTLCKA FVPTCIEQIH VVPPCRKLCE KVS DCKKLI DTFGIRWPPEE 120  
 LECDR LQYCD ETVPVTFDPH TEFLGPQKKT EQVQRDIGFW CPRHLKTS GG QGYKFLGIDQ 180  
 CAPPCPNMYF KSDELEFAKS FIGTVSIFCL CATLFTFLTF LIDVRRFRYP ERPIIYYSVC 240  
 YSIVSLMYFI GFLLDGSTAC NKADEKLELG DTVLVGSQNK ACTVLFMLLY FFTMAGTVVW 300  
 VILTITWFLA AGRKWSCEAI EQKAVWFHAV AWGTPGFLTV MLLALNKVEG DNISGVCVFG 360  
 LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHGRNQEKL KKFMRIGVF 420  
 SGLYLVLPIV LLGCYVYEQV NRITWEITW SDHCRQYHIP CPYQAKAKAR PELALFMIKY 480  
 LMTLIVGISA VFWVGSKTKT TEWAGFFKRN RKRDPISER RVLQESCEFF LKHNSKVKKH 540  
 KKHVKPSHHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQETLTIEI TSPETSMREV 600  
 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660  
 TGLAQSNLQ VPSSSEPSL KGSTSLLVHP VSGVRKEQGG GCHSDT 706

Seq ID NO: C385 Protein Sequence  
 Protein Accession #: NP\_000573

1 11 21 31 41 51  
 MRIAVICFCL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLAPQTL 60  
 PSKSNESH DH MDDMDEDD DHVDSQDSID SNDSDDVDDT DDSHQSDSH HSDESDELVT 120  
 DFPTDL PATE VFTPVVPTVD TYDGRGDSV YGLRSKSKKF RRPDIQYPA TDEDITSHME 180  
 SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240  
 NEHSDVIDSQ ELSKVSREFH SHEFHSHEM LVVDPKSKEE DKHLKFRISH ELDSASSEVN 300

Seq ID NO: C386 Protein Sequence  
 Protein Accession #: NP\_002812

1 11 21 31 41 51  
 MGAARGSPAR PRRLPLLSVL LLPLLGGTQT AIVFIKQPSS QDALQRRAL LRCEVEAPGP 60  
 VHVYWL DGA PVQDTERRFA QGSSLSFAAV DRLQDSGTFO CVARDDVTGE EARSANASFN 120  
 IKWIEAGPVV LKHPASEABI PQPTQVTLRC HIDGHPRTY QWFRDGTPLS DGQSNHTVSS 180  
 KERNLTLRPA GPEHSGLYSC CAHSAPGQAC SSQNF TSLIA DESFARVVLA PQDVVVARYE 240  
 EAMFHCQFSA QPPSLQWL F EDETPITNRS RPPHLRRATV FANGSLLLTQ VPRNAGIYR 300  
 CTGQQRG RPP IILEATLHLA EIEDMPLFEP RVFTAGSEER VTCLPPKGLP EPSVWWEHAG 360  
 VRLPTHGRVY QKGHELVLAN IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKKPQD 420  
 SQLEEGKPGY LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEVDGTWYR 480  
 CMSSTPAGSI EAQARVQVLE KLKFTPPPQP QOCMEFDKEA TVPCSATGRE KPTIKWERAD 540  
 GSSLPEWVTD NAGTLHFARV TRDDAGNYTC IASNGPQQQI RAHVQLTVAV FITFKVEPER 600  
 TTVYQGH TAL LQCEAQGDPK PLIQWKGKDR ILDP TKG LPR MHIFQNGSLV IHDVAPEDSG 660  
 RYTCIAGNSC NIKHTEAPLY VVDKPVPEES EGPSPPPPYK MIQTIGLSVG AAVAYIIAVL 720  
 GLMFYCKKRC KAKRLQKQPE GEEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780  
 KRHSTD KMH FPRSSLQPI T LKSGSEFGEV FLAKAQGLEE GVAETLVLVK SLQTKDEQQQ 840  
 LDPRELEMF KGLNHANVVR LLGLCREAEP HYMVLEYVDL GD LKQFLRIS KSKDEKLKSQ 900  
 PLSTKQKVAL CTQVALGMEH LSNNRVFKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960  
 YHFRQAWPV RWMSPEALE GDFSTKSDVW AFGVLMWEVF THGEMPHGGQ ADDEV LADLQ 1020  
 AGKARLPQPE GCPSKLYRLM QRCWALSPKD RPSFSEIASA LGDSTVDQSKP 1070

Seq ID NO: C387 Protein Sequence  
 Protein Accession #: NP\_002300.1

1 11 21 31 41 51  
 MKVLAAGVVP LLLVLHWKHG AGSPLPITPV NATCAIRHPC HNNLMNQIRS QLAQLNGSAN 60  
 ALFILIYTAQ GEPPFNLDK LCGPNVTDFF PFHANGTEKA KLVELYRIV YLGTSLGNIT 120  
 RDQKILNP SA LSLH SKLNAT ADILRGLLSN VLCRLCSKYH VGHVDVTYGP DTSGKDVFOK 180  
 KKLGCQLLGK YKQIIAVLAQ AF 202

Seq ID NO: C388 Protein Sequence  
 Protein Accession #: XP\_097508

1 11 21 31 41 51  
 MGRPRLTIVC HVSIISARD LSMNNLTQL PGLFHHRLFL EELRLSGNHL SHIPQAFSG 60  
 LYS LKILMLQ NNQLGGIPAE ALWELPSLQS LRLDANLISL VPERSFEGLS SLRHLWLDN 120  
 ALTEIPVRAL NNKALQAMT LALNRISHIP DYAFQNL TSL VVLHLHNNRI QHLGTHSFEG 180  
 LHNLETLDLN YNLKQEFFVA IRTLGR LQEL GFHNNNIKAI PEKAFMGNPL LQTIHFDYDN 240

IQFVGRSAFQ YLPKLHTLSL NGAMDIQEPF DLKGTTSLEI LTLTRAGIRL LPSGMCQQLP 300  
 RLRVLELSHN QIEELPSLHR CQKLEETGLQ HNRIWEIGAD TFSQLSSLQA LDLSWNAIRS 360  
 IHPEAFSTLH SLVKLDLTDN QLTTLPLAGL GGLMHLKLG NLALSQAFSK DSFFKLRILE 420  
 VPHYAYCCFPY GMCASFFKAS QQWEAEDLHL DDESSKRPL GLLARQENH YDQDLDELQL 480  
 EMEDSKPHPS VQCSPTPGPF KPCEYLFESW GIRLAVWAIV LLSVLCNGLV LLTVFAGGPV 540  
 PLPPVKFVVG AIAGANTITG ISCGLLASVD ALTFGQFSEY GARWETGLGC RATGFLAVLG 600  
 SEASVLLTL AAVQCSVSVS CVRAYGKSPS LGSVRAGVLG CLALAGLAAA LPLASVGEYG 660  
 ASPLCLPYAP PEGQPAALGF TVALVMMNSF CFLVVGAYI KLYCDLPRGD FEAVWDCAMV 720  
 RHVAWLIFAD GLLYCPVAVL SFASMLGLFP VTPEAVKSVL LVLPLPACL NPLLYLLFNP 780  
 HFRDDLRLR PRAGDSGPLA YAAAGELEKS SCDSTQALVA FSDVDLILEA SEAGRPPGLE 840  
 TYGFPSVTLI SCQPGAPRL EGSHCVPEEG NHFGNPQPSM DGEILLRAEG STPAGGGLSG 900  
 GGGFQPSGLA FASHV 915

Seq ID NO: C389 Protein Sequence  
 Protein Accession #: NP\_570901

1 11 21 31 41 51  
 MASLVSELEGL LLLAVLVVTA TASPPAGLLS LLTSGQGALD QEALGGLLNT LADRVHCTNG 60  
 PCGKCLSVED ALGLGEPEG GLPPGPVLEA RYVARLSAAA VLYLSNPEGT CEDTRAGLWA 120  
 SHADHLALL ESPKALTPLG SWLLQRMQAR AAGQTPKTAC VDIPQLLEEA VGAGAPGSAG 180  
 GVLAALLDHW RSGSCFHALP SPQYFVDFVF QHSSEVPMT LAELSALMQR LGVGREAHSD 240  
 HSHRHGASS RDPVPLISS NSSSVWDTVC LSARDVMAAY GLSEQAGVTP EAWAQLSPAL 300  
 LQQQLSGACT SQRSPVQDQ LSQSERYLYG SLATLLICLC AVFGLLLTTC TGCRCVAHYI 360  
 LQTFLSLAVG ALTGDVAVLH TPVKVLGLHTH SEEGLSPOPT WRLLAMLACL YAFFLFENLF 420  
 NLLLPDPDED LEDGPGCHSS HSHGGHSHGV SLQLAPSELR QPKPPHEGSR ADLVAEESPE 480  
 LLNPEPRRLS PELRLPLPMI TLGDVAVHFA DGLAVGAFA SSWKTGLATS LAVFCHELPH 540  
 ELGDFAALLH AGLSVRQALL LNLASALTAF AGLYVALAVG VSESESEWIL AVATGLFLYV 600  
 ALCDMLPAML KVRDPRPWLL FLLHNVGLLG GWTVLLLSL YEDDITF 648

Seq ID NO: C390 Protein Sequence  
 Protein Accession #: NP\_061844

1 11 21 31 41 51  
 MANASEPGGS GGGEAAALGL KLATLSLLLC VSLAGNVLFA LLIVRERSLH RAPPYLLLDL 60  
 CLADGLRALA CLPAVMLAAR RAAAAAGAPP GALGCKLLAF LAALFCFHAA FLLLVGVVTR 120  
 YLAIAHHRFY AERLAGWPCA AMLVCAAWAL ALAAAFPPVL DGGGDEDEDAP CALEQRPDGA 180  
 PGALGFLLLL AVVVGATHLV YLRLLFFIHD RRMKRPARLV PAVSHDWTFF GPGATQAAA 240  
 NWTAGFGRGP TPAALVGIRP AGPGRGARRL LVLEEFKTEK RLCKMFYAVT LFLFLWGPY 300  
 VVASYLRVLV RPAVLPQAYL TASVWLTFQA AGINPVVCFI FNRELRDCCR AQFPCCQSPR 360  
 TTQATHPCDL KGIGL 375

Seq ID NO: C391 Protein Sequence  
 Protein Accession #: NP\_005622

1 11 21 31 41 51  
 MAAARPARGP ELPLLGLLLL LLLGDPGRGA ASSGNATGPG PRSAGGSARR SAAVTGPPPP 60  
 LSHCGRAAPC EPLRYNVCLG SVLPYGATST LLAGDSDSQE EAHGKLVLS GLRNAPRCWA 120  
 VIQPLLCAVY MPKCENDRVE LPSRTLQCAT RGPCAIVERE RGWPDFLRCT PDRFPEGCTN 180  
 EVQNIKFNSS GQCEVPLVRT DNPKSWYEDV ECGGIQCONP LFTEAEHQDM HSYIAAFGAV 240  
 TGLCTLETLA TFVADWRNSN RYPAVILFYV NACFFVGSIG WLAQFMDGAR REIVCRADGT 300  
 MRLGEPTSNE TLSCVIFVI VYALMAGVV WFWVLTIAWH TSFKALGTTY QPLSGKTSYF 360  
 HLLTWSLPFV LTVAAILAVAQ VDGDSVSGIC FVGYKNYRIR AGFVLAPIGL VLVGGYFLI 420  
 RGVMTLFSIK SNHFGLLSEK AASKINETML RLGIFFGLAF GFVLITFSCH FYDFFNQAEW 480  
 ERSFRDYVLV QANVTIGLPT KQPIPDCEIK NRPSLLVEKI NLFAMFGTGI AMSTWVWTKA 540  
 TLLIWRRTWC RLTKQSDDEP KRIKSKMIA KAFSKRHELL QNPQQLSFS MHTVSHDGPV 600  
 AGLAFDLNRP SADVSSAWAQ HVTMVARRG AILPQDISVT PVATPVPPEE QANLWLVEAE 660  
 ISPQLQKRLK RKKKRRKRKK EVCPALPPE LHPPAPAPST IPRLPQLPRQ KCLVAAGAWG 720  
 AGDSCRQGAN TLVSNPFCPE PSPQDPFLP SAPAPVAWAH GRRQGLGPIH SRTNLMDEL 780  
 MDADSDF 788

Seq ID NO: C392 Protein Sequence  
 Protein Accession #: BAC04382

1 11 21 31 41 51  
 MGARSARGA LLLALLLWLD PRLSQAGRKR SGEVLPDSFP SAPAEPLPYF LQEPQDAYIV 60  
 KNKPVELRCR AFPATQIYFK CNGEWSQND HVTQEGLEDEA TLGARGGLRV REVQIEVSRQ 120  
 QVEELFGLD YWCQCVAWSS AGTTKSRRAY VRIAYLRKNF DQEPGLKEVP LDHEVLLQCR 180  
 PPEGVPVAEV EWLKNEDVID PTQDTNFLT IDHNLIIIRA RLSDTANYTC VAKNIVAKRR 240  
 STTATVIVYV NGGWSSWAEW SPCSNRGGRG WQKTRTRCTN PAPLNGGAF CEGQAFQKTAC 300  
 TTICPVDGAW TEWSKWSACS TECAHWSRE CMAPPQNGG RDCSGTLDS KNCTDGLCMQ 360  
 NKKTLSDPNS HLLASGDAA LYAGLVVAIF VVVAIIMAVG VVVYRNRCDR PDTDITDSSA 420  
 ALTGGFHEVN FKTRARSPNQ LLHPSVPPDL TASAGIYRGP VYALQDSTDK IPMTNSPLLD 480  
 PLPSLKVEVY SSSTTGSFGP LADGADLLGV LPPGTYPSPF ARDTFHLHLR SASLGSQQLL 540  
 GLPRDPGSSV SGTFCCLGGR LSIPGTGVS LVPNGAIPQG KFYEMYLLIN KAESTLPLSE 600  
 GTQTVLSPSV TCGPTGGLLC RPVILTMPHC AEVSARDWIF QLKTAHQHGH WEEVVTLDDE 660  
 TLNTPCYQL EPRACHILLD QLGTIVFTGE SYSRSVAVKRL QLAVFAPALC TSLEYSRLVY 720  
 CLEDTPVALK EVLEERLTG GYLVEEPKPL MFKDSYHNL LSLHDLPHAH WRSKLLAKYQ 780  
 EIPFYHIWSG SQKALHCTFT LERHSLASTE LTCKICVRQV EGEGQIFQLH TTLAETPAGS 840  
 LDTLCSAPGS TVTTQLGPYA FKIPLSIRQ ICNSLDAPNS RGNDWRMLAQ KLSMDRYLNY 900  
 FATKASPTGV ILDLWEALQQ DDGDLNSLAS ALEEMGKSEM LVAVATDGDC 950

Seq ID NO: C393 Protein Sequence  
Protein Accession #: NP\_004616

```

5      1      11      21      31      41      51
      |      |      |      |      |      |
MNRKARRCLG HLFSLGMVY LRIGGFSSVV ALGASII CNK IPGLAPRQRA ICQSRPDAIL 60
VIGEGSQMGL DECQFQFRNG RWNCSALGER TVFGKELKVG SREAAFTYAI IAAGVAHAIT 120
10    AACTQGNLSD CGCDKEKQGG YHRDEGKWKW GCSADIRYGI GFAKVFVDAR EIKQNARTLM 180
      NLHNEAGRK ILEENMKLEC KCHGVSGSCT TKTCWTTLPQ FRELGVVLKD KYNEAVHVEP 240
      VRASRNKRPT FLKIKKPLSY RKPMDTDLVY IEKSPNYCEE DPTVGSVGTQ GRACNKTA PQ 300
      ASGCDLMCCG RGYNTHQYAR VWQCNCCKFWH CCYVKCNTCS ERTEMYTCK 349

```

Seq ID NO: C394 Protein Sequence  
Protein Accession #: NP\_003777

```

15      1      11      21      31      41      51
      |      |      |      |      |      |
MDALCGSGEL GSKFWDNSNLS VHTENPDLTP CFQNSLLAWV PCIYLWVALP CYLLYLRRHHC 60
20    RGYIILSHLS KLMVLGVLL WCVSWADLFY SFHGLVHGRA PAPVFFVTPL VVGVTMLLAT 120
      LLTQYERLQG VQSSGVLIIF WFLCVVCAIV PFRSKILLAK AEGEISDPFR FTTFYIHFAL 180
      VLSALILACF REKPPFFSAK NVDPNPYPET SAGFLSRLFF WWFTKMAIYG YRHPLEEKDL 240
      WSLKEEDRSQ MVVQQLLEAW RKQEKQTARH KASAAPGKNA SGEDEVLLGA RPRPRKPSFL 300
25    KALLATFGSS FLISACFKLI QDLLSFINPQ LLSILIRFIS NPMAPSWWGF LVAGLMFLCS 360
      MMQSLILQHY YHYIFVTGVK FRTGIMGVIV RKALVITNSV KRASTVGEIV NLMVSVDQRF 420
      MDLAPFLNLL WSAFLQIILA IYFLWQNLGP SVLAGVAFMV LLIPLNGAVA VKMRAFQVKQ 480
      MKLKDSRIKL MSELINGIKV LKLYAWEPSF LKQVEGIRQG ELQLLRTAAY LHTTTTTFTWM 540
      CSPFLVLTIT LWVYVYVDPN NVLDAEKAFV SVSLFNILRL PLNMLPQLIS NLTAQASVSLK 600
30    RIQQFLSQEE LDPQSVERTK ISPGYAITIH SGTFTWAQDL PPTLHSLDIQ VPKGALVAVV 660
      GPVCGGKSSL VSALLGEMEK LEGKVHMKGS VAYVPQQAWI QNCTLQENVL FGKALNPKRY 720
      QQTLEACALL ADLEMLPGGD QTEIGEKGIN LSGGQQRQVS LARAVYSDAD IFLLDDPLSA 780
      VDSHVAKHIF DHVIGPEGVL AGKTRVLVTH GISFLPQTFD IIVLADGQVS EMGPYPALLQ 840
      RNSGFANFLC NYAPDEDQGH LEDSWTALEG AEDKEALLIE DTLSNHTDLT DNDPVTYVVQ 900
35    KQFMRQLSAL SSDGEGQGRP VPRRHLGPSE KVQVTEAKAD GALTQEEKAA IGTVELSVFW 960
      DYAKAVGLCT TLAICLLYVG QSAAAIKANV WLSAWTNDAM ADSRQNNNTSL RLGYYAALGI 1020
      LQGFLVMLAA MAMAAGGQA ARVLHQALLH NKIRSPQSFF DTTPSGRILN CFSKDIYVVD 1080
      EVLAPVILML LNSFFNAIST LVVIMASTPL FTVVILPLAV LYTILVQRFYA ATSRQLKRLE 1140
      SVSRSPIYSH FSETVTGASV IRAYNRSRDF EIIISDTKVA NQRSCYPYII SNRWLSIGVE 1200
40    FVGNCCVLFA ALFAVIGRSS LNPGLVGLSV SYSLQVTFAL NWMIRMMSDL ESNIVAVERV 1260
      KEYSKTETEA PMWVEGSRPP EGWPPRGEVE FRNYSVRYRP GLDLVLRLDS LHVHGGEKVG 1320
      IVGRGTGAGS SMTLCLFRIL EAAKGEIRID GLNVADIGLH DLRSQLTIIIP QDPILFSGTL 1380
      RMNLDPFGSY SEEDIWWALE LSHLHTFVSS QPAGLDFQCS EGGENLSVGG RQLVCLARAL 1440
      LRKSRILVLD EATAAIDLET DNLIQATIRT QFDTCTVLTI AHRLNTIMDY TRVLVLDKGV 1500
45    VAEDFSPANL IAARGIFYGM ARDAGLA 1527

```

Seq ID NO: C395 Protein Sequence  
Protein Accession #: NP\_004617

```

50      1      11      21      31      41      51
      |      |      |      |      |      |
MRARPQVCEA LLFALALQTG VCYGIKWLAL SKTPSALALN QTQHCQKLEG LVSAQVQLCR 60
      SNLELMHTVV HAAREVMKAC RRAFADMWRN CSSIELAPNY LLDLERGTRE SAFVYALSAA 120
      AISHAIARAC TSGDLPGCSC GPVPGEPPEP GNRWGGCADN LSYGLLMGAK FSDAPMKVKK 180
55    TGSQANKLMR LHNSEVGRQA LRASLEMKCK CHGVSGSCSI RTCWKGQLQEL QDVAADLKTR 240
      YLSATKVVHR PMGTRKHLVP KDLDIRPVKD SELVYLQSSP DFCMKNEKVG SHGTQDRQCN 300
      KTSNGSDSCD LMCCGRGYNP YTRDRVVERCH CKYHWCCYVT CRRCERTVER YVCK 354

```

Seq ID NO: C396 Protein Sequence  
Protein Accession #: NP\_114072

```

60      1      11      21      31      41      51
      |      |      |      |      |      |
MEWGYLLEVT SLLAALALLQ RSSGAAAASA KELACQEITV PLCKGIGYNY TYMPNQFNHD 60
65    TQDEAGLEVH QFWPLVEIQ SPDLKFFLCS MYTPICLEDY KKPLPPCRSV CERAKAGCAP 120
      LMRQYGFAPW DRMRCDRLPE QGNPDTLCMD YNRTDLTAA PSPRRRLPPP PGGEQPPSGS 180
      GHGRPPGARP PHRGGGGRGG GGDAAAAPPAR GGGGGGKARP PGGAAPCEP GCQCRAPMVS 240
      VSSERHPLYN RVKTGQIANC ALPCHNPFPS QDERAFTVFW IGLWSVLCFV STFATVSTFL 300
      IDMERFKYPE RPIIFLSACY LFVSVGYLVR LVAGHEKVAC SGGAPGAGGA GGAGGAAAGA 360
70    GAAGACAGGP GGRGEYBELG AVEQHVRVET TGPALCTVVF LLVYVFGMAS SIWWVILSLT 420
      WFLAAGMKWG NEAIIAGYSQY FHIAAWLVPS VKSIAVLALS SVDGDPVAGI CYVGNQSLDN 480
      LRGFVLAFLV IYLFIGTMFL LAGFVSLFRI RSVIKQDQGP TKTHKLEKLM IRLGLFTVLY 540
      TVPAAVVAC LFYBQHNRPR WEATHNCPCL RDLQPDQARR PDYAVFMLKY FMCLVVGITS 600
      GVWVWSGKTL ESWRSLCTRC CWASKGAAVG GGAGATAAGG GGGPGGGGGG GPGGGGGPGG 660
75    GGGSLYSVDS TGLTWRSGTA SSVYPKQMP LSQV 694

```

Seq ID NO: C397 Protein Sequence  
Protein Accession #: XP\_050625

```

80      1      11      21      31      41      51
      |      |      |      |      |      |
MLQGPGLSL LFLASHCCLG SARGFLFLGQ PDFSYKRSNC KPIPANLQLC HGIEYQNMRL 60
      PNLLGHETMK EVLEQAGAWI PLVMKQCHPD TKKFLCSLFA PVCLDDLDDET IQPCHSLCVQ 120
      VKDRCAPVMS AFGFPWPDML ECDRFPQDND LCIPLASSDH LLPATEEAPK VCEACKNKND 180
      DDNDIMETLC KNDFALKIKV KBITYINRDT KIILETKSKT TYKLVGVSER DLKKSVLWLK 240

```

DSLQCTCEEM NDINAPYLVM GQKQGGLVI TSVKRWQKGQ REFKRISRSI RKLQC 295

Seq ID NO: C398 Protein Sequence  
Protein Accession #: NP\_001297.1

1	11	21	31	41	51	
MSMGLEITGT	ALAVLWGLGT	IVCCALPMWR	VSAFIGSNII	TSQNIWEGWL	MNCVVQSTGQ	60
MQCKVYDSL	ALPQDLQAAR	ALIVVAILLA	AFGLLVALVG	AQCTNCVQDD	TAKAKITIVA	120
GVLFLAALL	TLVPVSWASN	TIIRDFYNPV	VPEAQKREMG	AGLYVGWAAA	ALQLLGALL	180
CCSCPPEKK	YTATKVYVSA	PRSTGPGASL	GTGYDRKDYV			220

Seq ID NO: C399 Protein Sequence  
Protein Accession #: NP\_036581.1

1	11	21	31	41	51	
MESRKDITNQ	EELWKMKPRR	NLEEDDYLHK	DTGETSMLKR	PVLLHLHQTA	HADEFDCPSE	60
LQHTQELFPQ	WHLPIKIAAI	IASLTFLYTL	LREVIHPLAT	SHQQYFYKIP	ILVINKVLPM	120
VSITLLALVY	LPGVIAAIVQ	LHNGTKYKKF	PHWLDKMWLT	RKQFGLLSFF	FAVLHAIYSL	180
SYPMRRSYRY	KLLNWAYQQV	QQNKEDAWIE	HDVWRMEIYV	SLGIVGLAIL	ALLAVTSIPS	240
VSDSLTWREF	HYIQSKLGIV	SLLLGTIHAL	IFAWNKWIDI	KQFVWYTPPT	FMIAVFLPIV	300
VLIFKSILFL	PCLRKKILKI	RHGVEDVTKI	NKTEICSQL			339

Seq ID NO: C400 Protein Sequence  
Protein Accession #: NP\_001766.1

1	11	21	31	41	51	
MANCEFSPVS	GDKPCCRLSR	RAQLCLGVSI	LVLILVVVLA	VVVPWRQWTW	SGPGTTKRFP	60
ETVLARCVKY	TEIHPEMRHV	DCQSVWDAFK	GAFISKHPCN	ITEEDYQPLM	KLGTQIVPCN	120
KILLWSRIKD	LAHQFTQVQR	DMFTLEDTL	GYLADDLTWC	GEFNTSKINY	QSCPDRWKDC	180
SNPVSVFVK	TVSRRFAEAA	CDVVHVMLNG	SRSKIFDKNS	TFGSVEVHNL	QPEKVQTLA	240
WVIHGGRS	RDLCDPTTIK	ELESIIKRN	IQFCKNIYR	PKFLQCVKN	PEDSSCTSEI	300

Seq ID NO: C401 Protein Sequence  
Protein Accession #: XP\_120513.2

1	11	21	31	41	51	
MVCTFSGPL	RETENVKKF	YALRAFMRM	SSEAAMLGES	RTFKPRKHRA	TTRAKIFKRF	60
FSEGESNSR	LVEELAVIHT	YSDDPAPITS	PSSVQPREFG	VMQAPRARF	GSRTPPAAAE	120
ASSPHLGIGE	AACQSGARAA	APRAGARRCQ	PQRQAAAAAA	TAQTHTLPH	RTRADPAGRR	180
RRHPRSPAPG	GEGTCEGPA	PRRMEEEMQ	PAEEGSPVVK	IYKQSPYVS	LKTFPSKRPA	240
LAKRYERPTL	VELPHGLRST	PAQPPASPA	ASSSSSFAAV	VRLGAPPRPP	RRGFRARGTI	300
PPLLPAPGVA	GTLPLPPTSS	SPPSPRPRFW	HAAAPRGTS	HTHMWSQST	LPGSDTMVSV	360
FGLMAQRWQ	HRSLLKQFEW	ILGSGWTWPC	GQDWLEKEGQ	VAVLLPRSEG	NTAPKKSRMI	420
LDFAQQCSR	VLSLLNCGGK	LDSNHSQSM	ISCVKQEGSS	YNERQEHCHI	GKGVHSQTS	480
NVDIEMQYMQ	RKQTSAPFLR	VFTDSLQNYL	LSGSFPTPNP	SSASEYGHLL	DVDPLSTSPV	540
HTLENIISLDS	TASLCKSRHL	SREPPVKSD	PNPLQQALAG	GASRPFSGAQ	QSIAYRVNSE	600
LEDGIRSPVP	LSCEALEMDL	TSLSGSKQLLN	NYPVYITSKQ	WDEAVNSSKK	DGRRLRLRYLI	660
RFVFTTDELK	YSCGLGKRKR	SVQSGETGPE	RRPLDPVKVT	CLRGATASFRS	VSPSVISFHR	720
IGCGSPRTSV	QPSVF					735

Seq ID NO: C402 Protein Sequence  
Protein Accession #: BAA92562.1

1	11	21	31	41	51	
METIVLSGIN	FEYKGMTGWE	VAGDHIYTAA	GASDNDFMIL	TLVVPGRFP	QSVMAADTENK	60
EVARITFVFE	TLCVSNCELY	FMVGVNSRTN	TPVETWKGSK	GKQSYTYIIE	ENTTTSFTWA	120
FQRTTFHEAS	RKYTNDVAKI	YSINVTNVMN	GVASYCRPCA	LEASDVGSSC	TSCPAGYYID	180
RDSGTCHSCP	PNTILKAHQ	YGVQACVPCG	PGTKNNKIHS	LCYNDCTFSR	NTPTRTFNYN	240
FSALANTVTL	AGGPSFTSKG	LKYFHHFTLS	LCGNQGRKMS	VCTDNVTDLR	IPEGESGFSK	300
SITAYVCQAV	IIPPEVTGYK	AGVSSQPVSL	ADRLIGVTTD	MTLDGITSQA	ELFHLESGLGI	360
PDVIFYRSN	DVTQSCSSGR	STTIRVRCSP	QKTVPGSLLL	PGTCSGTC	GCNFHFLWES	420
AAACPLCSVA	DYHAIVSSCV	AGIQKTTYVW	REPKLCSGGI	SLPEQRTVIC	KTIDFWLVKG	480
ISAGTCTAIL	LTVLTCYFWK	KNQKLEYKYS	KLVMNATLKD	CDLPAADSCA	IMEGEDVEDD	540
LIFTSKSLF	GKIKSFTSKQ	PAPVTISLSE	DS			572

Seq ID NO: C403 Protein Sequence  
Protein Accession #: NP\_055139.1

1	11	21	31	41	51	
MALQGISVVE	LSGLAPGRXC	AMVLADFGAR	VVRVDRPGSR	YDVSRLGRGK	RSLVLDLQKP	60
REPRAAASVQ	AVGCAAGALP	PRCHGETPAG	PRDSAAGKSK	AYLCQAEWIW	PVQESFCRLA	120
GHDNINLALS	GVLTKIGRSG	ENPYAPLNLV	ADFAGGGLMC	ALGIIMALFD	RTRTDKGQVI	180
DANMVEGTAY	LSSFLWKTQK	SSLWEAPRGQ	NMLDGGAPFY	TTYRTADGEF	MAVGAIEPQF	240
YELLIKGLGL	KSEDELPNQS	TDDWPEMKKK	FADVFAKTK	AEWCQIFDGT	DACVTPVLTF	300
EEVHHHDKND	ERGSFITSEE	QDVSPRLAPL	LLNTFAIPSS	KGDPFIGEHT	EEILEEFGFS	360
REEIYQLNSD	KIIESNKVKA	SL				382

Seq ID NO: C404 Protein Sequence

Protein Accession #: XP\_091332.1

	1	11	21	31	41	51	
5	MQRWTLWAAA	FLTLHSAQAF	PQTDISISPA	LPELPLPSLC	PLFWMEFKGH	CYRFFPLNKT	60
	WAEADLYCSE	FSVGRKSAKL	ASIHSEWENV	FVYDLVNSCV	PGIPADVWTG	LHDHRQEGQF	120
	EWTGSSSYDY	SYWDGSPDD	GVHADPEEED	CVQIWRPPTS	EQLQAPPEQL	PLSISEATDV	180
	YLPEDFPAEP	KLMDQSWVSR	KSLKPSKSHL	MEPPTPVAKH	QKAKTRHRS	RGVWVWPSGKA	240
	GSWKERMNAD	YGRRKRSAPR	QEGRLRCRER	RLRAASGQGR	PEGQRKQRRQ	ERQERGWEE	300
10	GGVSPMRGAQ	AWQHGLGAGS	QRGAAPCEGE	NHQAPELGST	WRGQRLQPT	AALCHFALRK	360
	LPGNAHGLAA	AFVQPALQVQ	EKKNNRTRFS	GAYFTMSDPT	CDQDSKEQSL	RRHGREAED	420
	GPYRLVKKKR	GPVACPSFFE	LQSGGEVCLD	FPVELRAGTW	IAREPP		466

Seq ID NO: C405 Protein Sequence  
Protein Accession #: XP\_054869.2

	1	11	21	31	41	51	
20	MHTCCPPVTL	EQDLHRKMHS	WMLQTLFAV	TSLVLSCAET	IDYYGEICDN	ACPCEEKDGI	60
	LTVSCENRGI	ISLSEISPPR	FPIYHLLLSG	NLLNRLYPNE	FVNYTGASIL	HLGSNVIQDI	120
	ETGAFFGLRG	LRRLHLNNNK	LELLRDDTFL	GLENLEYLQV	DVNYISVIEP	NAFGKLHLLQ	180
	VLIINDNLLS	SLPNNLFRFV	PLTHLDLRGN	RLKLLPYVGL	LQHMDKVVEL	QLEENPWNC	240
	CELISLKDWL	DSISYSALVG	DVVCETPFR	HGRDLDEVSK	QELCPRRLLS	DYEMRPQTPL	300
	STTGYLHTTP	ASVNSVATSS	SAVYKPLPK	PKGTRQENKP	RVRPTSRQPS	KDLGYSNYGP	360
25	STAYQTKSPV	PLECPTACSC	NLQISDLGLN	VNCQERKIES	IAELQPKPVN	PKMYLTENY	420
	IAVVRRTDFL	EATGLDLLHL	GNNRISMIQD	RAFGLDNLNR	RLYLNGNRIE	RLSPFLFYGL	480
	QSLQYLFLOQ	NLIRESQST	FDPVPNLQLL	FLNNNLLQAM	PSGVFSGGLT	LRLNLRSNHF	540
	TSLPVSGLVD	QLKSLQIDL	HNNPWCCTCD	IVGMKLWVEQ	LKGVVLVDEV	ICKAPKKFAE	600
	TDMRSIKSEL	LCEDYSDVVV	STPTPSSIQV	PARTSAVTPA	VRNLSTGAPA	SLGAGGGGSA	660
30	VPLSVLILSL	LLVFIMSVFV	AAGLFVLVMK	RRKKNSDHT	STNNSDVSSF	NMQYSVYGGG	720
	GGTGGHFAH	VHHRGPAALPK	VKTPAGHVYE	YIPHLGHMC	KNPIYRSREG	NSVEDYKDLH	780
	ELKVITYSSNH	HLQQQQQPPP	PPQQPQQPPP	PQLQLQPGEE	ERRESHHLRS	PAYSVSTIEP	840
	REDLLSPVQD	ADRFYRGILE	PDKHCSTTPA	GNSLPEYPKF	PCSPAAYTFS	PNYDLRRPHQ	900
35	YLHPGAGDSR	LREPVLYSPP	SAVFVEPNRN	EYLELKAKLN	VEPDYLEVLE	KQTTFSQF	958

Seq ID NO: C406 Protein Sequence  
Protein Accession #: NP\_000784.2

	1	11	21	31	41	51	
40	MGILSVDLLI	TLQILPVFFS	NCLFLALYDS	VILLKHVVLL	LSRSKSTRGE	WRRMLTSEGL	60
	RCVWKSFLLD	AYKQVKLGED	APNSSVHVVS	STEGGDNSGN	GTQEKIAEGA	TCHLLDFASP	120
	ERPLVNVFGS	ATUPPFTSQL	PAFRKLVEEF	SSVADFLLVY	IDEAHPSDGW	AIPGDSLSLF	180
45	EVKKHQNQED	RCAAAQQLLE	RFSLPPQCRV	VADRMNNAN	IAYGVAFERV	CIVQRQKIAI	240
	LGGKGPFPSYN	LQEVHRWLEK	NFSKRUKKTR	LAG			273

Seq ID NO: C407 Protein Sequence  
Protein Accession #: NP\_006540.2

	1	11	21	31	41	51	
50	MSSCVSSQPS	SNRAAPQDEL	GGRGSSSSSES	QKPCBALRGL	SSLSIHLGME	SFIVVTECEP	60
	GCAVDLGLAR	DPLEADGQE	VPLDSSGSQA	RPHLSGRKLS	LQERSQGGLA	AGGSLDMNGR	120
	CICPSLPYSP	VSSPQSSPRL	PRRPTVESHH	VSITGMQDCV	QLNQYTLKDE	IGKGSYGVVK	180
55	LAYNENDNTY	YAMKVLSSKK	LIRQAGFPRR	PPPRGTRPAP	GGCIQPRGPI	EQVYQEIAIL	240
	KKLDPNVVVK	LVEVLDDFNE	DHLYMVFEVL	NQGFVMEVPT	LKPLSEDAQAR	FYFQDLIKGI	300
	EYLYHQKIIH	RDIKPSNLLV	GEDGHIKIAD	FGVSNFPGKS	DALLSNTVGT	PAFMAPELSL	360
	ETRKIFSGKA	LDVWAMGVTL	YCFVFGQCPF	MDERIMCLHS	KIKSQALEFP	DQPDIAEDLK	420
60	DLITRMLDKN	PESRIVVPEI	KLHPWVTRHG	AEPLPSEDEN	CTLVEVTEEE	VENSVKHIPS	480
	LATVILVKTM	IRKRSFGNPF	EGSRREERSL	SAPGNLLTKK	PTRECESLSE	LKEARQRRQP	540
	PGHRPAPRGG	GGGSLVRGSP	CVESCWAPAP	GSPARMHPLR	PEEAMEPE		588

Seq ID NO: C408 Protein Sequence  
Protein Accession #: NP\_061116.2

	1	11	21	31	41	51	
65	MGLSLPKKEG	LILCLWSKFC	RWFQRRESWA	QSRDEQNLLQ	QKRIWESPLL	LAARDNDVQA	60
	LNKLLKYEDC	KVHQRGAMGE	TALHIAALYD	NLEAAMVLME	AAPELVFEPM	TSELYEGQTA	120
70	LHIAVNVQNM	NLVRALLARR	ASVSARATGT	AFRRSPCNLI	YFGEHPLSFA	ACVNSEEIVR	180
	LLIEHGADIR	AQDSLGNVT	HILILQPNKT	FACQMYNLLL	SYDRHGDHLQ	PLDLVPNHQG	240
	LTPPKLAGVE	GNTVMFQHLM	QKRKHTQWTY	GPLTSTLYDL	TEIDSSGDEQ	SLLELIITTK	300
	KREARQILDQ	TPVKELVSLK	WKRYGRPYFC	MLGAIYLLYI	ICFTMCCIYR	PLKPTNNRNT	360
75	SFRDNTLLQ	KLLQRAYMTP	KDDIRLVGEL	VTVIGAIIL	LVEVPDIFRM	GVTRFFGQTI	420
	LGGPFHVLI	TYAFMVLVTM	VMRLISASGE	VVPMFSFALV	GWCNVMYFAR	GFQMLGPFTI	480
	MIQKMIFGDL	MRFCWLMVAV	ILGFASAFYI	IFQTEDPEEL	GHFYDYPMAL	FSTFELFTI	540
	IDGPANYNDV	LFFMYSITYA	AFATIIATLLM	LNLLIAMMGD	THWRVAHERD	ELWRAQIVAT	600
	TVMLERKLPR	CLWPRSGICG	REYGLGDRWF	LRVEDRQDLN	RQRIQRYAQA	FHTRGSEDL	660
80	KDSVEKLELG	CPFSPHLSLP	MPSVSRSTSR	SSANWERLRQ	GTLRRDLRGI	INRGLEDGES	720
	WEYQI						725

Seq ID NO: C409 Protein Sequence  
Protein Accession #: NP\_068710.1

1 11 21 31 41 51  
 | | | | |  
 MQKVTLLGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSEW 60  
 RSSGEQAGRG WGSPPPLTTQL SPTGAKCKCK FGQKSGHHPG ETPPLITPGS AQS 113

Seq ID NO: C410 Protein Sequence  
 Protein Accession #: NP\_005962.1

1 11 21 31 41 51  
 | | | | |  
 MQKVTLLGLLV FLAGFPVLDA NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSAK 60  
 CKCKFGQKSG HHPGETPLLI TPGSAQS 87

Seq ID NO: C411 Protein Sequence  
 Protein Accession #: NP\_004952.1

1 11 21 31 41 51  
 | | | | |  
 MLSKVLPLVLL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60  
 TGSRVGKLEPE ASRIINTILS NYDHLKLRPGI GEKPTVVTVTE IAVNSLGPLS ILDMEYTTIDI 120  
 IFSQTYWYDER LCYNDFESL VLNQNVVSQL WIPDTFFRNS KRTHEHEITM PNQMVRIYKD 180  
 GKVLTYTIRM IDAGCSLHML RFPMDSHSCP LSFSSFSYPE NEMIYKWNF KLEINEKNSW 240  
 KLFQDFDTGV SNKTEIITP VGDPMVMTIF FNVSRFRGYV AFQNYVPSSV TTMLSWVSFW 300  
 IKTESAPART SLGITSVLTM TTLGTFSRKN FPRVSYITAL DFYIACFVF CFCALLEFAV 360  
 LNFLIYNQTK AHASPKLRHP RINSRAHART RARSACARQ HQEAFVCQIV TEGSDGGEER 420  
 PSCSAQQPPS PGSPGPRSL CSKLACCEWC KRFKKYFCMV PDCEGSTWQQ GRLCIHVYRL 480  
 DNYSRVVFPV TFFFNVLVW LVCLNL 506

Seq ID NO: C412 Protein Sequence  
 Protein Accession #: NP\_068819.1

1 11 21 31 41 51  
 | | | | |  
 MEYTDIIIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ 60  
 MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120  
 INEKNWKLFE QLDFTGVSNK TEIITTPVGD FMVMTIFFNV SRFRGYVAFQ NYVPSSVTM 180  
 LSWVSFWIKT ESAPARTSLG ITSVLMTTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240  
 ALLEFAVLNF LIYNQTKAHA SPKLHRPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE 300  
 GSDGEERPSC SAQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPDC EGSTWQQARL 360  
 CIHVYRLDNY SRVFPVPTFF FPNVLYWLVC LNL 393

Seq ID NO: C413 Protein Sequence  
 Protein Accession #: NP\_068822.1

1 11 21 31 41 51  
 | | | | |  
 MEYTDIIIFS QTWNSKRTHE HEITMPNQMV RIYKDGKVLV TIRMTIDAGC SLHMLRFPMD 60  
 SHSCPLSFSS FSYSPENEMIY KWENFKLEIN EKNSWKLFQF DFTGVSNKTE IITTPVGDFM 120  
 VMTIFFNVSR RFGYVAFQNY VPSSVTMLS WVSFWIKTES APARTSLGIT SVLMTTLTGT 180  
 FSRKNFPRVS YITALDFYIA ICFVFCFCAL LEFAVLNFLI YNQTKAHASP KLRHPRINSR 240  
 AHARTRARSR ACARQHQAFA VCQIVTTEGS DGEERPSCSA QPPSPGSPE GPRSLCSKLA 300  
 CCEWCKRFFK YFCMVPDCEG STWQQGRLCI HVYRLDNYSR VVFPVPTFFF NVLYWLVCNL 360  
 L 361

Seq ID NO: C414 Protein Sequence  
 Protein Accession #: NP\_068830.1

1 11 21 31 41 51  
 | | | | |  
 MEYTDIIIFS QTWYDERLCY NDTFESLVLN GNVVSQLWIP DTFFRNSKRT HEHEITMPNQ 60  
 MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSF SSFSYPENEM IYKWNFKLE 120  
 INEKNWKLFE QLDFTGVSNK TEIITTPVGD FMVMTIFFNV SRFRGYVAFQ NYVPSSVTM 180  
 LSWVSFWIKT ESAPARTSLG ITSVLMTTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240  
 ALLEFAVLNF LIYNQTKAHA SPKLHRPRIN SRAHARTRAR SRACARQHQE AFVCQIVTTE 300  
 GSDGEERPSC SAQPPSPGS PEGPRSLCSK LACCEWCKRF KKYFCMVPDC EGSTWQQGRL 360  
 CIHVYRLDNY SRVFPVPTFF FPNVLYWLVC LNL 393

Seq ID NO: C415 Protein Sequence  
 Protein Accession #: NP\_068591.1

1 11 21 31 41 51  
 | | | | |  
 MPAVSGPGPL FCLLLLLLDP HSPETGCPPL RFEYKLSFK GPRLALPGAG IPFWSHHGDA 60  
 ILGLEEVRLT PSMRNRSGAV WSRAVPPSA WEVEVQMRVT GLGRRGAHGM AVWYTRGRGH 120  
 VGSVLGGLAS WDGIIGIFDS PAEDTQDSPA IRVLASDGH I PSEQPGDGAS QGLGSCWDF 180  
 RNRPHFPRAR ITYWGQRLRM SLNSGLTPSD PGEFCVDVGP LLLVPGGFFG VSAATGTLD 240  
 DHDVLSFLT F SLSEPSPEVP PQPFLEMQLL RLARQLEGLW ARLGLGTRED VTPKSDSEAQ 300  
 GEGERLFDLE ETLGRHRRIL QALRLSKQL AQAERQWKQ LGPPGQARPD GGWALDASCQ 360  
 IPSTPGRGGH LSMSLNKDSA KVGALLHGQW TLLQALQEMR DAAMVMAEA QVSVPVGGIE 420  
 HHFLELDHIL GLLQBELRGP AKAAAKAPRP PGQPPRASSC LQPGIFLFYL LIQTGVGFFGY 480  
 VHFQELNKS LQECLESTGSL PLGPAHTPR ALGILRRQPL PASMPA 526

Seq ID NO: C416 Protein Sequence  
 Protein Accession #: XP\_117036.1

5  
1 11 21 31 41 51  
MERRTRGALG SRRPPPLPA LRHLCTGLQA AGMAWPGTLW RHTCQGRAXA AEGPWGLFRP 60  
HRCPREAGQA PVGSPETQG VAHVCSRARV SVDEREPGGG AYAMHVTPRW KGCHRHSGRT 120  
VRGSVSWKRP EQAAPETGRG PAVARGSGDG NECGWG 156

Seq ID NO: C417 Protein Sequence  
Protein Accession #: XP\_167803.2

10  
1 11 21 31 41 51  
MPGKGQRKTA TNKPGGLPGA PGVGIGGHCL YVLECKCFIK NKTKTHHHKK KNFAAKRNEE 60  
15  
KLKKKKQKEK KNHTKFFHHT YPLSQQDFLF AKSYFCGNGP CFLWQGLF 108

Seq ID NO: C418 Protein Sequence  
Protein Accession #: NP\_079056.1

20  
1 11 21 31 41 51  
MFRLVERYEM PRHEVYVLLI RNIFLKISII GILCYWLNT VALSGEECEW TLIGQDIYRL 60  
LLMDFVFSLV NSFLEFLRR IIGMQLITSL GLQEFDIARN VLELIYAQTL VWIGIFFCPL 120  
LPFIQMIMLF IMFYSKNISL MMNFQPPSKA WRASQMMTFF IFLFFPSFT GVLCTLAITI 180  
25  
WRLKPSADCG PFRGLPLFIH SIYSWIDTSL TRPGYLWVWV IYRNLIGSVH FFFILTLIVL 240  
IITYLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP SSLVLERREV 300  
EQQGFLHLGE HDGSLDLRSR RSVQEGNPRA 330

Seq ID NO: C419 Protein Sequence  
Protein Accession #: Eos sequence

30  
1 11 21 31 41 51  
MLSDDHVNEI IIQVENVSSG VQSHPSNQI FQEKVLLDSS INMVLISIDI DVIDSQTIVSK 60  
35  
RNDQKGNQVL RFSTSLNESM SQTLSLECM GIDTPGSSHE TVQGQKLIAS LIPMTSRDRI 120  
KAIRNQPRTM EEKRNLRKIV DKEKSKQTHR ILQLNCCIQC LNSISRAYRR SKNSLSEILN 180  
SISLWQKTLK IIGGKFGTSV LSYFNFLRWL LKFNIFSFIL NFSFIIIPQF TVAKKNTLQF 240  
TGLEFFTGVG YFRDVTVMYIG FYTNSTIQHG NSGASYNMQL AYIFTIGACL TTCFFSLLFS 300  
MAKYFRNNFI NPHIYSGGIT KLIFCWDFTV THEKAVKLKQ KNLSTEIREN LSELROENSK 360  
40  
LTFNQLLTRF SAYMVAVVVS TGVAIACCAA VYLAEYNLE FLKTHSNPGA VLLLPFVVS 420  
INLAVPCIYS MFRLVERYEM PRHEVYVLLI RNIFLKISII GILCYWLNT VALSGEECEW 480  
TLIGQDIYRL LLMDFVFSLV NSFLEFLRR IIGMQLITSL GLQEFDIARN VLELIYAQTL 540  
VWIGIFFCPL LPFIQMIMLF IMFYSKNISL MMNFQPPSKA WRASQMMTFF IFLFFPSFT 600  
GVLCTLAITI WRLKPSADCG PFRGLPLFIH SIYSWIDTSL TRPGYLWVWV IYRNLIGSVH 660  
45  
FFILTILIVL IITYLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP 720  
SSLVLERREV EQQGFLHLGE HDGSLDLRSR RSVQEGNPRA 760

Seq ID NO: C420 Protein Sequence  
Protein Accession #: NP\_002241.1

50  
1 11 21 31 41 51  
MGDDLVLGLG ALRRRKRLLE QEKSLAGWAL VLAGTGIGLM VLHAEMLWFG GCSWALYLF 60  
VKCTISISTF LLLCLIVAFH AKEVQLFMTD NGLRDWRVAL TGRQAAQIVL ELVVCGLHPA 120  
55  
PVRGPFCVQD LGAPLTSPQ WPGFLGQGEA LLSLAMLLRL YLVPRAVLLR SGVLLNASYR 180  
SIGALNQVRF RHWFAKLYM NTHPGRLLLG LTLGLNLTTA WVLSVAERQA VNATGHLSDT 240  
LWLIPITFLT IGYGDVVPQT MWGKIVCLCT GVMGVCTAL LVAVVARKLE FNKAEKHVHN 300  
FMMDIQTKE MKESAARVLQ EAWMFYKHTR RKESHAARRH QRKLLAANA FRQVRLKHRK 360  
LREQVNSMVD ISKMHMILYD LQQLNLSSSH ALEKQIDTLA GKLDALTELL STALGPRQLP 420  
60  
EPSQSK 427

Seq ID NO: C421 Protein Sequence  
Protein Accession #: NP\_079533.1

65  
1 11 21 31 41 51  
MGGKQRDEDD EAYGKPVKYD PSFRGPIKNR SCTDVICCVL FLLFILGYIV VGIVAWLYGD 60  
PRQVLYPRNS TGAYCGMGEN KDKPYLLYFN IFSCILSSNI ISVAENGLQC PTPQVCVSSC 120  
PEDPWTVGKN EFSQTVEGVF YTKNRNFCPL GVPWNMTVIT SLQQELCPSE LLPSAPALGR 180  
70  
CFPWTNITPP ALPGITNDTT IQQGISGLID SLNARDISVK IFEDFAQSWY WILVALGVAL 240  
VLSSLFILLL RLVAGPLVLV LILGVLGVLA YGIYYCWEEY RVLDRKGASI SQLGFTTNLS 300  
AYQSVQETWL AALIVLAVLE AILLLVLIFL RQRIRIAIAL LKEASKAVGQ MMSTMFYPLV 360  
TFVLLLICIA YWAMTALYPL PTQFATLGIV LWASNISSPG CEKVPINTSC NPTAHLVNSS 420  
CPGLMCFVQG YSSKGLIORS VFNLIYGVV GLFWTLNWVL ALGCQCVLAGA FASFYWAFHK 480  
75  
PQDIPTFPLI SAFIRTLRYH TGSALFAGALI LTLVQIARVI LEYIDHKLGR VQNPVARCIM 540  
CCFKCCLWCL EKFIKFLNRN AYIMIAIYK NFCVSAKNAF MLLMRNIVRV VVLDKVTDLL 600  
LFFGKLLVVG GVGVLSEFFF SGRIPGLGKD FKSPHLNYYW LPIMTSILGA YVIASGFFSV 660  
FGMCVDTLFL CFLEDLERNN GSLDRPYMS KSLKILGKK NEAPPDNKKR KK 712

80  
Seq ID NO: C422 Protein Sequence  
Protein Accession #: NP\_057264.1

1 11 21 31 41 51  
MGSNSGQAGR HIYKSLADDG PFDSVEPPKR PTSRLIMHSM AMFGREFCYA VEAAYVTPVL 60



LSVGLPSSLY SIVWFLSPIL GFLLPVVGVS ASDHCRSRWG RRRPYILTLG VMMLVGMALY 120  
 LNGATVVAAL IANPRRLKLVW AISVTMIGVV LFDFAADFID GPIKAYLFDV CSHQDKEKGL 180  
 HYHALFTGFG GALGYLLGAI DWAHLELGR LGEFQVMVF FSALVLTLCF TVHLCISEA 240  
 PLTEVAKGIP PQQTPQDPPL SSDGMYEYGS IEKVNGYVN PELAMQGAKN KNHAEQTRRA 300  
 MTLKSLRLAL VMMPPHYRYL CISHLIGWTA FLNMLFFTD FMQIVYRGD PYSAHNSTEF 360  
 LIYERGVEVG CWGFCINSVF SLSYSYFQKV LVSYIGLKGL YFTGYLLFGL GTGFIGLFPN 420  
 VYSTLVLCSL FGVMSSTLYT VPFNLITEYH REEEKERQQA PGGDPPNSVR KGKMDCATLT 480  
 CMVQLAQILV GGGGLFLVNT AGTVVVVVIT ASAVALIGCC FVALFVRYVD 530

Seq ID NO: C423 Protein Sequence  
 Protein Accession #: NP\_003264.1

1 11 21 31 41 51  
 | | | | |  
 MEGFGGVGGR GTRGFAAKGV WRGRAEEGPV LGAAERGFMV STGSRRRVFE GPGGGGLRWT 60  
 PGKGTGRQRG AWGPRAEAGV RRRRLGMPRG SRRDVRAPCG PAGSWGARGG RRRDGPSSRR 120  
 RGSATAAARH HVPPAPGGFF GPRAPAGSTR VPARAGGAVE PTGAAAVARL ARPAGGALPT 180  
 AGAQQAGPAR GRSGESEWA RRGKGRPGPY QSPLGPAVAE GQELKDKSRL RYPINGFQAL 240  
 VLTALLVLGL MSAGLPLGAL PEMLLPLAFV ATLTAFIFSL FLYMKAQVAP VSALAPGGNS 300  
 GNPIYDFFLG RELNPRICFF DFKYFCELRP GLIGWVLINL ALLMKEAELR GSPSLAMWL 360  
 NGFQLLYVGD ALWHEEAVLT TMDITHDGFG FMLAFGDMAW VPFTYSLQAG FLLHHPQLG 420  
 LPMASVICLI NATGYIYFRG ANSQKNTFRK NPSDPRVAGL ETISTATGRK LLVSGWVGW 480  
 RHPNYLGLDI MALAWSLPCG VSHLLPYFYL LYFTALLVHR EARDERSACR STAWPGRSTA 540  
 GVCLTASCPT STEAAPPQV GHVPTHPPAH PGPGASTHLG LKGLHPTQP 589

Seq ID NO: C424 Protein Sequence  
 Protein Accession #: NP\_056535.1

1 11 21 31 41 51  
 | | | | |  
 MGRLLRAARL PLLLSPLLLL LVGGAFLGAC VAGSDEPGPE GLTSTSLDDL LLPTGLEPLD 60  
 SEEPSETMGL GAGLGAPGSG FPSEENEESR LIQPPQYFWE EEEELNDSSL DLGPTADYVF 120  
 PDLTEKAGSI EDTSAQELP NLPSPLPKMN LVEPPWHMPP REEEEEEEEE EEREKEEVEK 180  
 QEEEEEEELL PVNGSQEEAK PQVRDFSLTS SSQTPGATKS RHEDSGDQAS SGVEVESSMG 240  
 PSLLLPSVTP TTVTPGDQDS TSQEAETVL PAAGLGVEFE APQEAEEAT AGAAGLSGQH 300  
 EEVPALPSFP OTTAPSGAEH PDEDPLGSRT SASSPLAPGD MELTPSSATL GQEDLNQQLL 360  
 EQAAAEASQR IPWDSQVIC KDWSNLAGKN YIILNMTENI DCEVFRQHRG PQLLALVEEV 420  
 LPRHSGSHHG AWHISLSKPS EKEQHLLMTL VGEQGVVPTQ DVLSMLGDIR RSLEEIGIQN 480  
 YSTTSSCQAR ASQVRSDYGT LFVVLVVIGA ICIIIIALGL LYNQCWRRLP KLKHVSHGEE 540  
 LRFVENGCHD NPTLDVASDS QSEMKEKHPN LGGGALNGP GSWGALMGK RDPEDSDVFE 600  
 EDTHL 605

Seq ID NO: C425 Protein Sequence  
 Protein Accession #: NP\_001188.1

1 11 21 31 41 51  
 | | | | |  
 MSEVRPLSRD ILMETLLYEQ LLEPPTMEVL GMTDSEEDLD PMEDFDSLEC MEGSDALALR 60  
 LACIGDEMVD SLRAPRLAQL SEVAMHSLGL AFYDQTEDI RDVLRFSFMDG FTTLKENIMR 120  
 FWRSPNPGSW VSCEQVLLAL LLLLALLLPL LSGGLHLLK 160

Seq ID NO: C426 Protein Sequence  
 Protein Accession #: AAF76225.1

1 11 21 31 41 51  
 | | | | |  
 MATPLPPSP RHLRLRLRL SGLVLGAALR GAAAGHPDVA ACPGSLDCAL KRRARCPFGA 60  
 HACGFCLOPF QEDQQLGCVF RMRRPPGGGR PQRLLEDEID FLAQELARKE SGQSTPPLPK 120  
 DRQRLPEPAT LGFSARGQGL ELGLPSTPGT PTPTPHTSLG SPVSSDPVHM SPLEPRGGQG 180  
 DGLALVLILA FCVAGAAALS VASLCWCRLQ REIRLTQKAD YATAKAPGSP AAPRISPGDQ 240  
 RLQAASAEYH YQHQRQMLC LERHKEPPKE LDTASSDEEN EDGDFTVYEC PGLAPTGE 300  
 VRNPLFDHAA LSAPLPAPSS PPALP 325

Seq ID NO: C427 Protein Sequence  
 Protein Accession #: NP\_004436.1

1 11 21 31 41 51  
 | | | | |  
 MVCSLWVLLL VSSVLALIEV LLDTTGETSE IGWLTYPFGG WDEVSVLDDQ RRLTRTFEAC 60  
 HVAGAPPGTG QDNWLQTHFV ERRGAQRAHI RLHFSVRACS SLGVSGGTCR ETFTLYYRQA 120  
 EEPDSDPSVS SWHLKRWTKV DTIAADESFP SSSSSSSSSS SAAWAVGPHG AGQRAGLQLN 180  
 VKERSFGPLT QRGFYVAFQD TGACIALVAV RLFSYTCPAV LRSFASFPET QASGAGGASL 240  
 VAAVGTCAVA AEPEEDGVGG QAGGSPPLRH CNGEGKMWVA VGGCRCQPGY QPARGDKACQ 300  
 ACPRGLYKSS AGNAPCSCP ARSHAAPNAA PVCPCLGIFY RASSDPPEAP CTGPPSAPQE 360  
 LWFEVQGSAL MLHWRLPREL GGRGDLLENV VCKECEGRQE PASGGGGTCH RCRDEVHFD 420  
 RQRGLTESRV LVGGLRAHVP YILEVQAVNG VSELSPDPFP AAAINVSTSH EVPSAVPVVH 480  
 QVSRASNSIT VSWPQPDQTN GNILDYQLRY YDQAEDESHS FTLTSETNTA TVTQLSPGHI 540  
 YGFQVRARTA AGHGYPGKV YFQTLPGEL SSQLEPRLSL VIGSILGALA FLLLAITVL 600  
 AVVFQRKRRG TGYTEQLQY SSPGLGVKYY IDPSTYEDPC QAIRELAREV DPAYIKIEV 660  
 IGTGSFGFVR QGRQLQPRGR EQTVAIQALW AGGAEGLQMT FLGRAAVLGQ FQHPNIRLE 720  
 GVVTKSRPLM VLTFERMELGP LDSFLRQREG QFSSLQLVAM QRGVAAAMQY LSSFAFVHRS 780  
 LSAHSVLVNS HLVCKVARLG HSPQGPSCLL RWAAPVIAH GKHTTSSDVW SFGILMWEVM 840  
 SYGERPYWDM SEQEVNLNIE QEFRLPPPPG CFFGLHLLML DTWQKDRARR PHFDQLVAAF 900  
 DKMIRKPDTL QAGGDPGERP SQALLTPVAL DFFCLDSPQA WLSAIGLECY QDNFSKFGLC 960

TFSDVAQLSL EDLPALGITL AGHQKKLLHH IQLLQQHLRQ QGSVEV 1006

Seq ID NO: C428 Protein Sequence  
Protein Accession #: XP\_043340.2

1	11	21	31	41	51	
MPFDFFRFDI	YRKVPKDLTQ	PTYTGAIISI	CCCLFILFLF	LSELTGFITT	EVVNELYVDD	60
PDKDSGGKID	VSLNISLPLN	HCELVGLDIQ	DEMGRHEVGH	IDNSMKIPLN	NGAGCRFEGQ	120
FSINKVPGNF	HVSTHSATAQ	FQNPDMTHVI	HKLSFGDTLQ	VQNIHGAFNA	LGGADRLTSN	180
PLASHDYILK	IVPTVYEDKS	GKQRYSYQYT	VANKEYVAYS	HTGRIIPAIW	FRYDLSPITV	240
KYTERRQPLY	RFITTICAI	GGFTTVAGIL	DSCIPTASEA	WKIKQLGKMH		290

Seq ID NO: C429 Protein Sequence  
Protein Accession #: NP\_002142.1

1	11	21	31	41	51	
MAQKEGGRTV	PCCSRPKVAA	LTAGTLLLLT	AIGAASWAIV	AVLLRSDQEP	LYPVQVSSAD	60
ARLMVFDKTE	GTWRLLCSSR	SNARVAGLSC	EEMGFRLALT	HSELDVRTAG	ANGTSGFFCV	120
DEGRLPHTQR	LLEVISVCD	PRGRFLAAIC	QDCGRRKLPV	DRIVGGDRDS	LGRWFWQVSL	180
RYDGAHLCCG	SLLSGDWLVT	AAHCFPERNR	VLSRWRVFAG	AVAQASPHGL	QLGVQAVVYH	240
GGYLPFRDPN	SEENSNDIAL	VHLSSPLPLT	EYIQPVCLPA	AGQALVDGKI	CTVTGWGNTQ	300
YYGQAGVLQ	EARVPIISND	VCNGADFYGN	QIKPKMFCAG	YPEGGIDACQ	GDSGGPFVCE	360
DSISRTPRWR	LCGIVSWGTV	CALAQKPGVY	TKVSDFREWI	FQAIKTHSEA	SGMVTQL	417

Seq ID NO: C430 Protein Sequence  
Protein Accession #: BAA92562.1

1	11	21	31	41	51	
METTIVLSGIN	FEYKGMTGWE	VAGDHIYTAA	GASDNDFMIL	TLVVPGFRPP	QSVMA DTENK	60
EVARITFVFE	TLCSVNCELY	FMVGVNSRTN	TPVETWKGSK	GKQSYTYIIE	ENTTTSFTWA	120
FQRTTFHEAS	RKYTNDVAKI	YSINVINVMN	GVASYCRPCA	LEASDVGSSC	TSCPAGYIID	180
RDSGTCHSCP	PNTILKAHQ	YGVQACVPCG	PGTKNNKIHS	LCYNDCTFSR	NTPTRTFNKN	240
FSALANTVTIL	AGGPSTFSKG	LKYFHHFTLS	LCGNQGRKMS	VCTDNVTDLR	IPEGESGFSK	300
SITAVVCAV	IIPPEVTGYK	AGVSSQPVSL	ADRLIGVTTD	MTLDGITSFA	ELFHLESGLI	360
PDVIFFYRSN	DVTQSCSSGR	STTIRVRCSP	QKTVPGLSL	PGTCSGDTCD	GCNFHFLWES	420
AAACPLCSVA	DYHAIVSSCV	AGIQKTTYVW	REPKLCSGGI	SLPEQRVTIC	KTIDFWLKV	480
ISAGTCTAIL	LTVLTCYFWK	KNQKLEYKYS	KLVNMATLKD	CDLPAADSCA	IMEGEDVEDD	540
LIFTSKSKSLF	GKIKSFTSKQ	PAPVTISLSE	DS			572

Seq ID NO: C431 Protein Sequence  
Protein Accession #: NP\_004855.1

1	11	21	31	41	51	
MPGQELRTVN	GSQMLLVLLV	LSWLPHGGAL	SLAEASRAS	PGPSELHSED	SRFRELKRY	60
EDLLTFLRRN	QSWEDNTDL	VPAPAVRILT	PEVRLGSGGH	LHLRISRAAL	PEGLPEASRL	120
HRALFRLSPT	ASRSWDVTRP	LRRQLSLARP	QAPALHLRLS	PPFSQSDQLL	AESSSARPQL	180
ELHLRPQAAR	GRRRRARARNG	DDCPLGPGRC	CRLHTVRSAL	EDLGWADWVL	SPREVQVTMC	240
IGACPSQFRA	ANMHAQIKTS	LHRLKPDTEP	APCCVPASYN	PMVLIQKTD	GVSLQTYDDL	300
LAKDCHCI						308

Seq ID NO: C433 Protein Sequence  
Protein Accession #: NP\_443090.1

1	11	21	31	41	51	
MEDPSGAREP	RARPRERDPG	RRPHPDQGR	HDRPRDRPGD	PRKRSSDGN	RRRDGDRDPK	60
RDQERDGNRD	RNRDRERERE	RERDPRDGR	RDTHRDAGPR	AGEHGVWEKP	RQSRTRDGR	120
GLTWDAAPP	GPAPWEAPEP	PQPQRKGDGP	RRRPESEPPS	ERYLPSTPRP	GREVEYYQS	180
EAEGGLECHK	CKYLCTGRAC	CQMLEVLLNL	LILACSSVSY	SSTGGYTGIT	SLGGIYYQF	240
GGAYSGFDGA	DGEKAQQLDV	QFYQLKLPV	TVAMACSGAL	TALCCLFVAM	GVLRVPWHCP	300
LLLVTGELL	MLIAGGYIPA	LYFYFHYLSA	AYGSPVCKER	QALYQSKGYS	GFGCSFHGAD	360
IGAGIFAALG	IVVFALGAVL	AIKGYRKVRK	LKEKPAEMFE	F		401

Seq ID NO: C435 Protein Sequence  
Protein Accession #: Eos sequence

1	11	21	31	41	51	
MGAAGRQDFL	FKAMLTISWL	TLTCFPGATS	TVAAGCPDQS	PELQPNWPGH	DQDHHVHIGQ	60
GKTLTLLTSSA	TVYSIHISEG	GKLVKIDHDE	PIVLRTRHIL	IDNGGELHAG	SALCPFQGNF	120
TIILYGRADE	GIQDPDYGL	KYIGVGKGA	LELHGQKKLS	WTFLNKTLHP	GGMAEGGYFF	180
ERSWGHGRVI	VHVIDPKSGT	VIHSDRFDY	RSKKESERLV	QYLNAPVDR	ILSVAVNDEG	240
SRNLDDMARK	AMTKLGSKHF	LHLGFRHPWS	FLTVKGNPSS	SVEDHIEYHG	HRGSAARVF	300
KLFQTEHGEY	FNVSLSSEW	QDVEWTEWED	HDKVSQTKGG	EKISDLWKAH	PGKICNRPID	360
IQATTMDGVN	LSTEVVYKKG	QDYRFACYDR	GRACRSYRVR	FLCGKPVPRK	LTVTIDTNVN	420
STILNLEDNV	QSWKPGDTLV	IASTDYSMYQ	AEEFQVLPCR	SCAPNQVQVA	GKPMYLIHGE	480
EIDGVMRAE	VGLLSRNIIIV	MGEMEDKCYP	YRNHCNFFD	FDTFGGHIKF	ALGFKAHLE	540
GTELKHMGOQ	LVGQYPIHFH	LAGDVDERGG	YDPPTYIRDL	SIHHTFSRCV	TVHGSNGLLI	600
KDVVGYNLSG	HCFTEDGPE	ERNTFDCHLG	LLVKSGLTLLP	SDRDSKMCKM	ITEDSYPGYI	660
PKPRQDCNAV	STFWMANPNN	NLINCAAAGS	EETGFWFIFH	HVPTGPSVGM	YSPGYSEHIP	720

LGKFYNNRAH	SNYRAGMIID	NGVKTTEASA	KDKRPFLSII	SARYSPHQDA	DPLKPREPAI	780
IRHFIAYKNQ	DHGAWLRGGD	VWLDSCHFRG	EAQEGFLLTG	MKAGGILLGG	DEAASGMAQG	840
FSPPCRCLLK	LVTGSEFFAH	VSLAHS				866

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein  
5 incorporated by reference as if each individual publication, accession number, or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1           1.       A method for determining the presence or absence of a pathological cell in a  
2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80%  
3 identical to a sequence as described in Tables 2A-80 in a biological sample from said patient,  
4 thereby determining the presence or absence of said pathological cell.

1           2.       The method of Claim 1, wherein:

- 2           a) said pathology is described in Table 1, including a cancer; and/or  
3           b) said biological sample comprises isolated nucleic acids.

1           3.       The method of Claim 1, wherein said biological sample is tissue from an organ  
2 which is affected by said pathology of Table 1, including a cancer.

1           4.       The method of Claim 2, wherein said nucleic acids are mRNA

1           5.       The method of Claim 2:

- 2           a) further comprising a step of amplifying nucleic acids before said step of detecting  
3           said nucleic acid; or  
4           b) where said detecting is of a protein encoded by said nucleic acid.

1           6.       The method of Claim 1, wherein said nucleic acid comprises a sequence as  
2 described in Tables 2A-80.

1           7.       The method of Claim 2, wherein:

- 2           a) said detecting step is carried out by:  
3           i) using a labeled nucleic acid probe;  
4           ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence  
5           as described in Tables 2A-80; or  
6           iii) detecting a polypeptide encoded by said nucleic acid; or  
7           b) said patient is:  
8           i) undergoing a therapeutic regimen to treat said pathology of Table 1; or  
9           ii) is suspected of having said pathology or cancer.

1           8.       An isolated nucleic acid molecule comprising a sequence as described in  
2 Tables 2A-80.

- 1           9.       The nucleic acid molecule of Claim 8, which is labeled.
- 1           10.      An expression vector comprising the nucleic acid of Claim 8.
- 1           11.      A host cell comprising the expression vector of Claim 10.
- 1           12.      An isolated polypeptide which is encoded by a nucleic acid molecule  
2 comprising a sequence as described in Tables 2A-80.
- 1           13.      An antibody that specifically binds a polypeptide of Claim 12.
- 1           14.      The antibody of Claim 13:  
2 a) conjugated to an effector component;  
3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a  
4 cytotoxic chemical;  
5 c) which is an antibody fragment; or  
6 d) which is a humanized antibody.
- 1           15.      A method for specifically targeting a compound to a pathological cell in a  
2 patient, said method comprising administering to said patient an antibody of Claim 13,  
3 thereby providing said targetting.
- 1           16.      A method for determining the presence or absence of a pathological cell in a  
2 patient, said method comprising contacting a biological sample with an antibody of Claim 13.
- 1           17.      The method of Claim 16, wherein:  
2 a) said antibody is conjugated to:  
3 i) an effector component; or  
4 ii) a fluorescent label; or  
5 b) said biological sample is a blood, serum, urine, or stool sample.
- 1           18.      A method for identifying a compound that modulates a pathology-associated  
2 polypeptide, said method comprising the steps of:

- 3 a) contacting said compound with a pathology-associated polypeptide, said  
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence  
5 at least 80% identical to a sequence as described in Tables 2A-80; and  
6 b) determining the functional effect of said compound upon said polypeptide.

1 19. A drug screening assay comprising the steps of:

- 2 a) administering a test compound to a mammal having a pathology of Table 1 or a  
3 cell isolated therefrom; and  
4 b) comparing the level of gene expression of a polynucleotide that selectively  
5 hybridizes to a sequence at least 80% identical to a sequence as described in  
6 Tables 2A-80 in a treated cell or mammal with the level of gene expression of said  
7 polynucleotide in a control cell or mammal, wherein a test compound that  
8 modulates said level of expression of the polynucleotide is a candidate for the  
9 treatment of said pathology.  
10

(19) World Intellectual Property  
Organization  
International Bureau



(43) International Publication Date  
22 May 2003 (22.05.2003)

PCT

(10) International Publication Number  
**WO 2003/042661 A3**

(51) International Patent Classification<sup>7</sup>: **C12Q 1/68**,  
C07H 21/02, 21/04

(21) International Application Number:  
PCT/US2002/036810

(22) International Filing Date:  
13 November 2002 (13.11.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/350,666	13 November 2001 (13.11.2001)	US
60/332,464	21 November 2001 (21.11.2001)	US
60/334,393	29 November 2001 (29.11.2001)	US
60/335,394	3 December 2001 (03.12.2001)	US
60/340,376	14 December 2001 (14.12.2001)	US
60/347,211	8 January 2002 (08.01.2002)	US
60/347,349	10 January 2002 (10.01.2002)	US
60/355,250	8 February 2002 (08.02.2002)	US
60/356,714	13 February 2002 (13.02.2002)	US
60/359,077	20 February 2002 (20.02.2002)	US
60/368,809	29 March 2002 (29.03.2002)	US
60/370,110	4 April 2002 (04.04.2002)	US
60/372,246	12 April 2002 (12.04.2002)	US
60/386,614	5 June 2002 (05.06.2002)	US
60/396,839	16 July 2002 (16.07.2002)	US
60/397,775	22 July 2002 (22.07.2002)	US
60/397,845	22 July 2002 (22.07.2002)	US
60/409,450	9 September 2002 (09.09.2002)	US

(71) Applicant (for all designated States except US): **PRO-TEIN DESIGN LABS, INC.** [US/US]; 34801 Campus Drive, Fremont, CA 94555 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **AFAR, Daniel** [CA/US]; 435 Visitacion Avenue, Brisbane, CA 94005 (US). **AZIZ, Natasha** [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). **GINSBURG, Wendy, M.** [US/US]; 655 Page Street, San Francisco, CA 94117 (US). **GISH, Kurt, C.** [US/US]; 37 Artuna Avenue, Piedmont, CA 94611 (US). **GLYNNE, Richard** [GB/US]; 2691 Palomino Circle, La Jolla, CA 92037 (US). **HEVEZI, Peter, A.** [GB/US]; 1360 11th Avenue, San Francisco, CA 94122 (US). **MACK, David, H.** [US/US]; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). **MURRAY,**

**Richard** [US/US]; 22643 Woodridge Court, Cupertino, CA 95014 (US). **WATSON, Susan, R.** [GB/US]; 805 Balra Drive, El Cerrito, CA 94530 (US). **WILSON, Keith, E.** [US/US]; 219 Jeter Street, Redwood City, CA 94062 (US). **ZLOTNIK, Albert** [US/US]; 507 Alger Drive, Palo Alto, CA 94306 (US).

(74) Agent: **KUNG, Viola, T.**; Howrey Simon Arnold White, LLP, Box 34, 301 Ravenswood Avenue, Menlo Park, CA 94025 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Declaration under Rule 4.17:**

— of inventorship (Rule 4.17(iv)) for US only

**Published:**

— with international search report  
— before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments

(88) Date of publication of the international search report:  
28 October 2004

**(15) Information about Correction:**

**Previous Correction:**

see PCT Gazette No. 42/2003 of 16 October 2003, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



WO 2003/042661 A3



# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; C07H 21/02, 21/04

US CL : 435/6; 536/23.1, 24.3

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6; 536/23.1, 24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
WEST, PubMed

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SATO, H. et al., Cloning and Expression of a Plasma Membrane Cystine/Glutamate Exchange Transporter Composed of Two Distinct Proteins, J. Biol. Chem. 23 April 1999, Vol. 247, No. 17, pp. 11455-11458.	1-7
A	KIM, J. Y. et al., Human cystine/glutamate transporter: cDNA cloning and upregulation by oxidative stress in glioma cells, B.B. Acta. June 2001, Vol. 1512, pp. 335-344.	1-7

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

\* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T"

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&"

document member of the same patent family

Date of the actual completion of the international search

04 August 2004(04.08.2004)

Date of mailing of the international search report

13 SEP 2004

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, Virginia 22313-1450

Facsimile No. (703) 872-9306

Authorized officer

Teresa Strzelecka

Telephone No. (571) 272-1600

*T. Roberts for*

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:  
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7, SEQ ID NO: 19

Remark on Protest

☐  
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

PCT/US02/36810

### BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-7, drawn to a special technical feature of a method for determining presence or absence of a pathological cell in a patient, said method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from said patient, thereby determining the presence or absence of said pathological cell.

Group II, claim(s) 8-11, drawn to a special technical feature of an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, expression vector comprising the nucleic acid and a host cell comprising the expression vector.

Group III, claim(s) 12, drawn to a special technical feature of an isolated polypeptide which is encoded by an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80.

Group IV, claim(s) 13, 14, drawn to a special technical feature of an antibody which specifically binds to polypeptide of claim 12.

Group V, claim(s) 15, drawn to a special technical feature of a method for specifically targeting a compound to a pathological cell in a patient, comprising administering to a patient an antibody of claim 13.

Group VI, claim(s) 16, 17, drawn to a special technical feature of a method for determining the presence or absence of a pathological cell in a patient, comprising contacting a biological sample with an antibody of claim 13.

Group VII, claim(s) 18, drawn to a special technical feature of a method for identifying a compound that modulates a pathology-associated polypeptide by contacting the compound with a pathology-associated polypeptide encoded by a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 and determining the functional effect of the compound on the polypeptide.

Group VIII, claim(s) 19, drawn to a special technical feature of a drug screening assay comprising the steps of: administering a test compound to a mammal having pathology of Table 1 or a cell isolated therefrom; comparing the level of gene expression of a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal.

The inventions listed as Groups I-VIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: claim 8 is anticipated by a sequence with accession No. BE440042 (Table 2A, first entry) (July 25, 2000), therefore there is no contribution of claim 8 over prior art.

CORRECTED VERSION

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
22 May 2003 (22.05.2003)

PCT

(10) International Publication Number  
**WO 03/042661 A2**

(51) International Patent Classification<sup>7</sup>: **G01N**

(21) International Application Number: PCT/US02/36810

(22) International Filing Date:  
13 November 2002 (13.11.2002)

(25) Filing Language: English

(26) Publication Language: English

## (30) Priority Data:

60/350,666	13 November 2001 (13.11.2001)	US
60/332,464	21 November 2001 (21.11.2001)	US
60/334,393	29 November 2001 (29.11.2001)	US
60/335,394	3 December 2001 (03.12.2001)	US
60/340,376	14 December 2001 (14.12.2001)	US
60/347,211	8 January 2002 (08.01.2002)	US
60/347,349	10 January 2002 (10.01.2002)	US
60/355,250	8 February 2002 (08.02.2002)	US
60/356,714	13 February 2002 (13.02.2002)	US
60/359,077	20 February 2002 (20.02.2002)	US
60/368,809	29 March 2002 (29.03.2002)	US
60/370,110	4 April 2002 (04.04.2002)	US
60/372,246	12 April 2002 (12.04.2002)	US
60/386,614	5 June 2002 (05.06.2002)	US
60/396,839	16 July 2002 (16.07.2002)	US
60/397,775	22 July 2002 (22.07.2002)	US
60/397,845	22 July 2002 (22.07.2002)	US
60/409,450	9 September 2002 (09.09.2002)	US

(71) Applicant (for all designated States except US): **EOS BIOTECHNOLOGY, INC.** [US/US]; 225A Gateway Boulevard, South San Francisco, CA 94080 (US).

## (72) Inventors; and

(75) Inventors/Applicants (for US only): **AFAR, Daniel** [CA/US]; 435 Visitacion Avenue, Brisbane, CA 94005 (US). **AZIZ, Natasha** [US/US]; 411 California Avenue, Palo Alto, CA 94306 (US). **GINSBURG, Wendy, M.** [US/US]; 655 Page Street, San Francisco, CA 94117 (US). **GISH, Kurt, C.** [US/US]; 37 Artuna Avenue, Piedmont, CA 94611 (US). **GLYNNE, Richard** [GB/US]; 2691 Palomino Circle, La Jolla, CA 92037 (US). **HEVEZI, Peter, A.** [GB/US]; 1360 11th Avenue, San Francisco, CA 94122 (US). **MACK, David, H.** [US/US]; 2076 Monterey Avenue, Menlo Park, CA 94025 (US). **MURRAY,**

**Richard** [US/US]; 22643 Woodridge Court, Cupertino, CA 95014 (US). **WATSON, Susan, R.** [GB/US]; 805 Balra Drive, El Cerrito, CA 94530 (US). **WILSON, Keith, E.** [US/US]; 219 Jeter Street, Redwood City, CA 94062 (US). **ZLOTNIK, Albert** [US/US]; 507 Alger Drive, Palo Alto, CA 94306 (US).

(74) Agents: **BASTIAN, Kevin, L.** et al.; Townsend and Townsend and Crew LLP, Two Embarcadero Center, Eighth Floor, San Francisco, CA 94111 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

## Declaration under Rule 4.17:

— of inventorship (Rule 4.17(iv)) for US only

## Published:

— without international search report and to be republished upon receipt of that report

## (48) Date of publication of this corrected version:

16 October 2003

## (15) Information about Correction:

see PCT Gazette No. 42/2003 of 16 October 2003, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



WO 03/042661 A2